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Genomic composition, gene action and genotype-enviromncnt interaction in hexaploid wheat (tritiecum aestivam L.)

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GENOMIC COMPOSITION, GENE ACTION AND GENOTYPE-ENVIRONMENT INTERACTION IN HEXAPLOID WHEAT (*Triticum aestivum* L.)

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CERTIFICATE

I have pleasure in certifying the thesis entitled "**Genomic composition, gene action and genotype-environment interaction in hexaploid wheat (*Triticum aestivum* L.)**" submitted by **Mr. Abdus Shahid** for the degree of **Doctor of Philosophy** in Botany of Rajshahi University.

I also certify that **i)** the candidate has fulfilled the residential requirement, **ii)** the works embodied in the thesis were carried out by the candidate, and **iii)** the data, to the best of my knowledge, are genuine and original. No part of the work has been submitted in substance for any degree.

Golam Kabir 18.5.

(*Golam Kabir*)
SUPERVISOR

Dedicated

to

my wife

Evany Lyzu

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THE AUTHOR

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ABSTRACT

The present study was carried out under three separate investigation in three parts. Part-I includes somatic karyotype, heterochromatin distribution and chromosome differentiation, and chromosome association and chiasma frequency under the head genomic composition. Somatic karyotypic analysis was carried out by quantitative method from selected dwarf plants of F_3-F_6 progenies of seven single crosses involving six varieties/lines of hexaploid wheat (Triticum aestivum L.). Heterochromatin distribution and chromosome differentiation of six parental genotypes were studied by banding technique. A comparative study was made to determine the effect of selection on the relationship between chiasma frequency and chromosome association of 12 Near Isogeneic Lines (NILs) from F_6 populations of four crosses.

*The proposed `**centromeric formulae**' comprised **19 m + 2 sm** in Aghrani, **11 m + 10 sm** in Akbar, **17 m + 4 sm** in Ananda, **16 m + 5 sm** in Kanchan, **16m + 5 sm** FM-32 and **14 m + 7 sm** in FM-139. In karyotypic composition, more submedian chromosomes were observed in FM-lines compared to those in Bangladeshi varieties except Akbar. In Ag X FM-32, the F_3 - F_6 progenies were found with **16m + 5sm** chromosome to make their haploid complement. In Ak X FM-32, haploid complements were found with **13m + 8sm, 12m n+ 8sm + 1st, 13m + 6sm + 2st** and **16m + 3sm + 2st** chromosomes for F_3, F_4, F_5 and F_6 progenies, respectively. The centromeric formula for F_3, F_4, F_5 and F_6 of An X FM-32 were found to comprise with **19m + 2sm, 14m + 6sm + 1st, 13m + 8sm** and **14m + 6sm + 1st** chromosomes, successively. For F_3, F_4, F_5 and F_6 progenies of Kan X FM-32 the centromeric formulae were consisted of **11m + 9sm + 1st, 16m + 4sm + 1st** and **16m + 3sm + 2st** chromosomes, respectively. The haploid complements of F_3, F_4, F_5 and F_6 progenies of Ak X FM-139 were found to consist of **12m + 9sm, 14m + 7sm, 12m + 9sm** and **16m + 3sm + 2st** chromosomes, successively. In An X FM-139 **15m + 6sm, 16m + 5sm, 13m + 7sm + 1st** and **15m + 5sm + 1st** chromosomes comprised the haploid complement for F_3, F_4, F_5 and F_6 progenies, respectively. The F_3, F_4, F_5 and F_6 progenies of Kan X FM-139 comprised **13m + 8sm, 13m + 7sm + 1st, 14m + 6sm + 1st** and **11m + 9sm + 1st** chromosomes successively for their haploid complement.*

It gave an idea about similarities and differences of the chromosome complement of six varieties/lines and their progenies under study. One pair of short chromosome (S_2^m) was invariably present in both the exotic dwarf lines, while it was absent in the indigenous lines. The occurrence of more than 5 pairs of long chromosome (L) were observed in all the indigenous varieties except Kanchan, whereas less than 5 pairs of long chromosome were

found in exotic lines. The F_3 progenies in most of the crosses and F_4 progenies of cross-1 & 2 did not posses any short chromosome (S_2) like their indigenous parent. However, the F_5 and F_6 progenies in most of the crosses have had at least one or more pair of S_2 chromosome/s like their exotic parent. All the progenies (F_3 - F_6) of crosses-3 & 5 were found to bear the S_2-chromosome. Moreover, the sub-terminal (st) chromosomes along with more sub-median chromosomes were frequently observed in the hybrid progenies of all crosses except Ag X FM-32, while it was fully absent in the parental genotypes. From the identified chromosomes of all the genotypes, it was confirmed that the chromosome nos. III & VIII were satellited. The significant difference in chromosome size of the genomes might have occurred by deletion in most of the cases and by unequal translocation in few cases. A very limited case of increased chromosome length was found, where duplication might be involved.

*Since some of the chromosome pairs in all the cases exhibited identical number of bands, the number of banding patterns become reduced to 9 in An, 10 in Ag and 11 in Ak, Kan, FM-32 and FM-139. This, in turn, was assumed that the later genotypes were derived from a more advanced progenitor compared to that of the former two. However, the chromosome pairs **XIV** and **XVIII** in Ag, **XX** in Ak and Kan, **XVI** and **XVII** in An, **IV** and **XV** in FM-32, and **VII** in FM-139 did not show any distinctly dark or faint band. The highly heterochromatic and mostly polymorphic but nearly identical banding patterns of the **B** genome chromosomes corresponded individually in all the genotypes. In the **D** genome, **6D** chromosome was identified individually and its banding pattern was almost identical in all the genotypes. **1D** in FM-139, **3D** in Ag and FM-32, **4D** in An, **5D** in Ag and An, and **7D** in Ak and Kan were not found to be banded and remained as unidentifiable, although their position in Karyotype were determined on the basis of probabilistic inferences. In the **A** genome chromosomes, the banding pattern of **3A**, **4A** and **6A** were quite similar in all the genotypes. However, the remaining chromosomes of **A** genome showed little difference in their heterochromatinization of different genotypes.*

*The mean performance of different meiotic features of **12 NILs** were compared with the check variety (Kanchan). Significantly increased bivalent frequency was noticed in all semidwarf (N) populations except Kan X FM-32 with a concurrent significant decrease in multivalent frequency compared to that of check variety. However, significantly increased bivalent and quadrivalent frequencies were found in dwarf **type-III** of An X FM-32, whereas significantly decreased bivalent frequency was observed in all the populations of Kan X FM-32 and in **type-II** of An X FM-32. The negative regression between multivalent and chiasmata in most of the studied populations was a feature of either genetic or chromosomal heterozygosity. On the other hand, the variance estimates of regression of chiasmata on other than bivalent*

configurations appeared to be significant in ***type-II*** *populations of most of the crosses indicating that there exists a great influence of chromosome differentiation in the variability in `pairs' in this population, which might provide the scope for increasing the frequency of bivalent. A significantly increased disjunction index and proportion of regular tetrads were regressed positively in most of the populations, while they were found to be significant simultaneously in* ***type-II*** *populations of Ak X FM-32. Moreover, the significant influence of chiasma frequency was detected in the variability of these meiotic features and thereby fertility status of the* ***type-II*** *populations. Therefore, their fertility status might be improved by progressive selection pressure for meiotic regularity in the advanced generations.*

Part-II includes gene action and it was studied on grain yield and its component traits in seven single crosses. The estimates of gene action were taken to determine the selection response of the crosses. Estimates of heritability and heterosis, and their genetic interpretations were also taken as counterpart of this study. The technique of generation mean analysis was used for the study of inheritance pattern. Simple scaling tests were applied for testing the presence or absence of epistasis and the joint scaling test was used for testing the adequacy of additive-dominance model. Genetic parameters were estimated based on six-parameter model in order to separate and identify different epistatic gene effect. Estimates of the fixable and non-fixable heritable components of variation were used to determine the nature of heritability. An attempt was made to estimate the magnitude of heterosis in relation to gene effects.

In this research programme, Aghrani X FM-32 (C_1) and Akbar X FM-139 (C_5) showed epistatic control for all characters (except fertile tillers/plant in C_1) and there were also appreciable amount of additive gene action. Therefore, these crosses might give best response to selection for yield. Kanchan X FM-32 (C_4) showed the significant additive gene action along with epistatic action for all the characters except fertile tillers and grains weight, which revealed better response to selection. In Akbar X FM-32 (C_2) and Ananda X FM-32 (C_3), Ananda X FM-139 (C_6) and Kanchan X FM-139 (C_7) lack of significant additive effect and presence of duplicate epistasis for grain yield and some yield components suggested that selection for them would not be effective in early segregating generation as in F_2.

The inheritance of the grain yield and its components were of predominantly dominant nature in most of the cases based on the components of variance analysis. Moreover, these characters were low to moderately heritable. Therefore, selection for them would be effective in F_3 or later generations. Although grain yield, harvest index and days to heading in C_4, C_5

and C_6 were controlled predominantly by additive gene action and was highly heritable, which indicated that selection for them might be effective in early segregating generations.

Significant heterotic performance in most of the traits in all crosses indicated good prospect of hybrid wheat. Significant positive better parent heterotic performances were observed for plant height in all crosses except C_2, for days to heading in C_1, C_2, C_3 and C_6, for fertile tillers in C_5 and C_6, for spikelets per ear in C_2 and C_5, and for grains per ear in C_5.

Part-III includes genotype-environment interaction and the magnitude of G x E interaction vis-a-vis stability parameters of twenty one NILs of F_6 progenies were estimated over six seeding dates for the grain yield and its component traits. The NILs were isolated from their photothermal sensitiveness and developmental characteristics. The genotype-environment (GE) interaction was found to be significant in all the cases and suggested for estimating the stability parameters. The significant E + (G x E) indicated the differential reaction of genotypes with the change of environments. Both the linear and non-linear (pooled deviation) components of GE interaction in most of the cases indicated that the genotypes differed significantly with respect to their response (b_i) and stability (S^2_{di}). The highly significant GE interaction along with their significant linear component for all the traits except the days to maturity, grains per ear and grain yield per plant predicted the feasibility of the genotypes under different environments. However, the prediction of the genotypes with the changing environments appeared to be difficult for DM, GE and GY. The linear relationship with the environment was found predominant for most of the characters studied, compared to that of non-linear relationship.

*From the estimation of stability parameters the genotype nos. **1, 5, 10** and **13** for almost all the developmental yield traits were found to be most stable and suitable with the change of environments. In case of morphological yield traits the genotype nos. **10-12** and **16** for SE and **3, 10** and **11** for GE and GY were proved to be most stable and suitable performer in any environment and could be used for the future breeding programme. On the other hand, the genotype nos. **8, 15-17** and **21** for developmental yield traits and the genotype nos. **7, 17** and **18** for most of the morphological yield traits might be stable and suitable performer under the unfavourable environments.*

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GENERAL INTRODUCTION

The genus *Triticum* L. belongs to subtribe Triticinae, tribe Triticeae and family Graminae. The polyploid series in *Triticum* includes diploid, tetraploid and hexaploid species with 2n=14, 28 and 42 chromosomes, respectively. The hexaploid wheat species is *Triticum aestivum* and it is generally called as 'common' or 'bread' wheat having the genomic constitution, AABBDD. The chromosome complement of hexaploid wheat is categorized into 7 groups with 3 pairs each and each group has one chromosome pair from each of the three genomes.

Wheat is the leading cereal crop, providing major food for one billion people or about 35 percent of the world's population. World wheat production is more than 520 million metric tons per anum (IWC, 1985). The most extensive production of wheat is in areas where the winter is cool and summer is comparatively less hot . Before 1974 wheat was not much favoured in Bangladesh but now it is the second most important crop, playing vital role in our agriculture based economy. All the wheat cultivars in Bangladesh are semidwarf spring type and they are grown successfully in the winter (from middle of November to early December). Moreover, the topography and soil texture, climatic conditions and the cropping pattern are such in Bangladesh that wheat can not be grown at the same time all over the country. Generally farmers sow wheat after the Aman rice harvest. It is oftenly delayed due to rainfall in November and December. Thus, its sowing time varies from one region to another and is delayed up to late December to early January. This delay results poor stand, reduced crop yield and low grain quality because of the heat stress of late spring. An endeavour for genetic improvement of this crop, with respect to

thermotolerance and good yield, may be helpful to boost up the wheat production in Bangladesh.

During the last thirty years, much attention has been focussed on the higher yields of bread wheat and it has been achieved with the introduction of semidwarf varieties into most wheat growing countries (Shamsuddin, 1990). Increase of yield with the concurrent decrease in height of the leading varieties of wheat has been achieved since middle of this century. The present day high yielding varieties (HYVs) of wheat are semidwarf in stature, which provide them resistance to lodging and increased yield to a substantial level. But now it is being thought that major dwarfing genes in wheat are associated with decrease in vegetative growth and restrict the leaf area development (Mackey, 1980), which ultimately results in source limitation. Therefore, the crosses between semidwarf and dwarf genotypes of wheat may provide the unification of improved yield and thermotolerance in a genotype.

Hybrid dwarfness usually defined as 'dwarf' is obtained in the segregating generations after crossing of normal genotypes of diverse gene pools. The F_1 plants produce a segregating F_2 population and does not agree with the expected ratio. But a number of normal F_2 plants which segregate dwarfs in the F_3 generation agrees with 13:3 ratio (Moore, 1969). However, some F_3 lines segregate dwarf plants again with different heights and spike lengths. It is also remarkable that a very few dwarf plants become vegetative in F_3 and successive generations. However, the dwarfing genes have been ascribed as a result of their complementary interaction in hybrid plants (Hermsen, 1967 and Moore, 1969).

Dwarfs are normally distinguished from semidwarfs by a characteristic tufted growth habit, short stature, very dark green leaves and remain in vegetative state at a photoperiod of below 8 hrs and a temperature below 16°C (Moore, 1966). Hermsen (1967) made a hypothesis that at least three dominant genes, *viz.* , D_1, D_2 and D_3, interact to produce dwarf phenotypes in hybrid dwarf wheat. Moore (1968) reported that D_1 and D_2 interact by complementation, D_2 being effective only in the homo- and hemizygous condition, but not at heterozygous. D_3 has an additive interaction with D_1 and D_2. Moreover, the genes (Ppd_1 and Ppd_2) responsible for photoperiod sensitivity in the dwarf lines are linked to the hybrid dwarf genes (D_1 and D_2) on chromosome 2D and 2B, respectively (Law, 1973). The genetic mechanisms responsible for semidwarfness have generally been considered independent of those which are responsible for dwarfness (Morrison, 1957; Hermsen, 1963 & 1967 and Moore, 1966 & 1969). Genes for dwarfism apparently are present in semidwarf wheat, as it exhibits a wide range in morphology and some of which are similar in appearance to the semidwarfs (Everson et al., 1957; McMillan, 1937 and Hermsen, 1967). However, it has been suggested that variants of dwarf-types may be ancestors of the present semidwarf varieties (Reitz, 1968 and Fick and Qualset, 1973).

Apical meristem of shoot is the region requiring optimum temperature (26°C) for the initiation of reproductive development in dwarf genotypes (Moore,1966). Three major types of dwarf genotype, *viz.*, Type I, Type II and Type III, may be classified according to their temperature requirements and phenotypic performance (Hermsen, 1967). Type I remains dwarf during their whole life cycle and normally do not produce seeds. Type II starts to grow as normal seedlings, become dwarfs while tillering, some produce seeds, others do not and die as

dwarfs. Type III emerges as normal seedlings, become dwarfs during the tillering stage, but after some time they start to shooting and develop into nearly or even completely normal plants. Type III and also vigorous Type II show some features. These are as follows:

1) Their high tillering capacity, advantageous for covering the soil very soon after the seedling emergence and for resisting soil moisture and temperature.
2) Their short straws give a high lodging resistance even after high N-application and the small leaf area reduces the rate of transpiration.
3) Few dwarf lines might have a chance of outcrossing due to open flowering tendency.
4) They become reproductive at high temperature and long photoperiod, and also tolerant to drought stress.

Therefore, dwarf wheats may be suitable material for use in breeding programme, which deserve high productivity with thermotolerance in the adverse environment of Bangladesh, specially the areas which suffer from the stresses of late planting.

Genetic and cytogenetic information has provided a framework for rapid and significant developments in characterizing the wheat genes and genomes not solely by their phenotypic effects but also by their structure and behaviour. This knowledge expands the traditional ways of transferring genes by crossing over or chromosome rearrangements, to include manipulation at molecular level. Consistently, a comparative study on somatic karyotype, heterochromatin distribution and chromosome differentiation in segregating populations of wheat

are essential aspect for a full understanding on the problems of multiple origin and diversity of wheat chromosomes. Identification of individual chromosomes and their homologue is complicated by variation in arm length and total length, between and within cells, particularly where more than one pair of chromosomes have similar length and arm ratio. Hence, to overcome this situation and aneuploid involvement in the segregating populations, a quantitative method for karyotype analysis may be applied. Analysis of heterochromatin distribution and chromosome differentiation may also be used to study the diversity and stability of genome in the advanced populations. Chiasma frequency may be used as a more precise parameter for comparing varieties/ lines as well as their progenies, since chiasma frequency reflects similarities both in genetic content and its arrangement.

Because of the great variability among the dwarfs from different crosses, there are good prospects for selection. It needs to find the best combinations of dwarfing genes and genetic backgrounds. This can be done by making crosses of selected dwarf lines with a few excellent Bangladeshi varieties, and therefore selecting dwarfs with valuable agronomic characters. In this regard, it is essential to study the inheritance of yield and its components of the crosses before starting the selection programme. Moreover, there are some genetical and environmental causes in the variation for the degree of dwarfness in segregating populations. Therefore, environmental effects on dwarfing genes and their interactions are needed to determine through the study of genotype-environment interactions. It may lead the successful selection and evaluation of the elite lines of segregating generations for use in the future breeding programme.

However, in the light of aforesaid attributes the present study was conducted with the following experiments under three parts:

Part I: GENOMIC COMPOSITION

1) Karyotypic analysis of dwarf progenies (F_3-F_6) and parental genotypes.
2) Heterochromatin distribution and Chromosome differentiation in parental genotypes.
3) Chiasma frequency and Chromosome association in Near Isogeneic Lines (NILs) of F_6 populations in four crosses.

Part II: GENE ACTION

1) Gene action for grain yield and its component traits in seven single crosses.
2) Heritability and heterosis for grain yield and its components.

Part III: GENOTYPE AND ENVIRONMENT INTERACTION

1) Genotype-environment (GE) interaction and *vis-a-vis* stability parameters in 21 NILs.
2) Evaluation of superior genotypes from the NILs of hybrid wheat.

PART - I

GENOMIC COMPOSITION

I. GENOMIC COMPOSITION

I.1. INTRODUCTION

The term genome was defined by Winkler (1920) for eukaryotes as the basic chromosome set of an organism, consisting of a species-specific number of linkage groups; hence the sum total of its genes. The smallest possible unit of the 'genome' in mutation and recombination is the individual nucleotide pair of deoxyribonucleic acid, and is referred to as a muton or recon, respectively. The chromosome may behave as units of genetic regulation in eukaryotes under particular circumstances.

In any crop improvement work involving chromosome manipulation, a karyotypic knowledge is necessary for full understanding to trace a comparative genetic and genomic status of that crop plant. On the basis of available information White (1978) classified six level of karyotype analysis. Among them the most common type found in the literature is the Beta-karyotype, in which chromosome numbers and lengths of chromosome arm are to be known. Karyotype analysis tends to suffer from the technical problems associated with the derivation of the data (Larsen and Kimber 1973) and consequently may lack both objective and subjective accuracy, mainly because of differences in chromosome contraction between and within cells.

Measurements of relative length of chromosome are somewhat better. Arm ratio is more reliable index (Kimber, 1971) particularly when strongly

heterobranchial chromosomes are present. The basic assumption made in karyotype analysis is that the homologous chromosomes have the same true length (Patau 1960). Because of the unavoidable length variation, it is necessary to measure the chromosomes in several cells of similar preparation and the use of mean to get an estimate of the true lengths of different chromosomes in a complement.

Patau (1965) proposed a quantitative method for human karyotypic analysis, based on obtaining an indicative estimate of lengths using the mean of several observations. Based on this method Ahmad et al. (1983) proposed a standard karyotype for soybean following the steps mentioned bellow:

1) Preparation of a two-dimensional scatter diagram of length and arm ratio for all the chromosomes in each cell, which reduce the diploid number of chromosomes to the haploid number and estimation of the mean values of haploid complement.
2) Construction of a combined scatter diagram of the haploid complements of all the studied cells to establish a standard morphology of those chromosomes which can be identified.
3) Characterization of the chromosomes through probabilistic inferences which can not be identified individually.

They stated also that this method can be used to propose the standard karyotypes of plant species with large number and small size of chromosome and also in aneuploid populations. Thus, the quantitative method may draw a valid result in case of the experimental materials used in the present study.

In the last two decades the most exciting developments in individual chromosome identification have been achieved by banding method (Hsu 1973). Among many specialized Giemsa banding methods, two techniques, namely C-banding and N-banding, have been most useful in cytogenetic studies of wheat. However, it is not possible to generalize the chromosome banding techniques in plants based on mammalian studies (Sharma 1975). Kimber and Sears (1987) reported that the differential staining of heterochromatin, DNA hybridization and other methods that mostly recognize repeated DNA sequences provide very clear and frequently beautiful patterns from which homology may be inferred. However, the very clarity of the preparations tends to obscure the fact that (1) the same sequence can appear at several locations throughout the genome, (2) the same sequences can often be found in distant non-lineal taxa, and (3) some 95% or more of the DNA may not be detected. Thus, it may not be considered in the phylogenetic conclusions. Nevertheless, a step toward the physical mapping of genes in relation to cytological landmarks on chromosome was taken by Dvorak and Chen (1984) and Dvorak *et al.* (1984). In spite of the innovation it prudently verifies any apparent chromosomal aberrations than by the conventional aneuploid and chromosome pairing analysis for the specific chromosome(s) implicated from banding analysis.

For identification and characterization of 21 individual chromosomes in wheat, the size and arm ratio of meiotic chromosomes were estimated using the monosomic series (Morrison 1953, Sears 1954 and Gill *et al.* 1963). However, chromosome length and arm ratio data from meiosis can not be reliably used for the identification of somatic chromosomes (Larsen and Kimber 1973). C-banding and N-banding technique for somatic chromosome identification in wheat were

reported by Gill and Kimber (1974) and Gerlach (1977), respectively. Both techniques differentially yielded constitutive heterochromatin regions and used widely in wheat cytogenetic research.

Dvorak and McGuire (1981) studied few substitution lines of common wheat by N-banding and observed nonstructural differentiation of wheat chromosomes as deduced from chromosome pairing relationships in intercultivar hybrids. However, they defined the structural differentiation in narrow sense and included only chromosomal changes, such as inversions, translocations, deletions and duplications, and their absence led them to conclude that nonstructural differentiation was the predominant mode of chromosome evolution in wheat group. However, changes in chromosome size and arm ratio may be caused by amplification of medium and highly repetitive DNA and repatterning of heterochromatin, and should also be considered as a form of structural differentiation. Endo and Gill (1984) reported that the reduced level of chromosome pairing is oftenly observed in intercultivar hybrids of wheat and this might be due to heterochromatic differentiation, genic and structural heterozygosity or hybrid dysgenesis. Therefore, a keen evaluation on the nature of heterochromatin distribution and chromosome differentiation in some of the materials used in the present study may be taken into consideration.

Ideally, the process of genomic analysis measures the total amount of chromosome pairing per cell. The determination of genomic homology becomes more difficult when there are not exactly the basic number of bivalents and multivalents are observed. Usually, reductions in total chromosome pairing are assumed to indicate some differentiation of otherwise identical genome (*i.e.*

becoming no longer homologous but homoeologous), and multivalents are taken to demonstrate residual homology or translocation heterozygosity.

Sensitivity of chiasma frequency to low temperature has already been shown to be controlled under the Ltp loci on chromosomes 5A and 5D of wheat (Riley 1966). The dominant allele, Ltp, at the locus 5A is present in the tetraploid wheats (AABB), maintaining chiasma frequency at low temperature in absence of the D genome (Riley and Hayter 1967). The lowering of chiasma frequency is found to be correlated with failure of zygotene chromosome pairing (asynapsis). The asynapsis might be due to a failure in the mechanism of chromosome pairing rather than of the prealignment of homologues. In euploid wheat the sensitivity of chiasma frequency to temperature could influence the cytological stability of the wheat crop (Bayliss and Riley 1972).

It has been generally accepted in a wide range of organisms that the temperature is an effective and convenient stimulus for altering the course of chromosome pairing and as well as crossing over (Wilson 1959, Henderson 1962, Peacock *et al.* 1981, Hossain 1978 and Church and Gilbert 1984). In common wheat, several studies have already manifested the reductional effect of both high (Fu and Sears 1973) and low (Riley *et al.* 1966) temperatures on homologous chromosome pairing. The high temperature (>30°C) disturbs the process of pairing at a step which controls premeiotic interhomologues attraction and this step may closely be connected with a peculiar stage, which is sensitive to the high temperature (Kato and Yamageta 1982).

Selection (for high seed set) had little or no effect on meiotic chromosome association (Muntzing 1951). Any increase in seed-set must have a genetical basis or some obscure physiological causes (Morrison 1956). Evidence of genotypic control of chromosome pairing strengthened the argument that fertility in autopolyploids could be improved by selection for meiotic regularity and *vice-versa* (Rees 1961). Both approaches had in fact been adopted for fertility improvement in tetraploid rye by Hossain and Moore (1975) and they concluded that the genetical control of the cytological factors is independent from that of plant vigour. They also indicated that selection for plant vigour (seed-set) is as important as the cytological factors for fertility improvement, while meiotic irregularity is lethal to semilethal and greatly limits the success of such selection.

Hybridization between population of diverse origin has been proved to be a source of improved meiotic regularity in tetraploid rye (Muntzing 1951). The heterosis effects in the hybrids are very obvious morphologically and are expected to increase the chiasma frequency (Rees and Thompson 1956). In many cases, it may be a more precise parameter than the karyotype itself, since chiasma formation reflects similarities both in genetic contents and in the arrangement of genes (Roy and Singh 1968). Therefore, the relationship between chiasma frequency and chromosome configuration may be very much useful for comparing the Near Isogeneic Lines (NILs) of wheat hybrid populations used in the present study. It may also be determined whether the chiasma frequency is under the control of genotype or environment or genotype-environment interaction.

I.2. REVIEW OF LITERATURE

The genome analysis has provided a framework to characterize genes and genomes not solely by their phenotypic effects but also by their structure and behaviour. This knowledge provides thrilling prospects for expanding the traditional ways of transferring genes. It has long been known that the cultivated wheats constitute an allopolyploid series, diploid through hexaploid. It was already clear that the genomes A, B and D were nowhere near as highly differentiated as had been believed. It has been established that each chromosome of hexaploid wheat has a homoeologue in each of the other two genomes to which it is closely related genetically. Okamoto (1957) and Riley and Chapman (1958) had discovered that meiotic pairing in hexaploid wheat is sufficiently suppressed by a gene or genes on the long arm of chromosome 5B that only homologues can pair, in the absence of chromosome 5B considerable pairing occurs between homologues. Thus, the polyploid wheats were shown to be more auto- than allopolyploid but to behave cytologically like diploids and thereby to maintain a high level of fertility and stability. In order to provide up-to-date and adequate coverage on this context, the available literatures are reviewed here under the following sub-heads.

I.2.1. Karyotype analysis:

a) Nomenclature:

In the identification of chromosome, location of centromere is the most useful landmark and it is characterized by great constancy. Designation of chromosomes is commonly done on the basis of centromeric location. Wilson (1928)

defined the location of centromere as attachment of chromosome to the spindle and commonly limited to a small area. He classified it generally into two types, namely 1) *terminal or telomitic* and 2) *non-terminal or atelomitic*. Different authors and even the same author on different occasions, used different terms for the same chromosome as well as the same term for different chromosome types, indicating that terminology of the centromeric position had become confused.

Ishing (1962) described the chromosomes as V-, L-, I-, j-shaped, median, metacentric and so on, without the centromeric position being clearly defined. Levan *et al.* (1964) proposed a standardized nomenclature for chromosomes. They divided half the length of a hypothetical chromosome into four equal sized regions, starting from the middle and called **m** (median region), **sm** (submedian), st (subterminal) and t (terminal region). The terms primarily referred to the location of centromere, but also indicated the location of all other morphological features of chromosomes. The location of the centromere has also been expressed as arm ratio, *i.e.* the length of the long arm divided by that of the short arm. The authors suggested to use the terms **m**, **sm**, **st** and **t** alone or in combination. The chromosome having the arm ratios 1.0-1.7 was designated as **m** chromosome, similarly arm ratios 1.7-3.0 for **sm**, 3.0-7.0 for st and 7.0-α for **t** chromosomes. However, it is possible to use the term *metacentric, submetacentric, subtelocentric* and *acrocentric* as synonyms to **m**, **sm**, **st** and **t**.

b) ***Constancy*** **:**

Each species possess a definite individuality for their somatic chromosomes in respect of their number, size, centromeric position and other additional

features. However, because of variation in the external appearance of the chromosomes in related species, Lewitsky (1931) and later on Stebbins (1950) defined the term karyotype as the phenotypic appearance of the somatic chromosomes in contrast to their genic content. Recent findings indicate that the constancy of the karyotype is a relative matter. Karyotypic variation may occur in a number of ways, such as the presence of B chromosomes, chromosomal polymorphism, genetic consequences and general fluctuations in size and shape of the chromosomes.

Rothfels and Siminovitch (1958) reported that the degree of mitotic chromosome contraction differed between long and short chromosomes as well as between the arms of a chromosome. Levan and Hsu (1959) observed that the homologous chromosomes within the same cell may show a considerable differences in length. They also found a variation in length up to 15% between the homologues in the same cell, the average being 6%. The length of that chromosome was found to be 5.5 to 7.9 μm in a sample of 10 cells. Maguire (1962) found a large variation in the length of pachytene chromosome in maize. The mean length of the longest chromosome was 83.5 μm and that of the shortest was 37.0 μm. The coefficient of variation in length of these two chromosomes was 23.2% and 23.8% respectively. And it ranged from 21.2% to 24.9% over the ten chromosomes. He also found that the arm ratio tended to be more variable in the chromosomes with higher arm ratios.

However, Sybenga (1972) insisted that although there may be variations, this does not necessarily take away the principle of karyotypic constancy. Lima-de-Faria (1975) asserted that the chromosome phenotype is a steric configuration

and it happens in a permanent state of change depending on the cell stage. The length of a somatic chromosome is only a fraction of its chromatin fibre length during interphase. The contraction of length is achieved by either coiling or folding of the chromatin fibre in association with various proteins and subsequent coiling (Du Praw 1966, and Rees and Jones 1977). Any factor that might affect the physico-chemical mechanics involved in chromosome contraction will cause the differences in chromosome size.

Dyer (1976) reported that a change in the amount of chromosomal protein may reflect the overall activity of the cell and may explain the observed differences in chromosome size between different tissues and even different genotypes. The inherent factors that influence the phenotypic change in chromosome form and behaviour may be the cellular and external environments or the genes which serve to control the activity of the chromosomes (Rees and Jones 1977). Recently it has been shown that the artificially induced constrictions and gaps on metaphase chromosomes are only stretched regions of the chromatids resulting from deficient folding of chromatin due to protein damage (Brogger and Waksvik 1978, and Mace *et al.* 1978).

According to Ahmad *et al.* (1983), chromosome length can be influenced by different methods and steps of the slide preparation tissue. Methods of flattening the cells and bringing the chromosomes in one plane during slide preparation may produce distortion. Measuring of chromosomes is another possible source of error. Because of limited resolving power of the light microscope there is a diffraction fringe at the two ends and sometimes at the centromere of a chromosome. This creates some uncertainty in the location of the proximal and

distal end of each chromosome arm. However, if the work is done carefully and in a consistent manner, the inaccuracy in measurement should not limit the usefulness of chromosome measurements. Improper printing of the photomicrographs may also produce some distortion in apparent chromosome size. It is clear that various factors may influence the length of a chromosome. While technical refinement may reduce this variation, it can not be eliminated completely.

c) *Techniques*:

In plants critical analysis of karyotype is essential for 1) assigning linkage groups, 2) identifying aneuploid individuals, 3) examining the effect of a specific chromosome in an alien background and 4) determining the phylogenetic relationships between and within taxa.

It is also essential to identify the chromosomes individually and properly for the karyotypic analysis. Variation in the length of chromosome complicates the identification of individual chromosomes and their homologues in any particular plate. The chromosome which may be longest in one cell may not be so in the next. Matching of chromosomes in homologous pairs becomes specially difficult when two or more pairs of chromosomes possess similar lengths and arm ratios. Patau (1960, 1965) made a survey on the problems of chromosome identification with special reference to human chromosomes. Because of the unavoidable length variation, he suggested to measure the chromosomes in several cells and to use the average to get an estimates of the true lengths of different chromosomes in a complement.

Sasaki (1961), however, pointed out that use of relative length would serve any real purpose only if the degree of contraction were uniform in all chromosomes. The degree of contraction or elongation was generally greater for longer chromosomes than the shorter ones. Torres (1968) used a non-parametric test based on rank sums, known as Mann-Whitney U-test, to assess the overall similarity between the karyotypes of different *Zinnia* species. The method is based on measurement of the distances in the scatter diagram between the pairs of points representing the homologous chromosomes of a real or simulated hybrid, and then comparing these distances by means of U-test with those similarly derived for the parents. Of course, all such comparisons are merely morphological and have no necessary genetic significance.

Compiling a good number of literatures White (1978) reported six types of karyotype analysis. These are mentioned bellow:

1) Alpha karyology - only chromosome numbers and approximate sizes were determined;
2) Beta karyology - chromosome numbers and lengths of chromosome arms were known;
3) Gamma karyology - geimsa and fluorescent banding techniques were adopted;
4) Delta karyology - location of satellite DNAs, nucleolar organizers and 5-s rRNA loci were determined;
5) Epsilon karyology - the main distinctive loops and other landmarks in lampbrush chromosome were mapped; and
6) Zeta karyology - morphology of the polytene chromosome was analysed.

Ahmad *et al.* (1983) used a quantitative method for karyotypic analysis in soybean. They used data from six cells selected on the basis of degree of contraction of the chromosomes and which were found to be homogeneous statistically. Scatter diagrams were prepared from data on total length and arm ratios of the chromosomes to determine the homologous pairs of chromosomes. The data from the haploid complement values of the six cells were then plotted to identify the chromosomes individually. They also stated that this method should be useful for karyotypic analysis of other plant species with large number and small size of chromosomes, specially when more pairs of chromosome posses similar length and arm ratios. They also suggest to use this method for identifying the chromosomes in aneuploid.

Despite genetical and breeding importance, relatively few karyotypic studies have been reported for the common wheat (*Triticum aestivum* L.). It might be due to large number (2n=42) and small size of the chromosomes, and allopolyploid genomic condition. These cytological difficulties suggest to use the quantitative technique for karyotypic analysis, which may throw a light on the genomic composition of hexaploid wheat.

I.1.2. Heterochromatin distribution and chromosome differentiation:

Plant chromosomes are coiled differentially into euchromatin and heterochromatin. DNA-nonhistone protein bands are stronger in heterochromatin and resistant to the disruptive chemicals (Sharma 1975). The differential staining of heterochromatin by Geimsa banding methods mostly recognize repeated DNA

sequences, provide clear bands and permit specific chromosome identification. The longitudinal differentiation of chromosomes revealed by the banding techniques provide a unique fingerprint of individual chromosomes for differentiation and evolutionary studies (Gill and Kimber 1974).

Direct identification of individual somatic chromosomes of wheat by C-banding technique was reported by Gill and Kimber (1974) and by N-banding was reported by Garlach (1977). From the evidence of usefulness of C-banding and N-banding techniques in chromosome identification, Zurabishvili *et al.* (1978) claimed that wheat chromosomes have diverse origins and that no unique karyotype exists in wheat cultivars. They also asserted that individual chromosome banding patterns can not be used to deduce homologous and homoeologous chromosome relationships among cultivars and species in the wheat group.

Following the reports on chromosome identification by C-banding (Natarajan and Sarma 1974, Zurabishvili *et al.* 1974) and N-banding (Garlach 1977, Jewell 1979), there has been widespread use of chromosome banding methods in various aspects of wheat cytogenetics research. Appels *et al.* (1978) and Dennis *et al.* (1980) stated that C- and N-banding differentiation of heterochromatin have a biochemical basis. C-banding technique is used for staining of all classes of heterochromatin and N-banding reveals only specialized heterochromatin containing polypyrimidine DNA sequences. Thus, C-banding might be a widely applicable technique across plant and animal taxa, and N-banding of limited use only to taxa containing significant amounts of polypyrimidine DNA sequences. On the other hand, Endo and Gill (1984) stated that N-banding does offer some

advantages over C-banding. The N-banding procedure is rapid, extremely reproducible, often stain some bands more intensely, and also provide excellent resolution of bands.

Particularly, polymorphic banding patterns among cultivars/lines (Iordansky *et al.* 1978, Seal 1982, Endo and Gill 1984, Friebe *et al.* 1990) and in numerous structural aberrations have been described in wheat (Endo 1988, Kota and Dvorak 1988). These advances have opened many possibilities for the genetic mapping of polymorphic C-bands (Jampates and Dvorak 1986, Curtis and Lukaszewski 1991) and the physical mapping of genes to specific bands on individual metaphase chromosome maps of wheat (Dvorak *et al.* 1984, Kota and Dvorak 1986, Mukai *et al.* 1990, 1991).

The observations of Dvorak and McGuir (1981) on the nonstructural differentiation of wheat chromosomes as deduced from chromosome pairing relationships in intercultivar hybrids are also of interest. Unfortunately, they used structural differentiation in the narrow sense to include only chromosomal changes such as inversions. translocations, deletions and duplications, and their absence led them to conclude that nonstructural differentiation was the predominant mode of chromosome evolution in the wheat group. However, changes in chromosome size and arm ratio, which may be caused by amplification of medium and highly repetitive DNA and repatterning of heterochromatin, should also be considered as a form of structural differentiation. Endo and Gill (1984) reported that the reduced level of chromosome pairing that is often observed in intercultivar hybrids of wheat may be due to heterochromatic differentiation, genic and structural heterozygosity or hybrid dysgenesis. Therefore, analysis of the nature of differentiation of wheat chromosomes needs reexamination.

Later on Lukaszewski and Gustafson (1983) presented idiograms of the 21 C-banded wheat chromosomes based on standard genetic nomenclature of wheat. However, no attempt was made to develop a nomenclature system for the description of bands. Iordansky *et al.* (1978) proposed the generalized Cytological Nomenclature for Cereal Chromosomes (GCNCC) after the Paris Conference on standardization in human cytogenetics. Under the GCNCC system, chromosomes were numbered on the basis of their length rather than the existing genetic nomenclature. Van Niekerk and Pienaar (1983) and Gill (1987) took initial steps in combining the genetic and GCNCC nomenclature and made proposals for a standard nomenclature system for the description of chromosome bands in wheat.

At the Seventh International Wheat Genetics Symposium (IWGS), Cambridge, England, an international chromosome banding nomenclature committee was formed and reached a consensus on nomenclature and designation of chromosome bands in 'Chinese Spring' wheat (*Triticum aestivum* L.). Following the instruction and in consultation with the committee Gill *et al.* (1991) developed a standard karyotype and nomenclature system for the description of the chromosome of 'Chinese spring' wheat. They also proposed the nomenclature for the polymorphic bands and frequently observed chromosome aberrations in wheat. Thus, the nomenclature system of chromosome bands of may be useful for the analysis of heterochromatin distribution and nature of chromosome differentiation, thereby individual chromosome identification in intraspecific hybrids of common wheat.

I.2.3. Chiasma frequency and chromosome association:

Chiasma frequency may be used as a more precise and distinctive parameter for comparing taxa/varieties/lines in respect to their genomic relationship, since chiasma frequency reflects similarities both in genetic content and its arrangements (Roy and Singh 1968). The primary association of homologous chromosomes into pairs (bivalent), and the non-random secondary associations of one or more bivalent into groups has been reported by numerous authors since the 1930's (Darlington and Moffett 1930), particularly in bread wheat by Riley (1960), Kempanna and Riley (1964) and Feldman and Avivi (1973).

The chiasma properties of nuclei are known to be genotypically determined and subjected to both continuous and discontinuous variation. An understanding of the principles governing this aspect of chromosome behaviour depends therefore upon a statistical evaluation of these properties, as well as on recognization of the consequences of mutation, segregation and recombination of genes. No organism has been more thoroughly investigated from this point of view than rye. It is known that :

1) Significant differences in chiasma frequency exists between individuals of different genotypes. The continuous nature of these differences show that they depend, at least partially, upon a polygenic control (Rees 1955).

2) Within certain genotypes there is a considerable variation in chiasma frequency both between and within pollen mother cells (PMCs). The amount of cell variation and bivalent variation has, however, shown to be dependent upon the genotype (Rees and Thompson 1956).

Jones and Rees (1964) described a rye genotype which had a highly abnormal and asymmetrical distribution of chiasmata between bivalents. This was interpreted as being due to breakdown of the normal control processes which operate in rye. According to John and Lewis (1965, meiosis is a complex process and this complexity has proved a consistent obstacle to progress in elucidating the precise nature of many meiotic events and its control mechanisms. A most promising approach for analysing the control mechanisms in the study of anomalous sequences are normal for the type concerned, others characterized abnormal cells or individuals and they all reflect the genotype. Jones (1969) proposed that two independent and fundamentally different control systems are involved in the maintenance of efficient chiasma conditions in rye. One of these simply gives competence for chiasma formation, and the other is evidently concerned with the regulation and distribution of chiasmata.

In some hexaploid wheat varieties a locus, probably on chromosome 5A has recessive allele Lpt and it is unable to stabilize the chiasma frequency to low temperature in absence of chromosome 5D. This allele revealed by plants tetrasomic 5A and nullisomic 5D exhibits a weak stabilizing activity and do not show reduction on chiasma frequency at temperatures below 20°C (Riley *et al.* 1966). The dominant allele Lpt at 5A chromosome of tetraploid wheat (AABB) maintains chiasma frequency at low temperature in the absence of the D genome (Riley and Hayter 1967). It may, thus, be generally concluded that in euploid wheat the presence of a gene or genes on chromosome 5D largely stabilizes chromosome pairing against extremes of temperature. Bayliss and Riley (1972) pointed out that in euploid wheat the sensitivity of chiasma frequency to temperature within the normal meteorological range could influence the cytological stability of the wheat crop.

The best result one may expect with a selection for meiotic irregularity is that the selected population will consist mainly of heterozygotes which may survive under normal growing condition. Hossain and Moore (1975) studied a population of tetraploid spring rye. They selected plants for high seed-set and regular meiosis, and for low seed-set and irregular meiosis, and referred as 'high' and 'low' populations respectively. A significant positive correlation between meiotic regularity and seed-set was found in the 'high' population while in the 'low' population the correlation was negative. This led to the conclusion that the genetical control of the cytological factors is independent from that of physiological factors. They also observed that in low population the regression of chiasma frequency on quadrivalent was negative and on bivalents was positive and significant based on plants mean, whereas the same regressions showed the opposite relationships based on cells mean.

Alonso and Kimber (1981) developed numerical methods for the analysis of chromosome pairing in hybrids and the consequent determination of genomic relationships. The essential features of these techniques are measure of how often the chromosome pairs (mean arm-pairing frequency, c) and the measures of the similarity of two or more of the genomes present (relative affinity, x). The value of c (which is not the same as chiasma frequency) is obtained from the frequencies of the observed meiotic figures. It ranges from 0.0 (when there is no chromosome pairing at all) to 1.0 (when every possible arm is paired in every cell). The frequencies expected from the various meiotic figures are calculated on the basis of various assumptions of synapsis, chiasma formation and the relative affinity of the genomes present. The relative affinity (x) ranges from 0.5 (when all the genomes are equally related to each other) to 1.0 (when two or more

genomes pair to the exclusion of all other genomes). These assumptions and definitions result in various models of chromosome pairing at increasing levels of ploidy. The optimum value of the relative affinity is calculated (by minimum sum of squares of differences between observed and expected pairing) for each of the appropriate models. The model that fits the observed data best, it's associated value of x, and the observed value of c are taken to describe the evolutionary relationships of the species involved. Together with the values of c and x, the determination of which pairing pattern fits best adds another dimension for recognizing the relationships of the chromosomes and the genomes present in the hybrid. Studies of genomic relationships based on this type of numerical analysis differ from the classical method by considering not only the amount but also the pattern of chromosome pairing.

In general, low temperature tends to decrease pairing and the number of chiasmata depending on the genetic makeup of the plant. On this basis, it is possible that the low temperature reduces irregular chromosomal behaviour at meiosis by restricting pairing and chiasmata formation within the inverted segments, thus reducing the frequency of bridges and fragments (Kato and Yamageta, 1982). They reported also the influence of genotype-environmental interaction on chiasma frequency in plants, where no structural change was involved. Ahmad *et al.* (1984) reported that meiosis in interspecific hybrids ranged from essentially normal to highly irregular, depending on the parentage and the temperature regime of the culture. Moreover, degeneration of pollen and seed was not, however, always proportional to meiotic irregularity. The degeneration may be caused by genetic inviability, unfertilization and/or zygotic undevelopment. They suggested that at least three factors influenced chromosome

behaviour and fertility. These factors were genotype, temperature and genotype-environment interaction.

Thus, the Near Isogeneic Lines (NILs) of intercultivar crosses along with their parents may be studied under a range of environments to determine the magnitude of meiotic pairing and comparing their genetic make up.

I.3. MATERIALS

The plant materials used for different experiments in the present study are as follows:

I.3.1. Somatic karyotype analysis:

For this experiment six parents and four generations (F_1, F_5 and F_6) of seven single crosses of wheat (*Triticum aestivum* L.) were evaluated.Four Bangladeshi varieties namely, Aghrani (Ag), Akbar (Ak), Ananda (An) and Kanchan (Kan), and two exotic selected dwarf lines of Falchetto X Maxicani crosses, FM-32 and FM-139 were used as parents in different crosses. The crosses were 1) Ag X FM-32, 2) Ak X FM-32, 3) An X FM-32, 4) Kan X FM-32, 5) Ak X FM-139, 6) An X FM-139 and 7) Kan X FM-139 were used. F_3 to F_6 materials were developed by selfing plants heterozygous for dwarfing genes alongwith the parental lines in a wheat breeding programme of Rajshahi University.

Bangladeshi varieties were procured from Regional Agricultural Research Station (RARS), Ishurdi, Bangladesh. The selected dwarf lines were supplied from the department of Agricultural and Environmental Sciences, University of Newcastle Upon Tyne, U.K.

I.3.2. Heterochromatin distribution:

Materials used for this experiment were four indigenous varieties (Aghrani, Akbar, Ananda and Kanchan) and two exotic selected dwarf lines (FM-32 and FM-139) of wheat.

I.3.3. Chromosome association and chiasma frequency:

Plants of 12 Near Isogeneic Lines (NILs) from F_6 progenies of four crosses of wheat along with a check variety (Kanchan) were used to conduct this experiment. Three NILs from each of the four crosses were considered as Semidwarf, Dwarf type-II and Dwarf type-III on the basis of their developmental performances (details in Part-III, Table 2). Their designation, developmental type and parentage are given

No.	Designation	Type	Parentage
1.	AgFM32903-1-6-3-5	Semidwarf (N)	Ag x FM32851-4-8-4-2
2.	AkFM32906-2-1-6-4	,,	Ak x FM32857-2-6-1-3
3.	AnFM32907-1-3-2-9	,,	An x FM32858-4-1-6-2
4.	KnFM32908-2-4-5-3	,,	Kn x FM32859-1-4-3-5
5.	AgFM32903-1-6-3-3	Dwarf type-II	Ag x FM32851-4-8-4-2
6.	AkFM32906-2-1-6-2	,,	Ak x FM32857-2-6-1-3
7.	AnFM32907-1-3-2-7	,,	An x FM32858-4-1-6-2
8.	KnFM32908-2-4-5-8	,,	Kn x FM32859-1-4-3-5
9.	AgFM32903-1-6-3-7	Dwarf type-III	Ag x FM32851-4-8-4-2
10.	AkFM32906-2-1-6-6	,,	Ak x FM32857-2-6-1-3
11.	AnFM32907-1-3-2-8	,,	An x FM32858-4-1-6-2
12.	KnFM32908-2-4-5-5	,,	Kn x FM32859-1-4-3-5

I.4. METHODS

I.4.1. Somatic karyotype:

I.4.1.1. Pretreatment, fixation and preservation of root tips:

Fresh and dry seeds of both indigenous and exotic varieties/lines of wheat and the hybrid progenies (F_3, F_4, F_5 and F_6) of seven crosses were allowed to germinate in petridishes with moistened Whatman filter paper at room temperature (22–24°C). When the radicle reached about 1.0–1.5 cm in length, they were treated with saturated solution of para-dichlorobenzene (PDB) for 5 hrs at 4°C. After thorough washing in running water the root tips were fixed in acetoalcohol (1:3) for 48 hrs at room temperature (22–24°C). Then they were preserved in 70% ethanol and kept in the refrigerator until they were used for study.

I.4.1.2. Staining of root tips and preparation of slide:

The root tips were stained using hematoxylin as stain and slides were prepared following the schedule as mentioned bellow:

a) The preserved roots were washed thoroughly for five minutes in distilled water.

b) Then they were hydrolyzed in 1N HCl for 12–15 minuets at 60°C.

c) The hydrolyzed roots were washed thrice for 10 minuets.

d) Then they were mordanted in 2% iron alum for 15 minuets.

e) The mordanted roots were then washed thrice for 10 minuets with frequent change of distilled water.

f) The root tips were then stained in 2% haematoxylon for 15 minuets.

g) After rinsing in 45% acetic acid, the stained root tip was excised and squashed in 0.5% acetocarmine on a clean slide.

h) Then a repeated heat-cool-press process were utilized until all chromosomes in cells were spread elsewhere.

I.4.1.3. Observation and Photomicrography:

Temporary slides were used for microscopic observation and photomicrography. However, the best of these were made semipermanent. Photomicrographs were made from the cells with well spread and properly contracted metaphase chromosomes using the Fuji photographic film and high contrast developer. Photomicrographs were printed at the magnification of 2000 X and chromosomes were measured using a divider and a millimeter scale. The values (millimeter) were then converted in micrometer (μm). Arm ratios were calculated by dividing the length of the long arm by that of the short arm. The chromosomes were then classified primarily by the arm length ratio according to Levan *et al.*(1964) as follows:

Chromosome with the arm ratio 1.0 to <7.0 as 'm'(metacentric), 1.7 to <3.0 as 'sm' (submetacentric), 3.0 to <7.0 as 'st'(subtelocentric) and 7.0 and above as 't'(telocentric) chromosome.

I.4.1.4. Analysis of data:

a) *Basis:*

The method of establishing the standard karyotype of a genotype required three conceptual basis and these are:

i) since the morphology of chromosomes was altered by differential contraction, the mean length and arm ratio of similar cytologically processed cells provided the best estimate of a **'standard morphology'**,

ii) in a two dimensional scatter diagram of total length and arm ratio of all chromosomes in studied cells, the points representing the same chromosome tended to cluster, and

iii) two homologous chromosomes became individually recognizable by the mean location of one chromosome occurred not less than one standard deviation away from that of the other. When such a difference did not exist, these two chromosomes could not be distinguished individually, unless particular marker feature (such as a satellite) existed on one of them. The indistinguishable chromosomes could be assigned to different morphological categories on a probabilistic basis.

b) *Standard chromosome morphology* :

A standard chromosome morphology was developed following three steps of analysis :

i) A scatter diagram was produced for all chromosomes of each cell, by use

of which the diploid number of chromosomes was reduced to the haploid and the mean values of each chromosome of haploid complement were determined.

ii) A combined scatter diagram of the haploid complements of all the cells was constructed to establish a standard morphology of those chromosomes which could be identified.

iii) These unidentified chromosomes were characterized individually through the probabilistic inferences.

c) *Derivation of the haploid values :*

i) A scatter diagram was prepared for each cell incorporating lengths and arm ratios of the 42 chromosomes. Each chromosome and its corresponding point on the diagram was numbered arbitrarily. The chromosomes were then paired by circling the corresponding two points on the basis of their proximity.

ii) In the cases, where more than two points occurred close together, the chromosomes were re-examined under the microscope to comprise a homologous pair on the basis of more alike staining intensity and physical appearance. Each pair of points were considered to represent a homologous chromosome pair.

iii) Average of the lengths and arm ratios of each pair of chromosomes constituted the haploid complement of that cell. The process was repeated for each of the five cells studied and thus, the haploid values were obtained. Chromosome pairs were then numbered from 1 to 21 within each cell approximately, but not strictly, in increasing order of length and arm

ratio.

iv) The average haploid total length, standard error and coefficient of variation were estimated over five cells. Furthermore, the degree of similarity of distribution of chromosomal morphology among different haploid complements was tested by using a 6 X 5 contingency table. The nonsignificant χ^2 -value indicated that the cells were homogeneous for the frequency of classes of chromosome based on haploid length and arm ratio. But in case of significant χ^2 -value the heterogeneity of cells were proved and indicated that those chromosomes (which were equated to be the corresponding ones in the different cells) were morphologically dissimilar in general.

d) *Chromosome identification :*

i) Although the differences between the cells for total haploid length were relatively small, it was necessary to standardize the lengths across the cells in order to minimise any anomalies in chromosome length due to differential contraction in the different cells. The haploid length for each chromosome was standardized using the following formula:

$X_{ij} = X_{ij}.(\Sigma X_i/5) \div X_i$,

Where,

X_{ij} = standardized length of the jth chromosome of the ith cell,

X_{ij} = unstandardized length of the jth chromosome of the ith cell,

X_i = the haploid total length of the ith cell,

i = 1 to 5 and j = 1 to 21.

Following this transformation, each complement was found to have equal haploid total length.

ii) Corresponding chromosomes in different haploid complements were determined through a grouping technique and applied to the combined scatter diagram of the five haploid complements involving 105 chromosomes.

iii) The data used were the original haploid values for arm ratio and the standardized haploid length values. Each point in the scatter diagram represented a specific chromosome in a particular haploid complement.

iv) Symbols in the diagram referred to specific chromosomes in a particular haploid complement, *i.e.* five different symbols referred to the studied five cells and numbers 1 to 21 represented the individual chromosomes characterized previously.

v) Ideally, if the morphology of all chromosome pairs were distinct and reproducible across the cells, the five points representing the haploid homologues of each chromosome should cluster closely, and 21 such clusters should be recognizable.

vi) Where the morphology of non-homologues was not distinct, their clusters would be expected to overlap and lack of reproducibility of morphology for a chromosome in different cells would result in diffuse clusters. Regardless, each cluster must contain one point (chromosome) from each cell studied (cell plates **a** to **e**).

vii) In reality, clear groups were existed for only some sets of five points. Some groups were distinct but somewhat diffused. Other groups were overlapped because of the occurrence of an outlying point. All clear groups (chromosomes) fall in the category of individually identifiable ones.

viii) For each of the chromosomes (clear groups) represented by the sets of five points the mean, standard error and coefficient of variation were determined for length and arm ratio, using the original diploid values.

ix) The identified chromosomes comprised **m, sm, st** or t (according to Levan *et al.* 1964) and an idiogram was made. The chromosomes within each type was numbered in decreasing order of mean length. Chromosome type together with this number constituted the specific name of the chromosome concerned. The identified chromosomes occupied approximately **50%** of the total complement length and that was consistent across the cells.

e) *Allocation of unidentified chromosomes:*

i) All chromosomes in five haploid complements were classified in different morphological categories based on total length and arm ratio within the length classes. The class interval of **0.5μm** for length was chosen arbitrarily and the ranges for arm ratio as recommended by Levan *et al.* (1964) were used. This classification was superimposed on the scatter diagram of the haploid complements as a grid of length and arm ratio classes.

ii) Since standard length was used in plotting which resulted in vertical displacement of the points in the combined scatter diagram, the count of points in cells of the scatter diagram may differed slightly from the number of chromosomes in that cells. However, the mean of the groups of identified chromosomes in the scatter diagram did not change as a result of standardization.

iii) The unidentified chromosomes were distributed to the various morphological classes using probabilistic inferences on –

1) the frequency of chromosomes in a given cells per haploid set,
2) occurrence of points in the combined scatter diagram and
3) the examination of the original total length and arm ratio of the chromosomes.

iv) The number of unidentified chromosomes were allocated to the various morphological classes and counted. Finally, all 21 chromosomes in the

haploid complement were numbered from 1 to 21 in decreasing order of total length and increasing order of arm ratio within each length class, following the convention of Rhoades (1955). These numbers were used as the identification of each chromosome in all subsequent discussion.

f) Centromeric formula:

i) After identification each chromosome was allocated a serial identification number and each carried a specific name based on its arm ratio. Then these identity of all the chromosomes over different plates were summarised for each genotype and was made a centromeric formula.

ii) The commonly identified were again plotted using their mean values for length and arm ratio to compare their structural changes over the studied genotypes.

g) Proposed standard karyotype:

Finally the standard karyotype was derived on the basis of centromeric formula, and range and general average of chromatin length per chromosome. The chromosomes were grouped as i) Long (L) whose chromatin length was above 7.0 μm, ii) Medium (M) whose chromatin length was between 5.01 – 7.0 μm, iii) Relatively short (S_1) whose chromatin length was between 3.01 – 5.0 μm, and iv) Short (S_2) whose chromatin length was below 3.0 μm.

I.4.2. Heterochromatin distribution:

I.4.2.1. Fixation and preservation of root tips:

Fresh and dry seeds of four local varieties and two exotic lines were allowed to germinate separately in petridishes containing moist filter paper at room temperature (20–22°C). When the roots attained the size about 1.0–1.5 cm length, the germinating seeds were immersed in ice cold water for 24 hours. The root tips were then fixed in acetoalcohol (1:3) for 2–3 days at room temperature (20–22°C). Then they were preserved in 70% ethyl alcohol and kept in refrigerator till use.

I.4.2.2. Staining schedule and slide preparation:

a) The preserved root tips were thoroughly washed in running water for 10 minutes.

b) Then they were soaked in a solution of 1N HCl and 1% acetocarmine (1:1) for 1.5 to 2 hours at room temperature (20–22°C).

c) Those moderately hydrolysed and lightly stained root tips were squashed in 45% acetic acid and they covered with coverslips.

d) Then coverslips were removed from the slides by freezing and was treated in hot 45% acetic acid at 60°C for 10 minuets, and then air dried overnight.

e) The air-dried slides and coverslips were treated in hot 1M NaH_2PO_4 at 94°C for 2 minuets and rinsed in distilled water.

f) Then the slides and coverslips were stained in freshly prepared 4% Geimsa solution for 30–50 minuets.

g) The slides were then rinsed briefly in distilled water. air dried and made semipermanent using euparol.

I.4.2.3. Observation and Photomicrography:

Semipermanent slides were used for observation and photomicrography. Cells with well-spread, properly contracted and banded chromosomes were studied and photomicrographs were made from the desired preparations. Five cells of uniform and satisfactory quality for each material were used for analysis. From photomicrographs chromosomes measured in millimeters and the values were then converted to micrometer (μm) and location and number of bands were determined. The data were then subjected for analysis.

I.4.2.4. Analysis of bands :

Number and kinds of bands (heterochromatin) were analysed as follows:

a) Position, size and intensity of individual bands were determined first.

b) Then the chromosome arms and bands were designated following the recommendations of Paris Conference, 1974. Under the proposed rules of nomenclature, short and long arm of each chromosome were designated as p and q, respectively. Each p and q arm was subdivided into regions based on landmark bands.

c) In designating a particular band, five items were required: i) the chromosome number, ii) the genome designation, iii) the arm symbol, iv) the region number and v) the band number within that region. These items were given in order without spacing or punctuation.

d) In present materials, dark and light bands represented heterochromatic and euchromatic regions, respectively. An attempt was made to subdivide most of the chromosomes into biologically meaningful regions. Dark bands which were not always reproducible in all chromosomes were designated by stippled bands and band numbers were not assigned.

e) Chromosome 1A was distinguished from chromosome 2A and 3A on the basis

of arm ratios and absence of any major landmark band. Chromosome 3A was distinguished from 2A by landmark band 3Ap21. The remaining A genome chromosomes were easily distinguishable.

f) In the B genome, 1B and 6B were the nucleolus organizer chromosomes. Chromosome 3B had a large number of landmark bands in the p arm and could be distinguished from 2B on this basis. Chromosome 7B had proximal large, dark bands and distal large, light bands in each arm. The remaining chromosome had many diagnostic landmarks and was easily distinguished from one another.

g) In the D genome, chromosome 1D was distinguished from 6D on the basis of arm ratio and bands 1Dq21 and 1Dq31. The banding pattern of chromosome 2D was found to be confused with chromosome 5A and was distinguished on the basis of arm ratio and size. Chromosomes 3D, 4D, 5D and 7D had highly diagnostic landmark bands and was identified easily.

h) The B genome chromosomes were highly heterochromatic and easily identifiable from others. D genome chromosomes was distinguished from A genome chromosomes by more distal diagnostic landmark bands at the p arm except 7D and 4A. Only chromosome 2D and 7D among the D genome chromosomes showed faint heterochromatins. The individual chromosomes were distinguished and numbered on the basis of length and arm ratios.

I.4.3. Chiasma frquency and chromosome association:

I.4.3.1. Experimental design:

Twelve Near Isogenic Lines (NILs) and the check variety (Kanchan) were raised in a Randomized Complete Block (RCB) design with three replications during the growing season 1993-94 at the experimentation field of Rajshahi University. Each block was of 6.6 m X 1.5 m with 0.5m space between and around

the blocks. Every block consisting of 15 rows, one for each of the 12 Nails and check variety, and two terminal rows were of non-experimental plants. An uniform row spacing of 30 cm and plant spacing of 10 cm within the row was maintained after seedling emergence for all the trials.

Fertilizers were applied @ 60 kg urea, 40 kg TSP, 40 kg MP and 1 ton cow dung per hectare. All fertilizers, except 50% of the urea, were applied at the time of final land preparation and the rest part of urea were applied as top dress in two equal splits during tillering and heading stage of the crop. Uniform and standard intercultural operations were done as and when necessary for all trials to raise the good crop. The weather records of the growing season of 1993-94 is given in Appendix 4.

I.4.3.2. Fixation and preservation of young inflorescence:

At the proper growth of plants, young inflorescences were fixed in Carnoy's solution (6 Ethanol : 3 Chloroform : 1 Acetic acid) at 8.30 - 9 AM. After 48 hours of fixation they were rinsed and preserved in 70% ethanol, and kept in a refrigerator till used.

I.4.3.3. Slide preparation :

Temporary slides were prepared from suitable anthers by aceto-orecine smear technique as follows:

i) Young anther was placed on a clean slide and a drop of 2% acto-orecine was added.

ii) The anther was ruptured by curved dissecting needle and the anther wall was removed.

iii) A coverslip was placed on the smear of PMCs and warmed gently over an alcohol flame.

iv) Then the slide was placed in a fold of blotting paper and a gentle pressure exerted by thumb to spread out the PMCs as well as the chromosomes. v) Additional 45% acetic acid and heat-cool-pressure was applied as needed until the cytoplasm became clear.

I.4.3.4. Recording of data :

The frequencies of chiasma from diakinesis and disjunction index from regular A-I cells (*i.e.* PMCs without bridges, lagards, fragments) were scored from the three anthers of a floret. The frequencies of regular tetrads (*i.e.* tetrads without micronuclei and polyads) from three florets of different regions of the spike were scored to take it into the account of the variations within the spike. For different meiotic features at least 50 PMCs were scored form each young spike and it was repeated in thirty different plants from each genotype. Other observed and recorded meiotic features were, 1) Bivalent frequency, 2) Quadrivalent frequency, 3) Trivalent frequency, 4) Univalent frequency, 5) No. of chromosomes in IV + II formations, 6) No. of chromosomes in III + I formations, 7) Regular tetrads (Ang. values) and 8) Disjunction index.

I.4.3.5. Analysis of data :

a) *Mean and standard error:*

Mean, variance and standard error for each meiotic feature under each

environmental regime (sowing) of all the Nails were calculated using the data over replications. The conventional formulae used for computation of these parameters are :

i) Mean, $\bar{X} = \Sigma X/n$

ii) Variance, $\sigma^2 = [\Sigma X^2 - (\Sigma X)^2/n] \div (n-1)$

iii) Standard error, $S.E. = (\sigma^2/n)^{\frac{1}{2}}$.

Where,

X = Individual observation and n = Total number of observations.

The mean performance of the Nails were compared with the check variety using the t-test.

b) *Simple linear regression (bivariate) analysis*:

A simple linear relationship between a dependent variable, Y (*i.e.* genotypic performance over environments for each meiotic feature) and an independent variable, X (*i.e.* environmental index for each meiotic feature) can be expressed mathematically as -

$$Y = \alpha + \beta X$$

Where,

α is the intercept of the line on Y-axis,

β is the slope of the line, indicating the change in Y for each unit change in X. β is usually referred to as the linear regression coefficient, since if β = 0, that indicated Y did not depend on X. The regression coefficient was estimated and represented graphically as follows :

1) Estimation procedure :

Using a set of data with n pairs of Y and X values, the simple linear regression equation were estimated based on the method of least squares as follows-

$$\hat{Y} = a + b\bar{X}$$

Where,

$\hat{Y}$ = estimated value of Y, a = estimates of α and b = estimates of β.

The values of a and b were computed as -

a $= \bar{Y} - b\bar{X}$ and

b $= \Sigma xy / \Sigma x^2$

Where, Σxy = corrected sum product of X and Y,

Σx^2 = corrected sum square of X,

$\bar{X}$ = arithmetic mean of X and

$\bar{Y}$ = arithmetic mean of Y.

2) Graphical representation :

Graphical representation of the estimated regression line were made adopting the following steps:

I) Computing two values of Y, as below -

$$\hat{Y}_1 = a + b\bar{X}_{(min)} \quad \text{and} \quad \hat{Y}_2 = a + b\bar{X}_{(max)}$$

where, $\bar{X}_{(min)}$ = smallest value of X and

$\bar{X}_{(max)}$ = largest value of X.

II) Two points, (X_{min}, Y_1) and (X_{max}, T_2) were plotted on the X and Y

plane, and drawn a line between the two points.

3) Test of Significance :

In testing the hypothesis concerning the values of α and β were carried out adopting the following steps:

I) Computed the residual mean square,

$S^2_{xy} = [\Sigma_i^n y_i^2 - (\Sigma x_i y_i)^2/\Sigma x_i^2)] \div (n-2)$.

II) To test hypothesis, $\beta = 0$, t_b computed as,

$t_b = b \div (\sqrt{S^2_{yx}/\Sigma x_i^2})$, and

compared with the corresponding tabular t-value .

Where, $t_{0.05}$ and $t_{0.01}$ are the tabular t-values with (n-2) degrees of freedom at 0.05 and 0.01 probability level of significance, respectively.

4) Analysis of simple regression :

The regression equation was measured by the coefficient of determination, (R^2) it was computed as follows:

$R^2 = SSR/\Sigma Y^2$, where $SSR = b.\Sigma xy$ (= sum of square due to regression).

The significance of R^2 was tested by computing an F-statistics as follows:

$F = (SSR/k) \div (SSE/n - k - 1)$,

Where,

$SSE = \Sigma y^2 - SSR$ (the residual or error sum of squares),

k = number of independent variable (X) and

n = total number of observation.

5) Variance analysis for homogeneity of regression :

The null hypothesis for testing homogeneity of the three regression coefficients (for seven trios of Nails) was stated as $H_0 : \beta_1 = \beta_2 = \beta_3$, where the three regression lines for each trios of Nails were –

$Y_1 = \alpha_1 + \beta_1$,

$Y_2 = \alpha_2 + \beta_2$ and

$Y_3 = \alpha_3 + \beta_3$.

For testing this null hypothesis the following steps were carried out –

I) by using the formula, $B = \Sigma A_i$,

where, A_i is the residual sum of squares of the ith set of data.

II) Then making computation by the following formula, $G = D - E^2/C$,

where, $C = \Sigma^k\Sigma^n x_{ij}$ (= sum of Σx^2 over **k** (=3) sets of data),

$D = \Sigma^k\Sigma^n y_{ij}$ (= sum of Σy^2 over **k** (=3) sets of data) and

$E = \Sigma^k\Sigma^n x_{ij}y_{ij}$ (= sum of Σxy over **k** (=3) sets of data).

III) Then the F-test was computed as follows:

$F = [(G-B) / (k-1)] \div [B / (\Sigma^k n_i - 2k)]$, where **n** is the number of observations in the ith set of data.

I.5. RESULTS

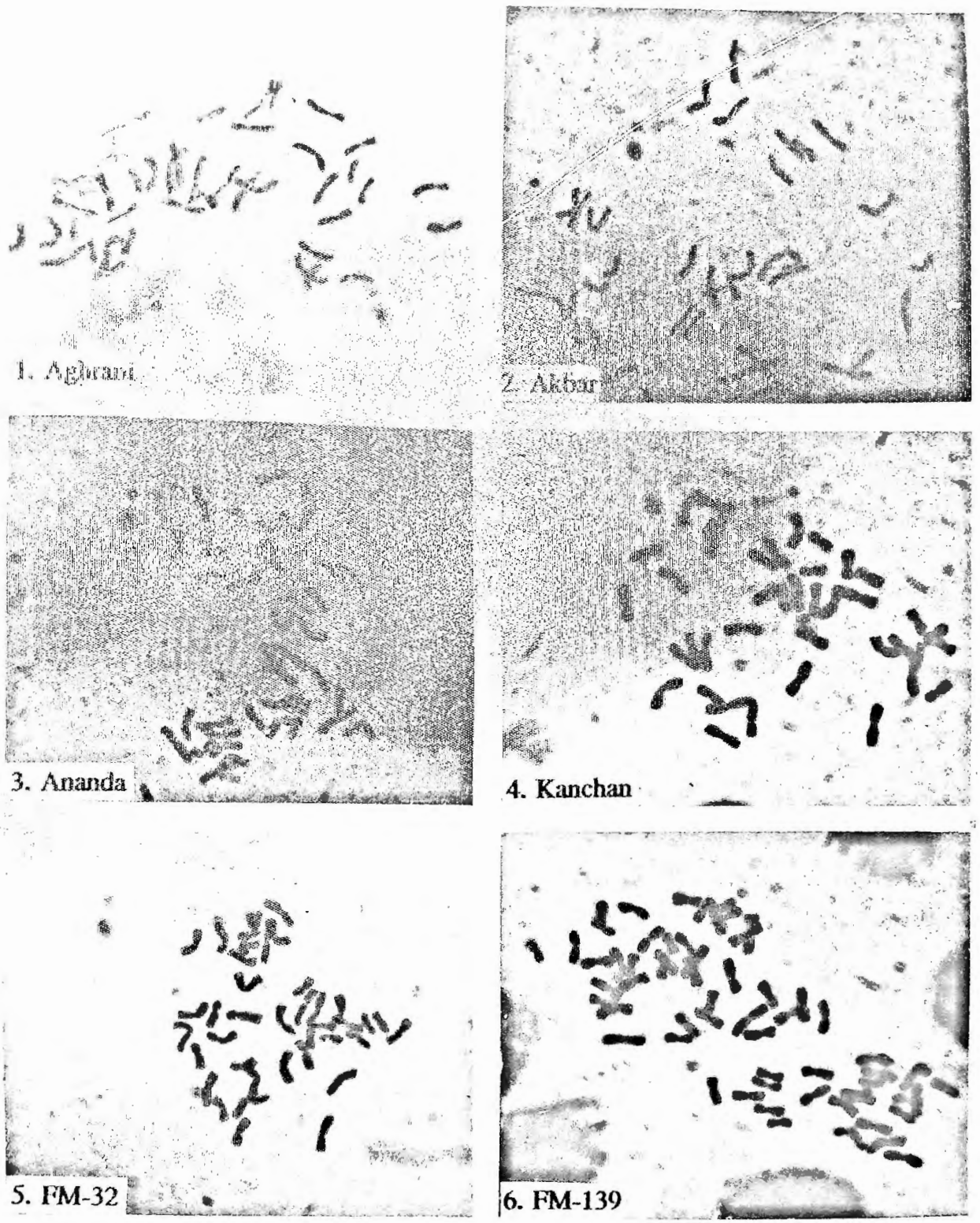
I.5.1. Somatic karyotype:

I.5.1.1. General considerations:

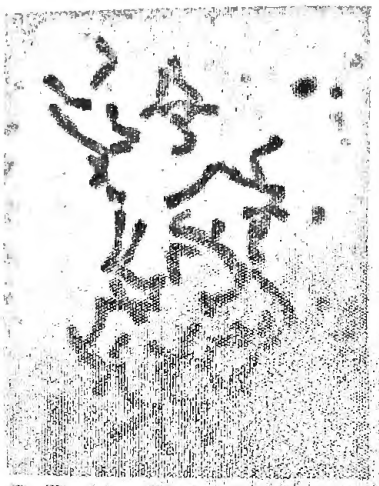
Cells with desirable state of chromosomes for karyotypic analysis were found moderately. In some cases, staining, contraction and dispersion of chromosomes were so poor that they were not suitable for karyotypic analysis. Thus, the choice of photomicrographic plates for karyotypic analysis was made by highly selective process (Figs. 1–34).

Values for lengths and arm ratios of all chromosomes from each of the five metaphase plates for all the genotypes were plotted separately on a two-dimensional scatter diagram. The number beside a point represented an arbitrary identity of the particular chromosome whose measurements produced that point. Pairs of adjacent points were considered to represent homologous chromosomes and were circled on the scatter diagram, a representative of which is shown in Fig. 35. Thus, the 21 pairs of chromosomes were determined and the averages values of total length and arm ratio for each pair were calculated constituting the haploid complement of that cell.

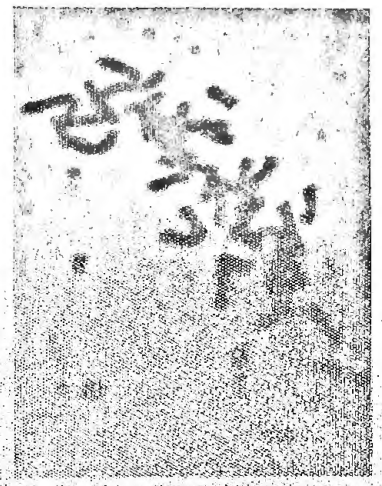
Then the chromosomes of haploid complement were numbered in decreasing order of length and increasing order of arm ratio within the same length. The uniformity of the degree of contraction of chromosomes in the studied five cells



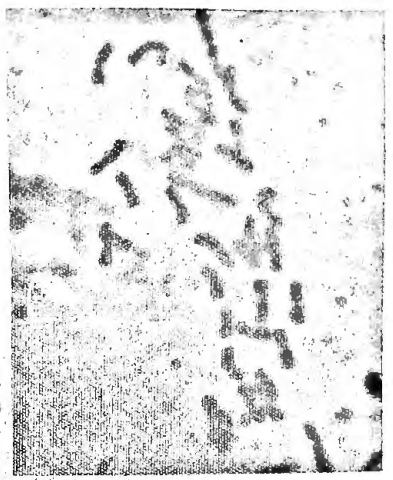
Figs. 1-6. Representative plate for metaphase chromosomes in six varieties/lines of wheat (Ca 750X).



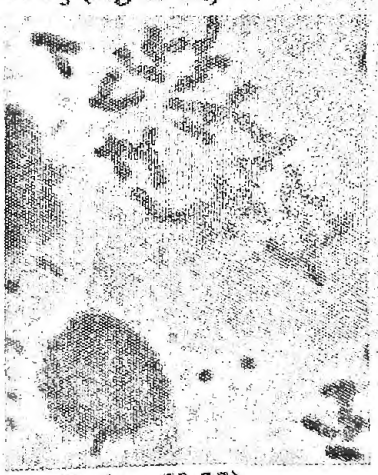
7. F_3 (Ag X 32)



8. F_4 (Ag X 32)

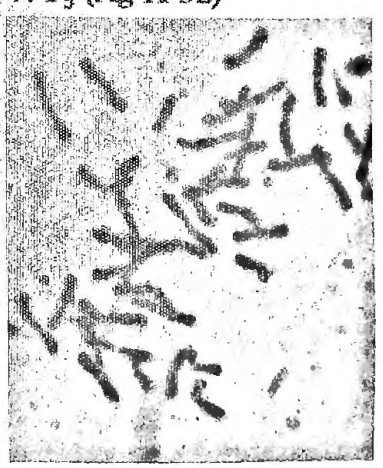


9. F_5 (Ag X 32)

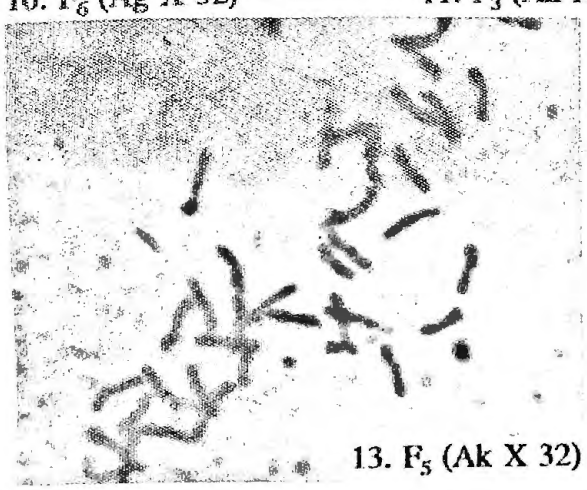


10. F_6 (Ag X 32)

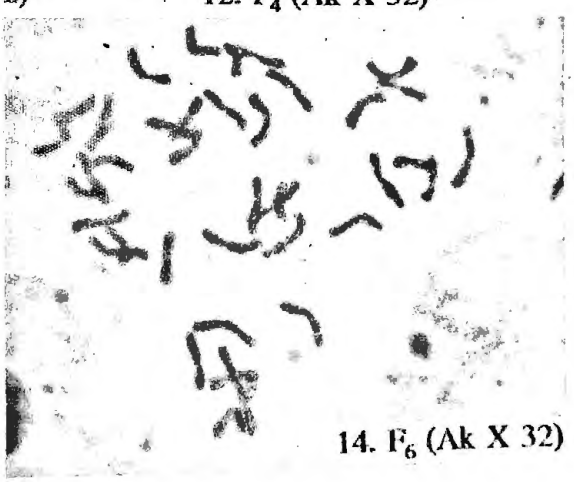
11. F_3 (Ak X 32)



12. F_4 (Ak X 32)

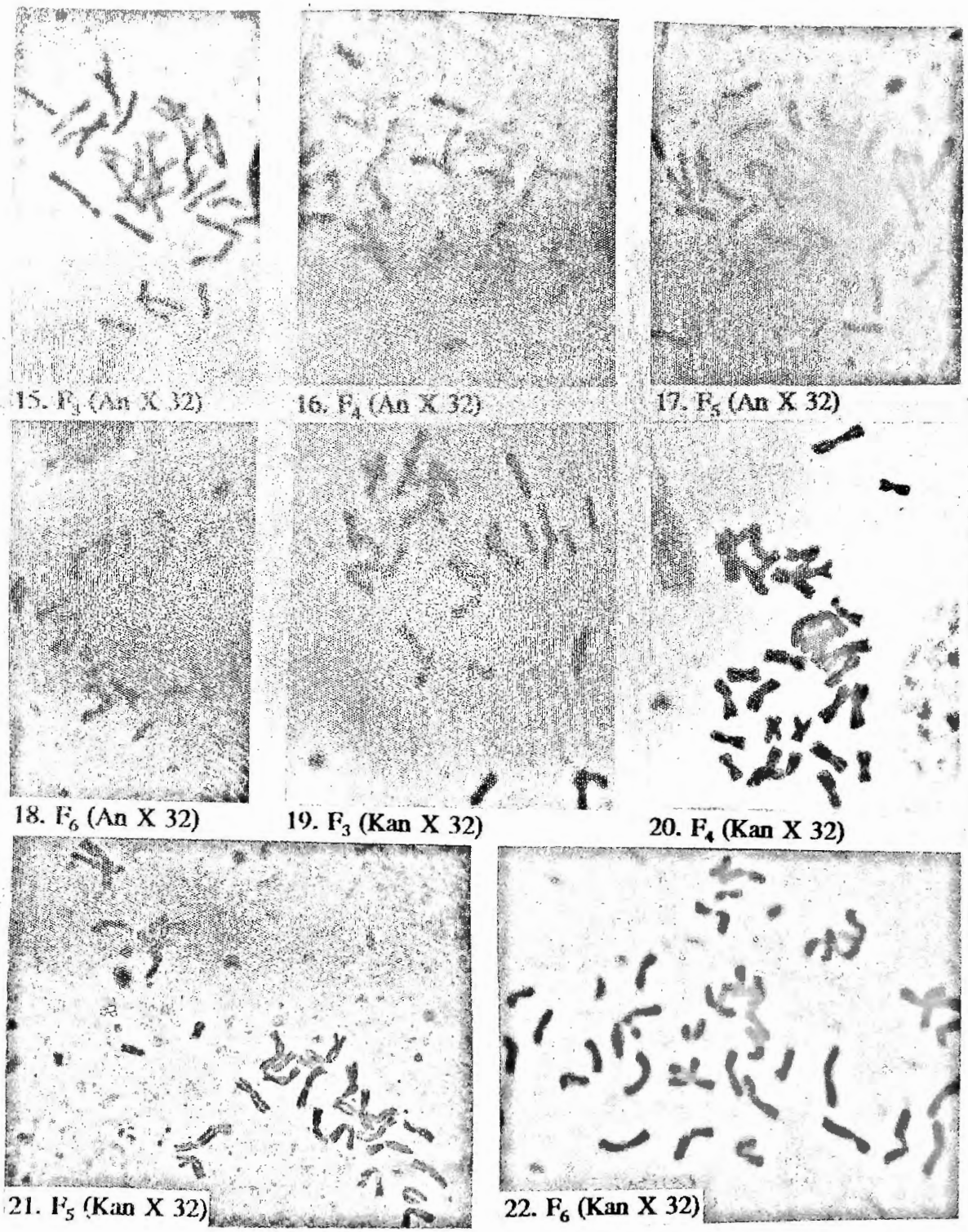


13. F_5 (Ak X 32)

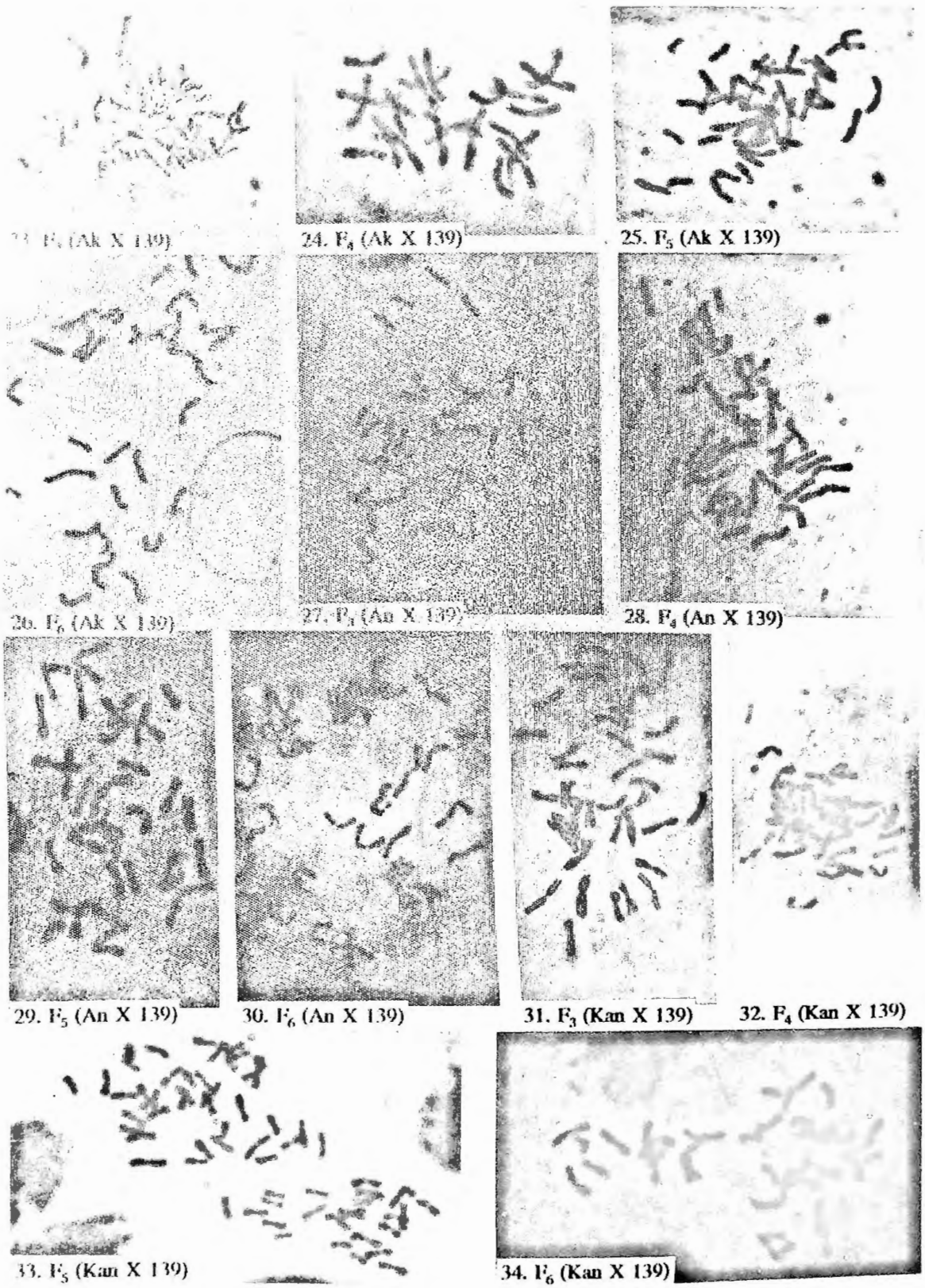


14. F_6 (Ak X 32)

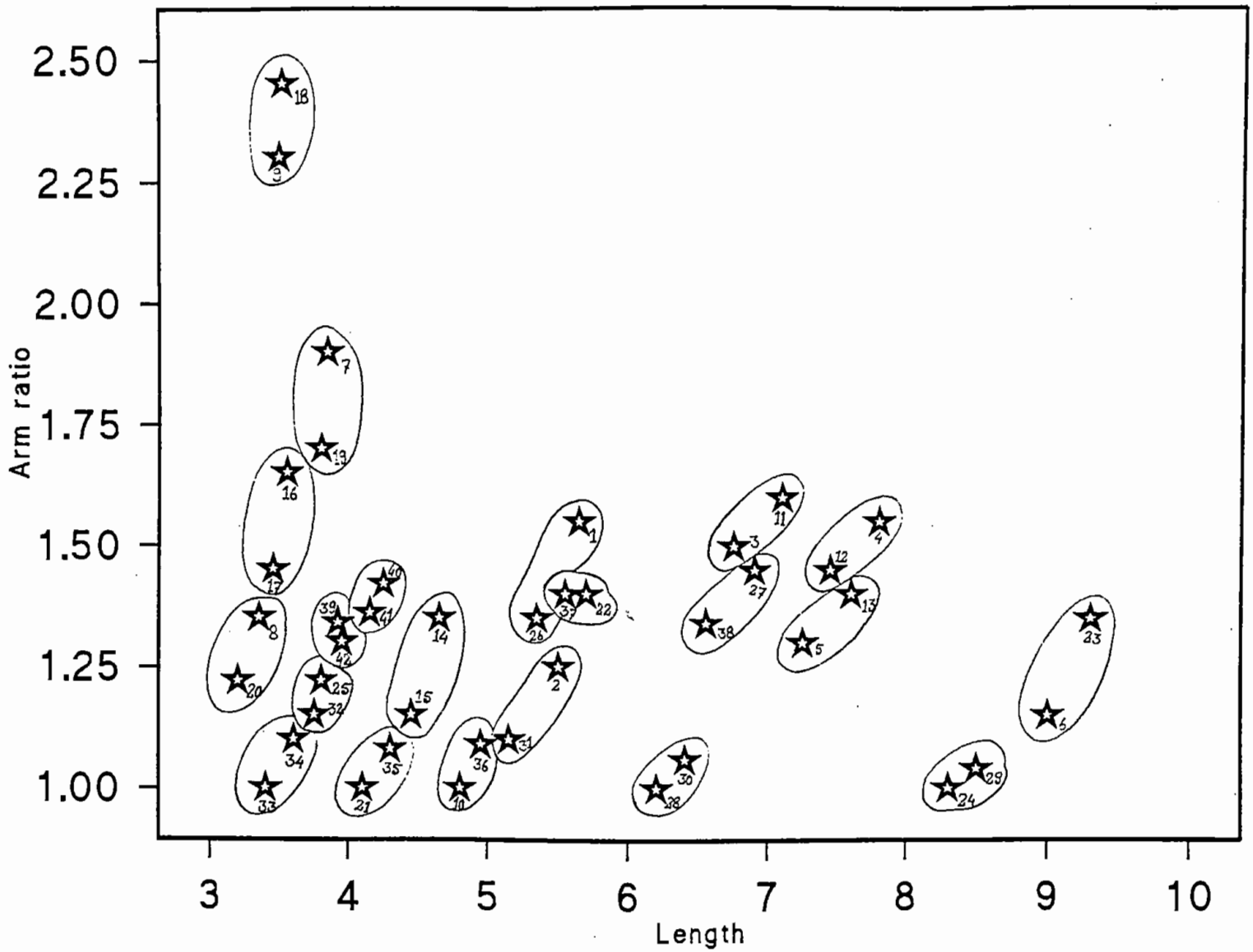
Figs. 7-14. Representative plate for metaphase chromosomes in F_3-F_6 hybrid progenies of two crosses of wheat (Ca 750X).



Figs. 15-22. Representative plate for metaphase chromosomes in F_3-F_6 hybrid progenies of two crosses of wheat (Ca 750X).



Figs. 23-34. Representative plate for metaphase chromosomes in F_3-F_6 hybrid progenies of three crosses of wheat (Ca 750X).



★=Position of a individual chromosome in a scatter diagram based on length and arm ratio.

Fig. 35: A representative scatter diagram for deriving the haploid complement values.

was determined by comparing the total haploid complement length of each cell. The homogeneity of chromosome distribution was tested by the use of haploid values in a contingency table. Moreover, the standardized chromosome lengths across the cells, as they were differentially contracted, were computed in order to provide a common basis of comparison of the morphology of each chromosome.

I.5.1.2. Comparison of chromosome length and distribution:

The average haploid total complement length of all studied cells and chromosome distribution in parents and their hybrid progenies of seven crosses of wheat are shown in Table 1. Among the parental genotypes the highest and lowest haploid total length were observed in **Ananda** and **FM-139**, and among the hybrid progenies in F_1 of **Ag** X **FM-32** and F_6 of **Kan** X **FM-139**, respectively. **Ananda** differed significantly from the over all mean of the parents. In all the hybrid progenies of all crosses except F_1 of **Ag** X **FM-32** and **Ak** X **FM-32** were found to differ nonsignificantly, in respect of haploid total length, from their respective over all mean values.

The ranges of coefficient of variation (C.V.) of the haploid total lengths within genotypes were from 1.33 to 6.84%, from 1.47 to 2.34%, form 2.17 to 4.13%, from 2.56 to 5.07%, from 2.85 to 7.79%, from 2.00 to 6.23%, from 2.36 to 5.86% and from 3.43 to 4.08% in parental varieties/lines, F_1 - F_6 progenies of Ag X FM-32, Ak X FM-32, An X FM-32, Kan X FM-32, Ak X FM-139, An X FM-139 and Kan X FM-139, respectively.

Table 1. Total haploid complement length and chromosome distribution in six parental varieties/lines and their hybrid progenies in seven crosses of wheat.

Varieties/ lines and hybrid Progenies	Total haploid complement length (µm) in five different plates					Statistics			Chromosome distribution	
	A	B	C	D	E	X	S.E.	C.V.	χ^2 - values	Probability
Parents:										
Ahrani	112.05	120.05	125.15	128.05	134.55	129.97	3.79	6.84	10.73	0.99-1.00
Akbar	128.80	125.95	125.45	126.00	126.25	126.49	0.59	1.05	10.84	0.95-0.99
Ananda	126.70	133.30	129.90	131.10	129.00	130.00	1.10	1.88	04.74	0.99-1.00
Kanchan	102.20	110.35	114.60	108.45	110.75	109.27	2.03	4.15	00.37	0.99-1.00
FW-32	113.05	116.70	116.10	114.60	116.45	115.38	0.69	1.33	00.59	0.99-1.00
FW-139	101.15	107.65	111.25	109.60	114.45	108.82	2.22	4.56	12.32	0.95-0.99
Over all						**118.99**	**3.71**	**7.64**	**28.34**	**0.50-0.75**
AgXFW-32/F_3	124.85	129.90	131.60	129.10	129.80	129.05	1.13	1.95	25.16	0.75-0.90
F_4	108.10	110.70	112.15	107.50	113.55	110.40	1.16	2.34	16.64	0.95-0.99
F_5	111.50	116.18	114.25	113.70	113.80	113.89	0.75	1.46	12.65	0.99-1.00
F_6	90.45	94.55	94.95	92.90	92.45	93.06	0.81	1.94	22.89	0.75-0.90
Over all						**111.60**	**7.39**	**13.24**	**31.92**	**0.10-0.25**
AkXFW-32/F_3	119.75	124.30	116.55	122.20	118.49	120.26	1.36	2.54	17.56	0.95-0.99
F_4	107.05	104.95	109.50	108.60	111.10	108.24	1.05	2.17	22.95	0.75-0.90
F_5	92.00	97.55	95.60	101.55	100.40	97.42	1.71	3.93	30.93	0.50-0.75
F_6	90.55	98.25	94.90	92.80	100.25	95.35	1.76	4.13	20.84	0.90-0.95
Over all						**105.32**	**5.73**	**10.88**	**100.42**	**0.001-0.01**
AnXFW-32/F_3	87.50	94.25	92.85	94.40	97.20	93.24	1.60	3.84	13.20	0.99-1.00
F_4	93.05	97.25	92.90	90.90	95.00	93.82	1.08	2.56	7.13	0.99-1.00
F_5	80.55	86.70	90.20	84.45	88.90	86.16	1.71	4.44	6.84	0.99-1.00
F_6	82.15	88.90	81.85	91.70	84.30	85.78	1.94	5.07	7.14	0.99-1.00
Over all						**89.75**	**2.19**	**4.87**	**9.42**	**0.95-0.99**

Table 1. (Continued).

Varieties/ lines and hybrid progenies	Total haploid complement length (µm) in five different cells					Statistics			Chromosome distribution	
	A	B	C	D	E	X	S.E.	C.V.	χ^2 values	Probability
KanXFM-32/F_3	89.60*	93.85	96.11	91.90	98.54*	94.00	1.56	3.72	9.24	0.99-1.00
F_4	103.25	99.40*	106.95*	101.60	105.10	103.21	1.32	2.85	2.07	0.99-1.00
F_5	108.55	113.45	104.80*	110.65	116.05	110.70	1.94	3.93	5.61	0.99-1.00
F_6	111.40	114.65	111.15	105.65*	115.20	111.61	1.70	3.41	9.62	0.99-1.00
Over all						104.88	4.09	7.79	15.41	0.75-0.90
AkXFM-139/F_3	121.30	124.50	117.40	114.70*	121.95	119.97	1.74	3.24	7.55	0.99-1.00
F_4	107.95	111.43*	105.45*	108.80	107.65	108.26	0.97	2.00	5.42	0.99-1.00
F_5	112.70	116.03*	109.50*	112.24	113.82	112.86	1.06	2.11	3.01	0.99-1.00
F_6	124.25	128.30	120.25*	122.98	126.90	124.54	1.43	2.56	4.69	0.99-1.00
Over all						116.41	3.24	6.23	7.65	0.99-1.00
AnXFM-139/F_3	105.50	110.10	101.25	103.70	108.17	105.74	1.57	3.32	4.21	0.99-1.00
F_4	95.55	99.12	91.95	97.37	93.77	95.55	1.27	2.97	5.29	0.99-1.00
F_5	112.35	117.41	107.02	112.42	110.25	109.89	1.16	2.36	8.16	0.99-1.00
F_6	105.90	111.03	100.45	108.60	103.02	105.80	1.89	3.99	8.85	0.99-1.00
Over all						104.25	3.06	5.86	7.30	0.99-1.00
KanXFM-139/F_3	115.50	120.67	110.08	117.26	113.66	115.43	1.77	3.43	15.35	0.99-1.00
F_4	123.50	129.10	115.55*	125.24	121.43	122.96	2.24	4.08	14.27	0.99-1.00
F_5	113.70	119.55	107.85	116.21	110.93	113.65	2.03	3.99	11.56	0.99-1.00
F_6	81.45	86.89*	78.68	83.64	80.14	82.16	1.44	3.91	11.96	0.99-1.00
Over all						108.55	9.03	16.63	26.76	0.90-0.95

The probability of chromosome distribution (χ^2 -values) of each haploid complement within and between the parental genotypes were found to range from 0.95-1.00 and 0.50-0.75, respectively. That for haploid complement within and between the generations of Ag X FM-32, Ak X FM-32, An X FM-32, Kan X FM-32, Ak X FM-139, An X Fm-139 and Kan X FM-139 were found to range from 0.75-1.00 and 0.10-0.25, from 0.50 to 0.99 and 0.001 to 0.01, from 0.99 to 1.00 and 0.95 to 0.99, from 0.99 to 1.00 and 0.75 to 0.90, from 0.99 to 1.00 and 0.99 to 1.00, from 0.99 to 1.00 and 0.99 to 1.00, and from 0.99 to 1.00 and 0.90 to 0.95, respectively. The chromosome distribution in respect to the length classes of each complement were found to be independent within and between the parental genotypes and all the progenies of all crosses except between the generations of Ag X FM-32.

1.5.1.3. Chromosome identification:

Corresponding chromosomes in different haploid complements of each genotype were determined through a grouping technique applied to a combined scatter diagram of the five haploid complements for each of the parents and their hybrid progenies (Figs. 36-69). In these scatter diagrams, each symbol was represented as a specific haploid complement and the number (1-21) of each symbol was represented as the individual identity of a specific chromosome in that complement. Morphologically distinct and reproducible chromosomes across the cells should give a cluster of five points, which representing the haploid homologues of each chromosome pair over the studied cells. Consequently, morphologically similar or near to similar chromosomes would be superimposed or overlapped and become individually indistinguishable, therefore the clustering or

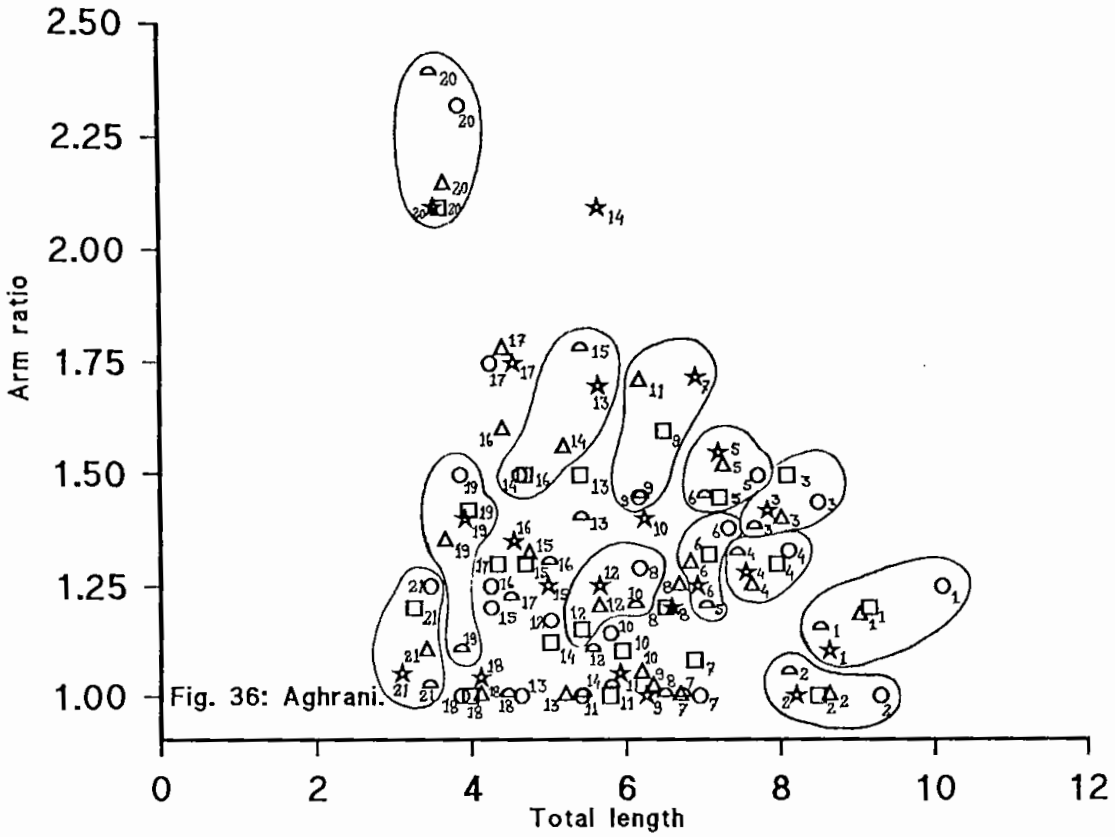


Fig. 36: Aghrani.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

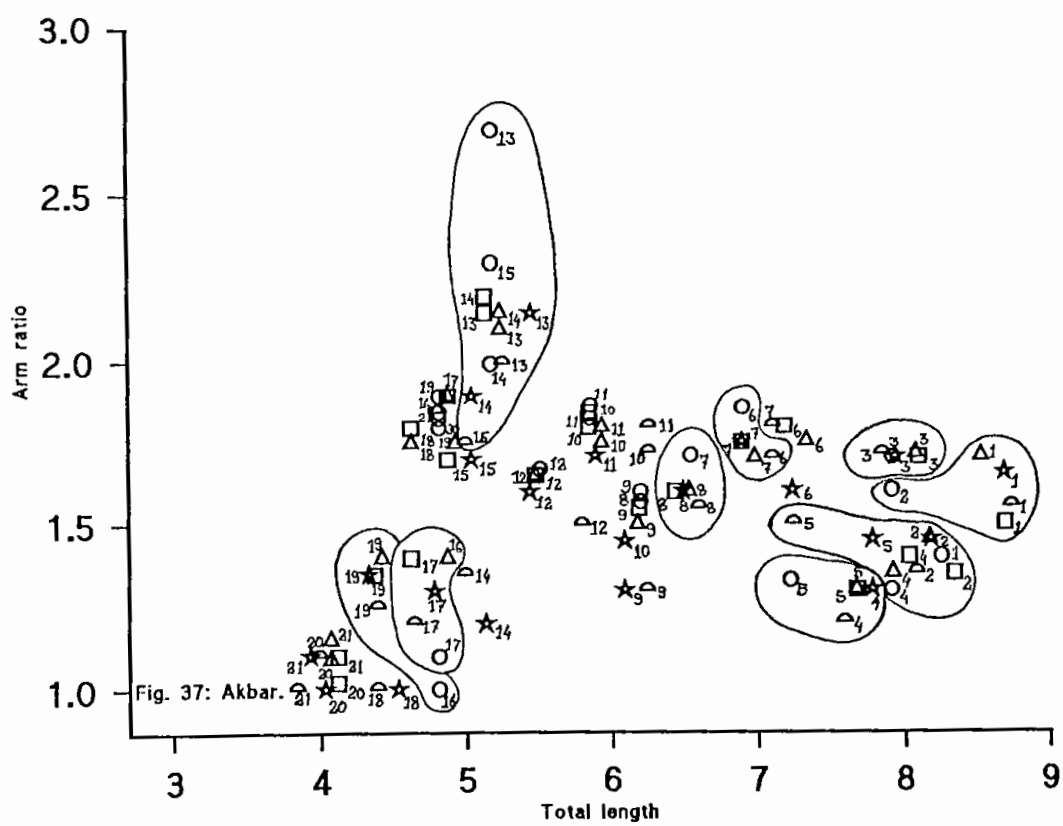
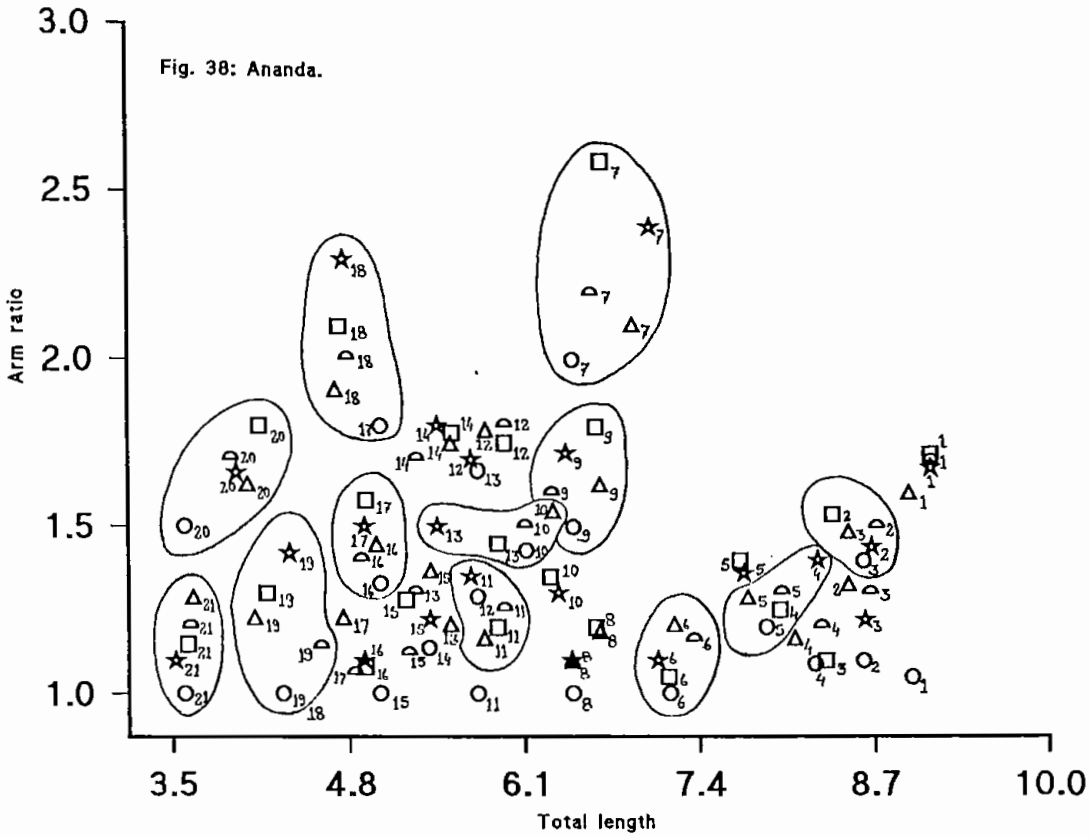


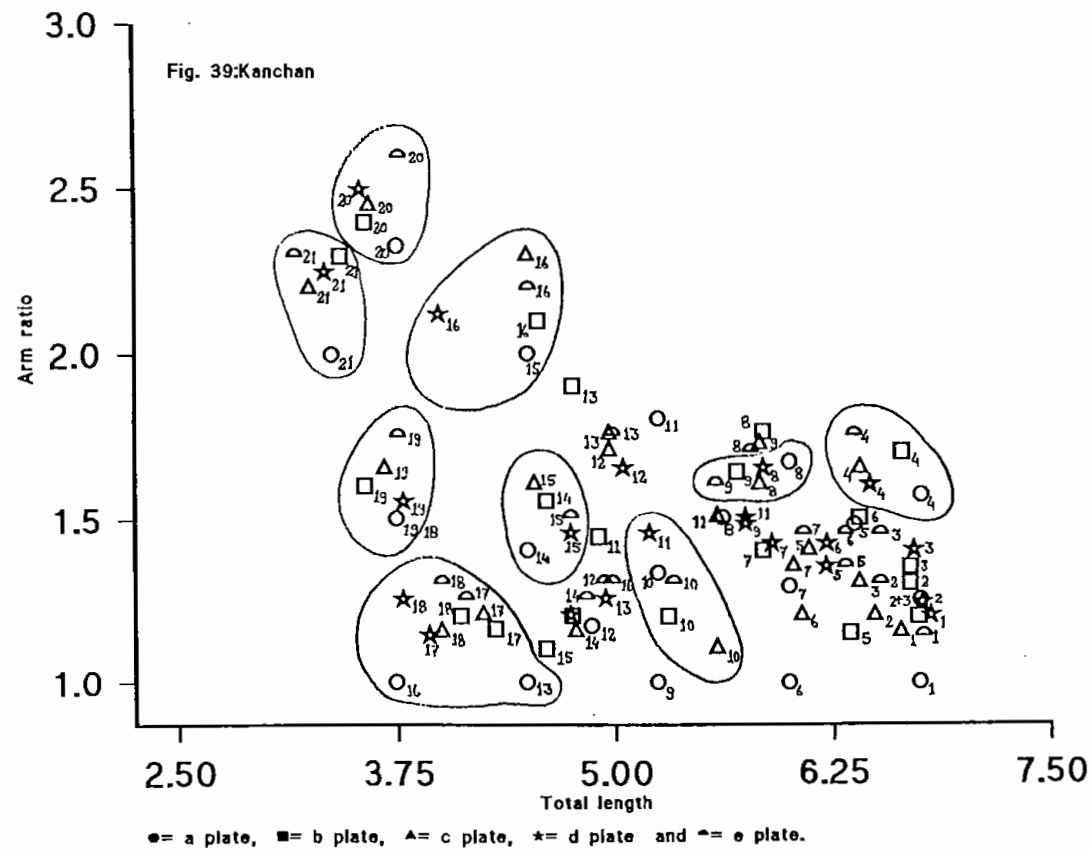
Fig. 37: Akbar.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Fig. 36 & 37: Combined scatter diagram of the 21 haploid chromosome values from five cells of Aghrani & Akbar.

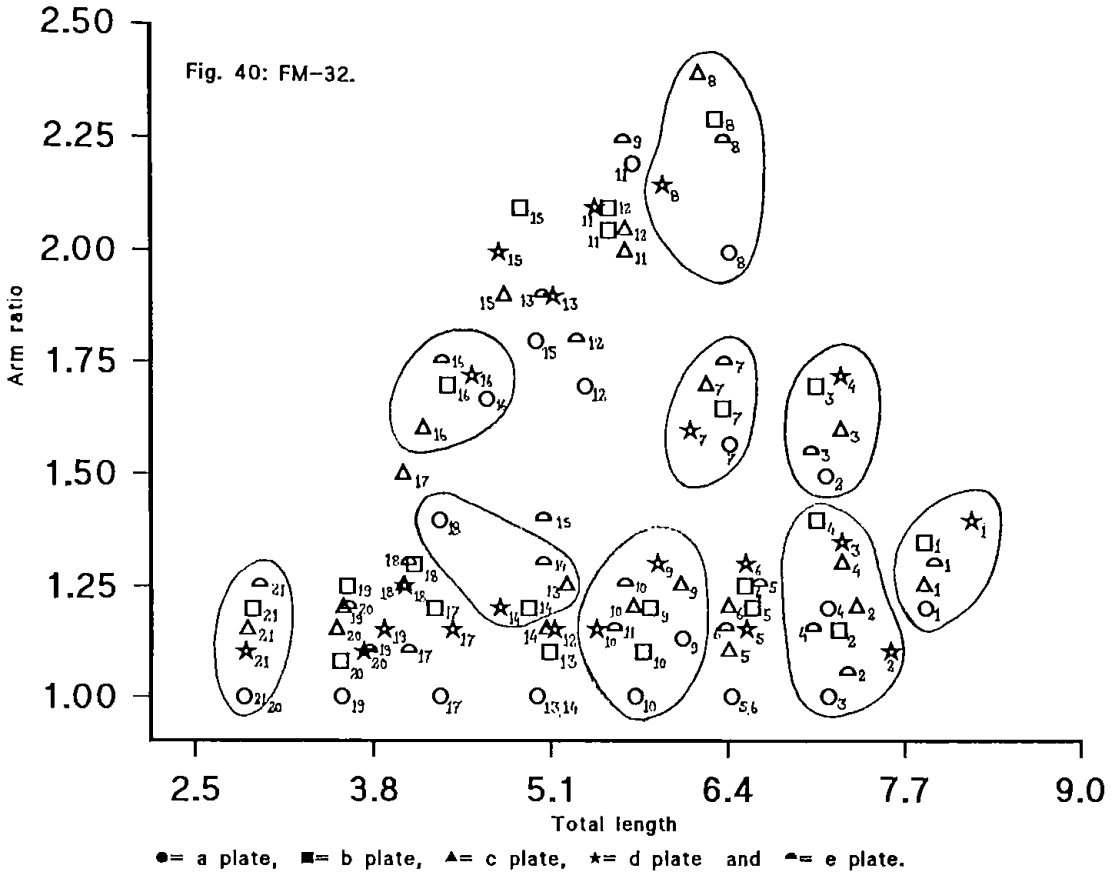


●= a plate, ■=b plate, ▲= c plate, ★= d plate and ◓= e plate.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Fig. 38 & 39: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ananda & Kanchan.



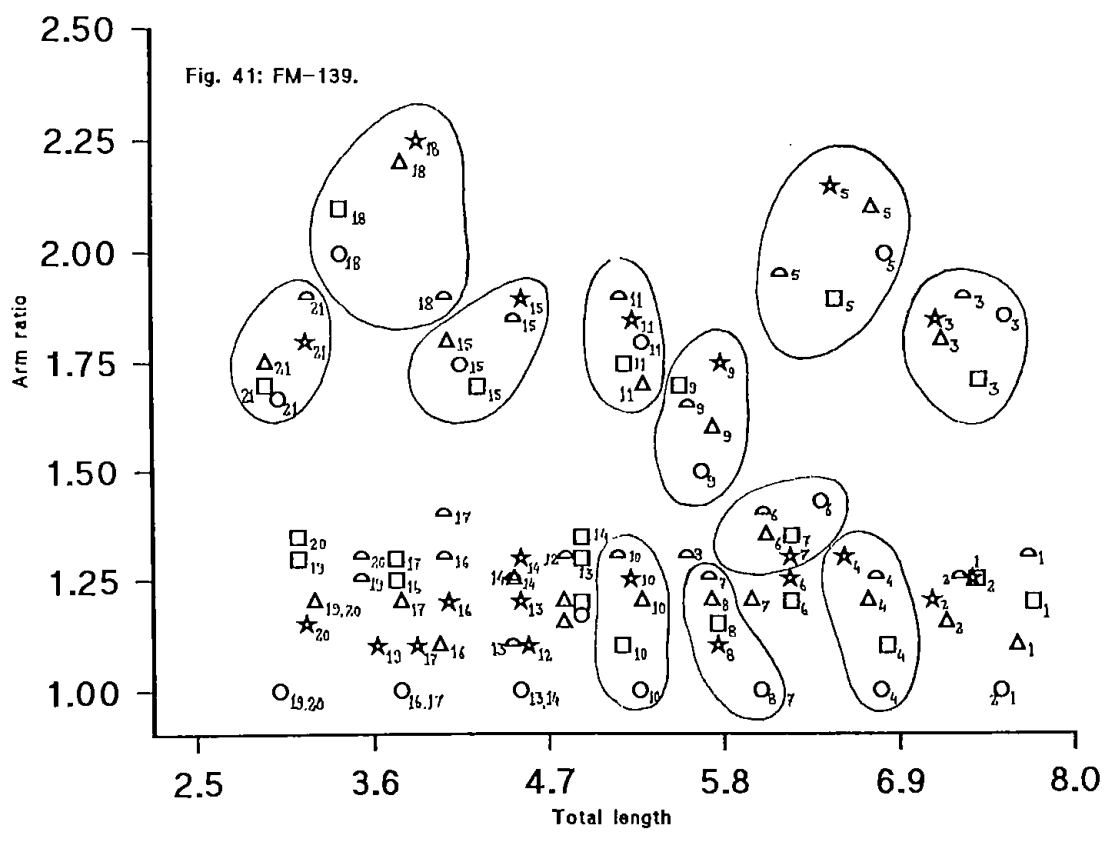
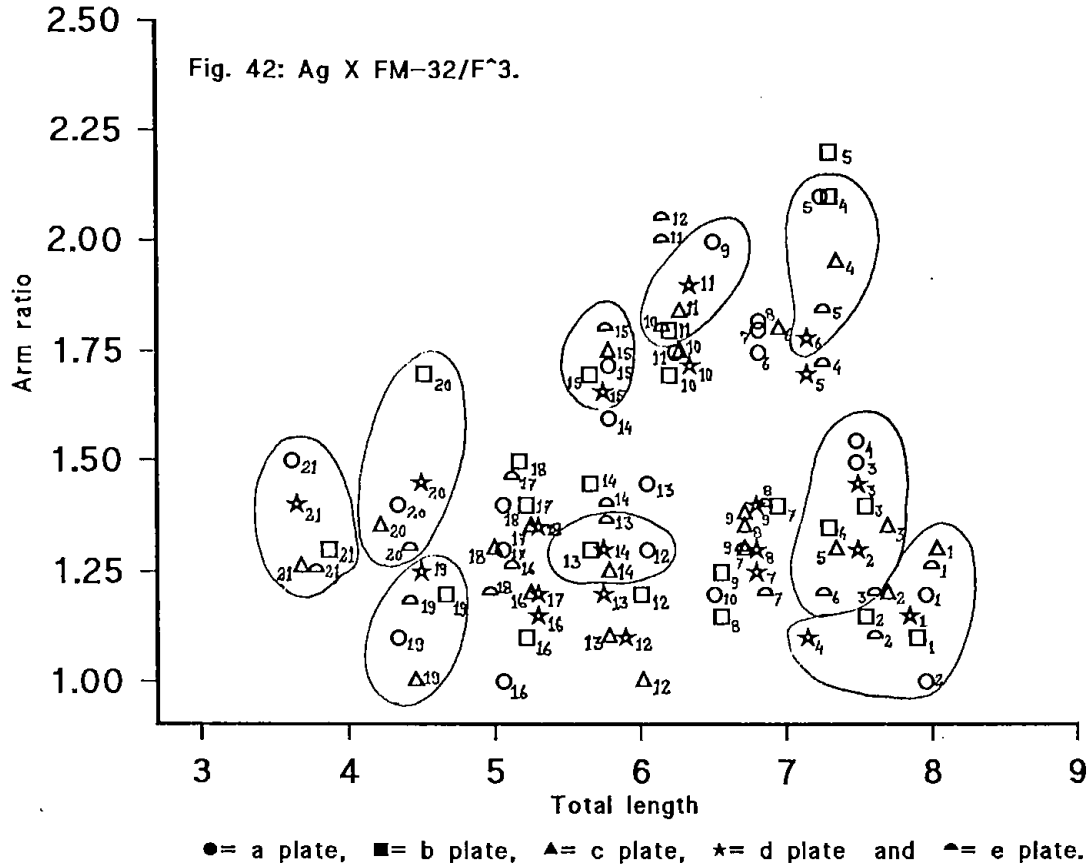


Fig. 40 & 41: Combined scatter diagram of the 21 haploid chromosomo values from five cells of FM-32 & FM-139.



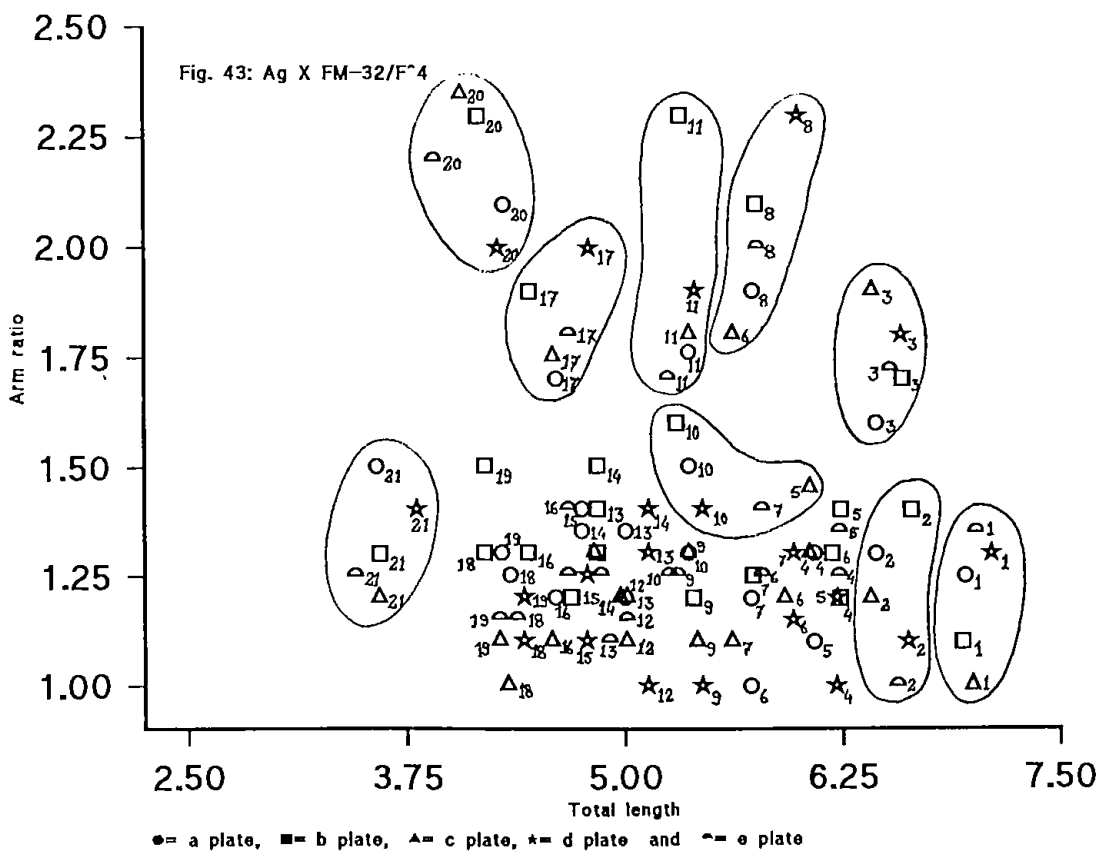
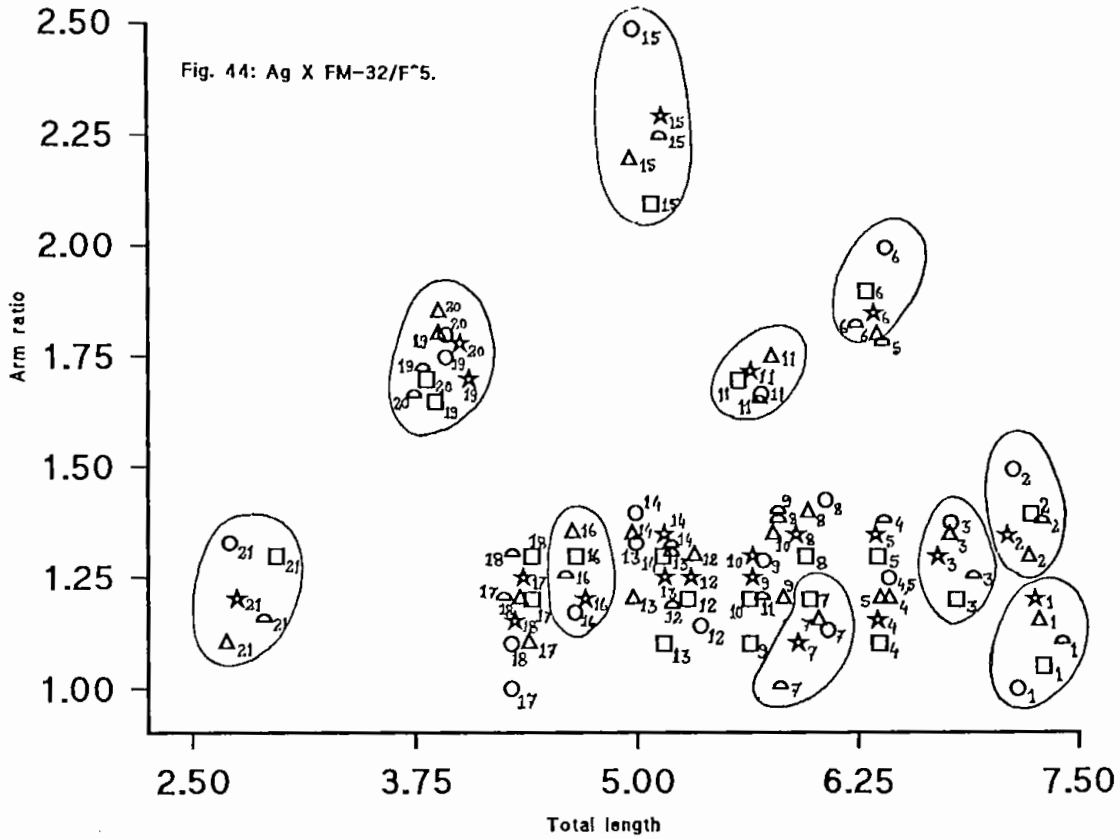
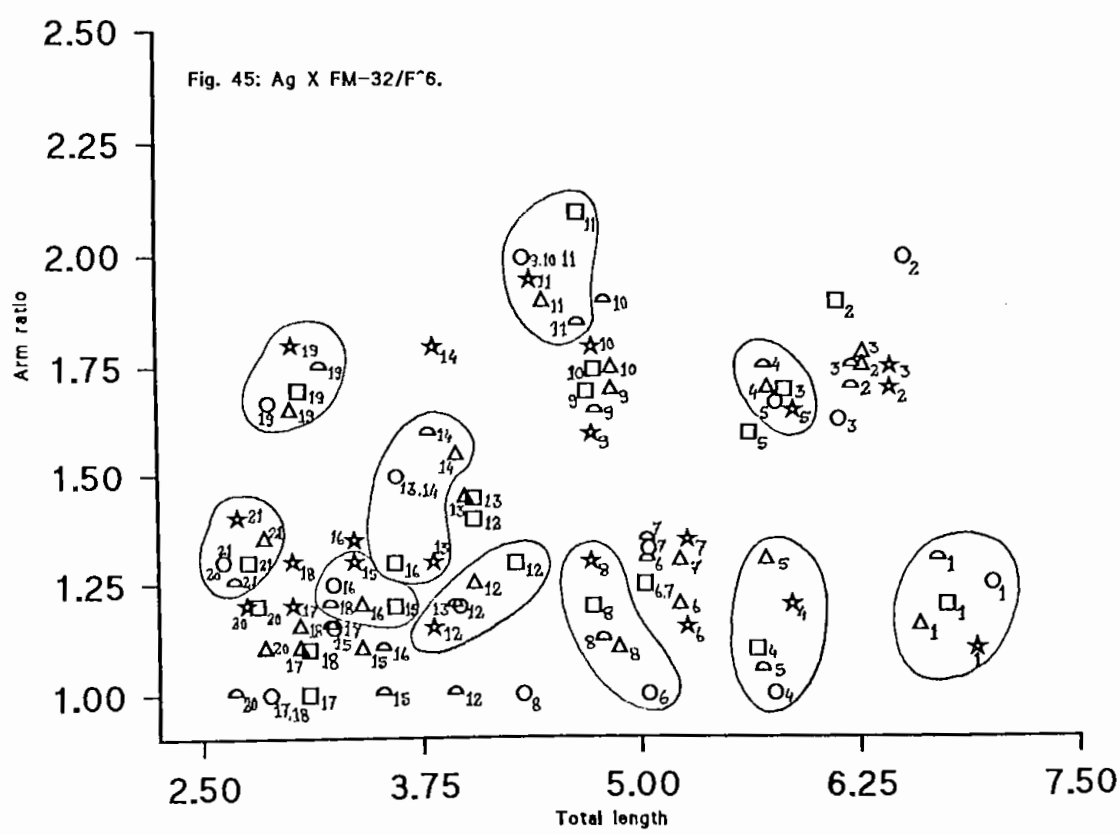
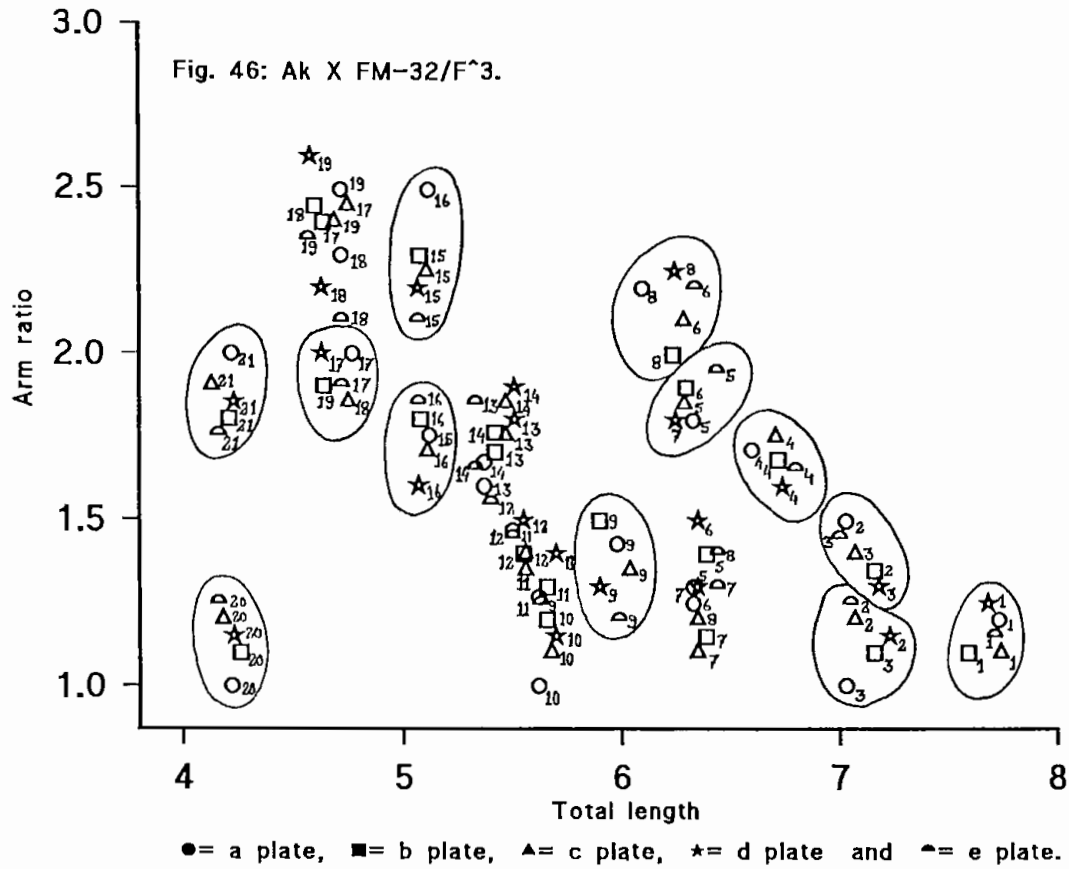


Fig. 42 & 43: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ag X FM-32/F^3 & F^4

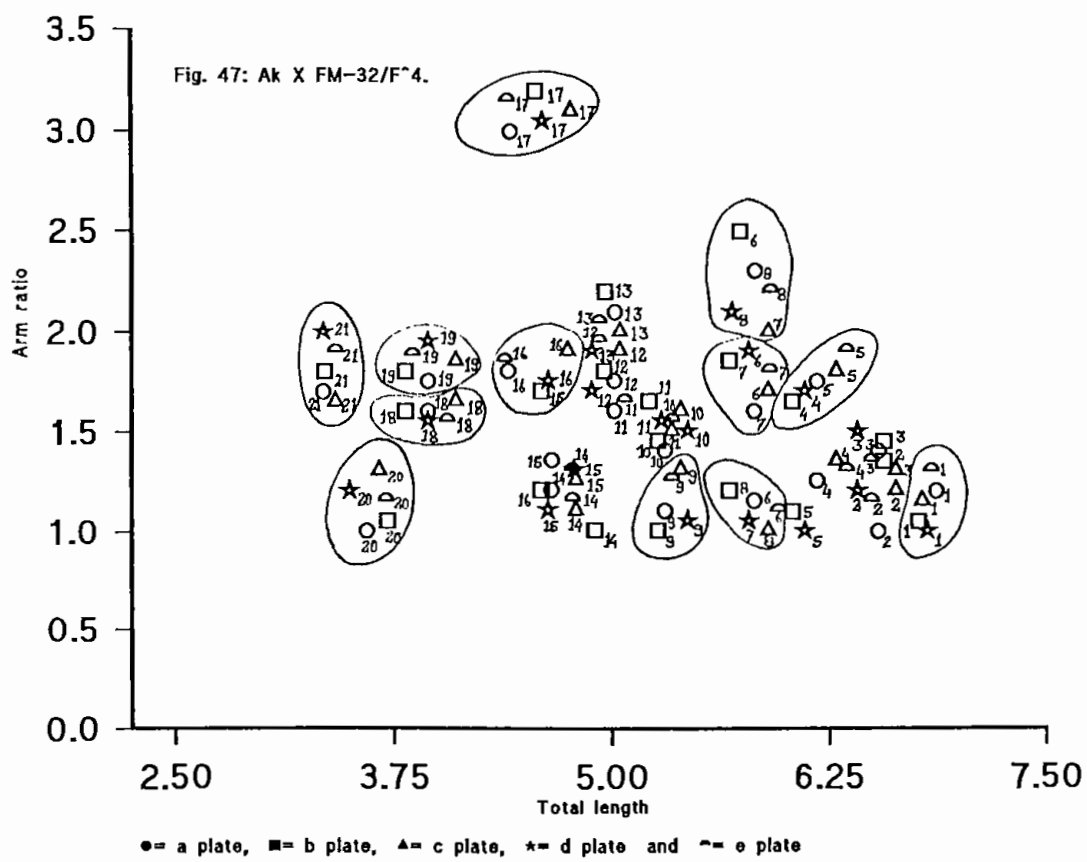




Figs. 44 & 45: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ag X FM-32/F^5 & F^6.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate

Figs. 46 & 47: Combined scatter diagram of the 21 haploid chromosome values from five cells of AK X FM-32/F^3

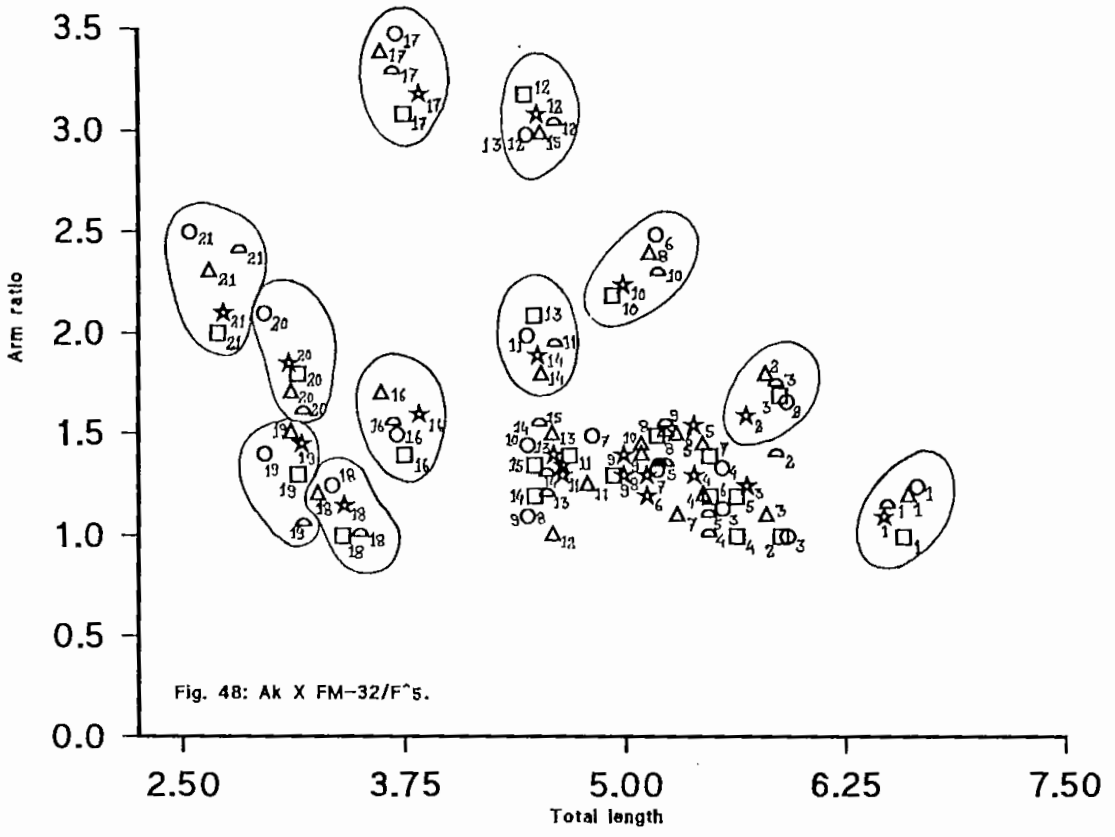


Fig. 48: Ak X FM-32/F^5.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate

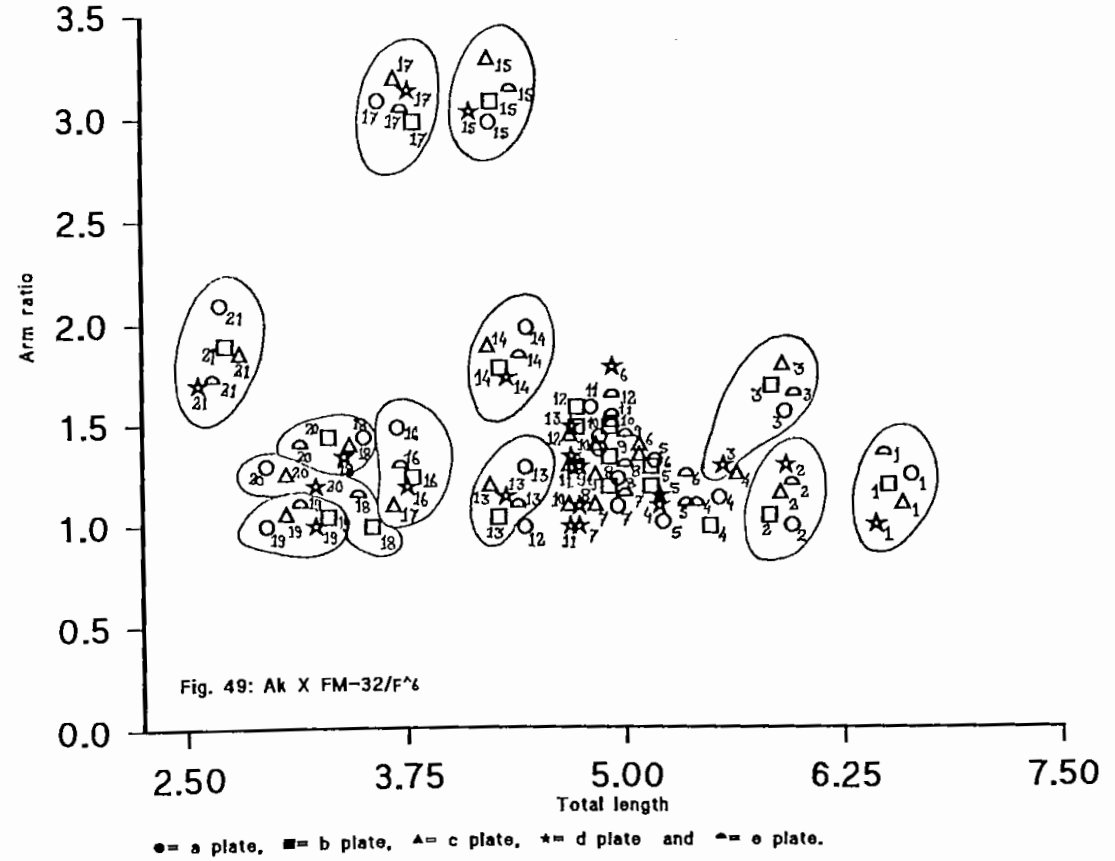
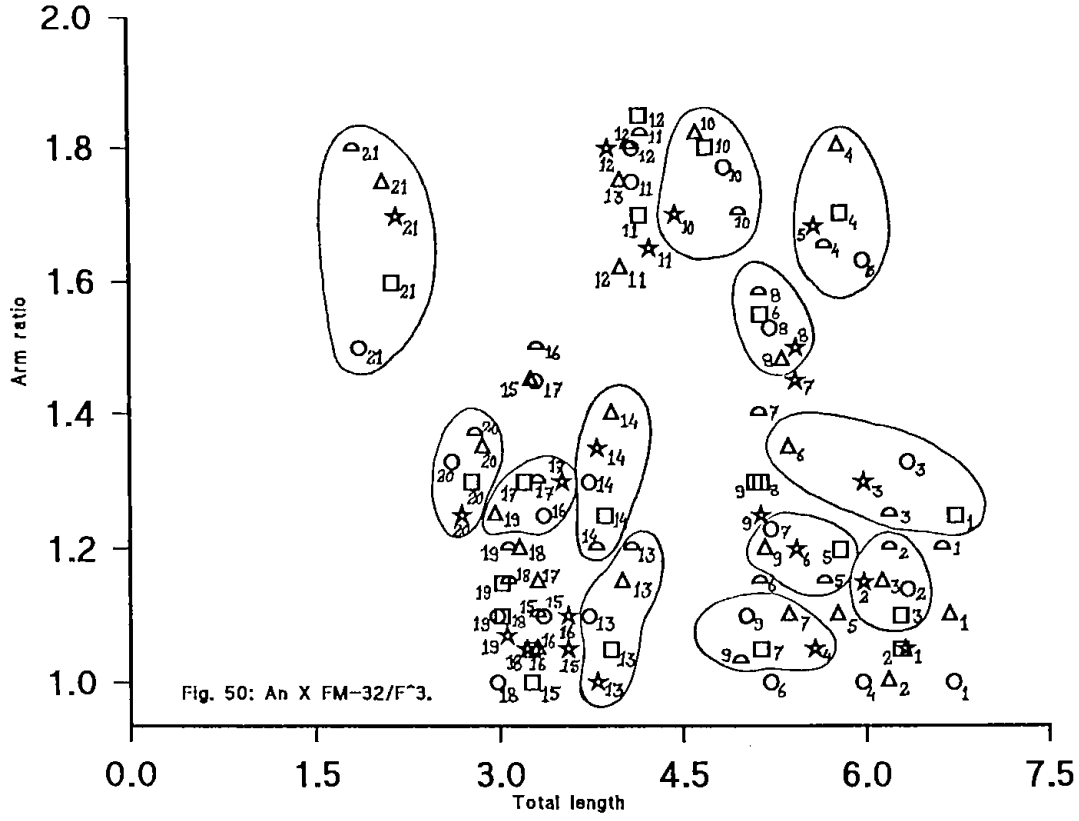


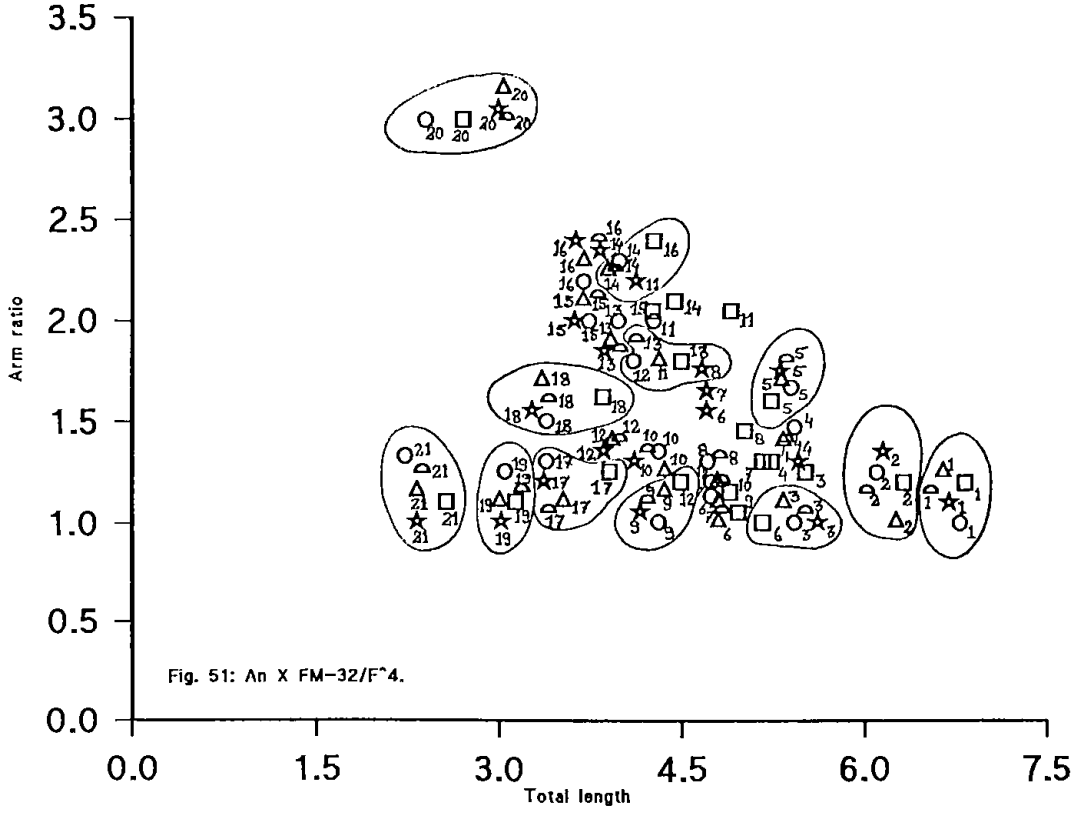
Fig. 49: Ak X FM-32/F^6

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

Fig. 48 & 49: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ak X FM-32/F^5 & F6.

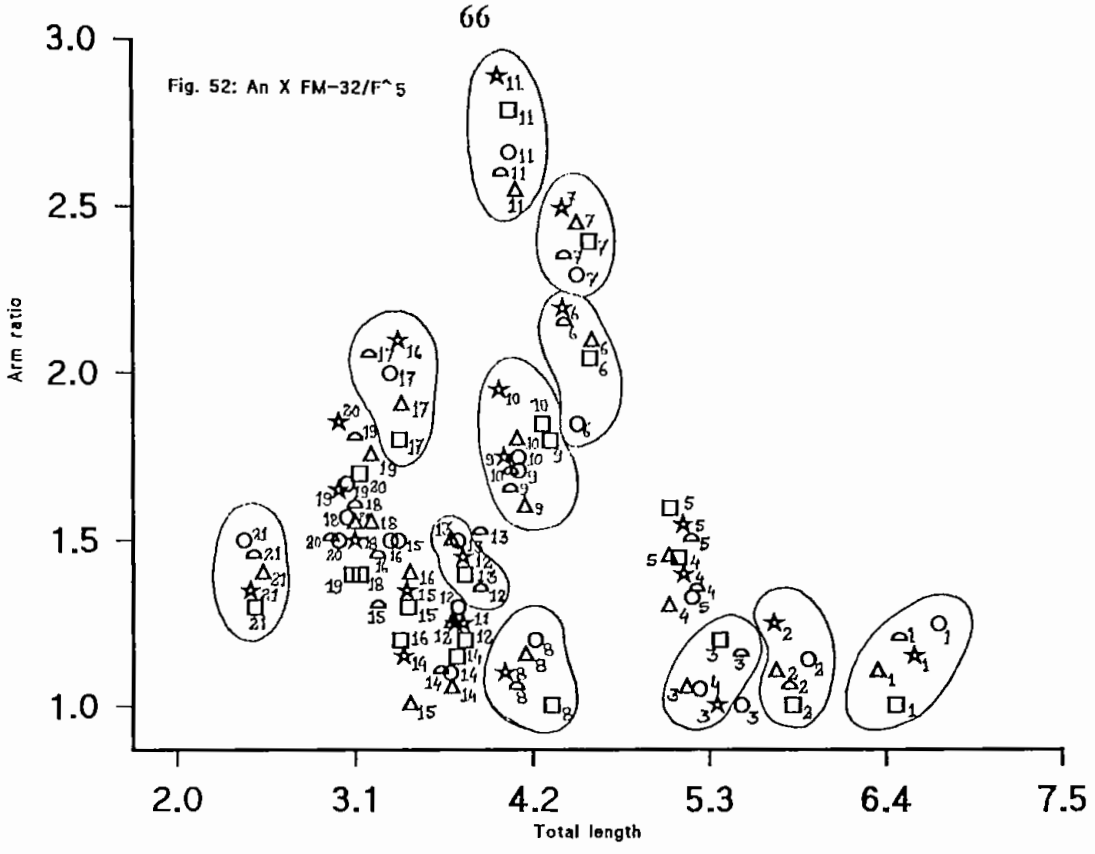


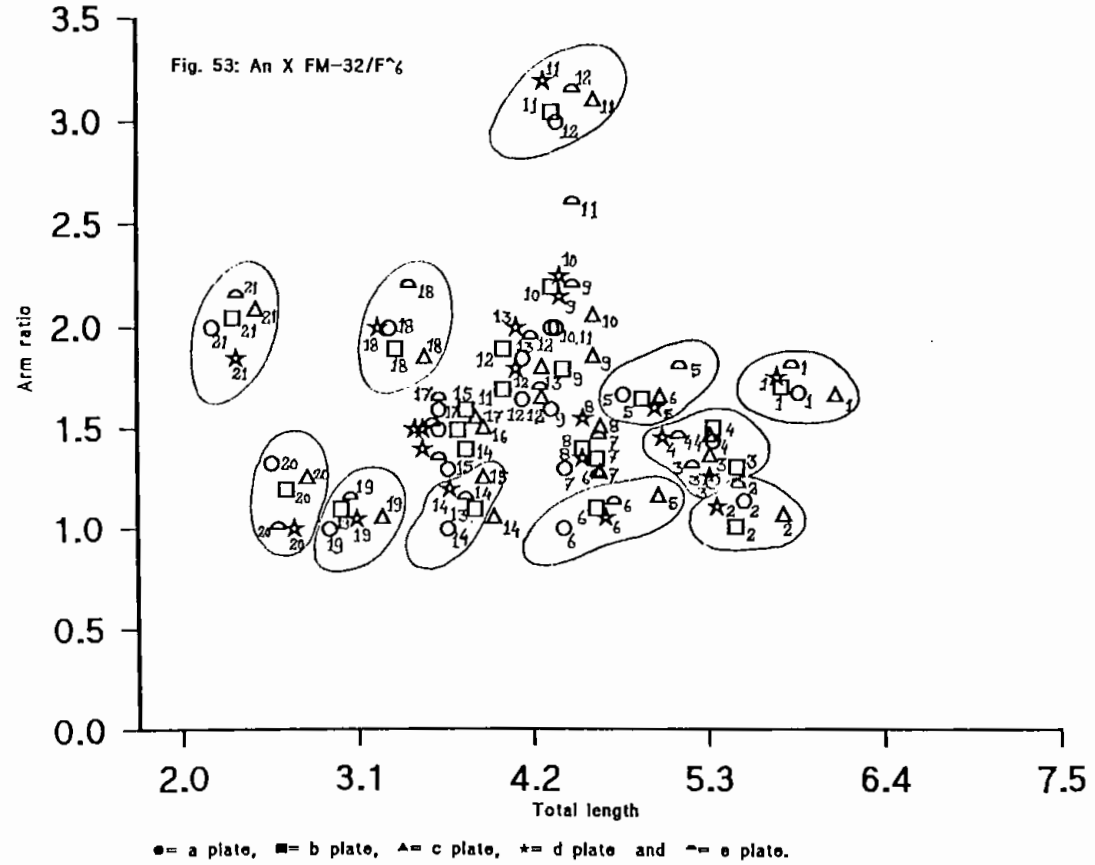
●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Figs. 50 & 51: Combined scatter diagram of the 21 haploid chromosome valuesfrom five cells of An X FM-32/F^3 & F^4.





Figs. 52 & 53: Combined scatter diagram of the 21 haploid chromosome values from five cells of An X FM-32/F^5 & F^6.

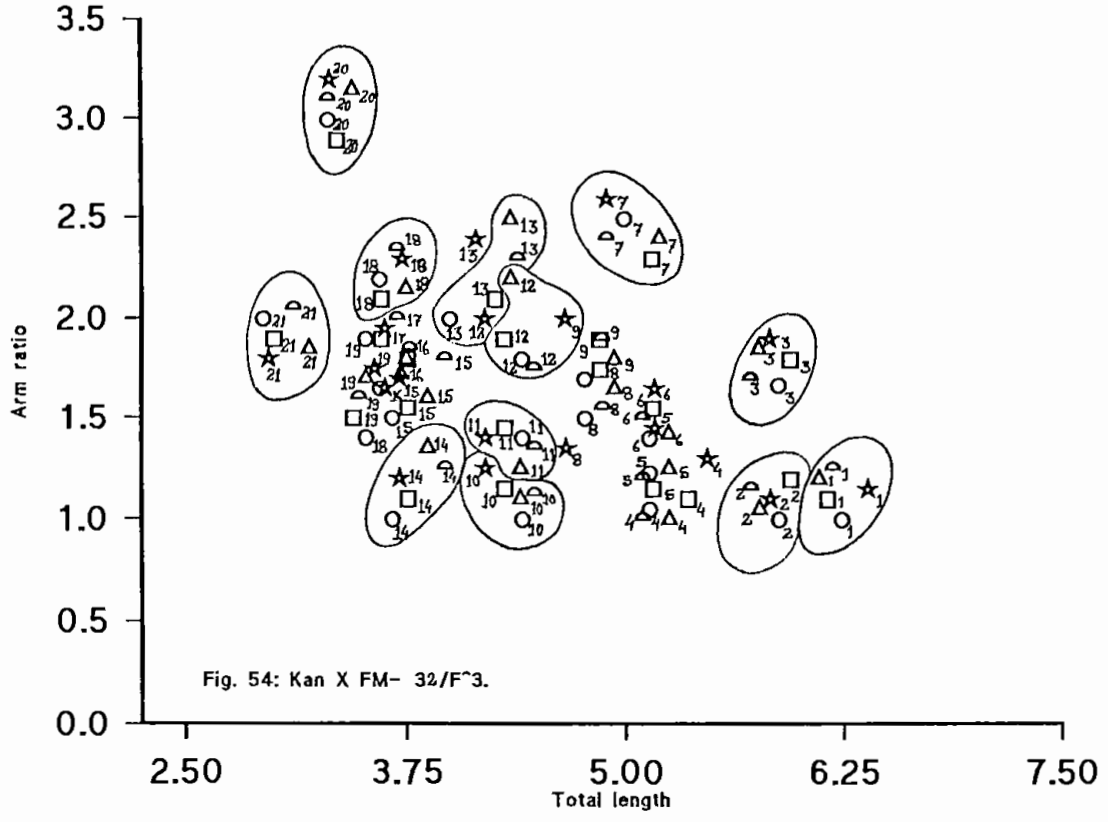


Fig. 54: Kan X FM- 32/F^3.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

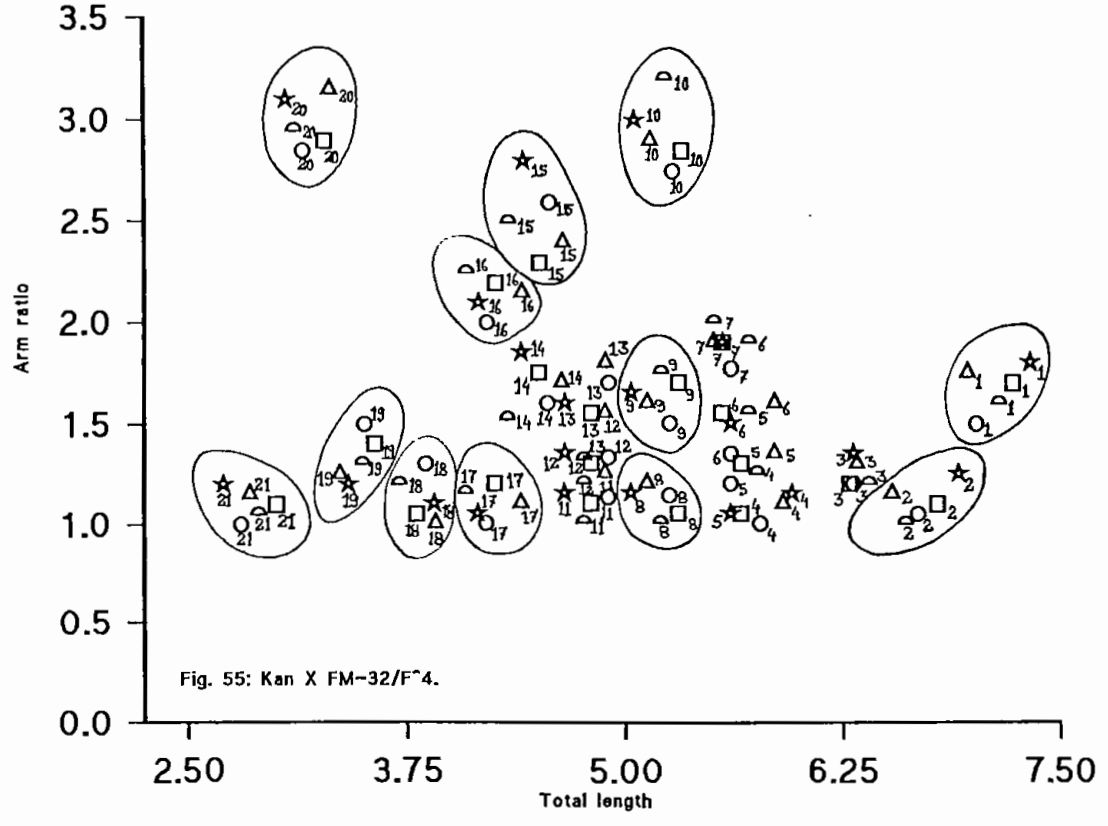


Fig. 55: Kan X FM-32/F^4.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

Fig. 54 & 55: Combined scatter diagram of the 21 haploid chromosome values from five cells of Kan X FM-32/F^3 & F4.

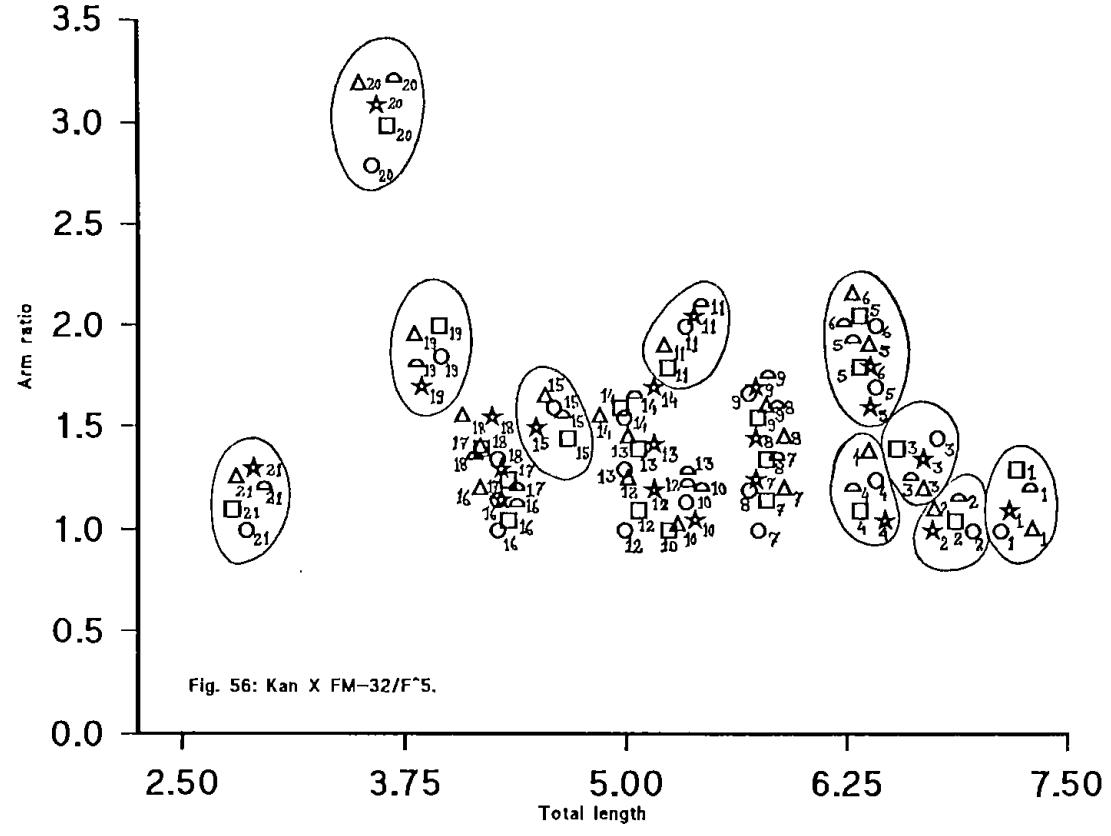


Fig. 56: Kan X FM-32/F^5.

●= a palte, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

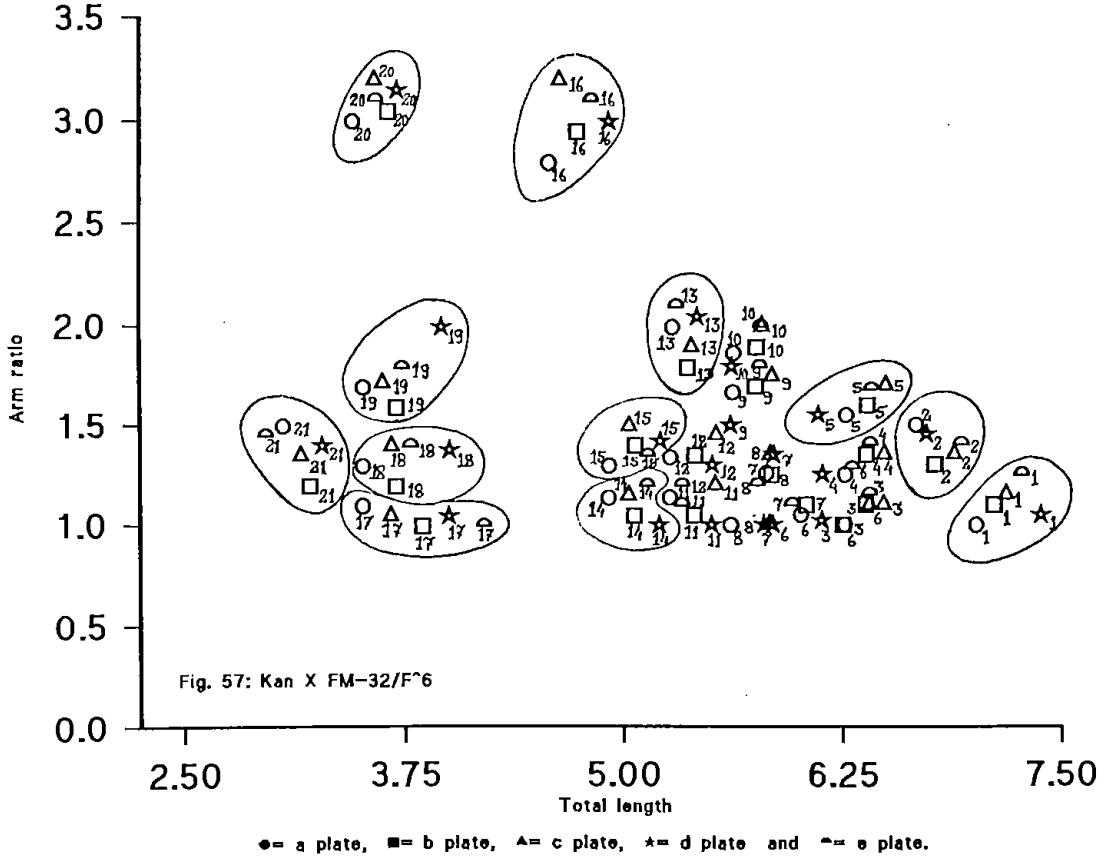
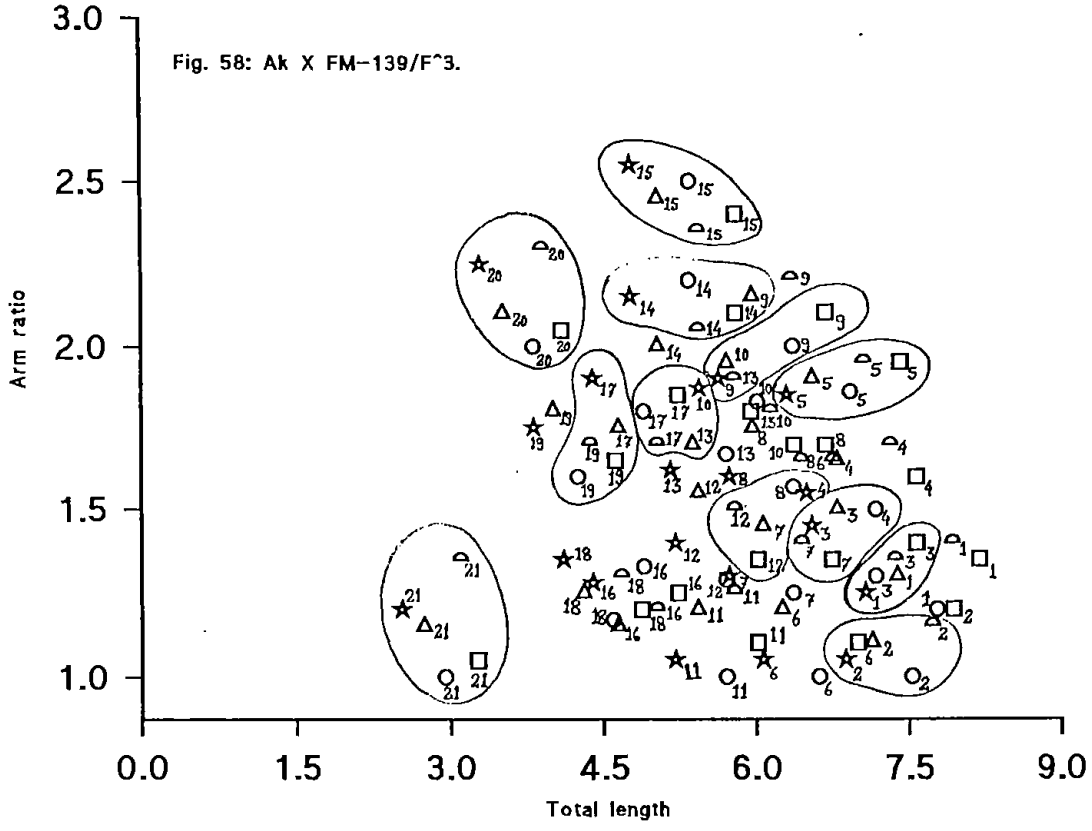


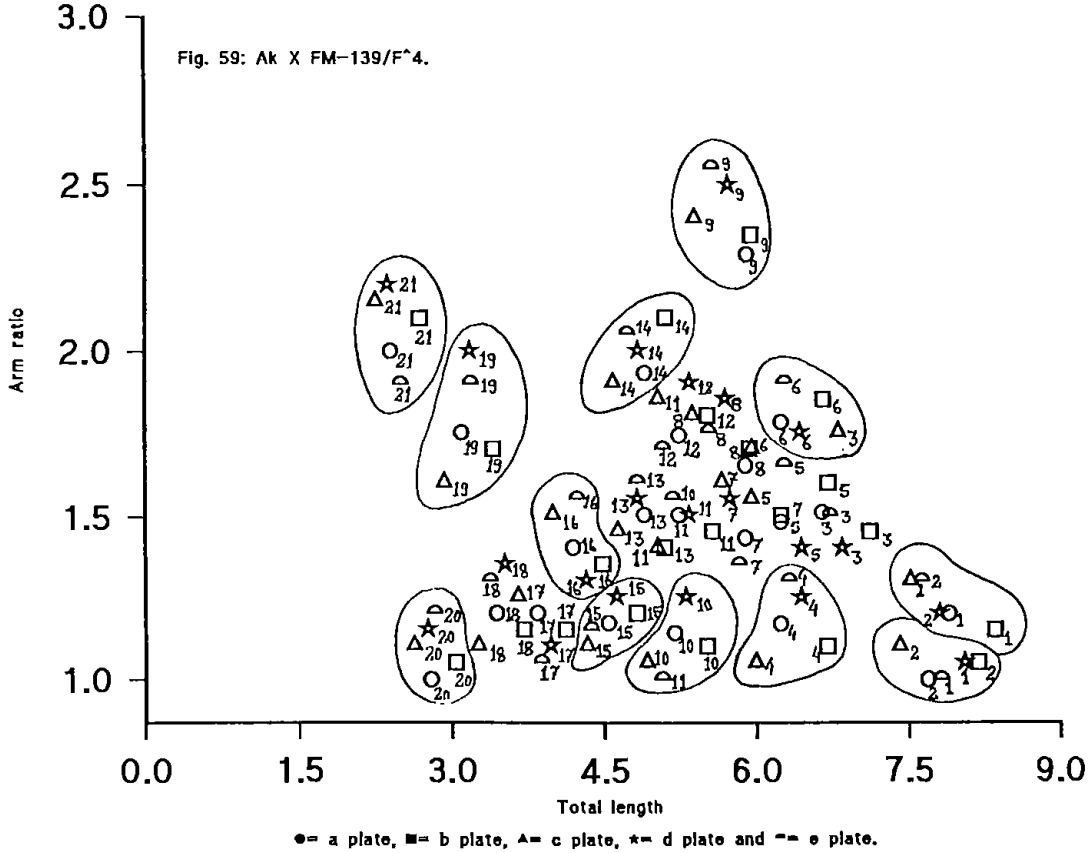
Fig. 57: Kan X FM-32/F^6

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

Fig. 56 & 57: Combined scatter diagram of the 21 haploid chromosome values from five cells of Kan X FM-32/F^5 & F^6.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ⁃= e plate.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ⁃= e plate.

Figs. 58 & 59: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ak X FM-139/F^3 & F^4.

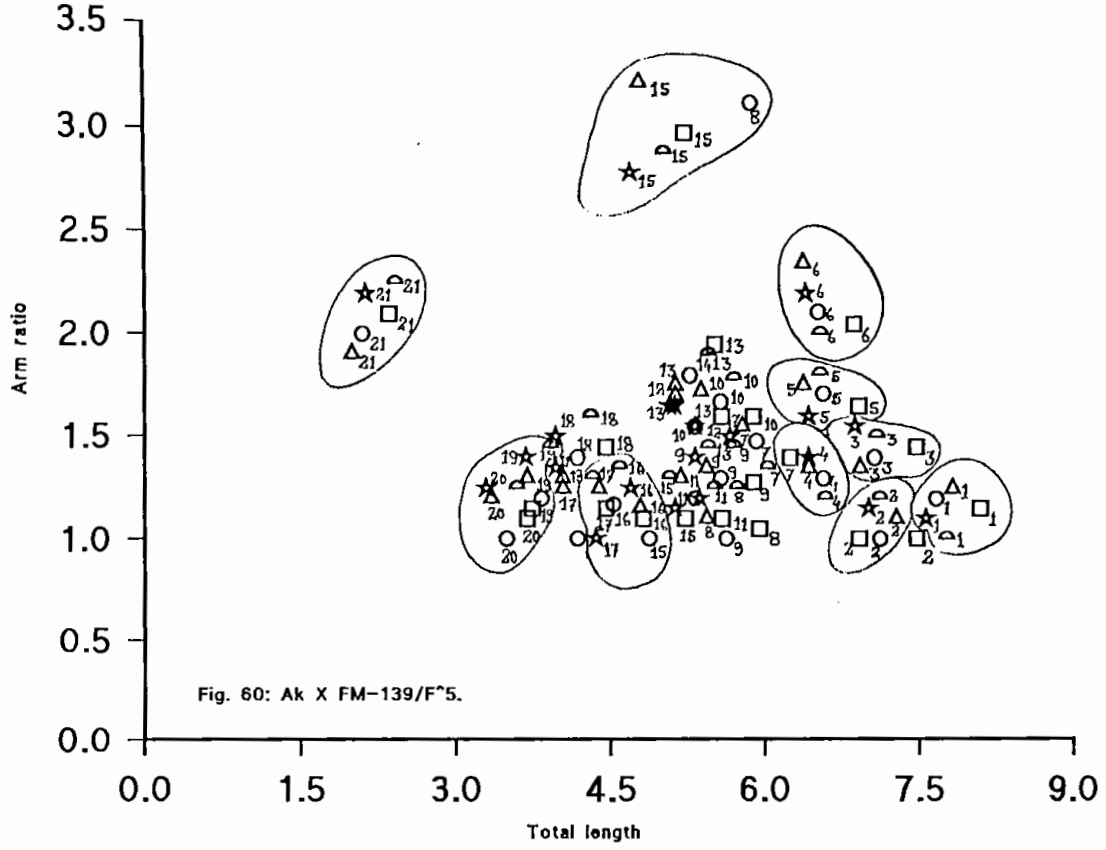


Fig. 60: Ak X FM-139/F^5.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

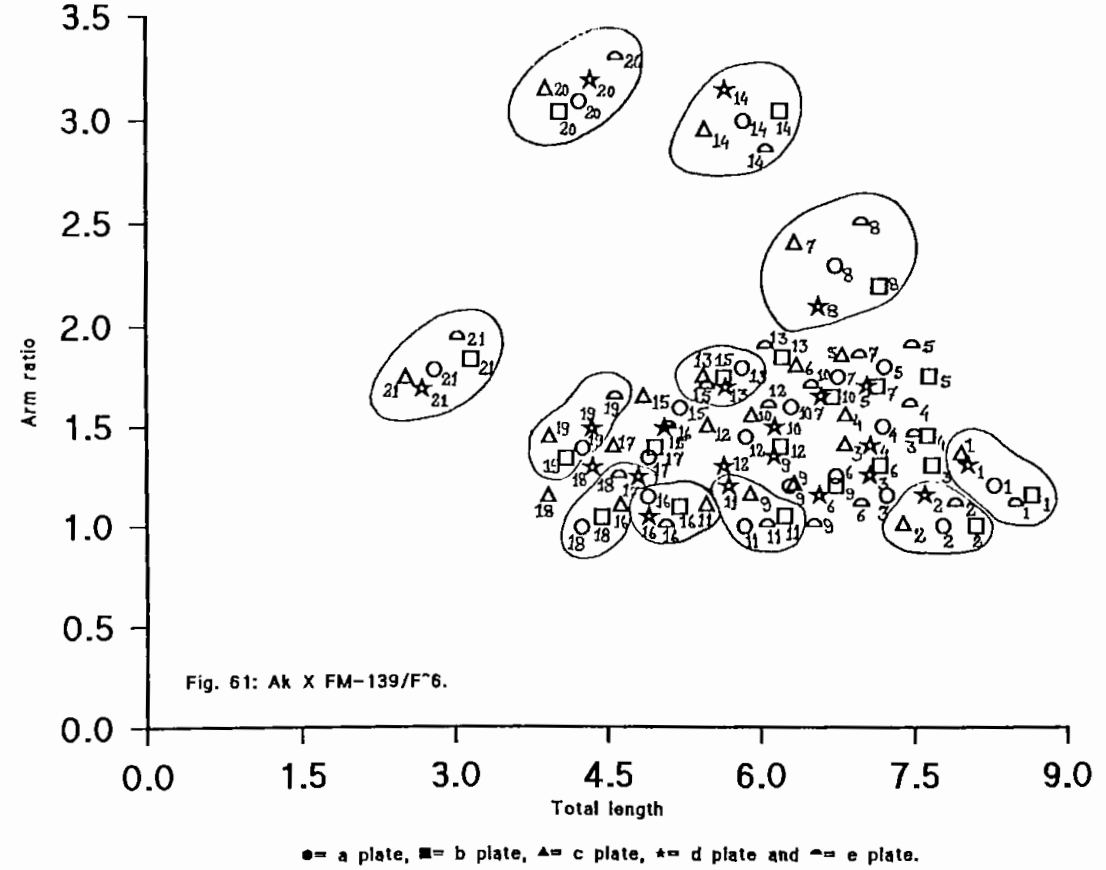
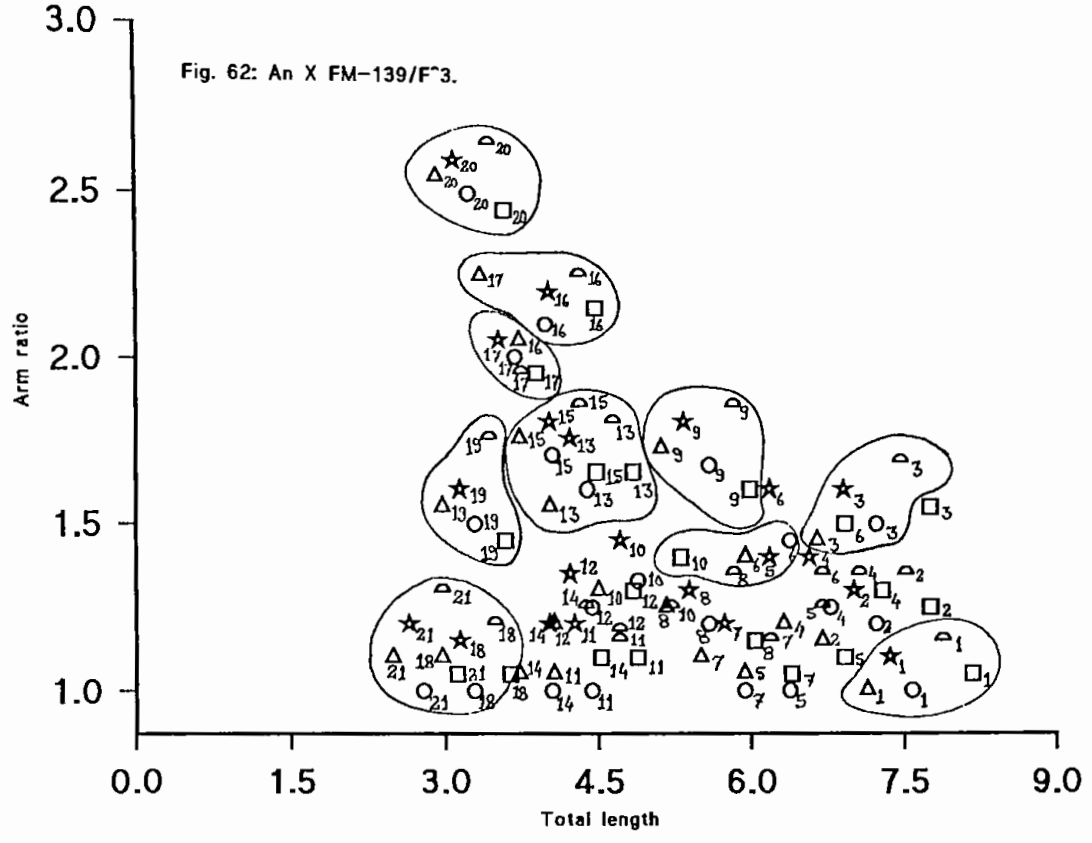


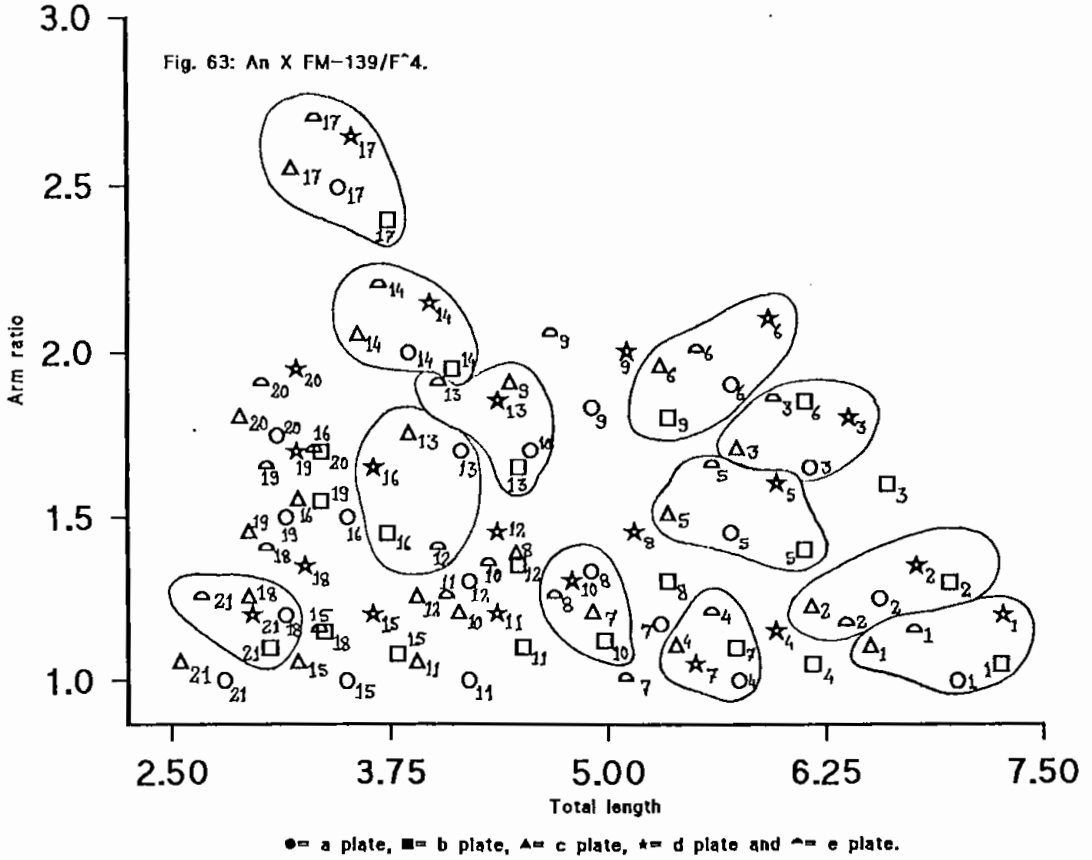
Fig. 61: Ak X FM-139/F^6.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Fig. 60 & 61: Combined scatter diagram of the 21 haploid chromosome values from five cells of Ak X FM-139/F^5 & F^6.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ^= e plate.

Fig. 62 & 63: Combined scattor diagram of tho 21 haploid chromosome values from five cells of An X FM-139/F^3 & F^4.

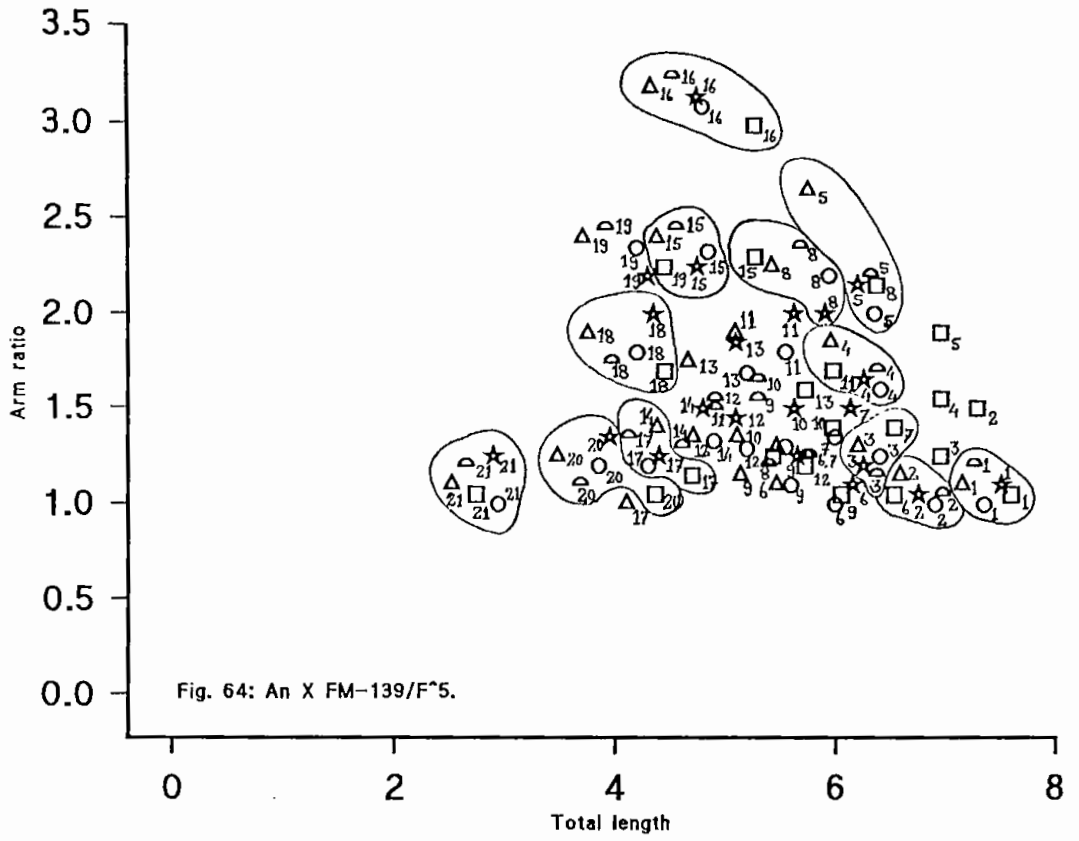


Fig. 64: An X FM-139/F^5.

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

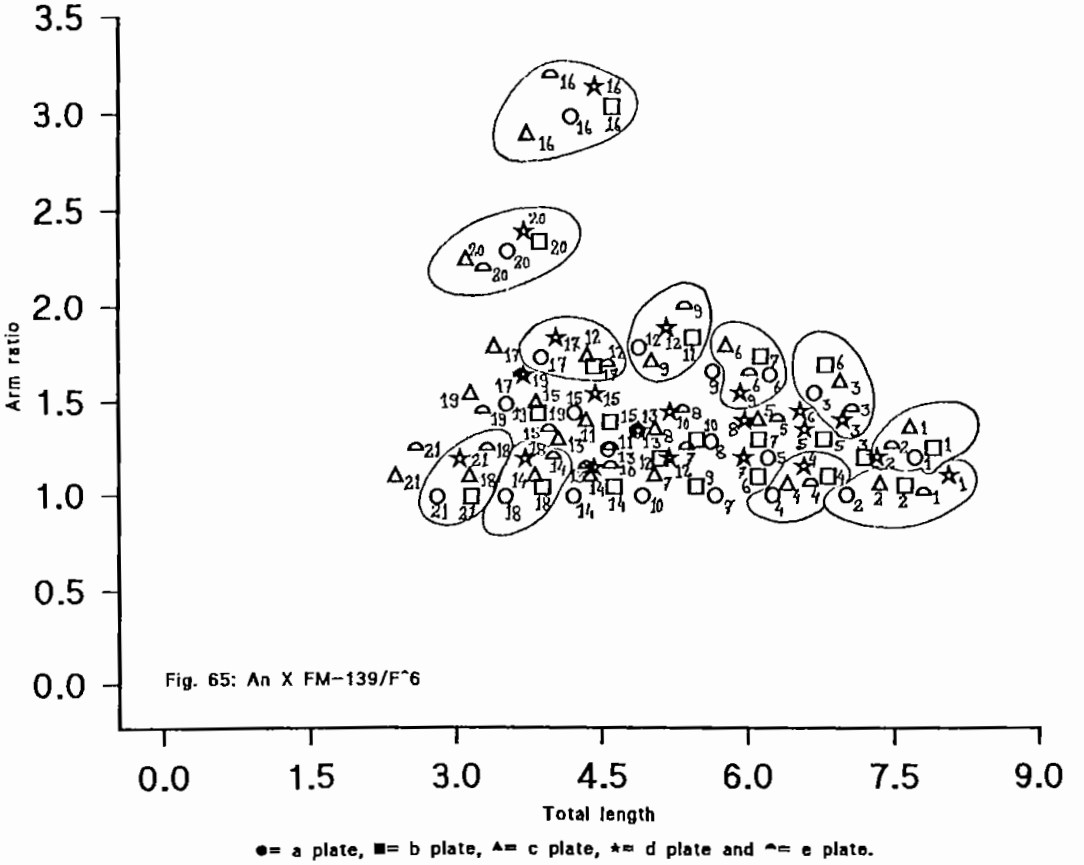
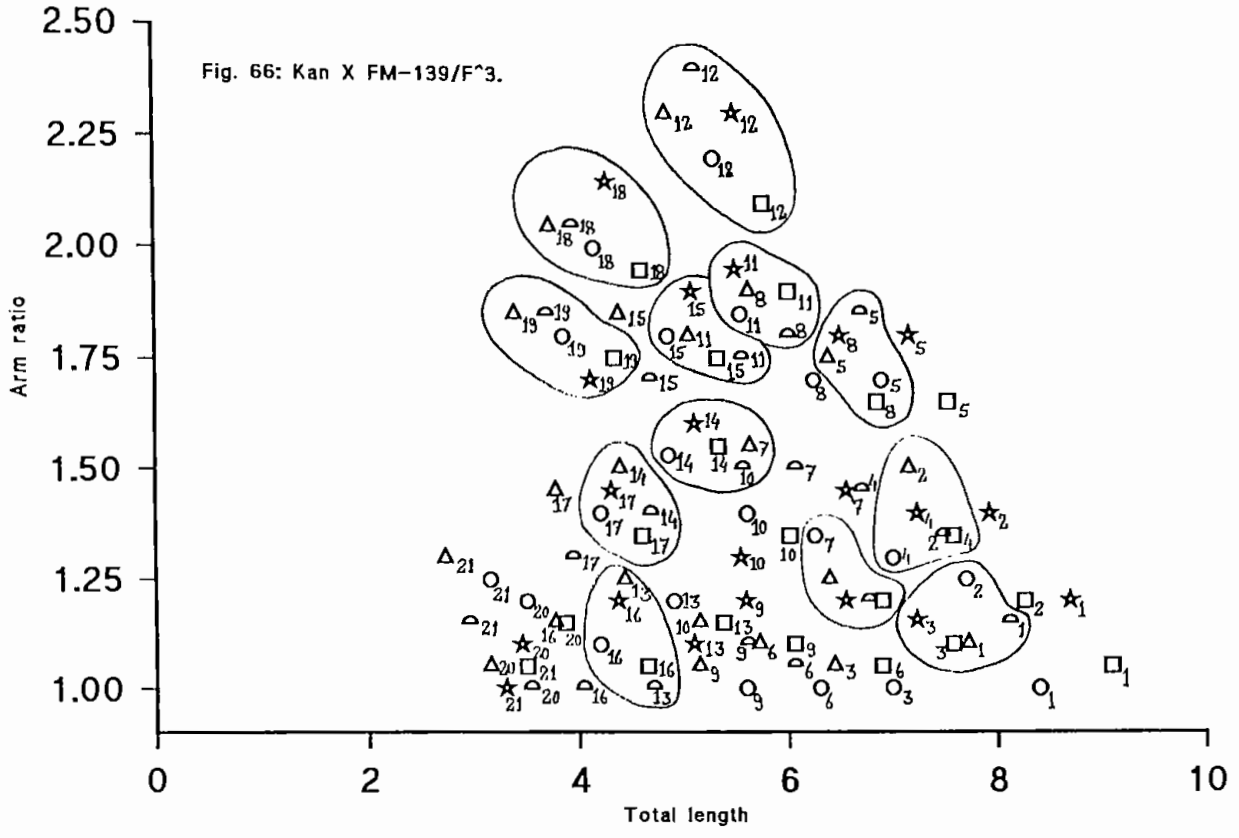


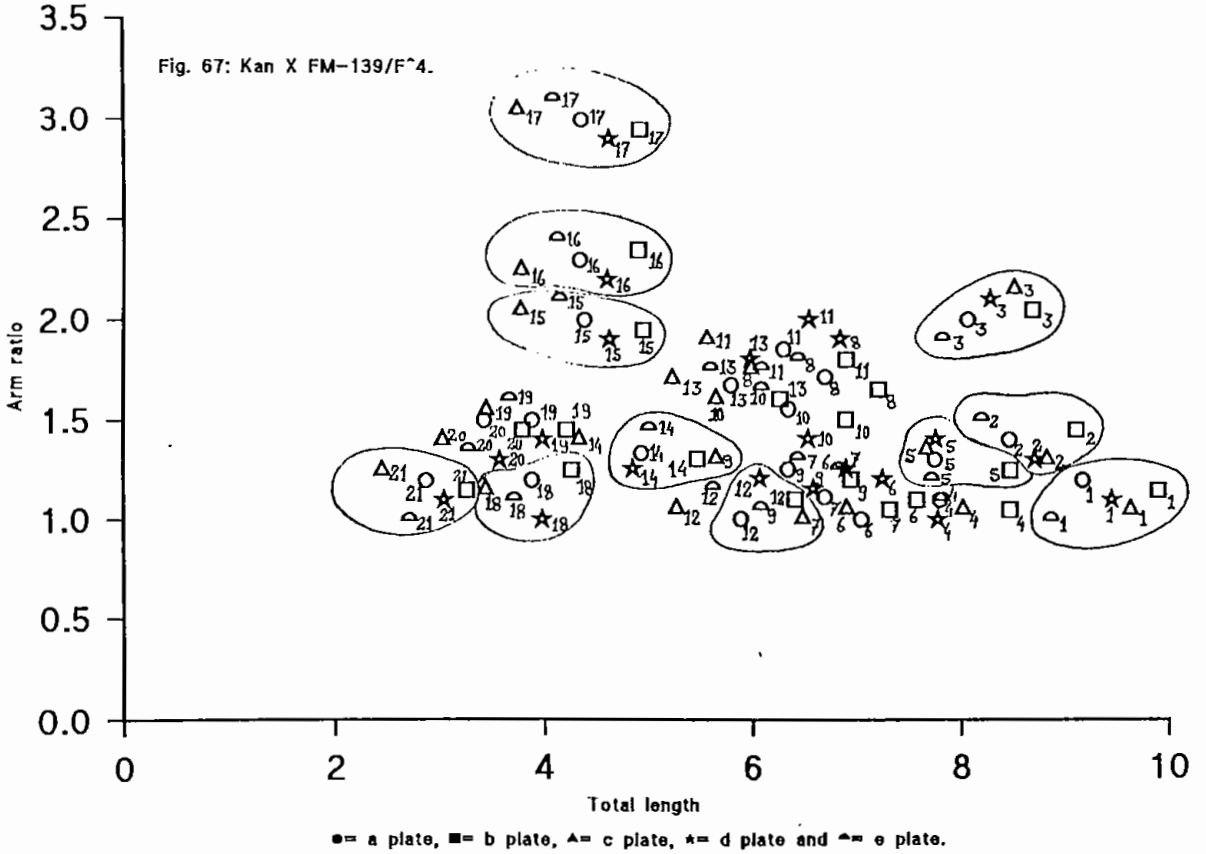
Fig. 65: An X FM-139/F^6

●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Fig. 64 & 65: Combined scatter diagram of the 21 haploid chromosome values from five cells of An X FM-139/F^5 & F^6.

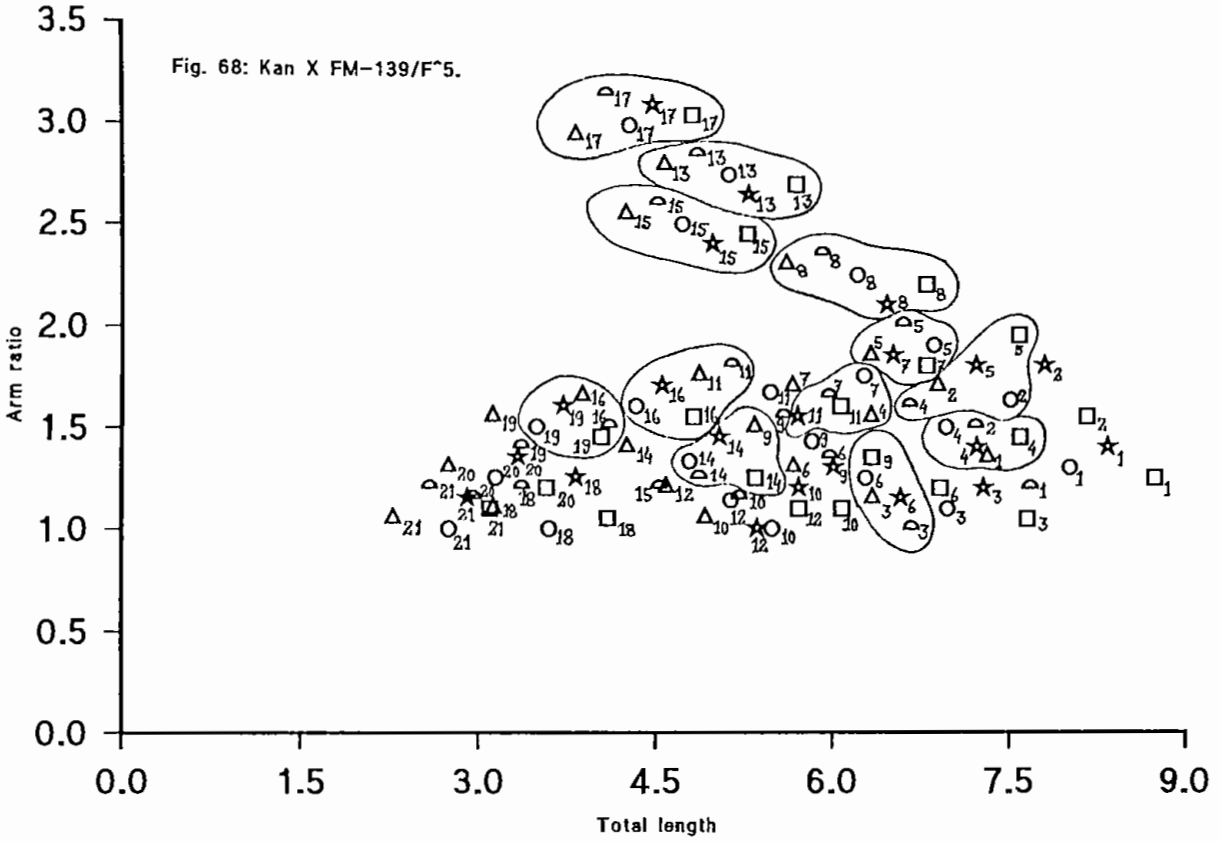


●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

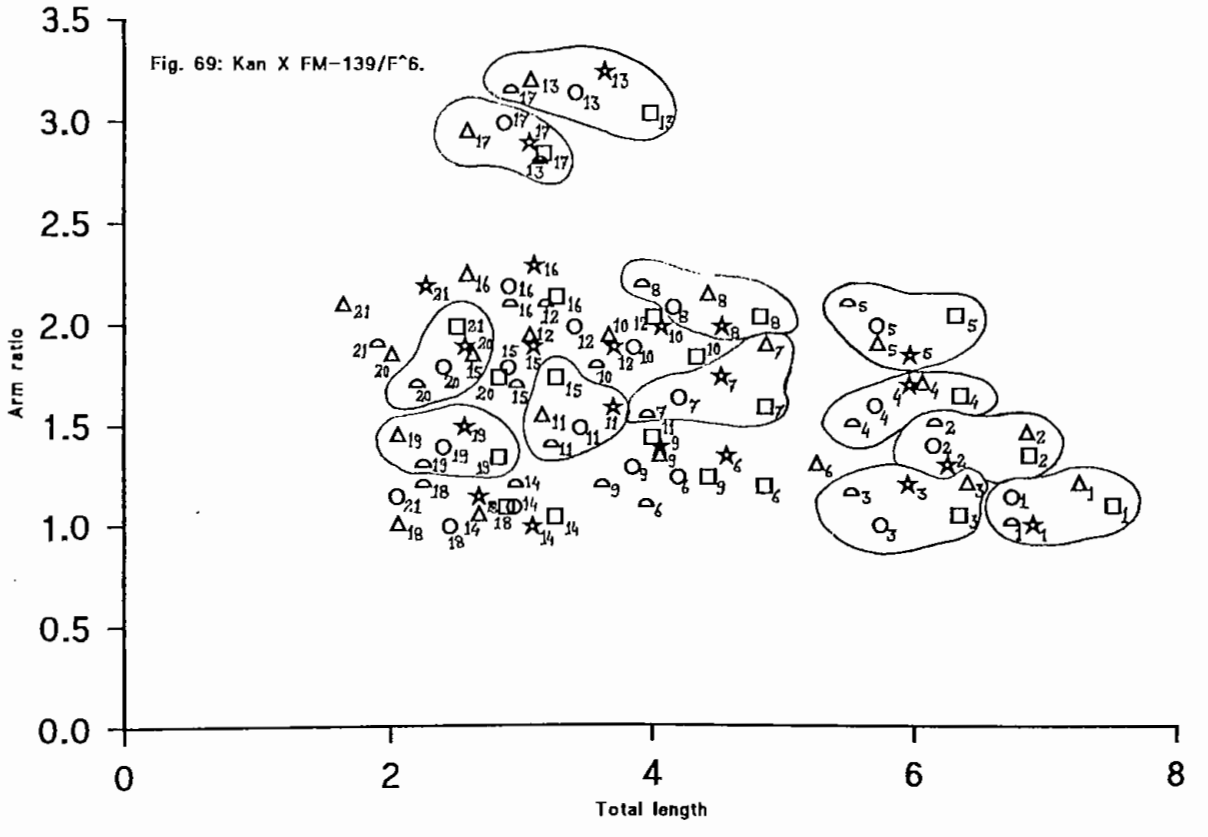


●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◓= e plate.

Fig. 66 & 67: Combined scatter diagram of the 21 haploid chromosome values from five cells of Kan X FM-139/F^3 & F^4.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◠= e plate.



●= a plate, ■= b plate, ▲= c plate, ★= d plate and ◠= e plate.

Figs. 68 & 69: Combined scatter diagram of the 21 haploid chromosome values from five cells of Kan X FM-139/F^5 & F^6.

grouping of such points would not be possible. The occurrence of distinct groups of points in the combined scatter diagram is one of the supporting evidence that this procedure in identifying the homologous chromosomes over different cells have had strong validity.

In these scatter diagrams, different number of groups of five points and groups of ten points were found to appear. These groups of five points indicated that the number of distinct and individually identifiable chromosomes in each genotype. Whereas the group of ten points is an indicator of two chromosomes are so similar morphologically that they could not be distinguished from each other but identifiable from the rest. The number of identified chromosome were 12, 11, 12, 10, 11 and 11 in Aghrani, Akbar, Ananda, Kanchan, FM-32 and FM-139, respectively. The identified chromosome numbers for F_3, F_4, F_5 and F_6 of Ag X FM-32, Ak X FM-32, An X FM-32, Kan XFM-32, Ak X FM-139, An X FM-139 and Kan X FM-139 were found to be 11, 9, 11 and 10; 12, 12, 11 and 12; 12, 12, 12 and 12; 12, 12, 11 and 12; 12, 12, 12 and 12; 12, 12, 12 and 11; and 12, 11, 12 and 12, respectively. Morphological features and idiogram of these chromosomes are given in Table 2 and Figs. 36-69, respectively.

The proportion of the total haploid complement length occupied by the identified chromosomes in different cells of the parental genotypes and their hybrid progenies are given in Table 3. The mean occupied proportions among the parental genotypes were observed highest in Aghrani (61.30%) and lowest in Kanchan (42.99%), and only Kanchan differed significantly from the over all parental genotypic mean (54.69%). In Ag X FM-32 the highest and lowest values for occupied proportions were found in F_3 and F_4 respectively. The progeny F_3

Table 2. Mean lengths and arm ratios of the identified chromosomes in parents and their hybrid progenies of seven crosses of wheat.

PARENTS:

Genotype/ Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
AGRHANI:						
m_1	9.05	0.08	1.87	1.18	0.03	4.76
m_2	8.51	0.11	2.83	1.01	0.01	2.21
m_3	8.02	0.11	3.14	1.43	0.02	3.22
m_4	7.73	0.12	3.47	1.30	0.01	2.48
m_5	7.29	0.13	3.92	1.49	0.02	2.94
m_6	7.04	0.17	5.46	1.29	0.03	5.31
m_7	6.27	0.19	6.73	1.64	0.05	7.18
m_8	5.81	0.23	8.93	1.22	0.02	4.40
m_9	5.15	0.34	14.8	1.61	0.06	7.85
m_{10}	3.86	0.12	7.18	1.35	0.07	11.22
sm_1	3.63	0.06	3.59	2.22	0.06	6.31
m_{11}	3.34	0.12	7.81	1.12	0.04	8.73
AKBAR:						
m_1	8.51	0.13	3.28	1.54	0.07	10.11
m_2	8.00	0.10	4.05	1.44	0.03	7.28
m_3	8.00	0.10	4.05	1.44	0.03	7.28
m_4	7.97	0.04	1.14	1.68	0.02	2.80
m_5	7.59	0.07	1.94	1.29	0.02	3.87
sm_1	6.94	0.05	1.56	1.75	0.03	3.73
m_6	6.51	0.05	1.67	1.61	0.03	3.65
sm_2	5.17	0.04	2.42	2.14	0.08	12.25
sm_3	5.17	0.04	2.42	2.14	0.08	12.25
m_7	4.74	0.05	2.52	1.28	0.06	10.19
m_8	4.46	0.11	5.57	1.27	0.07	12.64

Table 2. (Continued).

Genotype/ Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
ANANDA:						
m_1	8.58	0.06	1.57	1.44	0.04	5.97
m_2	7.99	0.13	3.52	1.29	0.03	5.76
m_3	7.20	0.06	1.9	1.01	0.04	7.33
sm_1	6.74	0.14	4.67	2.16	0.19	19.25
m_4	6.45	0.10	3.59	1.53	0.09	13.04
m_5	5.95	0.13	4.91	1.48	0.02	2.96
m_6	5.83	0.08	2.88	1.61	0.15	21.22
m_7	4.95	0.04	1.60	1.28	0.08	13.67
sm_2	4.80	0.04	1.65	1.86	0.22	27.04
m_8	4.45	0.13	6.74	1.38	0.12	18.79
m_9	3.94	0.12	7.03	1.66	0.05	6.64
m_{10}	3.60	0.04	2.20	1.15	0.05	9.19
KANCHAN:						
m_1	6.51	0.08	2.79	1.65	0.03	4.41
m_2	5.82	0.08	3.13	1.63	0.01	1.91
m_3	5.33	0.16	6.59	1.21	0.08	14.43
m_4	4.62	0.11	5.22	1.33	0.12	19.82
sm_1	4.40	0.14	7.14	2.02	0.16	17.67
m_5	4.18	0.08	5.76	1.28	0.08	20.08
m_6	4.18	0.08	5.76	1.28	0.08	20.08
m_7	3.70	0.07	3.94	1.61	0.04	5.97
sm_2	3.63	0.06	3.85	2.46	0.04	4.16
sm_3	3.30	0.06	3.85	2.21	0.06	5.63

Table 2. (Continued).

Genotype/ Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
FM-32:						
m_1	7.94	0.07	2.06	1.30	0.04	6.08
m_2	7.24	0.06	2.46	1.34	0.07	17.31
m_3	7.24	0.06	2.46	1.34	0.07	17.31
m_4	7.15	0.05	1.56	1.31	0.12	20.77
m_5	6.32	0.06	2.28	1.65	0.03	4.41
sm_1	6.26	0.10	3.48	2.22	0.07	6.87
m_6	5.74	0.07	3.96	1.36	0.14	31.97
m_7	5.74	0.07	3.96	1.36	0.14	31.97
m_8	4.85	0.13	8.56	1.29	0.03	7.94
sm_2	4.40	0.04	3.11	1.70	0.02	3.39
m_9	2.90	0.03	2.73	1.14	0.04	8.44
FM-139:						
sm_1	7.28	0.11	3.32	1.82	0.03	4.00
m_1	6.71	0.21	6.86	1.17	0.04	8.33
sm_2	6.50	0.09	3.22	2.02	0.05	5.13
m_2	6.17	0.08	2.72	1.34	0.03	5.01
m_3	5.79	0.07	2.62	1.14	0.04	8.44
m_4	5.64	0.12	4.87	1.64	0.04	5.86
m_5	5.21	0.10	4.09	1.17	0.05	10.29
sm_3	5.21	0.10	4.09	1.80	0.04	4.39
sm_4	4.29	0.15	7.88	1.80	0.04	4.39
sm_5	3.70	0.20	12.01	2.09	0.06	6.85
sm_6	3.05	0.10	7.33	1.76	0.04	5.14

Table 2. (Continued).

1. Ag X FM-32:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
$m_1 + m_2$	7.77	0.09	3.71	1.20	0.04	9.86
$m_3 + m_4$	7.48	0.06	2.59	1.36	0.04	8.63
sm_1	7.26	0.09	2.64	1.96	0.07	7.50
sm_2	6.30	0.04	1.25	1.87	0.04	4.52
m_5	5.80	0.04	1.36	1.29	0.01	1.73
sm_3	5.75	0.05	1.94	1.73	0.02	3.05
m_6	4.48	0.08	4.07	1.15	0.04	8.54
m_7	4.40	0.03	3.31	1.44	0.07	10.81
m_8	3.72	0.07	4.10	1.34	0.05	7.93
F_4:						
m_1	6.99	0.07	2.28	1.25	0.09	16.00
m_2	6.53	0.08	2.74	1.20	0.07	13.18
sm_1	6.5	0.07	2.43	1.74	0.05	6.46
sm_2	5.75	0.05	1.94	2.02	0.09	9.52
m_3	5.59	0.19	7.63	1.47	0.04	5.69
sm_3	5.33	0.04	1.70	1.89	0.11	12.65
sm_4	4.61	0.06	3.00	1.83	0.05	6.58
sm_5	4.12	0.03	1.84	2.19	0.06	6.54
m_4	3.60	0.04	2.20	1.33	0.05	9.05

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	7.28	0.08	2.41	1.10	0.04	7.19
m_2	7.21	0.07	2.21	1.39	0.03	5.34
m_3	6.80	0.06	1.87	1.30	0.03	5.63
sm_1	6.35	0.04	1.24	1.87	0.04	4.26
m_4	5.96	0.05	2.00	1.12	0.03	6.66
sm_2	5.69	0.03	1.30	1.70	0.02	2.33
sm_3	5.07	0.05	2.38	2.27	0.07	6.53
m_5	4.65	0.04	1.70	1.25	0.03	5.82
sm_4 + sm_5	3.89	0.03	2.43	1.74	0.02	3.79
m_6	2.77	0.05	3.74	1.22	0.04	8.03
F_6:						
m_1	6.78	0.05	1.53	1.20	0.04	6.59
m_2	5.76	0.06	2.25	1.69	0.02	2.23
m_3	5.73	0.05	1.81	1.13	0.05	10.66
m_4	4.68	0.13	6.07	1.14	0.05	9.84
sm_1	4.47	0.09	4.45	1.96	0.04	4.91
m_5	4.00	0.10	5.66	1.22	0.03	4.67
m_6	3.74	0.08	4.95	1.45	0.06	9.75
m_7	3.36	0.09	5.99	1.23	0.02	3.64
sm_2	3.02	0.06	4.47	1.71	0.03	3.56
m_8	2.72	0.06	4.97	1.32	0.03	4.32

Table 2. (Continued).

2. Ak X FM-32:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	7.69	0.06	1.86	1.16	0.03	5.62
m_2	7.11	0.11	3.50	1.14	0.04	8.44
m_3	7.09	0.11	3.47	1.40	0.04	5.65
m_4	6.73	0.08	2.61	1.68	0.03	3.41
sm_1	6.31	0.07	2.31	1.90	0.04	4.16
m_5	6.27	0.06	2.12	1.36	0.05	8.55
m_6	5.96	0.04	1.61	1.36	0.05	8.55
sm_2	5.09	0.05	2.35	1.74	0.04	5.531
sm_3	5.09	0.05	2.35	2.27	0.07	6.53
sm_4	4.70	0.04	1.68	1.93	0.03	3.48
m_7	4.21	0.06	3.40	1.14	0.04	8.44
sm_5	4.19	0.06	3.42	1.86	0.04	5.17
F_4:						
m_1	6.80	0.08	2.63	1.17	0.05	10.29
sm_1	6.18	0.11	4.04	1.76	0.04	5.46
m_2	5.82	0.10	3.89	1.10	0.04	7.19
sm_2	5.81	0.09	3.65	1.77	0.05	6.80
sm_3	5.80	0.09	3.48	2.22	0.09	8.66
m_3	5.34	0.07	2.83	1.14	0.06	11.35
sm_4	4.55	0.08	3.89	1.80	0.04	4.39
st_1	4.53	0.08	3.95	3.10	0.04	2.55
m_4	3.95	0.07	4.29	1.61	0.02	2.60
sm_5	3.95	0.08	4.29	1.70	0.02	2.15
m_5	3.63	0.05	3.32	1.14	0.05	10.47
m_6	3.37	0.05	3.08	1.83	0.05	6.58

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	6.57	0.08	2.72	1.14	0.04	8.44
sm_1	5.87	0.08	3.05	1.70	0.03	4.48
sm_2	5.08	0.08	3.31	2.33	0.05	5.17
sm_3	4.52	0.10	4.86	1.95	0.05	5.73
st_1	4.51	0.10	4.92	3.07	0.04	2.73
m_2	3.72	0.09	5.43	1.55	0.05	7.21
st_2	3.72	0.09	5.43	3.30	0.07	4.79
m_3	3.33	0.07	4.82	1.15	0.04	8.13
m_4	3.12	0.09	6.67	1.44	0.04	4.30
sm_4	3.12	0.09	6.67	1.80	0.08	9.82
sm_5	2.69	0.09	7.48	2.26	0.09	9.18
F_6:						
m_1	6.52	0.11	3.70	1.18	0.06	11.45
m_2	5.90	0.10	3.97	1.14	0.05	10.47
sm_1	5.89	0.11	4.22	1.70	0.04	5.82
m_3	4.32	0.08	4.14	1.16	0.04	8.29
sm_2	4.32	0.08	4.14	1.86	0.04	5.17
st_1	4.26	0.09	4.84	3.12	0.05	3.69
m_4	3.72	0.08	4.71	1.27	0.07	11.68
st_2	3.70	0.09	5.65	3.10	0.04	2.55
m_5	3.43	0.10	6.40	1.17	0.06	11.55
m_6	3.14	0.10	7.33	1.05	0.02	4.76
m_7	3.14	0.10	7.33	1.32	0.05	7.85
sm_3	2.68	0.06	5.30	1.83	0.06	6.85

Table 2. (Continued).

3. An X FM-32:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	6.18	0.09	3.41	1.15	0.02	3.10
m_2	6.12	0.24	8.94	1.32	0.04	7.16
m_3	5.75	0.06	2.22	1.69	0.03	3.91
m_4	5.48	0.18	7.49	1.20	0.01	2.41
m_5	5.26	0.10	4.22	1.12	0.03	5.09
m_6	5.25	0.10	4.15	1.53	0.02	2.59
sm_1	4.73	0.14	6.46	1.76	0.02	3.18
m_7	3.99	0.13	7.21	1.10	0.04	7.19
m_8	3.89	0.10	5.92	1.30	0.04	6.08
m_9	3.29	0.11	7.32	1.28	0.01	2.14
m_{10}	2.90	0.13	9.98	1.32	0.02	3.55
m_{11}	2.02	0.08	8.49	1.67	0.05	7.21
F_4:						
m_1	6.62	0.07	2.24	1.14	0.04	8.44
m_2	6.11	0.17	6.11	1.19	0.06	10.88
sm_1	5.48	0.07	2.78	1.70	0.03	4.48
m_3	5.38	0.16	6.79	1.06	0.04	8.44
m_4	4.34	0.06	2.98	1.10	0.04	7.19
sm_2	4.27	0.15	7.74	1.81	0.02	3.03
sm_3	4.04	0.11	6.03	2.28	0.03	3.33
m_5	3.47	0.04	2.81	1.18	0.05	8.79
m_6	3.43	0.06	3.80	1.59	0.03	4.73
m_7	3.12	0.06	4.18	1.12	0.04	8.11
st_1	2.81	0.18	14.47	3.04	0.03	2.14
m_8	2.35	0.05	4.76	1.17	0.06	11.03

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	6.52	0.07	2.46	1.15	0.05	9.22
m_2	5.56	0.11	4.42	1.11	0.04	8.60
m_3	5.21	0.09	3.87	1.15	0.04	6.87
sm_1	4.50	0.09	4.65	2.10	0.04	3.76
sm_2	4.49	0.09	4.34	2.40	0.04	3.29
m_4	4.12	0.08	4.51	1.10	0.04	7.17
$sm_3 + sm_4$	4.12	0.06	4.24	1.77	0.03	5.94
sm_5	4.07	0.08	4.56	1.83	0.04	4.96
m_5	3.77	0.08	4.74	1.40	0.05	7.58
sm_6	3.38	0.08	5.19	1.95	0.05	6.11
m_6	2.47	0.07	6.17	1.40	0.04	5.65
F_6:						
sm_1	5.83	0.09	3.41	1.71	0.03	3.56
m_1	5.17	0.07	3.03	1.10	0.03	6.97
$m_2 + m_3$	5.12	0.06	3.74	1.36	0.03	6.79
m_4	4.77	0.13	3.10	1.69	0.04	4.73
m_5	4.46	0.10	5.22	1.08	0.03	5.48
st_1	4.38	0.09	4.54	3.10	0.04	2.55
m_6	3.70	0.07	4.27	1.14	0.04	8.44
sm_2	3.35	0.07	4.72	1.99	0.06	6.74
m_7	3.06	0.08	5.94	1.10	0.04	7.19
m_8	2.65	0.07	5.97	1.16	0.05	10.57
sm_3	2.33	0.07	6.37	2.08	0.03	2.69

Table 2. (Continued).

4. Kan X FM-32:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	6.16	0.08	2.84	1.14	0.04	8.44
m_2	5.82	0.07	2.70	1.10	0.04	7.19
sm_1	5.80	0.07	2.73	1.78	0.04	5.47
sm_2	5.03	0.12	5.26	2.44	0.05	4.67
sm_3	4.44	0.09	4.46	1.93	0.08	9.27
m_3	4.36	0.11	5.52	1.15	0.05	8.91
m_4	4.36	0.11	5.52	1.32	0.03	4.32
sm_4	4.24	0.14	7.42	2.18	0.10	9.94
m_5	3.80	0.11	6.80	1.18	0.06	11.45
sm_5	3.67	0.08	4.98	2.16	0.08	7.57
st_1	3.35	0.07	4.64	3.10	0.04	2.55
sm_6	3.04	0.09	6.89	1.92	0.05	5.40
F_4:						
m_1	7.11	0.06	1.82	1.67	0.05	7.21
m_2	6.69	0.04	1.41	1.14	0.04	8.44
m_3	5.20	0.04	1.52	1.14	0.05	10.5
sm_1	5.20	0.04	1.52	1.73	0.06	7.58
sm_2	5.20	0.04	1.52	2.89	0.11	8.86
sm_3	4.57	0.08	3.99	2.14	0.04	4.49
m_4	4.19	0.05	2.85	1.10	0.04	7.19
sm_4	4.19	0.05	2.85	2.52	0.09	7.63
m_5	3.84	0.04	2.50	1.07	0.04	7.82
m_6	3.50	0.04	2.60	1.29	0.03	5.75
sm_5	3.16	0.04	3.047	2.92	0.11	8.78
m_7	2.77	0.05	4.16	1.10	0.04	7.19

Table 2: (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	7.18	0.11	3.29	1.12	0.06	11.64
m_2	6.86	0.15	4.77	1.05	0.02	4.36
m_3	6.67	0.10	3.28	1.33	0.05	7.80
m_4	6.39	0.10	3.39	1.26	0.05	9.47
$sm_1 + sm_2$	6.37	0.07	3.31	1.89	0.05	8.89
sm_3	5.35	0.12	5.13	1.97	0.05	6.11
m_5	4.60	0.11	5.11	1.52	0.03	3.75
sm_4	3.88	0.08	0.05	1.86	0.05	6.42
st_1	3.61	0.10	0.06	3.06	0.08	5.60
m_6	2.88	0.08	5.84	1.17	0.05	10.29
F_6:						
m_1	7.18	0.10	3.14	1.11	0.04	8.66
m_2	6.77	0.13	4.42	1.37	0.05	7.57
m_3	6.31	0.16	5.81	1.54	0.04	5.72
sm_1	5.12	0.27	11.83	1.97	0.05	6.11
m_4	5.02	0.11	4.76	1.11	0.04	7.32
m_5	5.02	0.11	4.76	1.39	0.03	5.41
st_1	4.71	0.08	3.82	3.01	0.07	5.04
m_6	3.79	0.10	5.77	1.04	0.02	4.02
m_7	3.74	0.08	4.65	1.27	0.03	5.17
sm_2	3.69	0.07	4.39	1.76	0.07	8.507
st_2	3.59	0.06	3.61	3.10	0.04	2.55
m_8	3.11	0.06	4.16	1.40	0.04	5.65

Table 2. (Continued).

5. Ak X FM-139:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	7.32	0.08	2.30	1.32	0.03	4.32
m_2	7.26	0.14	4.45	1.08	0.03	5.28
sm_1	6.85	0.10	3.14	1.89	0.03	3.37
m_3	6.75	0.14	4.66	1.44	0.03	4.53
m_4	6.16	0.20	7.13	1.48	0.04	5.94
sm_2	6.04	0.14	5.28	1.97	0.04	4.25
sm_3	5.47	0.18	7.53	2.13	0.03	2.68
sm_4	5.28	0.10	4.27	2.45	0.04	3.23
sm_5	5.21	0.17	7.10	1.78	0.04	4.53
sm_6	4.46	0.10	4.98	1.72	0.05	6.69
sm_7	3.73	0.09	5.38	2.14	0.06	6.05
m_5	2.91	0.09	6.80	1.15	0.06	11.91
F_4:						
m_1	7.82	0.08	2.15	1.04	0.02	4.02
m_2	7.82	0.08	2.33	1.19	0.03	6.23
sm_1	6.39	0.05	1.88	1.78	0.05	6.45
m_3	6.33	0.06	2.13	1.17	0.05	8.78
sm_2	5.61	0.04	1.71	2.42	0.05	4.41
m_4	5.24	0.05	2.28	1.51	0.05	7.55
sm_3	4.82	0.05	2.15	2.00	0.04	4.14
m_5	4.54	0.05	2.49	1.17	0.03	4.77
m_6	4.24	0.04	2.27	1.42	0.05	7.30
sm_4	3.15	0.05	3.55	1.79	0.07	8.92
m_7	2.81	0.04	3.42	1.10	0.04	7.19
sm_5	2.43	0.05	4.96	2.07	0.05	5.82

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	7.78	0.05	1.39	1.14	0.04	8.44
m_2	7.16	0.05	1.71	1.10	0.04	7.19
m_3	7.12	0.06	1.90	1.45	0.04	5.45
sm_1	6.58	0.06	2.05	1.70	0.04	4.65
sm_2	6.55	0.05	1.75	2.14	0.06	6.45
m_4	6.47	0.10	3.40	1.33	0.04	6.29
m_5	5.15	0.21	9.03	1.26	0.07	11.79
$m_6 + m_7$	4.60	0.07	4.64	1.20	0.04	9.52
$m_8 + m_9$	3.59	0.07	6.14	1.23	0.04	11.26
sm_3	2.20	0.07	7.19	2.09	0.06	6.85
F_6:						
m_1	8.28	0.10	2.13	1.22	0.05	8.50
m_2	7.80	0.06	1.59	1.05	0.03	6.73
m_3	7.11	0.07	2.13	1.61	0.04	5.55
sm_1	6.71	0.06	2.13	2.18	0.11	11.87
m_4	6.38	0.10	3.53	1.11	0.04	7.40
st_1	5.79	0.07	2.63	3.00	0.05	3.73
m_5	5.00	0.18	8.12	1.17	0.03	6.84
m_6	4.84	0.04	1.99	1.35	0.09	15.27
m_7	4.67	0.14	6.45	1.04	0.02	4.02
m_8	4.32	0.08	3.98	1.47	0.05	7.83
st_2	4.29	0.08	4.39	3.16	0.04	3.04
sm_2	2.82	0.08	6.47	1.81	0.04	5.31

Table 2. (Continued).

6. An X FM-139:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	7.60	0.09	2.51	1.08	0.04	8.41
m_2	7.04	0.12	3.70	1.55	0.04	5.99
m_3	5.94	0.24	9.11	1.40	0.02	2.53
sm_1	5.57	0.08	3.02	1.73	0.04	5.78
$sm_2 + sm_3$	4.27	0.07	5.32	1.71	0.03	5.65
sm_4	4.02	0.14	7.81	2.19	0.03	2.98
sm_5	3.72	0.05	3.04	1.99	0.03	3.28
m_4	3.28	0.06	4.12	1.57	0.05	7.33
sm_6	3.25	0.07	4.87	2.55	0.04	3.10
$m_5 + m_6$	3.06	0.10	10.36	1.12	0.03	8.73
F_4:						
m_1	7.00	0.09	2.80	1.10	0.04	7.18
m_2	6.55	0.05	1.81	1.26	0.03	5.55
sm_1	6.06	0.06	2.36	1.77	0.04	5.13
m_3	5.74	0.06	2.42	1.52	0.05	6.82
m_4	5.59	0.06	2.51	1.09	0.03	6.82
sm_2	5.55	0.11	4.50	1.95	0.05	5.73
m_5	4.86	0.07	3.17	1.24	0.04	6.72
sm_3	4.50	0.09	4.39	1.78	0.06	7.91
m_6	3.89	0.12	7.09	1.59	0.07	9.79
sm_4	3.83	0.05	2.71	2.07	0.05	5.01
sm_5	3.43	0.05	3.26	2.56	0.05	4.66
m_7	2.80	0.06	4.42	1.12	0.05	9.26

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	7.35	0.05	1.48	1.09	0.03	6.80
m_2	6.88	0.07	2.33	1.06	0.02	5.17
m_3	6.34	0.05	1.71	1.26	0.04	7.63
sm_1	6.23	0.08	2.70	2.21	0.09	9.25
sm_2	6.18	0.14	5.01	1.70	0.04	5.50
sm_3	5.69	0.17	6.50	2.20	0.06	6.09
st_1	4.75	0.09	4.06	3.14	0.04	3.069
sm_4	4.62	0.10	4.94	2.34	0.04	3.82
m_4	4.40	0.07	3.59	1.27	0.05	8.166
sm_5	4.16	0.07	3.84	1.83	0.05	6.58
m_5	3.87	0.09	5.06	1.19	0.05	10.03
m_6	2.81	0.06	5.10	1.12	0.05	9.28
F_6:						
m_1	7.51	0.16	4.66	1.18	0.06	11.45
m_2	7.19	0.26	8.22	1.04	0.02	4.02
m_3	6.57	0.06	2.18	1.46	0.05	8.18
m_4	6.29	0.18	6.56	1.09	0.04	7.54
m_5	5.94	0.11	4.04	1.58	0.09	12.43
sm_1	5.16	0.10	4.36	1.85	0.05	5.68
sm_2	4.45	0.20	9.97	1.75	0.03	3.50
st_1	4.14	0.08	4.34	3.06	0.05	3.907
m_6	3.78	0.12	6.85	1.11	0.04	8.06
sm_3	3.47	0.07	4.74	2.30	0.04	3.44
m_7	3.11	0.11	7.91	1.11	0.05	10.27

Table 2. (Continued).

7. Kan X FM-139:

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_3:						
m_1	7.97	0.23	6.35	1.16	0.03	5.62
m_2	7.29	0.11	3.46	1.38	0.03	5.49
sm_1	6.67	0.09	2.98	1.75	0.04	4.52
m_3	6.58	0.11	3.65	1.24	0.03	5.26
sm_2	5.75	0.12	4.66	1.88	0.03	3.03
m_4	5.30	0.20	8.45	1.55	0.02	2.36
sm_3	5.30	0.08	3.22	2.26	0.05	5.05
sm_4	5.18	0.14	5.97	1.80	0.03	3.40
m_5	4.48	0.11	5.36	1.12	0.05	9.26
m_6	4.45	0.10	5.026	1.42	0.03	4.01
sm_5	4.10	0.09	4.64	2.04	0.03	3.64
sm_6	3.87	0.11	2.87	1.79	0.03	3.65
F_4:						
m_1	9.10	0.11	2.61	1.10	0.04	7.18
m_2	8.40	0.09	2.35	1.39	0.04	6.43
sm_1	8.00	0.09	2.38	2.04	0.04	4.71
m_3	7.71	0.11	3.12	1.30	0.04	6.08
m_4	6.06	0.10	3.52	1.07	0.04	7.82
m_5	5.18	0.22	9.42	1.33	0.03	5.66
sm_2	4.35	0.12	6.36	2.00	0.04	3.95
sm_3	4.32	0.12	6.05	2.30	0.04	3.44
st_1	4.30	0.13	6.23	3.00	0.04	2.64
m_6	3.84	0.07	3.95	1.14	0.04	8.44
m_7	2.85	0.09	6.88	1.14	0.04	8.44

Table 2. (Continued).

Generation Chromosome name	Total length			Arm ratio		
	Mean (X)	Standard error (S.E)	Coefficient of variation	Mean (X)	Standard error (S.E)	Coefficient of variation
F_5:						
m_1	7.31	0.13	4.06	1.44	0.03	4.53
sm_1	7.21	0.12	3.58	1.74	0.06	8.19
sm_2	6.66	0.09	3.11	1.88	0.03	4.03
m_2	6.47	0.14	4.91	1.18	0.06	11.05
sm_3	6.23	0.10	3.43	2.24	0.04	4.29
m_3	5.97	0.12	4.65	1.65	0.04	4.79
sm_4	5.13	0.10	4.39	2.75	0.04	2.87
m_4	5.10	0.15	6.39	1.36	0.05	8.47
m_5	4.77	0.19	8.89	1.68	0.05	6.17
sm_5	4.77	0.10	4.48	2.50	0.04	3.16
st_1	4.31	0.09	4.81	3.05	0.04	2.59
m_6	3.86	0.13	7.77	1.54	0.04	5.33
F_6:						
m_1	6.79	0.08	2.67	1.09	0.04	8.08
m_2	6.23	0.08	2.69	1.40	0.04	5.65
m_3	5.78	0.05	1.88	1.12	0.04	8.11
m_4	5.70	0.09	3.50	1.63	0.04	5.13
sm_1	5.66	0.10	4.00	1.98	0.05	5.24
m_5	4.32	0.09	4.53	1.69	0.06	8.21
sm_2	4.21	0.10	5.47	2.10	0.04	3.76
st_1	3.35	0.13	8.88	3.16	0.03	2.35
m_6	3.31	0.10	6.70	1.56	0.06	8.30
sm_3	2.96	0.08	5.79	2.90	0.04	2.73
sm_4	2.46	0.09	8.55	1.85	0.05	6.04
m_7	2.41	0.08	7.25	1.40	0.04	5.65

Table 3. Proportion of the haploid complement length occupied by the identified chromosomes in five different cells of six parental varieties/lines and their hybrid progenies in seven crosses of wheat.

Varieties/ lines and hybrid progenies	Mean total length (µm)		Proportion of the haploid complement occupied by identified chromosomes in five different cells (%)							
			Different plates					Statistics		
	Haploid complement (n)	All identified chr.	A	B	C	D	E	X	S.E.	C.V.
Parents/										
Aghrani	123.97	75.70	64.03	61.11	60.65	60.60	60.09	61.30	0.70	2.55
Akbar	126.49	73.06	57.34	58.00	58.03	57.90	57.47	57.75	0.14	0.54
Ananda	130.00	70.48	54.97	54.09	54.35	53.97	54.50	54.38	0.18	0.74
Kanchan	109.27	45.67	43.15	41.87	47.75	40.76	41.44	42.99	1.25	6.50
FM-32	115.38	65.78	56.97	56.98	57.41	56.68	56.93	56.99	0.12	0.47
FM-139	108.82	59.55	55.36	54.25	54.56	54.97	54.61	54.75	0.19	0.78
Over all								54.69	2.55	11.43
AgXFM-32/ F_3	129.05	68.21	53.30	52.85	52.36	52.40	52.73	52.73	0.17	0.73
F_4	110.40	49.02	44.13	44.04	44.40	45.21	44.25	44.41	0.21	1.06
F_5	113.80	59.56	52.29	52.25	52.21	52.37	52.33	52.29	0.03	0.12
F_6	93.06	44.26	46.71	48.18	47.66	47.69	47.54	47.56	0.24	1.12
Over all								49.25	1.99	8.09
AkXFM-32/ F_3	120.26	70.44	58.75	58.49	58.60	58.59	58.65	58.58	0.03	0.10
F_4	108.24	59.73	54.91	54.41	56.24	54.83	55.47	55.17	0.32	1.28
F_5	97.42	46.25	47.12	47.46	47.33	47.76	47.66	47.47	0.11	0.54
F_6	95.35	51.02	53.18	53.82	53.58	53.61	53.72	53.58	0.11	0.45
Over all								53.70	2.32	8.65
AnXFM-32/ F_3	93.24	54.86	58.40	59.68	57.51*	58.81	59.26	58.73	0.37	1.42
F_4	89.82	51.42	55.89	48.89*	56.51	57.22	56.47	55.00	1.54	6.27
F_5	86.16	48.21	60.89	60.90	60.64	60.92	60.43*	60.76	0.10	0.35
F_6	85.78	44.82	57.58	57.54	60.84*	57.74	57.66	58.27	0.64	2.47
Over all								58.19	1.19	4.10

Table 3. (Continued).

Varieties/lines and hybrid progenies	Mean total length (µm)		Proportion of the haploid complement occupied by identified chromosomes in five different cells (%)							
	Haploid complement	All identified chr.	Different plates					Statistics		
			A	B	C	D	E	X	S.E.	C.V.
KanXFM-32:										
F_3	94.00	54.07	57.12	57.27	58.10*	57.14	57.89	57.50	0.20	0.80
F_4	103.26	55.62	53.92	54.98*	53.70	53.75	53.03	53.88	0.31	1.30
F_5	110.70	60.16	54.66*	54.16	54.01*	54.45	54.41	54.34	0.11	0.47
F_6	111.61	58.05	50.72*	52.46	52.09	53.09	52.62	52.20	0.40	1.72
Over all								**54.48**	**1.11**	**4.06**
AkXFM-139:										
F_3	119.97	67.44	55.61	54.42	58.30	58.54	54.49	56.27	0.90	3.59
F_4	108.26	61.20	56.42	56.52	56.80	56.46	56.43	56.53	0.07	0.28
F_5	112.86	65.39	58.43	56.31	57.85	58.62	57.27	57.70	0.42	1.62
F_6	124.54	68.01	54.25	53.34	56.32	55.44	54.66	54.80	0.51	2.08
Over all								**56.33**	**0.60**	**2.12**
AnXFM-139:										
F_3	105.74	55.08	52.75	50.59*	52.54	52.70	51.82	52.08	0.41	1.75
F_4	95.55	59.80	63.37	60.17*	64.27	61.48	63.86	62.63	0.78	2.78
F_5	111.89	63.28	57.10	56.52	57.97	56.88	57.80	57.25	0.28	1.07
F_6	105.80	57.61	53.40	52.31*	54.83	55.59	56.56	54.54	0.76	3.11
Over all								**57.51**	**2.48**	**8.62**
KanXFM-139:										
F_3	115.43	66.94	56.10	55.13	61.57	56.47	61.07	58.07	1.35	5.19
F_4	122.96	64.11	51.50	51.74	54.22*	51.56	51.91	52.19	0.51	2.20
F_5	113.65	67.79	59.06	56.88	63.70	57.28	61.80	59.74	1.32	4.92
F_6	82.16	53.18	64.95	63.46*	65.81	64.47	65.14	64.77	0.39	1.35
Over all								**58.69**	**2.59**	**8.84**

and F_5 in Ak X FM-32, F_5 and F_4 in An X FM-32, F_3 and F_6 in Kan X FM-32, F_5 and F_6 in Ak X FM-139, F_4 and F_3 in An X FM-139, and F_6 and F_4 in Kan X FM-139 were found to show the highest and lowest values, respectively. However, no significant difference was observed within the genotypes in every case. The coefficient of variation (C.V.) of this feature within and between the generations of all the crosses and their parents, which indicated that the uniformity of chromosome distribution in the studied cells of all genotypes.

I.5.1.4. Allocation of unidentified chromosomes:

The allocation of unidentified chromosomes of each parental genotypes and their hybrid progenies are given in **Table 4.** All the chromosomes in five haploid complements of each genotype were classified in different morphological categories based on their total length and arm ratio classes. It was a second order classification based on original haploid chromosome's length and arm ratio. The class interval (0.5μ) for the length was chosen arbitrarily, whereas to describe the chromosome types recommendations of Levan *et al.* (1954) was followed for the arm ratio classification within each length class. Thus, two arm ratio classes and several length classes were determined (**Table 4**).

The unidentified chromosomes were distributed to the various morphological categories using probabilistic inferences, specially on the chromosome frequency in a given class per haploid set. The number of unidentified chromosomes allocated to various morphological classes based on the unsaturated frequency of occurrence of points in those classes, due to lack of identifiable chromosomes as in column 6. All chromosomes, identified as well as unidentified, in the haploid

Table 4: Allocation of unidentified chromosomes to different morphological categories in parents and their hybrid progenies of seven crosses of wheat.

PARENTS:

Genotype/ Length class (X)	Arm ratio class (Y)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
AGRANI:							
9.51-10	<1.7	1	0.2				
	>1.7	0	0				
9.01-9.5	<1.7	3	0.6	1(m_1)		1	1
	>1.7	0	0				
8.51-9.0	<1.7	2	0.4	1(m_2)		1	2
	>1.7	0	0				
8.01-8.5	<1.7	8	1.6	1(m_3)	1	2	3, 4
	>1.7	0	0				
7.51-8.0	<1.7	6	1.2	2(m_4)		1	5
	>1.7	0	0				
7.01-7.5	<1.7	8	1.6	2(m_5, m_6)		2	6, 7
	>1.7	0	0				
6.51-7.0	<1.7	8	1.6		2	2	8, 9
	>1.7	1	0.2				
6.01-6.5	<1.7	11	2.2	1(m_7)	1	2	10, 11
	>1.7	1	0.2				
5.51-6.0	<1.7	8	1.6	1(m_8)	1	2	12, 13
	>1.7	2	0.4				
5.01-5.5	<1.7	7	1.4	1(m_9)		1	14
	>1.7	1	0.2				
4.51-5.0	<1.7	10	2.0		2	2	15, 16
	>1.7	1	0.2				
4.01-4.5	<1.7	8	1.6		2	2	17, 18
	>1.7	2	0.4				
3.51-4.0	<1.7	7	1.4	1(m_{10})		2	19, 20
	>1.7	5	1.0	1(sm_1)			
3.01-3.5	<1.7	5	1.0	1(m_{11})			21
	>1.7	0	0				
Total		105	21	12	9	21	

Table 4: (Continued).

Genotype/ Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
AKBAR:							
8.51-9.0	<1.7	2	0.4	1(m_1)		1	1
	>1.7	2	0.4				
8.01-8.5	<1.7	6	1.2		1	1	2
	>1.7	2	0.4				
7.51-8.0	<1.7	8	1.6	4(m_2..m_5)		4	3, 4, 5,
	>1.7	3	0.6				6
7.01-7.5	<1.7	3	0.6			1	7
	>1.7	4	0.8		1		
6.51-7.0	<1.7	2	0.4	1(m_6)		2	8, 9
	>1.7	5	1.0	1(sm_1)			
6.01-6.5	<1.7	9	1.8		2	2	10, 11
	>1.7	2	0.4				
5.51-6.0	<1.7	1	0.2			1	12
	>1.7	7	1.4		1		
5.01-5.5	<1.7	2	0.4	2(sm_2,		3	13, 14,
	>1.7	13	2.6	sm_3)	1		15
4.51-5.0	<1.7	8	1.6	1(m_7)		4	16, 17
	>1.7	13	2.6		3		18, 19
4.01-4.5	<1.7	10	2.0	1(m_8)	1	2	20, 21
	>1.7	0	0				
3.51-4.0	<1.7	3	0.6				
	>1.7	0	0				
Total		105	21	11	10	21	

Table 4: (Continued).

Genotype/ Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromo-some number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
ANANDA:							
9.01-9.5	<1.7	1	0.2				
	>1.7	2	0.4				
8.51-9.0	<1.7	7	1.4	$1(m_1)$		1	1
	>1.7	0	0				
8.01-8.5	<1.7	8	1.6		2	2	2, 3
	>1.7	0	0				
7.51-8.0	<1.7	6	1.2	$1(m_2)$		1	4
	>1.7	0	0				
7.01-7.5	<1.7	5	1.0	$1(m_3)$		1	5
	>1.7	0	0				
6.51-7.0	<1.7	3	0.6		1	2	6, 7
	>1.7	5	1.0	$1(sm_1)$			
6.01-6.5	<1.7	10	2.0	$1(m_4)$	1	2	8, 9
	>1.7	2	0.4				
5.51-6.0	<1.7	10	2.0	$2(m_5, m_6)$		3	10, 11,
	>1.7	5	1.0		1		12
5.01-5.5	<1.7	10	2.0		2	3	13, 14,
	>1.7	3	0.6		1		15
4.51-5.0	<1.7	10	2.0	$1(m_7)$	1	3	16, 17,
	>1.7	4	0.8	$1(sm_2)$			18
4.01-4.5	<1.7	5	1.0	$1(m_8)$		1	19
	>1.7	1	0.2				
3.51-4.0	<1.7	7	1.4	$2(m_9, m_{10})$		2	20, 21
	>1.7	1	0.2				
Total		105	21	12	9	21	

Table 4: (Continued).

Genotype/ Length class (X)	Arm ratio class (Y)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
KANCHAN:							
6.51-7.0	<1.7	15	3.0	1(m_1)	2	3	1, 2, 3
	>1.7	1	0.2				
6.01-6.5	<1.7	15	3.0		3	3	4, 5, 6
	>1.7	3	0.6				
5.51-6.0	<1.7	9	1.8	1(m_2)	1	3	7, 8, 9
	>1.7	5	1.0		1		
5.01-5.5	<1.7	5	1.0	1(m_3)		1	10
	>1.7	2	0.4				
4.51-5.0	<1.7	15	3.0	1(m_4)	2	4	11, 12,
	>1.7	5	1.0		1		13, 14
4.01-4.5	<1.7	6	1.2	3(sm_1,		3	15, 16,
	>1.7	3	0.6	m_5, m_6)			17
3.51-4.0	<1.7	9	1.8	2(sm_2, m_7)	1	3	18, 19,
	>1.7	7	1.4				20
3.01-3.5	<1.7	0	0	1(sm_3)		1	21
	>1.7	5	1.0				
Total		105	21	10	11	21	

Table 4: (Continued).

Genotype/ Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromo-some number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
FM-32:							
8.01-8.5	<1.7	1	0.2				
	>1.7	0	0				
7.51-8.0	<1.7	5	1.0	1(m_1)	0	1	1
	>1.7	0	0				
7.01-7.5	<1.7	10	2.0	3(m_2, m_3,	0	3	2, 3, 4
	>1.7	1	0.2	m_4)			
6.51-7.0	<1.7	5	1.0		1	1	5
	>1.7	0	0				
6.01-6.5	<1.7	14	2.8	2(m_5,sm_1)	1	3	6, 7, 8
	>1.7	5	1.0				
5.51-6.0	<1.7	7	1.4	2(m_6,m_7)		3	9, 10,
	>1.7	5	1.0		1		11
5.01-5.5	<1.7	9	1.8		2	3	12, 13,
	>1.7	6	1.2		1		14
4.51-5.0	<1.7	4	0.8	1(m_8)		2	15, 16
	>1.7	5	1.0		1		
4.01-4.5	<1.7	13	2.6	1(sm_2)	2	3	17, 18,
	>1.7	1	0.2				19
3.51-4.0	<1.7	9	1.8		1	1	20
	>1.7	0	0				
3.01-3.5	<1.7					0	
	>1.7						
2.51-3.0	<1.7	5	1.0	1(m_9)		1	21
	>1.7	0	0				
Total		105	21	11	10	21	

Table 4: (Continued).

Genotype/ Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
FM-139:							
7.51-8.0	<1.7	2	0.4		0	0	
	>1.7	0	0				
7.01-7.5	<1.7	6	1.2	1(sm_1)	1	2	1, 2
	>1.7	5	1.0				
6.51-7.0	<1.7	5	1.0	1(m_1)		2	3, 4
	>1.7	4	0.8		1		
6.01-6.5	<1.7	6	1.2	2(m_2,sm_2)		2	5, 6
	>1.7	4	0.8				
5.51-6.0	<1.7	10	2.0	2(m_3,m_4)		2	7, 8
	>1.7	1	0.2				
5.01-5.5	<1.7	7	1.4	2(m_5,sm_3)		2	9, 10
	>1.7	6	1.2				
4.51-5.0	<1.7	8	1.6		2	2	11, 12
	>1.7	0	0				
4.01-4.5	<1.7	8	1.6	1(sm_4)	2	3	13, 14,
	>1.7	5	1.0				15
3.51-4.0	<1.7	10	2.0	1(sm_5)	2	3	16, 17,
	>1.7	3	0.6				18
3.01-3.5	<1.7	6	1.2	1(sm_6)	1	2	19, 20
	>1.7	5	1.0				
2.51-3.0	<1.7	3	0.6		1	1	21
	>1.7	1	0.2				
Total		105	21	11	10	21	

Table 4. (Continued).

Table 4. (Continued).

1. Ag X FM-32:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
7.51-8.0	<1.7	10	2.0	2(m_1,m_2)		2	1, 2
	>1.7	0	0			0	
7.01-7.5	<1.7	10	2.0	2(m_3,m_4)		2	3, 4
	>1.7	7	1.4	1(sm_1)	0	1	5
6.51-7.0	<1.7	12	2.4		2	2	6, 7
	>1.7	4	0.8	1(sm_2)		1	8
6.01-6.5	<1.7	5	1.0		1	1	9
	>1.7	10	2.0		2	2	10, 11
5.51-6.0	<1.7	13	2.6	1(m_5)	1	2	12, 13
	>1.7	4	0.8	1(sm_3)		1	14
5.01-5.5	<1.7	13	2.6		3	3	15, 16 17
	>1.7	0	0			0	
4.51-5.0	<1.7	3	0.6		1	1	18
	>1.7	0	0			0	
4.01-4.5	<1.7	9	1.8	2(m_6,m_7)		2	19, 20
	>1.7	0	0			0	
3.51-4.0	<1.7	5	1.0	1(m_8)		1	21
	>1.7	0	0			0	
Total		105	21	11	10	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
7.01-7.5	<1.7	1	0.2		0	0	
	>1.7	0	0			0	
6.51-7.0	<1.7	8	1.6	2(m_1, m_2)		2	1, 2
	>1.7	0	0			0	
6.01-6.5	<1.7	15	3.0		3	3	3, 4, 5
	>1.7	2	0.4	1(sm_1)		1	6
5.51-6.0	<1.7	10	2.0	1(m_3)	1	2	7, 8
	>1.7	5	1.0	1(sm_2)		1	9
5.01-5.5	<1.7	13	2.6		2	2	10, 11
	>1.7	5	1.0	1(sm_3)		1	12
4.51-5.0	<1.7	22	4.4		4	4	13, 14, 15, 16
	>1.7	3	0.6	1(sm_4)		1	17
4.01-4.5	<1.7	11	2.2		2	2	18, 19
	>1.7	5	1.0	1(sm_5)		1	20
3.51-4.0	<1.7	4	0.8	1(m_4)		1	21
	>1.7	0	0			0	
3.01-3.5	<1.7	1	0.2		0	0	
	>1.7	0	0			0	
Total		105	21	9	12	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
7.01-7.5	<1.7	10	2.0	2(m_1, m_2)		2	1, 2
	>1.7	0	0			0	
6.51-7.0	<1.7	5	1.0	1(m_3)		1	3
	>1.7	0	0			0	
6.01-6.5	<1.7	11	2.2		2	2	4, 5
	>1.7	6	1.2	1(sm_1)	0	1	6
5.51-6.0	<1.7	18	3.6	1(m_4)	3	4	7, 8, 9, 10
	>1.7	4	0.8	1(sm_2)		1	11
5.01-5.5	<1.7	11	2.2		2	2	12, 13
	>1.7	4	0.8	1(sm_3)		1	14
4.51-5.0	<1.7	9	1.8	1(m_5)	1	2	15, 16
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	10	2.0		2	2	17, 18
	>1.7	1	0.2		0	0	
3.51-4.0	<1.7	2	0.4		0	0	
	>1.7	7	1.4	2(sm_4, sm_5)		2	19, 20
3.01-3.5	<1.7	0	0			0	
	>1.7	0	0			0	
2.51-3.0	<1.7	5	1.0	1(m_6)		1	21
	>1.7	0	0			0	
Total		105	21	11	10	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
6.51-7.0	<1.7	8	1.6	1(m_1)	1	2	1, 2
	>1.7	0	0			0	
6.01-6.5	<1.7	3	0.6		1	1	3
	>1.7	8	1.6		2	2	4, 5
5.51-6.0	<1.7	9	1.8	2(m_2,m_3)		2	6, 7
	>1.7	2	0.4		0	0	
5.01-5.5	<1.7	10	2.0		2	2	8, 9
	>1.7	0	0			0	
4.51-5.0	<1.7	7	1.4	1(m_4)	0	1	10
	>1.7	7	1.4		1	1	11
4.01-4.5	<1.7	5	1.0		1	1	12
	>1.7	3	0.6	1(sm_1)		1	13
3.51-4.0	<1.7	13	2.6	2(m_5,m_6)	0	2	14, 15
	>1.7	1	0.2		0	0	
3.01-3.5	<1.7	13	2.6	1(m_7)	1	2	16, 17
	>1.7	1	0.2	1(sm_2)		1	18
2.51-3.0	<1.7	14	2.8	1(m_8)	2	3	19, 20, 21
	>1.7	1	0.2		0	0	
Total		105	21	10	11	21	

Table 4. (continued).

2. Ak X FM-32:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
7.51-8.0	<1.7	5	1.0	1(m_1)		1	1
	>1.7	0	0			0	
7.01-7.5	<1.7	9	1.8	2(m_2,m_3)		2	2, 3
	>1.7	0	0			0	
6.51-7.0	<1.7	4	0.8	1(m_4)		1	4
	>1.7	2	0.4		0	0	
6.01-6.5	<1.7	10	2.0	1(m_5)	1	2	5, 6
	>1.7	10	2.0	1(sm_1)	1	2	7, 8
5.51-6.0	<1.7	19	3.8	1(m_6)	3	4	9, 10, 11, 12
	>1.7	1	0.2		0	0	
5.01-5.5	<1.7	8	1.6		2	2	13, 14
	>1.7	12	2.4	2(sm_2,sm_3)	0	2	15, 16
4.51-5.0	<1.7	0	0			0	
	>1.7	15	3.0	1(sm_4)	2	3	17, 18, 19
4.01-4.5	<1.7	5	1.0	1(m_7)		1	20
	>1.7	5	1.0	1(sm_5)		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
6.51-7.0	<1.7	10	2.0	1(m_1)	1	2	1, 2
	>1.7	0	0			0	
6.01-6.5	<1.7	11	2.2		2	2	3, 4
	>1.7	4	0.8	1(sm_1)		1	5
5.51-6.0	<1.7	6	1.2	1(m_2)	0	1	6
	>1.7	9	1.8	2(sm_2,sm_3)		2	7, 8
5.01-5.5	<1.7	14	2.8	1(m_3)	2	3	9, 10, 11
	>1.7	5	1.0		1	1	12
4.51-5.0	<1.7	10	2.0		2	2	13, 14,
	>1.7	12	2.4	2(sm_4,st_1)	0	2	15, 16
4.01-4.5	<1.7	2	0.4		0	0	
	>1.7	5	1.0		1	1	17
3.51-4.0	<1.7	7	1.4	2(m_4,m_5)		2	18, 19
	>1.7	4	0.8	1(sm_5)		1	20
3.01-3.5	<1.7	2	0.4		0	0	
	>1.7	4	0.8	1(sm_6)		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
6.51-7.0	<1.7	5	1.0	1(m_1)		1	1
	>1.7	0	0			0	
6.01-6.5	<1.7	0	0			0	
	>1.7	0	0			0	
5.51-6.0	<1.7	12	2.4		2	2	2, 3
	>1.7	4	0.8	1(sm_1)		1	4
5.01-5.5	<1.7	18	3.6		4	4	5, 6, 7, 8
	>1.7	5	1.0	1(sm_2)		1	9
4.51-5.0	<1.7	13	2.6		2	2	10, 11
	>1.7	7	1.4	2(sm_3,st_1)		2	12, 13
4.01-4.5	<1.7	5	1.0		1	1	14
	>1.7	7	1.4		1	1	15
3.51-4.0	<1.7	5	1.0	1(m_2)		1	16
	>1.7	5	1.0	1(st_2)		1	17
3.01-3.5	<1.7	11	2.2	2(m_3,m_4)	0	2	18, 19
	>1.7	2	0.4	1(sm_4)		1	20
2.51-3.0	<1.7	0	0			0	
	>1.7	6	1.2	1(sm_5)	0	1	21
Total		105	21	11	10	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
6.51-7.0	<1.7	4	0.8	$1(m_1)$		1	1
	>1.7	0	0			0	
6.01-6.5	<1.7	4	0.8		1	1	2
	>1.7	0	0			0	
5.51-6.0	<1.7	9	1.8	$1(m_2)$	1	2	3, 4
	>1.7	2	0.4	$1(sm_1)$		1	5
5.01-5.5	<1.7	13	2.6		2	2	6, 7
	>1.7	0	0			0	
4.51-5.0	<1.7	27	5.4		5	5	8,9,10, 11,12
	>1.7	1	0.2		0	0	
4.01-4.5	<1.7	7	1.4	$1(m_3)$	0	1	13
	>1.7	10	2.0	$2(sm_2, st_1)$		2	14,15
3.51-4.0	<1.7	8	1.6	$1(m_4)$	0	1	16
	>1.7	5	1.0	$1(st_2)$		1	17
3.01-3.5	<1.7	10	2.0	$3(m_5, m_6, m_7)$		3	18, 19, 20
	>1.7	0	0			0	
2.51-3.0	<1.7	1	0.2		0	0	
	>1.7	4	0.8	$1(sm_3)$		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

3. An X FM-32.

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
6.51-7.0	<1.7	4	0.8		1	1	1
	>1.7	0	0			0	
6.01-6.5	<1.7	10	2.0	$2(m_1, m_2)$		2	2, 3
	>1.7	0	0			0	
5.51-6.0	<1.7	10	2.0	$1(m_3)$	1	2	4, 5
	>1.7	1	0.2		0	0	
5.01-5.5	<1.7	20	4.0	$3(m_4, m_5, m_6)$	1	4	6, 7, 8, 9
	>1.7	1	0.2		0	0	
4.51-5.0	<1.7	0	0		0	0	
	>1.7	4	0.8	$1(sm_1)$		1	10
4.01-4.5	<1.7	4	0.8		1	1	11
	>1.7	6	1.2		1	1	12
3.51-4.0	<1.7	13	2.6	$2(m_7, m_8)$	1	3	13, 14, 15
	>1.7	1	0.2		0	0	
3.01-3.5	<1.7	19	3.8	$1(m_9)$	3	4	16, 17, 18, 19
	>1.7	0	0			0	
2.51-3.0	<1.7	7	1.4	$1(m_{10})$	0	1	20
	>1.7	0				0	
2.01-2.5	<1.7	3	0.6	$1(m_{11})$		1	21
	>1.7	2	0.4		0	0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
6.51-7.0	<1.7	4	0.8	1(m_1)		1	1
	>1.7	0	0			0	
6.01-6.5	<1.7	5	1.0	1(m_2)		1	2
	>1.7	0	0			0	
5.51-6.0	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
5.01-5.5	<1.7	13	2.6	1(m_3)	1	2	3, 4
	>1.7	3	0.6	1(sm_1)		1	5
4.51-5.0	<1.7	15	3.0		3	3	6, 7,8
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	9	1.8	1(m_4)	1	2	9, 10
	>1.7	9	1.8	2(sm_2,sm_3)		2	11, 12
3.51-4.0	<1.7	5	1.0		1	1	13
	>1.7	16	3.2		3	3	14, 15, 16
3.01-3.5	<1.7	11	2.2	3(m_5,m_6,m_7)		3	17, 18, 19
	>1.7	2	0.4		0	0	
2.51-3.0	<1.7	1	0.2	1(st_1)		1	20
	>1.7	3	0.6		0	0	
2.01-2.5	<1.7	4	0.8	1(m_8)		1	21
	>1.7	1	0.2		0	0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
6.51-7.0	<1.7	4	0.8	1(m_1)		1	1
	>1.7	0	0			0	
6.01-6.5	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
5.51-6.0	<1.7	6	1.2	1(m_2)		1	2
	>1.7	0	0			0	
5.01-5.5	<1.7	12	2.4	1(m_3)	1	2	3, 4
	>1.7	0	0			0	
4.51-5.0	<1.7	0	0			0	
	>1.7	6	1.2		1	1	5
4.01-4.5	<1.7	6	1.2	1(m_4)		1	6
	>1.7	18	3.6	5(sm_1, sm_2, sm_3, sm_4, sm_5)		5	7, 8,9, 10, 11
3.51-4.0	<1.7	15	3.0	1(m_5)	2	3	12, 13, 14
	>1.7	0	0			0	
3.01-3.5	<1.7	21	4.2		4	4	15, 16, 17,18
	>1.7	9	1.8	1(sm_6)	1	2	19, 20
2.51-3.0	<1.7	2	0.4			0	
	>1.7	0	0		0	0	
2.01-2.5	<1.7	4	0.8	1(m_6)		1	21
	>1.7	0	0			0	
Total		105	21	12	9	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
6.01-6.5	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
5.51-6.0	<1.7	7	1.4		1	1	1
	>1.7	2	0.4	1(sm_1)		1	2
5.01-5.5	<1.7	12	2.4	3(m_1, m_2, m_3)		3	3, 4, 5
	>1.7	1	0.2		0	0	
4.51-5.0	<1.7	15	3.0	1(m_4)	2	3	6, 7, 8
	>1.7	6	1.2		1	1	9
4.01-4.5	<1.7	8	1.6	1(m_5)	1	2	10, 11
	>1.7	15	3.0	1(st_1)	2	3	12, 13, 14
3.51-4.0	<1.7	17	3.4	1(m_6)	2	3	15, 16, 17
	>1.7	2	0.4		0	0	
3.01-3.5	<1.7	4	0.8	1(m_7)		1	18
	>1.7	4	0.8	1(sm_2)		1	19
2.51-3.0	<1.7	5	1.0	1(m_8)		1	20
	>1.7	0	0			0	
		0	0			0	
		5	1.0	1(sm_3)		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

4. Kan X FM-32:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_1:							
6.01-6.5	<1.7	5	1.0	1(m_1)		1	1
	>1.7	0	0			0	
5.51-6.0	<1.7	6	1.2	1(m_2)	0	1	2
	>1.7	4	0.8	1(sm_1)		1	3
5.01-5.5	<1.7	15	3.0		3	3	4, 5, 6
	>1.7	3	0.6	1(sm_2)		1	7
4.51-5.0	<1.7	5	1.0		1	1	8
	>1.7	7	1.4		1	1	9
4.01-4.5	<1.7	10	2.0	2(m_3,m_4)		2	10, 11
	>1.7	10	2.0	2(sm_3,sm_4)		2	12, 13
3.51-4.0	<1.7	11	2.2	1(m_5)	1	2	14, 15,
	>1.7	16	3.2	1(sm_5)	2	3	16, 17, 18
3.01-3.5	<1.7	3	0.6		1	1	19
	>1.7	8	1.6	2(sm_6,sm_7)		2	20, 21
2.51-3.0	<1.7	0	0			0	
	>1.7	2	0.4		0	0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
7.01-7.5	<1.7	3	0.6	1(m_1)		1	1
"	>1.7	1	0.2		0	0	
6.51-7.0	<1.7	5	1.0	1(m_2)		1	2
	>1.7	1	0.2		0	0	
6.01-6.5	<1.7	5	1.0		1	1	3
	>1.7	0	0			0	
5.51-6.0	<1.7	12	2.4		2	2	4, 5
	>1.7	5	1.0		1	1	6
5.01-5.5	<1.7	9	1.8	1(m_3)	1	2	7, 8
	>1.7	9	1.8	2(sm_1,sm_2)		2	9, 10
4.51-5.0	<1.7	16	3.2		3	3	11, 12, 13
	>1.7	5	1.0		1	1	14
4.01-4.5	<1.7	6	1.2	1(m_4)		1	15
	>1.7	8	1.6	2(sm_3,sm_4)		2	16, 17
3.51-4.0	<1.7	6	1.2	1(m_5)	0	1	18
	>1.7	0	0			0	
3.01-3.5	<1.7	4	0.8	1(m_6)		1	19
	>1.7	5	1.0	1(sm_5)		1	20
2.51-3.0	<1.7	5	1.0	1(m_8)		1	21
	>1.7	0	0			0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
7.01-7.5	<1.7	5	1.0	1(m_1)		1	1
	>1.7	0				0	
6.51-7.0	<1.7	10	2.0	2(m_2,m_3)		2	2, 3
	>1.7	0	0			0	
6.01-6.5	<1.7	6	1.2	1(m_4)	0	1	4
	>1.7	9	1.8	2(sm_1,sm_2)		2	5, 6
5.51-6.0	<1.7	13	2.6		3	3	7, 8, 9
	>1.7	2	0.4		0	0	
5.01-5.5	<1.7	18	3.6		4	4	10, 11, 12, 13
	>1.7	5	1.0	1(sm_3)		1	14
4.51-5.0	<1.7	6	1.2	1(m_5)	0	1	15
	>1.7	0	0			0	
4.01-4.5	<1.7	16	3.2		3	3	16, 17, 18
	>1.7	0	0			0	
3.51-4.0	<1.7	1	0.2		0	0	
	>1.7	9	1.8	2(sm_4,st_1)		2	19, 20
3.01-3.5	<1.7	0	0			0	
	>1.7	0	0			0	
2.51-3.0	<1.7	5	1.0	1(m_6)		1	21
	>1.7	0	0			0	
Total		105	21	11	10	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
7.01-7.5	<1.7	6	1.2	1(m_1)	0	1	1
	>1.7	0				0	
6.51-7.0	<1.7	6	1.2	1(m_2)	0	1	2
	>1.7	0				0	
6.01-6.5	<1.7	18	3.6	1(m_3)	3	4	3, 4, 5, 6
	>1.7	0	0			0	
5.51-6.0	<1.7	16	3.2		3	3	7, 8, 9
	>1.7	7	1.4		1	1	10
5.01-5.5	<1.7	16	3.2	2(m_4,m_5)	1	3	11, 12, 13
	>1.7	5	1.0	1(sm_1)		1	14
4.51-5.0	<1.7	2	0.4		0	0	
	>1.7	5	1.0	1(st_1)		1	15
4.01-4.5	<1.7	3	0.6		1	1	16
	>1.7	0				0	
3.51-4.0	<1.7	9	1.8	2(m_6,m_7)		2	17, 18,
	>1.7	6	1.2	2(sm_2,st_2)		2	19, 20
3.01-3.5	<1.7	4	0.8	1(m_8)		1	21
	>1.7	1	0.2		0	0	
2.51-3.0	<1.7	1	0.2		0	0	
	>1.7	0				0	
Total		105	21	12	9	21	

Table 4. (Continued).

5. Ak X FM-139:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
8.01-8.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
7.51-8.0	<1.7	7	1.4		1	1	1
	>1.7	0				0	
7.01-7.5	<1.7	8	1.6	$2(m_1, m_2)$		2	2, 3
	>1.7	2	0.4		0	0	
6.51-7.0	<1.7	8	1.6	$1(m_3)$	1	2	4, 5
	>1.7	4	0.8	$1(sm_1)$		1	6
6.01-6.5	<1.7	10	2.0	$1(m_4)$	1	2	7, 8
	>1.7	6	1.2	$1(sm_2)$		1	9
5.51-6.0	<1.7	7	1.4		1	1	10
	>1.7	7	1.4		1	1	11
5.01-5.5	<1.7	7	1.4		1	1	12
	>1.7	10	2.0	$3(sm_3, sm_4, sm_5)$		3	13, 14, 15
4.51-5.0	<1.7	6	1.2		1	1	16
	>1.7	4	0.8		1	1	17
4.01-4.5	<1.7	4	0.8		1	1	18
	>1.7	4	0.8	$1(sm_6)$		1	19
3.51-4.0	<1.7	0				0	
	>1.7	4	0.8	$1(sm_7)$		1	20
3.01-3.5	<1.7	2	0.4		0	0	
	>1.7	1	0.2		0	0	
2.51-3.0	<1.7	3	0.6	$1(m_5)$		1	21
	>1.7	0				0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
8.01-8.5	<1.7	3	0.6		1	1	1
	>1.7	0				0	
7.51-8.0	<1.7	5	1.0	2(m_1, m_2)		2	2, 3
	>1.7	0				0	
7.01-7.5	<1.7	3	0.6		1	1	4
"	>1.7	0				0	
6.51-7.0	<1.7	5	1.0		1	1	5
	>1.7	2	0.4		0	0	
6.01-6.5	<1.7	7	1.4	1(m_3)		1	6
	>1.7	3	0.6	1(sm_1)		1	7
5.51-6.0	<1.7	10	2.0		2	2	8, 9
	>1.7	7	1.4	1(sm_2)		1	10
5.01-5.5	<1.7	9	1.8	1(m_4)	1	2	11, 12
	>1.7	7	1.4		1	1	13
4.51-5.0	<1.7	7	1.4	1(m_5)		1	14
	>1.7	5	1.0	1(sm_3)		1	15
4.01-4.5	<1.7	7	1.4	1(m_6)		1	16
	>1.7	0				0	
3.51-4.0	<1.7	7	1.4		1	1	17
	>1.7	0	0			0	
3.01-3.5	<1.7	5	1.0	1(sm_4)		1	18
	>1.7	3	0.6		1	1	19
2.51-3.0	<1.7	5	1.0	1(m_7)		1	20
	>1.7	1	0.2		0	0	
2.01-2.5	<1.7	0				0	
	>1.7	4	0.8	1(sm_5)		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
8.01-8.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
7.51-8.0	<1.7	4	0.8	1(m_1)		1	1
	>1.7	0				0	
7.01-7.5	<1.7	5	1.0	2(m_2, m_3)		2	2, 3
	>1.7	2	0.4		0	0	
6.51-7.0	<1.7	4	0.8		1	1	4
	>1.7	8	1.6	2(sm_1, sm_2)		2	5, 6
6.01-6.5	<1.7	1	0.2	1(m_4)		1	7
	>1.7	7	1.4		1	1	8
5.51-6.0	<1.7	7	1.4		1	1	9
	>1.7	10	2.0		2	2	10, 11
5.01-5.5	<1.7	7	1.4	1(m_5)		1	12
	>1.7	12	2.4		2	2	13, 14
4.51-5.0	<1.7	8	1.6	2(m_6, m_7)		2	15, 16
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	7	1.4		1	1	17
	>1.7	3	0.6		1	1	18
3.51-4.0	<1.7	8	1.6	2(m_8, m_9)		2	19, 20
	>1.7	2	0.4		0	0	
3.01-3.5	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
2.51-3.0	<1.7	0				0	
	>1.7	0				0	
2.01-2.5	<1.7	0				0	
	>1.7	5	1.0	1(sm_3)		1	21
Total		105	21	12	9	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
8.51-9.0	<1.7	1	0.2		0	0	
	>1.7	0				0	
8.01-8.5	<1.7	4	0.8	1(m_1)		1	1
	>1.7	0				0	
7.51-8.0	<1.7	5	1.0	1(m_2)		1	2
	>1.7	2	0.4		0	0	
7.01-7.5	<1.7	4	0.8	1(m_3)		1	3
	>1.7	8	1.6		2	2	4, 5
6.51-7.0	<1.7	4	0.8		1	1	6
	>1.7	10	2.0	1(sm_1)	1	2	7, 8
6.01-6.5	<1.7	5	1.0	1(m_4)		1	9
	>1.7	11	2.2		2	2	10, 11
5.51-6.0	<1.7	4	0.8		1	1	12
	>1.7	10	2.0	1(st_1)	1	2	13, 14
5.01-5.5	<1.7	2	0.4		0	0	
	>1.7	7	1.4		1	1	15
4.51-5.0	<1.7	8	1.6	3(m_5, m_6, m_7)		3	16, 17, 18
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	4	0.8	1(m_8)		1	19
	>1.7	6	1.2	1(st_2)		1	20
3.51-4.0	<1.7	1	0.2		0	0	
	>1.7	2	0.4		0	0	
3.01-3.5	<1.7	0				0	
	>1.7	1	0.2		0	0	
2.51-3.0	<1.7	0			0	0	
	>1.7	4	0.8	1(sm_2)		1	21
Total		105	21	12	9	21	

Table 4. (Continued).

6. An X FM-139:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
8.01-8.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
7.51-8.0	<1.7	5	1.0	$1(m_1)$		1	1
	>1.7	0				0	
7.01-7.5	<1.7	7	1.4	$1(m_2)$		1	2
	>1.7	0				0	
6.51-7.0	<1.7	11	2.2		2	2	3, 4
	>1.7	0				0	
6.01-6.5	<1.7	7	1.4		1	1	5
	>1.7	0				0	
5.51-6.0	<1.7	7	1.4	$1(m_3)$		1	6
	>1.7	1	0.2	$1(sm_1)$		1	7
5.01-5.5	<1.7	7	1.4		1	1	8
	>1.7	1	0.2		0	0	
4.51-5.0	<1.7	7	1.4		1	1	9
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	12	2.4		2	2	10, 11
	>1.7	6	1.2	$3(sm_2, sm_3, sm_4)$		3	12, 13, 14
3.51-4.0	<1.7	6	1.2		1	1	15
	>1.7	7	1.4	$1(sm_5)$		1	16
3.01-3.5	<1.7	6	1.2	$3(m_4, m_5, m_6)$		3	17, 18, 19
	>1.7	5	1.0	$1(sm_6)$		1	20
2.51-3.0	<1.7	5	1.0		1	1	21
	>1.7	1	0.2		0	0	
2.01-2.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
7.01-7.5	<1.7	3	0.6		1	1	1
"	>1.7	0				0	
6.51-7.0	<1.7	5	1.0	$2(m_1, m_2)$		2	2, 3
	>1.7	0				0	
6.01-6.5	<1.7	6	1.2		1	1	4
	>1.7	2	0.4	$1(sm_1)$		1	5
5.51-6.0	<1.7	8	1.6	$2(m_3, m_4)$		2	6, 7
	>1.7	3	0.6	$1(sm_2)$		1	8
5.01-5.5	<1.7	7	1.4		1	1	9
	>1.7	4	0.8		1	1	10
4.51-5.0	<1.7	7	1.4	$1(m_5)$		1	11
	>1.7	2	0.4			0	
4.01-4.5	<1.7	12	2.4		2	2	12, 13
	>1.7	4	0.8	$1(sm_3)$		1	14
3.51-4.0	<1.7	7	1.4	$1(m_6)$		1	15
	>1.7	7	1.4	$1(sm_4)$		1	16
3.01-3.5	<1.7	15	3.0		3	3	17, 18, 19
	>1.7	5	1.0	$1(sm_5)$		1	20
2.51-3.0	<1.7	6	1.2	$1(m_7)$		1	21
	>1.7	2	0.4		0	0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
7.51-8.0	<1.7	2	0.4		0	0	
	>1.7	0				0	
7.01-7.5	<1.7	7	1.4	$1(m_1)$		1	1
	>1.7	1	0.2		0	0	
6.51-7.0	<1.7	5	1.0	$1(m_2$		1	2
	>1.7	0				0	
6.01-6.5	<1.7	12	2.4	$1(m_3)$	2	3	3, 4, 5
	>1.7	8	1.6	$2(sm_1, sm_2)$		2	6, 7
5.51-6.0	<1.7	11	2.2		2	2	8, 9
	>1.7	6	1.2	$1(sm_3)$		1	10
5.01-5.5	<1.7	9	1.8		2	2	11, 12
	>1.7	5	1.0		1	1	13
4.51-5.0	<1.7	7	1.4		1	1	14
	>1.7	6	1.2	$2(st_1, sm_4)$	2	2	15, 16
4.01-4.5	<1.7	7	1.4	$1(m_4)$		1	17
	>1.7	7	1.4	$1(sm_5)$		1	18
3.51-4.0	<1.7	3	0.6	$1(m_5)$		1	19
	>1.7	3	0.6		1	1	20
3.01-3.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
2.51-3.0	<1.7	5	1.0	$1(m_6)$		1	21
	>1.7	0				0	
Total		105	21	12	9	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
8.01-8.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
7.51-8.0	<1.7	5	1.0	$1(m_1)$		1	1
	>1.7	0				0	
7.01-7.5	<1.7	5	1.0	$1(m_2)$		1	2
	>1.7	0	0			0	
6.51-7.0	<1.7	10	2.0	$1(m_3)$	1	2	3, 4
	>1.7	0	0			0	
6.01-6.5	<1.7	9	1.8	$1(m_4)$	1	2	5, 6
	>1.7	1	0.2		0	0	
5.51-6.0	<1.7	7	1.4	$1(m_5)$		1	7
	>1.7	1	0.2		0	0	
5.01-5.5	<1.7	7	1.4		1	1	8
	>1.7	3	0.6	$1(sm_1)$		1	9
4.51-5.0	<1.7	7	1.4		1	1	10
	>1.7	2	0.4	$2(sm_1, st_1)$		2	11, 12
4.01-4.5	<1.7	12	2.4		2	2	13, 14
	>1.7	4	0.8		1	1	15
3.51-4.0	<1.7	10	2.0	$1(m_6)$	1	2	16, 17
	>1.7	6	1.2		1	1	18
3.01-3.5	<1.7	8	1.6	$1(m_7)$	1	2	19, 20
	>1.7	2	0.4	$1(sm_3)$		1	21
2.51-3.0	<1.7	2	0.4		0	0	
	>1.7	1	0.2		0	0	
2.01-2.5	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
Total		105	21	11	10	21	

Table 4. (Continued)

7. Kan X FM-139:

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_3:							
9.01-9.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
8.51-9.0	<1.7	1	0.2		0	0	
	>1.7	0				0	
8.01-8.5	<1.7	3	0.6		1	1	1
	>1.7	0				0	
7.51-8.0	<1.7	6	1.2	1(m_1)		1	2
	>1.7	0				0	
7.01-7.5	<1.7	6	1.2	1(m_2)		1	3
	>1.7	1	0.2		0	0	
6.51-7.0	<1.7	7	1.4	1(m_3)		1	4
	>1.7	3	0.6	1(sm_1)		1	5
6.01-6.5	<1.7	8	1.6		2	2	6, 7
	>1.7	5	1.0		1	1	8
5.51-6.0	<1.7	7	1.4		1	1	9
	>1.7	5	1.0	1(sm_2)		1	10
5.01-5.5	<1.7	7	1.4	1(m_4)		1	11
	>1.7	6	1.2	2(sm_3, sm_4)		2	12, 13
4.51-5.0	<1.7	6	1.2		1	1	14
	>1.7	4	0.8		1	1	15
4.01-4.5	<1.7	7	1.4	2(m_5, m_6)		2	16, 17
	>1.7	5	1.0	1(sm_5)		1	18
3.51-4.0	<1.7	7	1.4		1	1	19
	>1.7	4	0.8	1(sm_6)		1	20
3.01-3.5	<1.7	3	0.6		1	1	21
	>1.7	1	0.2		0	0	
2.51-3.0	<1.7	2	0.4		0	0	
	>1.7	0	0			0	
Total		105	21	12	9	21	

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_4:							
9.51-10.0	<1.7	2	0.4		0	0	
	>1.7	0				0	
9.01-9.5	<1.7	3	0.6	1(m_1)		1	1
	>1.7	0				0	
8.51-9.0	<1.7	3	0.6		1	1	2
	>1.7	1	0.2		0	0	
8.01-8.5	<1.7	4	0.8	1(m_2)		1	3
	>1.7	2	0.4		0	0	
7.51-8.0	<1.7	9	1.8	1(m_3)	1	2	4, 5
	>1.7	2	0.4	1(sm_1)		1	6
7.01-7.5	<1.7	4	0.8		1	1	7
"	>1.7	0				0	
6.51-7.0	<1.7	7	1.4		1	1	8
	>1.7	2	0.4		0	0	
6.01-6.5	<1.7	10	2.0	1(m_4)	1	2	9, 10
	>1.7	5	1.0		1	1	11
5.51-6.0	<1.7	6	1.2		1	1	12
	>1.7	2	0.4		0	0	
5.01-5.5	<1.7	2	0.4	1(m_5)		1	13
	>1.7	2	0.4		0	0	
4.51-5.0	<1.7	2	0.4		0	0	
	>1.7	7	1.4		1	1	14
4.01-4.5	<1.7	2	0.4		0	0	
	>1.7	7	1.4	3(sm_2, sm_3, st_1)		3	15, 16, 17
3.51-4.0	<1.7	7	1.4	1(m_6)		1	18
	>1.7	3	0.6		1	1	19
3.01-3.5	<1.7	7	1.4		1	1	20
	>1.7	0				0	
2.51-3.0	<1.7	4	0.8	1(m_7)		1	21
	>1.7	0				0	
Total		105	21	11	10	21	0

Table 4. (Continued).

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_5:							
8.51-9.0	<1.7	1	02		0	0	
	>1.7	0				0	
8.01-8.5	<1.7	3	0.6		1	1	1
	>1.7	0				0	
7.51-8.0	<1.7	3	0.6		1	1	2
	>1.7	2	0.4		0	0	
7.01-7.5	<1.7	5	1.0	$1(m_1)$		1	3
	>1.7	1	0.2	$1(sm_1)$		1	4
6.51-7.0	<1.7	6	1.2		1	1	5
	>1.7	5	1.0	$1(sm_2)$		1	6
6.01-6.5	<1.7	7	1.4	$1(m_2)$		1	7
	>1.7	5	1.0	$1(sm_3)$		1	8
5.51-6.0	<1.7	6	1.2	$1(m_3)$		1	9
	>1.7	5	1.0		1	1	10
5.01-5.5	<1.7	8	1.6	$1(m_4)$	1	2	11, 12
	>1.7	4	0.8	$1(sm_4)$		1	13
4.51-5.0	<1.7	6	1.2	$1(m_5)$		1	14
	>1.7	7	1.4	$1(sm_5)$		1	15
4.01-4.5	<1.7	6	1.2		1	1	16
	>1.7	5	1.0	$1(st_1)$		1	17
3.51-4.0	<1.7	4	0.8	$1(m_6)$		1	18
	>1.7	2	0.4		0	0	
3.01-3.5	<1.7	8	1.6		2	2	19, 20
	>1.7	0				0	
2.51-3.0	<1.7	5	1.0		1	1	21
	>1.7	0				0	
2.01-2.5	<1.7	1	0.2		0	0	
	>1.7	0				0	
Total		105	21	12	9	21	

Table 4. (Continued)

Length class (X)	Arm ratio class (X)	Number of chromosomes					Assigned chromosome number
		Total in six haploid sets	Mean per haploid set	Identified chromosome with name	Proposed unidentified chromosomes	Total	
F_6:							
7.01-7.5	<1.7	2	0.4		0	0	
	>1.7	0					
6.51-7.0	<1.7	5	1.0	1(m_1)		1	1
	>1.7	0				0	
6.01-6.5	<1.7	6	1.2	1(m_2)		1	2
	>1.7	2	0.4		0	0	
5.51-6.0	<1.7	6	1.2	2(m_3, m_4)		2	3, 4
	>1.7	4	0.8	1(sm_1)		1	5
5.01-5.5	<1.7	1	0.2		0	0	
	>1.7	1	0.2		0	0	
4.51-5.0	<1.7	3	0.6		1	1	6
	>1.7	2	0.4		0	0	
4.01-4.5	<1.7	5	1.0	1(m_5)		1	7
	>1.7	6	1.2	1(sm_2)		1	8
3.51-4.0	<1.7	5	1.0		1	1	9
	>1.7	8	1.6		2	2	10, 11
3.01-3.5	<1.7	5	1.0	1(m_6)		1	12
	>1.7	11	2.2	1(st_1)	1	2	13, 14
2.51-3.0	<1.7	7	1.4		1	1	15
	>1.7	12	2.4	1(sm_3)	1	2	16, 17
2.01-2.5	<1.7	8	1.6	1(m_7)	1	2	18, 19
	>1.7	3	0.6	1(sm_4)		1	20
1.51-2.0	<1.7	0				0	
	>1.7	3	0.6		1	1	21
Total		105	21	12	10	21	

complement were numbered from 1-21 (column 8) following the convention of Rhoades (1955), *i.e.*, in decreasing order of length and increasing order of arm ratio within the length class. Thus, the identity of each chromosome of the haploid complements for all the genotypes might be indicated by assigning the serial number. Then these identity of all the chromosomes were used to propose a 'standard karyotype' for each genotype.

I.5.1.5. Centromeric formulae:

Morphological features of the chromosomes of haploid complements of parental genotypes as well as hybrid progenies were summarized as karyotypic composition and are presented in Table 5. The specific roman number (column 1) and names (column 5) were represented as the identity of all 21 chromosomes for each genotype. The proposed 'centromeric formulae' comprised 19 m + 2 sm in Aghrani, 11 m + 10 sm in Akbar, 17 m + 4 sm in Ananda, 16 m + 5 sm in Kanchan, 16m + 5 sm FM-32 and 14 m + 7 sm in FM-139. In karyotypic composition, more submedian chromosomes were observed in FM-lines compared to those in Bangladeshi varieties except Akbar.

In Ag X FM-32, the F_3 - F_6 progenies were found with 16m + 5sm chromosome to make their haploid complement. In Ak X FM-32, haploid complements were found with 13m + 8sm, 12m n+ 8sm + 1st, 13m + 6sm + 2st and 16m + 3sm + 2st chromosomes for F_3, F_4, F_5 and F_6 progenies, respectively. The centromeric formula for F_3, F_4, F_5 and F_6 of An X FM-32 were found to comprise with 19m + 2sm, 14m + 6sm + 1st, 13m + 8sm and 14m + 6sm + 1st, chromosomes successively. For F_3, F_4, F_5 and F_6 progenies of Kan X FM-32 the centromeric

Table 5: Morphological features of the proposed karyotype in parents and their hybrid progenies of seven crosses of wheat.

PARENTS:

Chro-mosome Number	Aghrani				Akbar			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	9.05	1.18	m	m_1	8.51	1.54	m
II	m_2	8.51	1.01	m		8.01-8.5	>1.7	sm
III		8.01-9.0	<1.7	m	m_2	8.00	1.44	m
IV	m_3	8.02	1.43	m	m_3	8.00	1.44	m
V	m_4	7.73	1.30	m	m_4	7.97	1.68	m
VI	m_5	7.29	1.49	m	m_5	7.59	1.29	m
VII	m_6	7.04	1.29	m		7.01-7.5	>1.7	sm
VIII		6.51-7.0	<1.7	m	sm_1	6.94	1.75	sm
IX		"	"	m	m_6	6.51	1.61	m
X	m_7	6.27	1.64	m		6.01-6.5	<1.7	m
XI		6.01-6.5	<1.7	m		"	"	m
XII	m_8	5.81	1.22	m		5.51-6.0	>1.7	sm
XIII	m_9	5.15	1.61	m	sm_2	5.17	2.14	sm
XIV		4.51-5.0	<1.7	m	sm_3	5.17	2.14	sm
XV		"	"	m		5.01-5.5	>1.7	sm
XVI		4.01-4.5	"	m	m_7	4.74	1.28	m
XVII		"	"	m		4.51-5.0	>1.7	sm
XVIII		"	>1.7	sm		"	"	sm
XIX	m_{10}	3.86	1.35	m		"	"	sm
XX	sm_1	3.63	2.22	sm	m_8	4.46	1.27	m
XXI	m_{11}	3.34	1.12	m		4.01-4.5	<1.7	m
Centromeric formula: 19 m + 2 sm					Centromeric formula: 11 m + 10sm			

Table 5: (Continued).

Chromosome Number	Ananda				Kanchan			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	8.51	1.44	m	m_1	6.51	1.65	m
II		8.01-8.5	<1.7	m		6.51-7.0	<1.7	m
III		"	"	m		"	"	m
IV	m_2	7.99	1.29	m		6.01-6.5	"	m
V	m_3	7.20	1.01	m		"	"	m
VI		6.51-7.0	<1.7	m		"	"	m
VII	sm_1	6.74	2.16	sm	m_2	5.82	1.63	m
VIII	m_4	6.45	1.53	m		5.51-6.0	<1.7	m
IX		6.01-6.5	<1.7	m		"	>1.7	sm
X	m_5	5.95	1.48	m	m_3	5.33	1.21	m
XI	m_6	5.83	1.61	m	m_4	4.62	1.33	m
XII		5.51-6.0	>1.7	sm		4.51-5.0	<1.7	m
XIII		5.01-5.5	<1.7	m		"	"	m
XIV		"	"	m		"	>1.7	sm
XV		"	>1.7	sm	sm_1	4.40	2.02	sm
XVI	m_7	4.95	1.28	m	m_5	4.18	1.18	m
XVII		4.51-5.0	<1.7	m	m_6	4.18	1.28	m
XVIII	sm_2	4.80	1.86	sm	m_7	3.70	1.61	m
XIX	m_8	4.45	1.38	m	sm_2	3.63	2.46	sm
XX	m_9	3.94	1.66	m		3.51-4.0	<1.7	m
XXI	m_{10}	3.60	1.15	m	sm_3	3.30	2.21	sm
Centromeric formula: 17 m + 4 sm					Centromeric formula: 16 m + 5sm			

Table 5: (Continued).

Chromosome Number	Ananda				Kanchan			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	8.51	1.44	m	m_1	6.51	1.65	m
II		8.01-8.5	<1.7	m		6.51-7.0	<1.7	m
III		"	"	m		"	"	m
IV	m_2	7.99	1.29	m		6.01-6.5	"	m
V	m_3	7.20	1.01	m		"	"	m
VI		6.51-7.0	<1.7	m		"	"	m
VII	sm_1	6.74	2.16	sm	m_2	5.82	1.63	m
VIII	m_4	6.45	1.53	m		5.51-6.0	<1.7	m
IX		6.01-6.5	<1.7	m		"	>1.7	sm
X	m_5	5.95	1.48	m	m_3	5.33	1.21	m
XI	m_6	5.83	1.61	m	m_4	4.62	1.33	m
XII		5.51-6.0	>1.7	sm		4.51-5.0	<1.7	m
XIII		5.01-5.5	<1.7	m		"	"	m
XIV		"	"	m		"	>1.7	sm
XV		"	>1.7	sm	sm_1	4.40	2.02	sm
XVI	m_7	4.95	1.28	m	m_5	4.18	1.18	m
XVII		4.51-5.0	<1.7	m	m_6	4.18	1.28	m
XVIII	sm_2	4.80	1.86	sm	m_7	3.70	1.61	m
XIX	m_8	4.45	1.38	m	sm_2	3.63	2.46	sm
XX	m_9	3.94	1.66	m		3.51-4.0	<1.7	m
XXI	m_{10}	3.60	1.15	m	sm_3	3.30	2.21	sm
Centromeric formula: 17 m + 4 sm					Centromeric formula: 16 m + 5sm			

Table 5: (Continued).

Chromosome Number	FM-32				FM-139			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.94	1.30	m	sm_1	7.28	1.82	sm
II	m_2	7.24	1.34	m		7.01-7.5	<1.7	m
III	m_3	"	"	m	m_1	6.71	1.17	m
IV	m_4	7.15	1.31	m		6.51-7.0	>1.7	sm
V		6.51-7.0	<1.7	m	sm_2	6.50	2.02	sm
VI	m_5	6.32	1.65	m	m_2	6.17	1.34	m
VII	sm_1	6.26	2.22	sm	m_3	5.79	1.14	m
VIII		6.01-6.5	<1.7	m	m_4	5.64	1.64	m
IX	m_6	5.74	1.36	m	m_5	5.21	1.17	m
X	m_7	"	"	m	sm_3	5.21	1.80	sm
XI		5.51-6.0	>1.7	sm		4.51-5.0	<1.7	m
XII		5.01-5.5	<1.7	m		"	"	m
XIII		"	>1.7	sm	sm_4	4.29	1.80	sm
XIV	m_8	4.85	1.29	m		4.01-4.5	<1.7	m
XV		4.51-5.0	>1.7	sm		"	"	m
XVI	sm_2	4.40	1.70	sm	sm_5	3.70	2.09	sm
XVII		4.01-4.5	<1.7	m		3.51-4.0	<1.7	m
XVIII		"	"	m		"	"	m
XIX		3.51-4.0	<1.7	m	sm_6	3.05	1.76	sm
XX		"	"	m		3.01-3.5	<1.7	m
XXI	m_9	2.90	1.14	m		2.51-3.0	<1.7	m
Centromeric formula: 16m + 5sm					Centromeric formula: 14m + 7sm			

Table 5. (Continued)

1. Ag X FM-32:

Chromosome Number	F_3				F_4			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.7	1.20	m	m_1	6.99	1.25	m
II	m_2	7.7	1.20	m	m_2	6.53	1.20	m
III	m_3	7.48	1.36	m		6.01-6.5	<1.7	m
IV	m_4	7.48	1.36	m		"	"	m
V	sm_1	7.26	1.95	sm		"	"	m
VI		6.51-7.0	<1.7	m	sm_1	6.50	1.74	sm
VII		"	"	m	sm_2	5.75	2.02	sm
VIII	sm_2	6.30	1.87	sm		5.51-6.0	<1.7	m
IX		6.01-6.5	<1.7	m	m_3	5.59	1.47	m
X		"	>1.7	sm		5.01-5.5	<1.7	m
XI		"	"	sm		"	"	m
XII	m_5	5.80	1.29	m	sm_3	5.33	1.89	sm
XIII		5.51-6.0	<1.7	m		4.51-5.0	<1.7	m
XIV	sm_3	5.75	1.73	sm		"	"	m
XV		5.01-5.5	<1.7	m		"	"	m
XVI		"	"	m		"	"	m
XVII		"	"	m	sm_4	4.61	1.83	sm
XVIII		4.51-5.0	"	m		4.01-4.5	<1.7	m
XIX	m_6	4.48	1.15	m		"	"	m
XX	m_7	4.40	1.44	m	sm_5	4.12	2.19	sm
XXI	m_8	3.72	1.34	m	m_4	3.60	1.33	m
Centromeric formula: 16 m + 5 sm					Centromeric formula: 16 m + 5 sm			

Table 5: (Continued).

Chro-mosome Number	F_5				F_6			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.28	1.10	m	m_1	6.78	1.20	m
II	m_2	7.21	1.39	m		6.51-7.0	<1.7	m
III	m_3	6.80	1.30	m		6.01-6.5	"	m
IV		6.01-6.5	<1.7	m		"	>1.7	sm
V		"	"	m		"	"	sm
VI	sm_1	6.35	1.87	sm	m_2	5.76	1.69	m
VII	m_4	5.96	1.12	m	m_3	5.73	1.13	m
VIII		5.51-6.0	<1.7	m		5.01-5.5	<1.7	m
IX		"	"	m		"	"	m
X		"	"	m	m_4	4.68	1.14	m
XI	sm_2	5.69	1.70	sm		4.51-5.0	>1.7	sm
XII		5.01-5.5	<1.7	m		4.01-4.5	<1.7	m
XIII		"	"	m	sm_1	4.47	1.96	sm
XIV	sm_3	5.07	2.27	sm	m_5	4.00	1.22	m
XV	m_5	4.65	1.25	m	m_6	3.74	1.45	m
XVI		4.51-5.0	<1.7	m	m_7	3.36	1.23	m
XVII		4.01-4.5	"	m		3.01-3.5	<1.7	m
XVIII		"	"	m	sm_2	3.02	1.71	sm
XIX	sm_4	3.89	1.74	sm	m_8	2.72	1.32	m
XX	sm_5	3.89	1.74	sm		2.51-3.0	<1.7	m
XXI	m_6	2.77	1.22	m		"	"	m
Centromeric formula: 16 m + 5 sm					Centromeric formula: 16 m +5m			

Table 5. (Continued).

2. Ak X FM-32:

Chromosome Number	F_3				F_4			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.69	1.16	m	m_1	6.80	1.17	m
II	m_2	7.11	1.14	m		6.51-7.0	<1.7	m
III	m_3	7.09	1.40	m		6.01-6.5	"	m
IV	m_4	6.73	1.68	m		"	"	m
V	sm_1	6.31	1.90	sm	sm_1	6.18	1.76	sm
VI	m_5	6.27	1.36	m	m_2	5.82	1.10	m
VII		6.01-6.5	<1.7	m	sm_2	5.81	1.77	sm
VIII		"	>1.7	sm	sm_3	5.80	2.22	sm
IX	m_6	5.96	1.36	m	m_3	5.34	1.14	m
X		5.51-6.0	<1.7	m		5.01-5.5	<1.7	m
XI		"	"	m		"	"	m
XII		"	"	m		"	>1.7	sm
XIII		5.01-5.5	<1.7	m		4.51-5.0	<1.7	m
XIV		"	"	m		"	"	m
XV	sm_2	5.09	1.74	sm	sm_4	4.55	1.80	sm
XVI	sm_3	5.09	2.27	sm	st_1	4.53	3.10	st
XVII	sm_4	4.70	1.93	sm		4.01-4.5	>1.7	sm
XVIII		4.51-5.0	>1.7	sm	m_4	3.95	1.61	m
XIX		"	"	sm	sm_5	3.95	1.70	sm
XX	m_7	4.21	1.14	m	m_5	3.63	1.14	m
XXI	sm_5	4.19	1.86	sm	sm_6	3.37	1.83	sm
Centromeric formula: 13 m + 8 sm					C. formula: 12 m + 8 sm + 1 st			

Table 5. (Continued).

Chromosome Number	F_5				F_6			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	6.57	1.14	m	m_1	6.52	1.18	m
II		5.51-6.0	<1.7	m		6.01-6.5	<1.7	m
III		"	"	m	m_2	5.90	1.14	m
IV	sm_1	5.87	1.70	sm		5.51-6.0	<1.7	m
V		5.01-6.0	<1.7	m	sm_1	5.89	1.70	sm
VI		"	"	m		5.01-5.5	<1.7	m
VII		"	"	m		"	"	m
VIII		"	"	m		4.51-5.5	"	m
IX	sm_2	5.08	2.33	sm		"	"	m
X		4.51-5.5	<1.7	m		"	"	m
XI		"	"	m		"	"	m
XII	sm_3	4.52	1.95	sm		"	"	m
XIII	st_1	4.51	3.07	st	m_3	4.32	1.16	m
XIV		4.01-5.0	<1.7	m	sm_2	4.32	1.86	sm
XV		"	>1.7	sm	st_1	4.26	3.12	st
XVI	m_2	3.72	1.55	m	m_4	3.72	1.27	m
XVII	st_2	3.72	3.30	st	st_2	3.70	3.10	st
XVIII	m_3	3.33	1.15	m	m_5	3.43	1.17	m
XIX	m_4	3.12	1.44	m	m_6	3.14	1.05	m
XX	sm_4	3.12	1.80	sm	m_7	3.14	1.32	m
XXI	sm_5	2.69	2.26	sm	sm_3	2.68	1.83	sm
C. formula: 13 m + 6 sm + 2st					C. formula:16 m + 3 sm + 2st			

Table 5. (Continued).

3. An X FM-32:

Chro-mosome Number	F_3				F_4			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I		6.51-7.0	<1.7	m	m_1	6.62	1.14	m
II	m_1	6.18	1.15	m	m_2	6.11	1.19	m
III	m_2	6.12	1.32	m	sm_1	5.48	1.70	sm
IV	m_3	5.75	1.69	m		5.01-5.5	<1.7	m
V		5.51-6.0	<1.7	m	m_3	5.38	1.06	m
VI	m_4	5.48	1.20	m		4.51-5.0	<1.7	m
VII	m_5	5.26	1.12	m		"	"	m
VIII	m_6	5.25	1.53	m		"	"	m
IX		5.01-5.5	<1.7	m	m_4	4.34	1.10	m
X	sm_1	4.73	1.76	sm		4.01-4.5	<1.7	m
XI		4.01-4.5	<1.7	m	sm_2	4.27	1.81	sm
XII		"	>1.7	sm	sm_3	4.04	2.28	sm
XIII	m_7	3.99	1.10	m		3.51-4.0	<1.7	m
XIV	m_8	3.89	1.30	m		"	>1.7	sm
XV		3.51-4.0	<1.7	m		"	"	sm
XVI	m_9	3.29	1.28	m		"	"	sm
XVII		3.01-3.5	<1.7	m	m_5	3.47	1.18	m
XVIII		"	"	m	m_6	3.43	1.59	m
XIX		"	"	m	m_7	3.12	1.12	m
XX	m_{10}	2.90	1.32	m	st_1	2.81	3.04	st
XXI	m_{11}	2.02	1.67	m	m_8	2.35	1.17	m
Centromeric formula: 19 m + 2 sm					C. formula: 14 m + 6 sm + 1 st			

Table 5. (Continued).

Chromosome Number	F_5				F_6			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	6.52	1.15	m		5.51-6.0	<1.7	m
II	m_2	5.56	1.11	m	sm_1	5.83	1.71	sm
III	m_3	5.21	1.15	m	m_1	5.17	1.10	m
IV		5.01-5.5	<1.7	m	m_2	5.12	1.36	m
V		4.51-5.0	>1.7	sm	m_3	5.12	1.36	m
VI	sm_1	4.50	2.10	sm	m_4	4.77	1.69	m
VII	sm_2	4.49	2.40	sm		4.51-5.0	<1.7	m
VIII	m_4	4.12	1.10	m		"	"	m
IX	sm_3	4.12	1.77	sm		"	>1.7	sm
X	sm_4	4.12	1.77	sm	m_5	4.46	1.08	m
XI	sm_5	4.07	1.83	sm		4.01-4.5	<1.7	m
XII	m_5	3.77	1.40	m	st_1	4.38	3.10	st
XIII		3.51-4.0	<1.7	m		4.01-4.5	>1.7	sm
XIV		"	"	m		"	"	sm
XV		3.01-3.5	"	m	m_6	3.70	1.14	m
XVI		"	"	m		3.51-4.0	<1.7	m
XVII		"	"	m		"	"	m
XVIII		"	"	m	sm_2	3.35	1.99	sm
XIX	sm_6	3.38	1.95	sm	m_7	3.06	1.10	m
XX		3.01-3.5	>1.7	sm	m_8	2.65	1.16	m
XXI	m_6	2.47	1.40	m	sm_3	2.33	2.08	sm
C. formula: 13 m + 8 sm					C. formula: 14 m + 6 sm + 1st			

Table 5. (Continued).

4. Kan X FM-32:

Chro-mosome Number	F_3				F_4			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	6.16	1.14	m	m_1	7.11	1.67	m
II	m_2	5.82	1.10	m	m_2	6.69	1.14	m
III	sm_1	5.80	1.78	sm		6.01-6.0	<1.7	m
IV		5.01-5.5	<1.7	m		5.51-6.0	"	m
V		"	"	m		"	"	m
VI		"	"	m		"	"	m
VII	sm_2	5.03	2.44	sm		"	>1.7	sm
VIII		4.51-5.0	<1.7	m	m_3	5.20	1.14	m
IX		"	>1.7	sm	sm_1	5.20	1.73	sm
X	sm_3	4.44	1.93	sm	sm_2	5.20	2.89	sm
XI	m_3	4.36	1.15	m		4.51-5.0	<1.7	m
XII	m_4	"	1.32	m		"	"	m
XIII	sm_4	4.24	2.18	sm		"	"	m
XIV	m_5	3.80	1.18	m		"	>1.7	sm
XV		3.51-4.0	<1.7	m	sm_3	4.57	2.14	sm
XVI	sm_5	3.67	2.16	sm	m_4	4.19	1.10	m
XVII		3.51-4.0	>1.7	sm	sm_4	4.19	2.52	sm
XVIII		"	"	sm	m_5	3.84	1.07	m
XIX		3.01-3.5	<1.7	m	m_6	3.50	1.29	m
XX	st_1	3.35	3.10	st	sm_5	3.16	2.92	sm
XXI	sm_6	3.04	1.92	sm	m_7	2.77	1.10	m
Centromeric formula: 11 m + 9 sm + 1st					C. formula: 14 m + 7 sm			

Table 5. (Continued).

Chromosome Number	F_5				F_6			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.18	1.12	m	m_1	7.18	1.11	m
II	m_2	6.86	1.05	m	m_2	6.77	1.37	m
III	m_3	6.67	1.33	m	m_3	6.31	1.54	m
IV	m_4	6.39	1.26	m		6.01-6.5	<1.7	m
V	sm_1	6.37	1.89	sm		"	"	m
VI	sm_2	6.37	1.89	sm		"	"	m
VII		5.51-6.0	<1.7	m		5.51-6.0	"	m
VIII		"	"	m		"	"	m
IX		"	"	m		"	"	m
X		5.01-5.5	"	m		"	>1.7	sm
XI		"	"	m	sm_1	5.12	1.97	sm
XII		"	"	m	m_4	5.02	1.11	m
XIII		"	"	m	m_5	5.02	1.39	m
XIV	sm_3	5.35	1.97	sm		5.01-5.5	<1.7	m
XV	m_5	4.60	1.52	m	st_1	4.71	3.01	st
XVI		4.01-4.5	<1.7	m		4.01-4.5	<1.7	m
XVII		"	"	m	m_6	3.79	1.04	m
XVIII		"	"	m	m_7	3.74	1.27	m
XIX	sm_4	3.38	1.86	sm	sm_2	3.69	1.76	sm
XX	st_1	3.61	3.06	st	st_2	2.59	3.10	st
XXI	m_6	2.88	1.17	m	m_8	3.11	1.40	m
C. formula: 16 m + 4 sm + 1st					C. formula: 16 m + 3 sm + 2st			

Table 5. (Continued).

5. Ak X FM-139:

Chro-mosome Number	F_3				F_4			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I		7.51-8.0	<1.7	m		8.01-8.5	<1.7	m
II	m_1	7.32	1.32	m	m_1	7.82	1.04	m
III	m_2	7.26	1.08	m	m_2	7.82	1.19	m
IV	sm_1	6.85	1.89	sm		7.01-7.5	<1.7	m
V		6.51-7.0	<1.7	m		6.51-7.0	"	m
VI	m_3	6.75	1.44	m	sm_1	6.39	1.78	sm
VII	m_4	6.16	1.48	m	m_3	6.33	1.17	m
VIII		6.01-6.5	<1.7	m		5.51-6.0	<1.7	m
IX	sm_2	6.04	1.97	sm		"	"	m
X		5.51-6.0	<1.7	m	sm_2	5.61	2.42	sm
XI		"	>1.7	sm	m_4	5.24	1.51	m
XII		5.01-5.5	<1.7	m		5.01-5.5	<1.7	m
XIII	sm_3	5.47	2.13	sm		"	>1.7	sm
XIV	sm_4	5.28	2.45	sm	sm_3	4.82	2.00	sm
XV	sm_5	5.21	1.78	sm	m_5	4.54	1.17	m
XVI		4.51-4.5	<1.7	m	m_6	4.24	1.42	m
XVII		"	>1.7	sm		3.51-4.0	<1.7	m
XVIII		4.01-4.5	<1.7	m	sm_4	3.15	1.79	sm
XIX	sm_6	4.46	1.72	m		3.01-3.5	>1.7	sm
XX	sm_7	3.73	2.14	sm	m_7	2.81	1.10	m
XXI	m_5	2.91	1.15	m	sm_5	2.43	2.07	sm
Centromeric formula: 12 m + 9 sm					C. formula: 14 m + 7 sm			

Table 5. (Continued).

Chro-mosome Number	F_5				F_6			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.78	1.14	m	m_1	8.28	1.22	m
II	m_2	7.16	1.10	m	m_2	7.80	1.05	m
III	m_3	7.12	1.45	m	m_3	7.11	1.61	m
IV		6.51-7.0	<1.7	m		7.01-7.5	<1.7	m
V	sm_1	6.58	1.70	sm		"	>1.7	sm
VI	sm_2	6.55	2.14	sm		6.51-7.0	<1.7	m
VII	m_4	6.47	1.33	m	sm_1	6.71	2.18	sm
VIII		6.01-6.5	>1.7	sm		6.51-7.0	>1.7	sm
IX		5.51-6.0	<1.7	m	m_4	6.38	1.11	m
X		"	>1.7	sm		6.01-6.5	>1.7	sm
XI		"	"	sm		"	"	sm
XII	m_5	5.15	1.26	m		5.51-6.0	<1.7	m
XIII		5.01-5.5	>1.7	sm	st_1	5.79	3.00	st
XIV		"	"	sm		5.51-6.0	>1.7	sm
XV	m_6	4.60	1.20	m		5.01-5.5	"	sm
XVI	m_7	4.60	1.20	m	m_5	5.00	1.17	m
XVII		4.01-4.5	<1.7	m	m_6	4.86	1.35	m
XVIII		"	>1.7	sm	m_7	4.67	1.04	m
XIX	m_8	3.59	1.23	m	m_8	4.32	1.47	m
XX	m_9	3.59	1.23	m	st_2	4.29	3.16	st
XXI	sm_3	2.20	2.09	sm	sm_2	2.82	1.81	sm
C. formula: 12 m + 9 sm					C. formula:16 m + 3 sm + 2st			

Table 5. (Continued).

6. An X FM-139:

Chromosome Number	F_3				F_4			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.60	1.08	m		7.01-7.5	<1.7	m
II	m_2	7.04	1.55	m	m_1	7.00	1.10	m
III		6.51-7.0	<1.7	m	m_2	6.55	1.26	m
IV		"	"	m		6.01-6.5	<1.7	m
V		6.01-6.5	"	m	sm_1	6.06	1.77	sm
VI	m_3	5.94	1.40	m	m_3	5.74	1.52	m
VII	sm_1	5.57	1.73	sm	m_4	5.59	1.09	m
VIII		5.01-5.5	<1.7	m	sm_2	5.55	1.95	sm
IX		4.51-5.0	"	m		5.01-5.5	<1.7	m
X		4.01-4.5	"	m		"	"	m
XI		"	"	m	m_5	4.86	1.24	m
XII	sm_2	4.27	1.71	sm		4.01-4.5	<1.7	m
XIII	sm_3	4.27	1.71	sm		"	"	m
XIV	sm_4	4.02	2.19	sm	sm_3	4.50	1.78	sm
XV		3.51-4.0	<1.7	m	m_6	3.89	1.59	m
XVI	sm_5	3.72	1.99	sm	sm_4	3.83	2.07	sm
XVII	m_4	3.28	1.57	m		3.01-3.5	<1.7	m
XVIII	sm_6	3.25	2.55	sm		"	"	m
XIX	m_5	3.06	1.12	m		"	"	m
XX	m_6	3.06	1.12	m	sm_5	3.43	2.56	sm
XXI		2.51-3.0	<1.7	m	m_7	2.80	1.12	m
Centromeric formula: 15 m + 6 sm					C. formula: 16 m + 5 sm			

Table 5. (Continued).

Chromosome Number	F_5				F_6			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I	m_1	7.35	1.09	m	m_1	7.51	1.18	m
II	m_2	6.88	1.06	m	m_2	7.19	1.04	m
III	m_3	6.34	1.26	m	m_3	6.57	1.46	m
IV		6.01-6.5	<1.7	m		6.51-7.0	<1.7	m
V		"	"	m	m_4	6.29	1.09	m
VI	sm_1	6.23	2.21	sm		6.01-6.5	<1.7	m
VII	sm_2	6.18	1.70	sm	m_5	5.94	1.58	m
VIII		5.51-6.0	<1.7	m		5.01-5.5	<1.7	m
IX		"	"	m	sm_1	5.16	1.85	sm
X	sm_3	5.69	2.20	sm		4.51-5.0	<1.7	m
XI		5.01-5.5	<1.7	m	sm_2	4.45	1.75	sm
XII		"	"	m	st_1	4.14	3.06	st
XIII		"	>1.7	sm		4.01-4.5	<1.7	m
XIV		4.51-5.0	<1.7	m		"	"	m
XV	st_1	4.75	3.14	st		"	>1.7	sm
XVI	sm_4	4.62	2.34	sm	m_6	3.78	1.11	m
XVII	m_4	4.40	1.27	m		3.51-4.0	<1.7	m
XVIII	sm_5	4.16	1.83	sm		"	>1.7	sm
XIX	m_5	3.87	1.19	m	m_7	3.47	2.30	sm
XX		3.51-4.0	>1.7	sm		3.01-3.5	<1.7	m
XXI	m_6	2.81	1.12	m	sm_3	3.11	1.11	m
C. formula: 13 m + 7 sm + 1st					C. formula: 15 m + 5 sm + 1st			

Table 5. (Continued).

7. Kan X FM-139:

Chro-mosome Number	F_3				F_4			
	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type	Identi-fied chr.	Length (X)	Arm ratio (Y)	Chr. type
I		8.01-8.5	<1.7	m	m_1	9.10	1.10	m
II	m_1	7.97	1.16	m		8.51-9.0	<1.7	m
III	m_2	7.29	1.38	m	m_2	8.40	1.39	m
IV	sm_1	6.67	1.75	sm	sm_1	8.00	2.04	sm
V	m_3	6.58	1.24	m		7.51-8.0	<1.7	m
VI		6.01-6.5	<1.7	m	m_3	7.71	1.30	m
VII		"	"	m		7.01-7.5	<1.7	m
VIII		"	>1.7	sm		6.51-7.0	"	m
IX		5.51-6.0	<1.7	m	m_4	6.06	1.07	m
X	sm_2	5.75	1.88	sm		6.01-6.5	<1.7	m
XI	m_4	5.30	1.55	m		"	>1.7	sm
XII	sm_3	5.30	2.26	sm		5.51-6.0	<1.7	m
XIII	sm_4	5.18	1.80	sm	m_5	5.18	1.33	m
XIV		4.51-5.0	<1.7	m		4.51-5.0	>1.7	sm
XV		"	>1.7	sm	sm_2	4.35	2.00	sm
XVI	m_5	4.48	1.12	m	sm_3	4.32	2.30	sm
XVII	m_6	4.45	1.42	m	st_1	4.30	3.00	st
XVIII	sm_5	4.10	2.04	sm	m_6	3.84	1.14	m
XIX		3.51-4.0	<1.7	m		3.51-4.0	>1.7	sm
XX	sm_6	3.87	1.79	sm		3.01-3.5	<1.7	m
XXI		3.01-3.5	<1.7	m	m_7	2.85	1.14	m
Centromeric formula: 13 m + 8 sm					C. formula: 13 m + 7 sm + 1st			

Table 5. (Continued).

Chromosome Number	F_5				F_6			
	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type	Identified chr.	Length (X)	Arm ratio (Y)	Chr. type
I		8.01-8.5	<1.7	m	m_1	6.79	1.09	m
II		7.51-8.0	"	m	m_2	6.23	1.40	m
III	m_1	7.31	1.44	m	m_3	5.78	1.12	m
IV	sm_1	7.21	1.74	sm	m_4	5.70	1.63	m
V		6.51-7.0	<1.7	m	sm_1	5.66	1.98	sm
VI	sm_2	6.66	1.88	sm		4.51-5.0	<1.7	m
VII	m_2	6.47	1.18	m	m_5	4.32	1.69	m
VIII	sm_3	6.23	2.24	sm	sm_2	4.21	2.10	sm
IX	m_3	5.97	1.65	m		3.51-4.0	<1.7	m
X		5.51-6.0	>1.7	sm		"	>1.7	sm
XI	sm_4	5.13	2.75	sm		"	"	sm
XII		5.01-5.5	<1.7	m	st_1	3.35	3.16	st
XIII	m_4	5.10	1.36	m	m_6	3.31	1.56	m
XIV	m_5	4.77	1.68	m		3.01-3.5	>1.7	sm
XV	sm_5	4.77	2.50	sm		2.51-3.0	<1.7	m
XVI		4.01-4.5	<1.7	m	sm_3	2.96	2.90	sm
XVII	st_1	4.31	3.05	st		2.51-3.0	>1.7	sm
XVIII	m_6	3.86	1.54	m	sm_4	2.46	1.85	sm
XIX		3.01-3.5	<1.7	m		2.01-2.5	<1.7	m
XX		"	"	m	m_7	2.41	1.40	m
XXI		2.51-3.0	"	m		1.51-2.0	>1.7	sm
C. formula: 14 m + 6 sm + 1st					C. formula: 11 m + 9 sm + 1st			

formulae were consisted of 11m + 9sm + 1st, 16m + 4sm + 1st and 16m + 3sm + 2st chromosomes, respectively. The haploid complements of F_3, F_4, F_5 and F_6 progenies of Ak X FM-139 were found to consist of 12m + 9sm, 14m + 7sm, 12m + 9sm and 16m + 3sm + 2st chromosomes, successively. In An X FM-139 15m + 6sm, 16m + 5sm, 13m + 7sm + 1st and 15m + 5sm + 1st chromosomes comprised the haploid complement for F_3, F_4, F_5 and F_6 progenies, respectively. The F_3, F_4, F_5 and F_6 progenies of Kan X FM-139 comprised 13m + 8sm, 13m + 7sm + 1st, 14m + 6sm + 1st and 11m + 9sm + 1st, successively for their haploid complement.

I.5.1.6. Proposed standard karyotype:

Standard karyotype of parents and their hybrid progenies in seven crosses were derived on the basis of centromeric formula, and range and average chromatin length per chromosome (Table 6). It gives an idea about similarities and differences of the chromosomes of six varieties/lines and their progenies under study. One pair of short chromosome ($S_1^{\blacksquare}$) was invariably present in both the exotic dwarf lines, while it was absent in the indigenous lines. The occurrence of more than 5 pairs of long chromosome (L) were observed in all the indigenous varieties except Kanchan, whereas less than 5 pairs of long chromosome were found in exotic lines.

The F_3 progenies of most of the crosses and F_4 progenies of cross-1 & 2 did not posses any short chromosome (S_1) like their indigenous parent. However, the F_5 and F_6 progenies of most of the crosses have had at least one or more pair of S_1 chromosome/s like their exotic parent. All the progenies (F_3 - F_6) of cross-3 & 5 found to bear the S_1-chromosome. Moreover, the sub-terminal (st)

Table 6. Proposed standard karyotype of parents and hybrid progenies in seven crosses of wheat.

Cross/ Generation	Large (L) (>7.01μm)	Medium (M) (5.01–7.0μm)	Relatively short (S_1) (3.01–5.0μm)	Short (S_2) (<3.0μm)
1. Ag X FM-32:				
P_1	7 L^m	6 M^m	6 S_1^m + 2 S_1^{sm}	-
F_3	4 L^m + 1 L^{sm}	8 M^m + 4 M^{sm}	4 S_1^m	-
F_4	-	9 M^m + 3M^{sm}	7 S_1^m + 2 S_1^{sm}	-
F_5	2 L^m	9 M^m + 3 M^{sm}	4 S_1^m + 2 S_1^{sm}	1 S_2^m
F_6	-	7 M^m + 2 M^{sm}	6S_1^m + 3 S_1^{sm}	3 S_2^m
P_2	4 L^m	6 M^m + 3 M^{sm}	5S_1^m + 2 S_1^{sm}	1 S_2^m
2. Ak X FM-32:				
P_1	5 L^m + 2L^{sm}	3 M^m + 5 M^{sm}	3 S_1^m + 3 S_1^{sm}	-
F_3	3 L^m	9 M^m + 4 M^{sm}	1 S_1 + 4 S_1^{sm}	-
F_4	-	8 M^m + 4 M^{sm}	4 S_1^m + 4 S_1^{sm} + 1 S_1^{st}	-
F_5	-	7 M^m + 2 M^{sm}	6 S_1^m + 3 S_1^{sm} + 2 S_1^{st}	1 S_2^{sm}
F_6	-	6 M^m + 1 M^{sm}	10 S_1^m + 1 S_1^{sm} + 2 S_1^{st}	1 S_2^{sm}
P_2	4 L^m	6 M^m + 3 M^{sm}	5 S_1^m + 2 S_1^{sm}	1 S_2^m
3. An X FM-32:				
P_1	5 L^m	7 M^m + 3 M^{sm}	5 S_1^m + 1 S_1^{sm}	-
F_3	-	9 M^m	8 S_1^m + 2 S_1^{sm}	2 S_2^m
F_4	-	4 M^m + 1 M^{sm}	9 S_1^m + 5 S_1^{sm}	1 S_2^{sm} + 1S_2^{st}
F_5	-	4 M^m	8 S_1^m + 8 S_1^{sm}	1 S_2^m
F_6	-	4 M^m + 1 M^{sm}	9 S_1^m + 4 S_1^{sm} + 1 S_1^{st}	1 S_2^m + 1 S_2^{sm}
P_2	4 L^m	6 M^m + 3 M^{sm}	5 S_1^m + 2 S_1^{sm}	1 S_2^m
4. Kan X FM-32:				
P_1	-	9 M^m + 1 M^{sm}	7 S_1^m + 4 S_1^{sm}	-
F_3	-	5 M^m + 2 M^{sm}	6 S_1^m + 7 S_1^{sm} + 1 S_1^{st}	-
F_4	1 L^m	6 M^m + 3 M^{sm}	6 S_1^m + 4 S_1^{sm}	1 S_2^m
F_5	1 L^m	10 M^m + 3 M^{sm}	4 S_1^m + 1 S_1^{sm} + 1 S_1^{st}	1 S_2^m
F_6	1 L^m	11 M^m + 2 M^{sm}	4 S_1^m + 1 S_1^{sm} + 2 S_1^{st}	-
P_2	4 L^m	6 M^m + 3 M^{sm}	5 S_1^m + 2 S_1^{sm}	1 S_2^m

Table 6. (Continued).

Cross/ Generation	Large (L) (>7.01μm)	Medium (M) (5.01–7.0μm)	Relatively short (S_1) (3.01–5.0μm)	Short (S_1) (<3.0μm)
5. Ak X FM-139:				
P_1	5 L^m + 2 L^{sm}	3 M^m + 5 M^{sm}	3 S_1^m + 3 S_1^{sm}	–
F_3	3 L^m	6 M^m + 6 M^{sm}	2 S_1^m + 3 S_1^{sm}	1 S_2^m
F_4	4 L^m	6 M^m + 3 M^{sm}	3 S_1^m + 3 S_1^{sm}	1 S_2^m + 1 S_2^{sm}
F_5	3 L^m	4 M^m + 7 M^{sm}	5 S_1^m + 1 S_1^{sm}	1 S_2^{sm}
F_6	4 L^m + 1 L^{sm}	3 M^m + 6 M^{sm} + 1 M^{st}	4 S_1^m + 1 S_1^{st}	1 S_2^{sm}
P_2	1 L^m + 1 L^{sm}	5 M^m + 3 M^{sm}	7 S_1^m + 3 S_1^{sm}	1 S_2^m
6. An X FM-139:				
P_1	2 L^m	5 M^m + 1 M^{sm}	7 S_1^m + 5 S_1^{sm}	1 S_2^m
F_3	1 L^m	7 M^m + 2 M^{sm}	7 S_1^m + 3 S_1^{sm}	1 S_2^m
F_4	1 L^m	7 M^m + 2 M^{sm}	7 S_1^m + 3 S_1^{sm}	1 S_2^m
F_5	1 L^m	8 M^m + 4M^{sm}	3 S_1^m + 3 S_1^{sm} + 1 S_1^{st}	1 S_2^m
F_6	2 L^m	6M^m + 1 M^{sm}	7 S_1^m + 4 S_1^{sm} + 1 S_1^{st}	–
P_2	1 L^m + 1 L^{sm}	5 M^m + 3 M^{sm}	7 S_1^m + 3 S_1^{sm}	1 S_2^m
7. Kan X FM-139				
P_1	–	9 M^m + 1 M^{sm}	7 S_1^m + 4 S_1^{sm}	–
F_3	3 L^m	5 M^m + 5 M^{sm}	5 S_1^m + 3 S_1^{sm}	–
F_4	6 L^m + 1 L^{sm}	5 M^m + 1 M^{sm}	2 S_1^m + 4 S_1^{sm} + 1 S_1^{st}	1 S_2^m
F_5	3 L^m + 1 L	5 M^m + 4 M^{sm}	5 S_1^m + 1 S_1^{sm} + 1 S_1^{st}	1 S_2^m
F_6	–	4 M^m + 1 M^{sm}	4 S_1^m + 4 S_1^{sm} + 1 S_1^{st}	3 S_2^m + 4 S_2^{sm}
P_2	1 L^m + 1 L^{sm}	5 M^m + 3 M^{sm}	7 S_1^m + 3 S_1^{sm}	1 S_2^m

chromosomes along with more sub-median chromosomes were frequently observed in the hybrid progenies of all crosses except Ag X FM-32, while it was fully absent in the parental genotypes.

I.5.1.7. Satellited chromosomes:

Satellited chromosomes with a visible state were found occasionally. Usually two in parental genotype and never more than four satellited chromosome in hybrid progenies were found in any cell. Satellited chromosomes were allocated to the morphological categories based on the chromosome frequency per haploid set (Table 4). The trabant was always found to bear by the short arm of the chromosomes in all the cases. From identified chromosomes of all genotypes, it was confirmed that the chromosome-III & -VIII were confined with this character.

Chromosome pair-III was found to be satellited in Akbar, FM-32 and FM-139, and chromosome pair-VIII in Akbar, Ananda and FM-139 was identified as satellited. In Aghrani and Kanchan the sat-chromosomes were not detected individually across the cells. The satellited chromosome pair-III was found in all the progenies of An X FM-32, Ak X FM-32, Ak X FM-139 and Kan X FM-139. The sat-chromosome pair-VIII was not found in any of the generations of Ak X FM-139. Not in all but in most of the progenies of all the crosses sat-chromosome pair-III was found to found to identifiable individually (Table 7). Length and arm ratio of the identified sat-chromosomes are given in Table 8. The t-test indicated that there was no significant difference between the identified sat-chromosomes of the mentioned genotypes, in respect of the arm lengths and ratios. However, in few cases of the hybrid progenies significant difference among the sat-chromosomes in respect of arm lengths and arm ratios were found to appear.

Table 7: Distribution of the individually identified chromosomes in parents and their hybrid progenies of seven crosses of wheat.

Chromosome number	Parental varieties/lines						No. of genotypes where the chromosome identified
	Aghrani	Akbar	Ananda	Kanchan	FM-32	FM-139	
I	+	+	+	+	+	+	6
II	+	–	–	–	+	–	2
III*	–	+	–	–	+	+	3*
IV	+	+	+	–	+	–	4
V	+	+	+	–	–	+	4
VI	+	+	–	–	+	+	4
VII	+	–	+	+	+	+	5
VIII*	–	+	+	–	–	+	3*
IX	–	+	–	–	+	+	3
X	+	–	+	+	+	+	5
XI	–	–	+	+	–	–	2
XII	+	–	–	–	–	–	1
XIII	+	+	–	–	–	+	3
XIV	–	+	–	–	+	–	2
XV	–	–	–	+	–	–	1
XVI	–	+	+	+	+	+	5
XVII	–	–	–	+	–	–	1
XVIII	–	–	+	+	–	–	2
XIX	+	–	+	+	–	+	4
XX	+	+	+	–	–	–	3
XXI	+	–	+	+	+	–	4

'+' and '–' indicating the presence and absence of specified chromosome, respectively.

Table 7. (Continued).

Chromosome number	1. Ag X FM-32						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	+	+	+	+	+	+	6
II	+	+	+	-	+	+	5
III*	-	+	-	+	-	+	3*
IV	+	+	-	-	+	+	3
V	+	-	-	-	+	-	2
VI	-	+	+	+	+	+	5
VII	-	+	+	+	+	+	5
VIII*	+	-	-	-	-	-	1*
IX	-	+	-	-	-	+	2
X	-	-	-	+	+	+	3
XI	-	-	+	-	-	-	1
XII	+	+	-	-	+	-	3
XIII	-	-	-	+	+	-	2
XIV	+	-	+	+	-	+	4
XV	-	-	+	+	-	-	2
XVI	-	-	-	+	-	+	2
XVII	-	+	-	-	-	-	1
XVIII	-	-	-	+	-	-	1
XIX	+	-	+	+	+	-	4
XX	+	+	+	-	+	-	4
XXI	+	+	+	-	+	+	5

Table 7. (Continued).

Chromosome number	2. Ak X FM-32						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	+	+	+	+	+	+	6
II	+	-	-	-	-	+	2
III*	+	-	-	+	+	+	4*
IV	+	-	+	-	+	+	4
V	+	+	-	+	+	-	4
VI	+	+	-	-	+	+	4
VII	-	+	-	-	-	+	2
VIII*	-	+	-	-	+	-	2*
IX	+	+	+	-	+	+	5
X	-	-	-	-	-	+	1
XI	-	-	-	-	-	-	0
XII	-	-	+	-	-	-	1
XIII	-	-	+	+	+	-	3
XIV	-	-	-	+	+	+	3
XV	+	+	-	+	-	-	3
XVI	+	+	+	+	+	+	6
XVII	+	-	+	+	-	-	3
XVIII	-	+	+	+	-	-	3
XIX	-	+	+	+	-	-	3
XX	+	+	+	+	+	-	5
XXI	+	+	+	+	-	+	5

Table 7. (Continued).

Chromosome number	3. An X PM-32						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	-	+	+	-	+	+	4
II	+	+	+	+	-	+	5
III*	+	+	+	+	-	+	5*
IV	+	-	-	+	+	+	4
V	-	+	-	+	+	-	3
VI	+	-	+	+	-	+	4
VII	+	-	+	-	+	+	4
VIII*	+	-	+	-	+	-	3*
IX	-	+	+	-	-	+	3
X	+	-	+	+	+	+	5
XI	-	+	+	-	+	-	3
XII	-	+	+	+	-	-	3
XIII	+	-	-	-	-	-	1
XIV	+	-	-	-	-	+	2
XV	-	-	-	+	-	-	1
XVI	+	-	-	-	+	+	3
XVII	-	+	-	-	-	-	1
XVIII	-	+	-	+	+	-	3
XIX	-	+	+	+	+	-	4
XX	+	+	-	+	+	-	4
XXI	+	+	+	+	+	+	6

Table 7. (Continued).

Chromosome number	4. Kan X FM-32						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	+	+	+	+	+	+	6
II	+	+	+	+	-	+	5
III*	+	-	+	+	-	+	4*
IV	-	-	+	-	-	+	2
V	-	-	+	-	-	-	1
VI	-	-	+	-	-	+	2
VII	+	-	-	-	+	+	3
VIII*	-	+	-	-	-	-	1*
IX	-	+	-	-	-	+	2
X	+	+	-	-	+	+	4
XI	+	-	-	+	+	-	3
XII	+	-	-	+	-	-	2
XIII	+	-	-	+	-	-	2
XIV	+	-	+	-	-	+	3
XV	-	+	+	+	+	-	4
XVI	+	+	-	-	+	+	4
XVII	-	+	-	+	+	-	3
XVIII	-	+	-	+	+	-	3
XIX	-	+	+	+	+	-	4
XX	+	+	+	+	-	-	4
XXI	+	+	+	+	+	+	6

Table 7. (Continued).

Chromosome number	5. Ak X FM-139						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	-	-	+	+	+	+	4
II	+	+	+	+	-	-	4
III*	+	+	+	+	+	+	6*
IV	+	-	-	-	+	-	2
V	-	-	+	-	+	+	3
VI	+	+	+	-	+	+	5
VII	+	+	+	+	-	+	5
VIII*	-	-	-	-	+	+	2*
IX	+	-	-	+	+	+	4
X	-	+	-	-	-	+	2
XI	-	+	-	-	-	-	1
XII	-	-	+	-	-	-	1
XIII	+	-	-	+	+	+	4
XIV	+	+	-	-	+	-	3
XV	+	+	+	-	-	-	3
XVI	-	+	+	+	+	+	5
XVII	-	-	-	+	-	-	1
XVIII	-	+	-	+	-	-	2
XIX	+	-	+	+	-	+	4
XX	+	+	+	+	+	-	5
XXI	+	+	+	+	-	-	4

Table 7. (Continued).

Chromosome number	6. An X FM-139						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	+	–	+	+	+	+	5
II	+	+	+	+	–	–	4
III*	–	+	+	+	–	+	4*
IV	–	–	–	–	+	–	1
V	–	+	–	+	+	+	4
VI	+	+	+	–	–	+	4
VII	+	+	+	+	+	+	6
VIII*	–	+	–	–	+	+	3*
IX	–	–	–	+	–	+	2
X	–	–	+	–	+	+	3
XI	–	+	–	+	+	–	3
XII	+	–	–	+	–	–	2
XIII	+	–	–	–	–	+	2
XIV	+	+	–	–	–	–	2
XV	–	+	+	–	–	–	2
XVI	+	+	+	+	+	+	6
XVII	+	–	+	–	–	–	2
XVIII	+	–	+	–	+	–	3
XIX	+	–	+	+	+	+	5
XX	+	+	–	–	+	–	3
XXI	–	+	+	+	+	–	4

Table 7. (Continued).

Chromosome number	7. Knn X PM-139						No. of genotypes where the chromosome identified
	F_3	F_4	F_5	F_6	P_1	P_2	
I	-	+	-	+	+	+	4
II	+	-	-	+	-	-	2
III*	+	+	+	+	-	+	5*
IV	+	+	+	+	-	-	4
V	+	-	-	+	-	+	3
VI	-	+	+	-	-	+	3
VII	-	-	+	+	+	+	4
VIII*	-	-	+	+	-	+	3*
IX	-	+	+	-	-	+	3
X	+	-	-	-	+	+	3
XI	+	-	+	-	+	-	3
XII	+	-	-	+	-	-	2
XIII	+	+	+	+	-	+	5
XIV	-	-	+	-	-	-	1
XV	-	+	+	-	+	-	3
XVI	+	+	-	+	+	+	5
XVII	+	+	+	-	+	-	4
XVIII	+	+	+	+	+	-	5
XIX	-	-	-	-	+	+	2
XX	+	-	-	+	-	-	2
XXI	-	+	-	-	+	-	2

Table 8. Morphological features of commonly identified chromosomes in six varieties/lines and their hybrid progenies in seven crosses of wheat.

Chr.No.	Morphology		Parental varieties/lines						Mean	S.E.
			Aghrani	Akbar	Ananda	Kanchan	FM-32	FM-139		
I	Length	L	4.90*	5.16	5.02	4.05*	4.49	4.70	4.72	0.17
		S	4.15*	3.35	3.49	2.45*	3.45	2.58	3.25	0.26
		T	9.05*	8.51	8.51	6.51*	7.94	7.28	7.97	0.38
	Arm ratio		1.18*	1.54	1.44	1.65	1.30	1.82*	1.49	0.10
VII	Length	L	3.97	-	4.61	3.61	4.32	3.08*	3.92	0.27
		S	3.07*	-	2.13	2.21	1.94	2.71	2.41	0.21
		T	7.04*	-	6.74	5.82	6.26	5.79	6.33	0.25
	Arm ratio		1.29	-	2.16	1.63	2.22	1.14	1.69	0.22
X	Length	L	3.90*	-	3.55	2.92*	3.31	3.35	3.41	0.16
		S	2.38	-	2.40	2.41	2.43	1.86*	2.30	0.11
		T	6.27*	-	5.95	5.33	5.74	5.21	5.70	0.20
	Arm ratio		1.64	-	1.48	1.21*	1.36	1.80*	1.50	0.10
XVI	Length	L	-	2.66	2.78	2.35*	2.77	2.50	2.61	0.08
		S	-	2.08	2.17	1.83	1.63	1.20*	1.78	0.17
		T	-	4.74	4.95	4.18	4.40	3.70*	4.39	0.22
	Arm ratio		-	1.28	1.28	1.28	1.70	2.09*	1.53	0.16
III	Length	L	-	4.72	-	-	4.15	3.62	4.16	0.32
		S	-	3.28	-	-	3.09	3.09	3.15	0.06
		T	-	8.00	-	-	7.24	6.71	7.32	0.37
	Arm ratio		-	1.44	-	-	1.34	1.17	1.32	0.08
VIII	Length	L	-	4.42	3.90	-	-	3.50	3.94	0.27
		S	-	2.52	2.55	-	-	2.14	2.40	0.13
		T	-	6.94	6.45	-	-	5.64	6.34	0.38
	Arm ratio		-	1.75	1.53	-	-	1.64	1.64	0.06

Table 8. (Continued).

Chromosome number	Morphology		1. Ag X PM-32						Statistics		
			F_2	F_3	F_4	F_5	P_1	P_2	X	S.E.	C.V.
I	Length	L	4.20	3.88	3.81	3.70	4.90*	4.49	4.16	0.19	11.19
		S	3.50	3.11	3.47	3.08	4.15*	3.45	3.46	0.16	11.33
		T	7.70	6.99	7.28	6.78	9.05*	7.94	7.62	0.34	10.77
	Arm ratio		1.20	1.25	1.10*	1.20	1.18	1.30*	1.21	0.03	5.60
II	Tength	L	4.20	3.56*	4.19	-	4.28	4.15	4.08	0.13	7.17
		S	3.50	2.97	3.02	-	4.23*	3.09	3.36	0.24	15.72
		T	7.70	6.53	7.21	-	8.51*	7.24	7.44	0.33	9.82
	Arm ratio		1.20	1.20	1.39	-	1.01*	1.34	1.23	0.07	12.07
III*	Length	L	4.31	-	3.84	-	-	4.15	4.10	0.14	5.83
		S	3.17	-	2.96	-	-	3.09	3.07	0.06	3.45
		T	7.48	-	6.80	-	-	7.24	7.17	0.20	4.81
	Arm ratio		1.36	-	1.30	-	-	1.34	1.33	0.02	2.29
VI	Length	L	-	4.13	4.14	3.62*	4.36	3.94	4.04	0.12	6.86
		S	-	2.37	2.21	2.14	2.93*	2.38	2.41	0.14	12.91
		T	-	6.50	6.35	5.76	7.29*	6.32	6.44	0.25	8.54
	Arm ratio		-	1.74	1.87*	1.69	1.49*	1.65	1.69	0.06	8.19
VII	Length	L	-	3.85	3.15	3.04	3.97	4.32	3.67	0.25	15.02
		S	-	1.90	2.81	2.69	3.07	1.94	2.48	0.24	21.41
		T	-	5.75	5.96	5.73	7.04*	6.26	6.15	0.24	8.82
	Arm ratio		-	2.02	1.12	1.13	1.29	2.22*	1.56	0.23	33.68
VIII*	Length	L	4.10	-	-	-	-	-			
		S	2.20	-	-	-	-	-			
		T	6.30	-	-	-	-	-			
	Arm ratio		1.87	-	-	-	-	-			
XXI	Length	L	2.13	2.05	1.52	-	1.76	1.54	1.80	0.13	15.69
		S	1.59	1.55	1.25*	-	1.58	1.36	1.47	0.07	10.42
		T	3.72	3.60	2.77	-	3.34	2.90	3.27	0.19	12.82
	Arm ratio		1.34	1.33	1.22	-	1.12	1.14	1.23	0.05	8.37

Table 8. (Continued).

Chromosome number	Morphology		2. Ak X FM-32						Statistics		
			F_2	F_3	F_4	F_5	P_1	P_2	X	S.E.	C.V.
I	Length	L	4.13	3.67	3.50	3.53	5.16*	4.49	4.08	0.27	16.05
		S	3.56*	3.13	3.07	2.99	3.35*	3.45*	3.26	0.09	7.00
		T	7.69	6.80	6.57	6.52	8.51*	7.94	7.34	0.34	11.25
	Arm ratio		1.16	1.17	1.14	1.18	1.54*	1.30	1.25	0.06	12.31
III*	Tength	L	3.55	-	-	3.14	4.72	4.15	3.89	0.35	17.78
		S	2.54	-	-	2.76	3.28	3.09	2.92	0.17	11.34
		T	6.09	-	-	5.90	8.00	7.24	6.81	0.50	14.56
	Arm ratio		1.40	-	-	1.14	1.44	1.34	1.33	0.07	10.01
VIII*	Length	L	-	4.00	-	-	4.42	-	4.21	0.21	7.05
		S	-	1.80	-	-	2.52	-	2.16	0.36	23.57
		T	-	5.80	-	-	6.94	-	6.37	0.57	12.65
	Arm ratio		-	2.22	-	-	1.75	-	1.99	0.24	16.74
IX	Length	L	3.43	2.84*	3.55	-	4.02*	3.31	3.43	0.19	12.41
		S	2.53	2.50	1.53*	-	2.49	2.43	2.30	0.19	18.72
		T	5.96	5.34	5.08	-	6.51*	5.74	5.73	0.25	9.714
	Arm ratio		1.36	1.14	2.33*	-	1.61	1.36	1.56	0.21	29.58
XVI	Length	L	3.53*	3.43*	2.26	2.08	2.08	2.77	2.69	0.27	24.58
		S	1.56	1.10*	1.46	1.64	2.66*	1.63	1.68	0.21	31.18
		T	5.09*	4.53	3.72*	3.72*	4.74	4.40	4.37	0.23	12.65
	Arm ratio		2.27	3.10*	1.55	1.27	1.28	1.70	1.86	0.29	38.07
XX	Length	L	2.24	1.93	2.01	1.79	2.50*	-	2.09	0.13	13.35
		S	1.97	1.70	1.11*	1.35	1.96	-	1.62	0.17	23.48
		T	4.21	3.63	3.12	3.14	4.46*	-	3.71	0.27	16.45
	Arm ratio		1.14	1.14	1.80	1.32	1.27	-	1.33	0.12	20.42
XXI	Length	L	2.72*	2.18	1.86	1.73	-	1.54	2.01	0.21	23.04
		S	1.47	1.19	0.83	0.95	-	1.36	1.16	0.12	23.21
		T	4.19*	3.37	2.69	2.68	-	2.90	3.17	0.28	20.12
	Arm ratio		1.86	1.83	2.26	1.83	-	1.14*	1.78	0.18	22.62

Table 8. (Continued).

Chromosome number	Morphology		3. An X FM-32						Statistics		
			F_3	F_4	F_5	F_6	P_1	P_2	X	S.E.	C.V.
II	Length	L	3.31	3.32	2.92	4.59*	-	4.15	3.66	0.31	16.05
		S	2.87	2.79	2.64	1.24*	-	3.09	2.53	0.33	7.00
		T	6.18	6.11	5.56	5.83	-	7.24*	6.18	0.29	11.25
	Arm ratio		1.15	1.19	1.11	1.71*	-	1.34	1.30	0.11	12.31
III*	Tength	L	3.48	3.45	2.79	2.71	-	4.15*	3.32	0.26	17.78
		S	2.64	2.03*	2.42	2.46	-	3.09*	2.53	0.17	11.34
		T	6.12	5.48	5.21	5.17	-	7.24*	5.84	0.39	14.56
	Arm ratio		1.32	1.70*	1.15	1.10	-	1.34	1.32	0.11	10.01
VIII*	Length	L	3.17	-	2.16	-	3.90	-	3.08	0.50	7.05
		S	2.08	-	1.96	-	2.55	-	2.20	0.18	23.57
		T	5.25	-	4.12	-	6.45	-	5.27	0.67	12.65
	Arm ratio		1.53	-	1.10	-	1.53	-	1.39	0.14	16.74
X	Length	L	3.02	-	2.63	2.32*	3.55	3.31	2.97	0.22	12.41
		S	1.71	-	1.49*	2.14	2.40	2.43	2.03	0.19	18.72
		T	4.73	-	4.12	4.46	5.95	5.74	5.00	0.36	9.714
	Arm ratio		1.76	-	1.77	1.08*	1.48	1.36	1.49	0.13	29.58
XXI	Length	L	1.26	1.27	1.44	1.57	1.93*	1.54	1.50	0.10	24.58
		S	0.76	1.08	1.03	0.76	1.67*	1.36	1.11	0.14	31.18
		T	2.02	2.35	2.47	2.33	3.60*	2.90	2.61	0.23	12.65
	Arm ratio		1.67	1.17	1.40	2.08*	1.15	1.14	1.44	0.15	38.07

Table 8. (Continued).

Chromosome number	Morphology		4. Kan X FM-32						Statistics		
			F_3	F_4	F_5	F_6	P_1	P_2	X	S.E.	C.V.
I	Length	L	3.28*	4.45	3.79	3.78	4.05	4.49	3.97	0.19	11.72
		S	2.88	2.66	3.39	3.40	2.46*	3.45	3.04	0.18	14.16
		T	6.16*	7.11	7.18	7.18	6.51	7.94*	7.01	0.25	8.80
	Arm ratio		1.14	1.67	1.12	1.11	1.65*	1.30	1.33	0.11	19.80
II	Tength	L	3.05*	3.56	3.51	3.91	-	4.15	3.64	0.19	11.54
		S	2.77	3.13	3.35*	2.86	-	3.09	3.04	0.10	7.57
		T	5.82*	6.69	6.86	6.77	-	7.24	6.68	0.23	7.83
	Arm ratio		1.10	1.14	1.05	1.37	-	1.34	1.20	0.07	12.12
III*	Length	L	3.71	-	3.87	3.83	-	4.15	3.89	0.09	4.79
		S	2.09	-	2.86	2.48	-	3.09	2.63	0.22	16.70
		T	5.80	-	6.67	6.31	-	7.24	6.51	0.30	9.32
	Arm ratio		1.78	-	1.33	1.54	-	1.34	1.50	0.11	14.14
VIII*	Length	L	-	2.77	-	-	-	-			
		S	-	2.43	-	-	-	-			
		T	-	5.20	-	-	-	-			
	Arm ratio		-	1.14	-	-	-	-			
XXI	Length	L	2.00	1.19*	1.55	1.81	2.27*	1.54	1.73	0.16	22.14
		S	1.04	1.08	1.33	1.30	1.03*	1.36*	1.19	0.06	13.06
		T	3.04	2.27*	2.88	3.11	3.30*	2.90	2.92	0.14	12.07
	Arm ratio		1.92	1.10	1.17	1.40	2.21*	1.14	1.49	0.19	31.31

Table 8. (Continued).

Chromosome number	Morphology		S. Ak X PM-139						Statistics		
			F_3	F_4	F_5	F_6	P_1	P_2	X	S.E.	C.V.
III*	Length	L	3.77	4.25	4.21	4.39	4.72*	3.62*	4.16	0.17	9.74
		S	3.49	3.57*	2.91	2.72*	3.28	3.09	3.18	0.14	10.45
		T	7.26	7.82	7.12	7.11	8.00*	6.71*	7.34	0.20	6.95
	Arm ratio		1.08*	1.19	1.45	1.61*	1.44	1.17	1.32	0.08	15.57
VI	Length	L	3.98	4.09	4.46	-	4.28	3.53*	4.07	0.16	8.66
		S	2.77	2.30	2.09	-	3.31*	2.64	2.62	0.21	17.91
		T	6.75	6.39	6.55	-	7.59*	6.17	6.69	0.24	8.17
	Arm ratio		1.44	1.78	2.14*	-	1.29	1.34	1.60	0.16	22.42
VII	Length	L	3.68	3.41	3.69	4.60*	-	3.08	3.69	0.25	15.31
		S	2.48	2.92	2.78	2.11*	-	2.71	2.60	0.14	12.18
		T	6.16	6.33	6.47	6.71*	-	5.79*	6.29	0.15	5.49
	Arm ratio		1.48	1.17	1.33	2.18*	-	1.14	1.46	0.19	29.10
VIII*	Length	L	-	-	-	-	4.42	3.50	3.96	0.46	16.43
		S	-	-	-	-	2.52	2.14	2.33	0.19	11.53
		T	-	-	-	-	6.94	5.64	6.29	0.65	14.61
	Arm ratio		-	-	-	-	1.75	1.64	1.70	0.06	4.59
XVI	Length	L	-	2.49	2.51	2.70*	2.66	2.50	2.57	0.04	3.88
		S	-	1.75	2.09	2.30	1.08	1.20*	1.88	0.19	22.83
		T	-	4.24	4.60	5.00	4.74	3.70*	4.46	0.23	11.31
	Arm ratio		-	1.42	1.20	1.17	1.28	2.09*	1.43	0.17	26.56
XX	Length	L	2.54	1.47*	1.98	3.26*	2.50	-	2.35	0.29	28.52
		S	1.19	1.34	1.61	1.03	1.96*	-	1.43	0.16	25.74
		T	3.73	2.81	3.59	4.29	4.46	-	3.78	0.44	17.27
	Arm ratio		2.14	1.10	1.23	3.16*	1.27	-	1.78	0.39	49.13

Table 8. (Continued).

Chromosome number	Morphology		6. An X FM-139						Statistics		
			F_3	F_4	F_5	F_6	P_1	P_2	X	S.E.	C.V.
I	Length	L	3.95	-	3.83	4.07	5.02*	4.70	4.31	0.23	12.01
		S	3.65	-	3.52	3.44	3.49	2.58*	3.34	0.19	12.88
		T	7.60	-	7.35	7.51	8.51*	7.28	7.65	0.22	6.50
	Arm ratio		1.08	-	1.09	1.18	1.44	1.82*	1.32	0.14	23.75
III*	Length	L	-	3.65	3.53	3.90	-	3.62	3.68	0.08	4.31
		S	-	2.90	2.81	2.67	-	3.09	2.87	0.09	6.14
		T	-	6.55	6.34	6.57	-	6.71	6.55	0.08	2.33
	Arm ratio		-	1.26	1.26	1.46	-	1.17	1.29	0.06	9.52
VII	Length	L	3.35	2.92*	3.89	3.64	4.61*	3.08	3.58	0.25	17.21
		S	2.04*	2.67	2.29	2.30	2.13	2.71*	2.36	0.11	11.73
		T	5.57	5.59	6.18	5.94	6.74*	5.79	5.97	0.18	7.40
	Arm ratio		1.73	1.09*	1.70	1.58	2.16*	1.14*	1.57	0.16	25.63
VIII*	Length	L	-	3.67	-	-	3.90	3.50	3.69	0.12	5.44
		S	-	1.88	-	-	2.55	2.14	2.19	0.20	15.42
		T	-	5.55	-	-	6.45	5.64	5.88	0.29	8.43
	Arm ratio		-	1.95	-	-	1.53	1.64	1.71	0.13	12.76
XVI	Length	L	2.48	2.58	3.24*	1.99*	2.78	2.50	2.60	0.17	15.78
		S	1.24	1.25	1.38	1.79	2.17	1.20	1.51	0.16	26.03
		T	3.72	3.83	4.62	3.78	4.95*	3.70	4.10	0.22	13.24
	Arm ratio		1.99	2.07	2.34*	1.11*	1.28*	2.09	1.81	0.20	27.35
XIX	Length	L	1.62*	-	2.10	2.42	2.58	1.94	2.13	0.17	17.92
		S	1.44	-	1.77	1.05	1.87	1.11	1.45	0.17	25.71
		T	3.06	-	3.87	3.47	4.45*	3.05	3.58	0.26	16.55
	Arm ratio		1.12	-	1.19	2.30*	1.38	1.76	1.55	0.22	31.44

Table 8. (Continued)

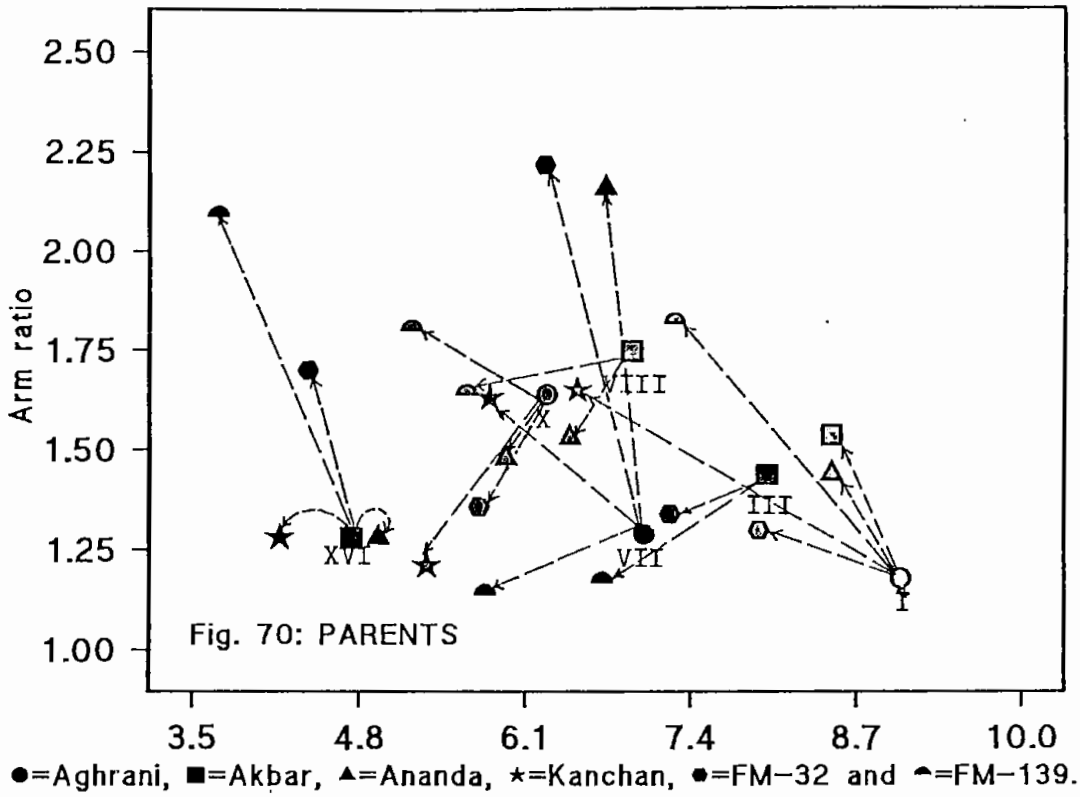
Chromosome number	Morphology		7. Kan X PM-139						Statistics		
			F_3	F_4	F_5	F_6	P_1	P_2	X	S.E.	C.V.
III*	Length	L	4.23	4.89	4.31	3.05*	-	3.62	4.02	0.32	17.53
		S	3.06	3.51*	3.00	2.73	-	3.09	3.08	0.13	9.11
		T	7.29	8.40*	7.31	5.78*	-	6.71	7.10	0.43	13.49
	Arm ratio		1.38	1.39	1.44	1.12*	-	1.17	1.30	0.06	11.11
VIII*	Length	L	-	-	4.31	2.85	-	3.50	3.55	0.42	20.59
		S	-	-	1.92	1.36	-	2.14	1.81	0.23	22.26
		T	-	-	6.23	4.21	-	5.64	5.36	0.60	19.38
	Arm ratio		-	-	2.24	2.10	-	1.64	1.99	0.18	15.75
XIII	Length	L	3.33	2.96	2.94	2.02*	-	2.76	2.80	0.22	17.26
		S	1.85	2.22	2.16	1.29*	-	1.53	1.81	0.18	22.12
		T	5.18	5.18	5.10	3.31*	-	4.29	4.61	0.37	17.76
	Arm ratio		1.80	1.33	1.36	1.56	-	1.80	1.57	0.10	14.51
XVI	Length	L	2.37	3.01*	-	2.20	2.26	2.50	2.47	0.14	13.12
		S	2.11*	1.31	-	0.76*	1.92	1.20	1.46	0.23	37.73
		T	4.48	4.32	-	2.96*	4.18	3.70	3.93	0.27	15.65
	Arm ratio		1.12	2.30	-	2.90*	1.18	2.09	1.92	0.34	39.71
XVIII	Length	L	2.48	2.05	2.34	1.60*	2.28	-	2.15	0.15	16.02
		S	1.39	1.79	1.52	0.86*	1.42	-	1.40	0.15	24.25
		T	3.87	3.84	3.86	2.46*	3.70	-	3.55	0.27	17.23
	Arm ratio		1.79	1.14*	1.54	1.85	1.61	-	1.59	0.13	17.64

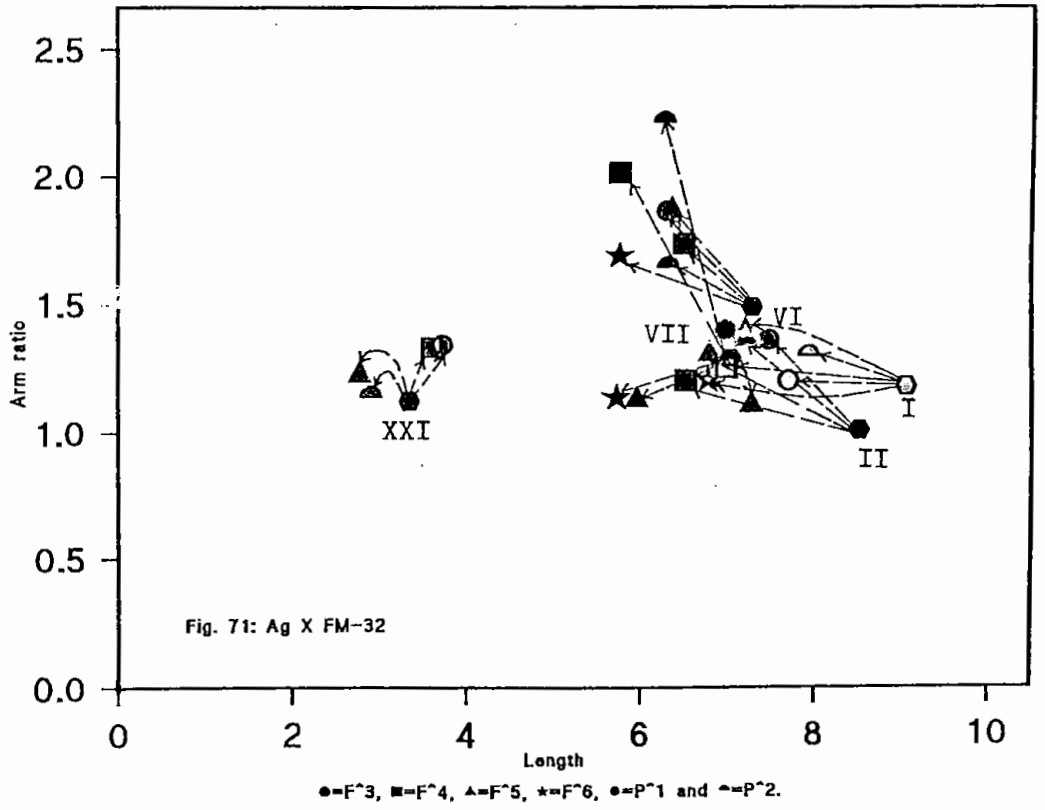
I.5.1.8. Possible pathways of structural changes in commonly identified chromosomes:

The sets of values of the commonly identified chromosomes of six parental genotypes and hybrid progenies were plotted on a two-dimensional scatter diagram (Figs. 70-77). Those points (chromosomes), which were close to each other and belonged to different symbols (genotypes) on the diagram were considered as homologous. Morphological features of the commonly identified chromosomes of parents and their hybrid progenies in seven crosses are given in Table 8. The test of significance was also carried out by t-test for their morphological differences. The significant difference in chromosome size of the genomes might have occurred either by deletion or unequal translocation for decreasing the chromosome size and through duplication for increased size. The possible pathways of structural changes in those chromosomes were indicated with arrows. However, the results obtained for possible pathways of structural changes are described below:

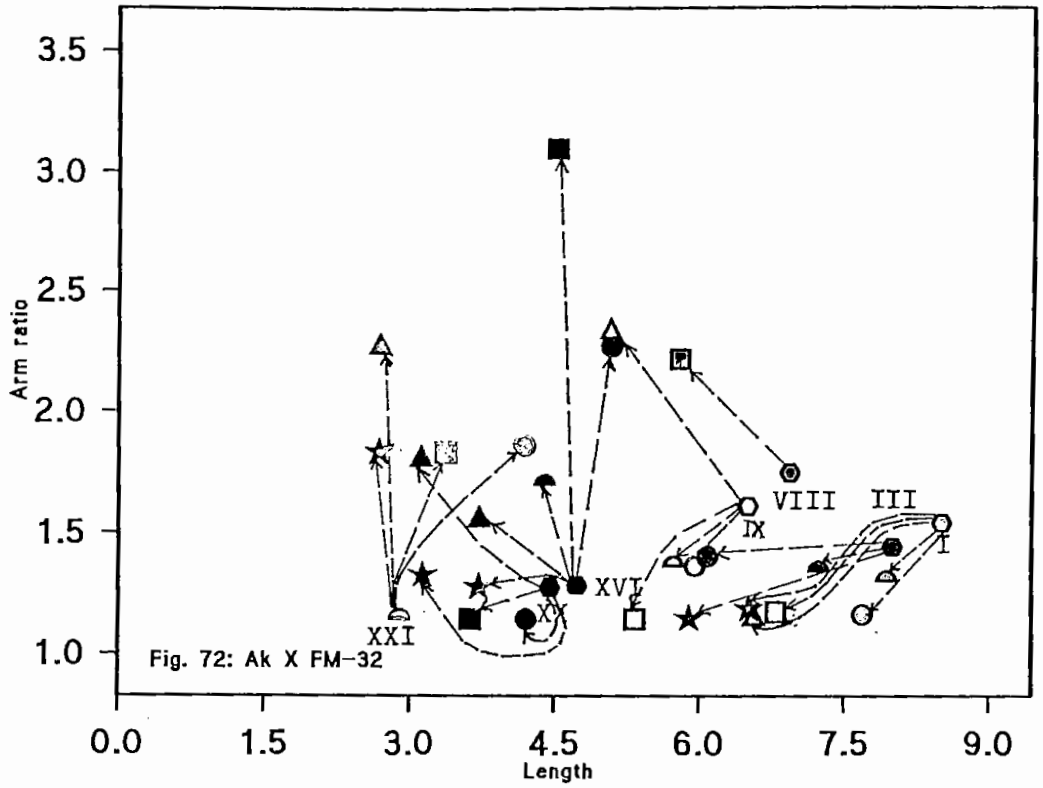
Parents:

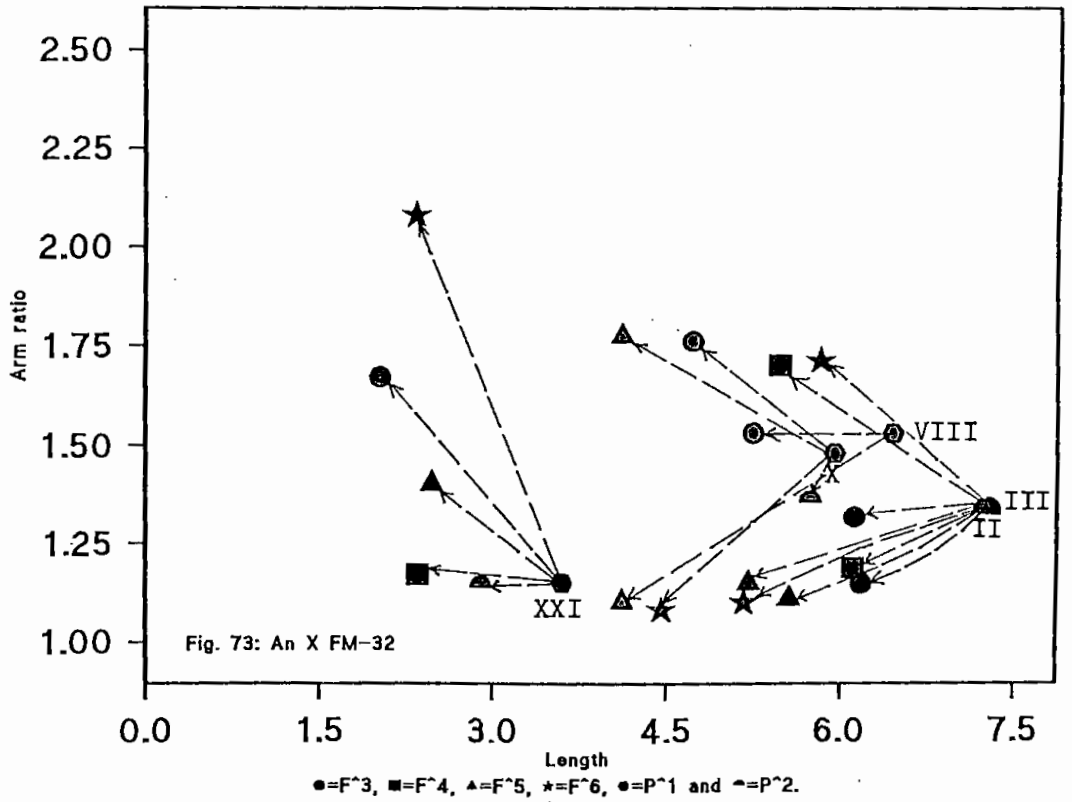
The chromosome-I in all the genotypes, chr.-VII & X in all except Akbar and chr.-XVI in all except Aghrani were identified individually (Table 7), and their morphological features are given in Table 8. In Aghrani, the total length of chromosome-I, VII & X were found to differ significantly due to difference in the short arm of former two and for long arm of later one. However, they were found to differ significantly in respect their arm ratio only in case of chr.-I. In Akbar, Ananda and FM-32 no significant difference was found in any chromosome in respect of their arm length and ratio. In Kanchan, the total length of chr.-I





Figs. 70 & 71: Changes in the commonly identified chromosomes of parental genotypes and Ag X FM-32 cross.





Figs. 72 & 73: Changes in the commonly identified chromosomes of Ak X FM-32 and An X FM-32 crosses.

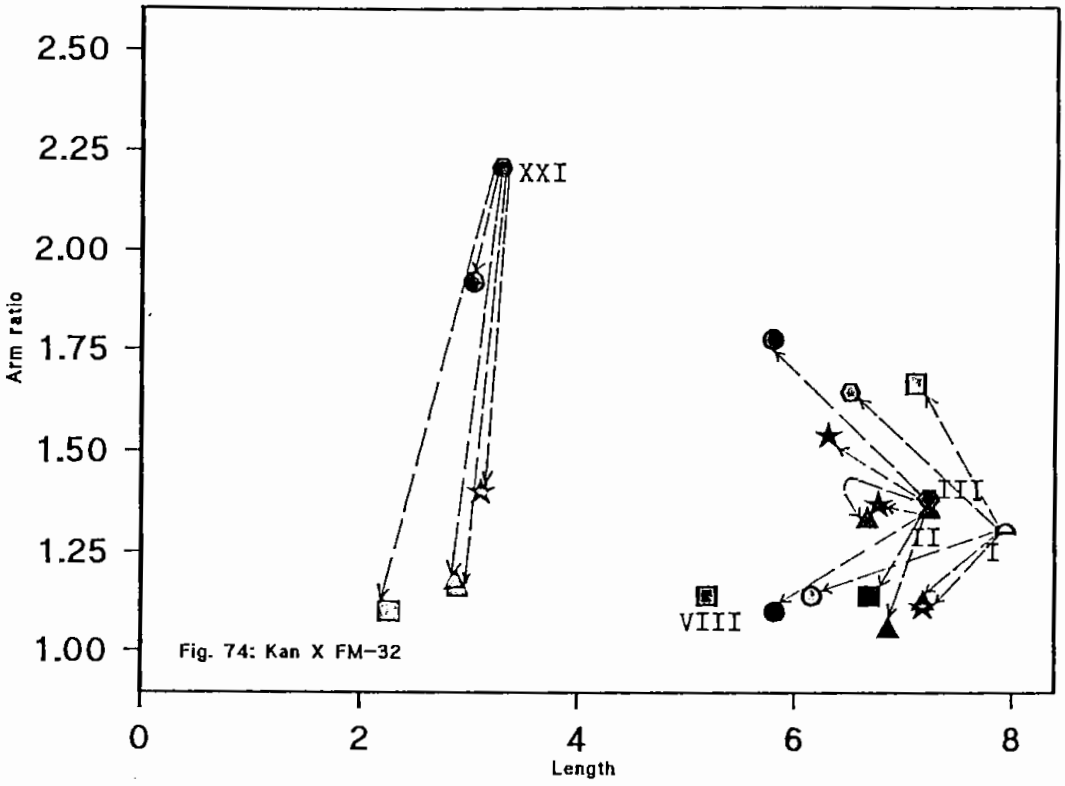


Fig. 74: Kan X FM-32

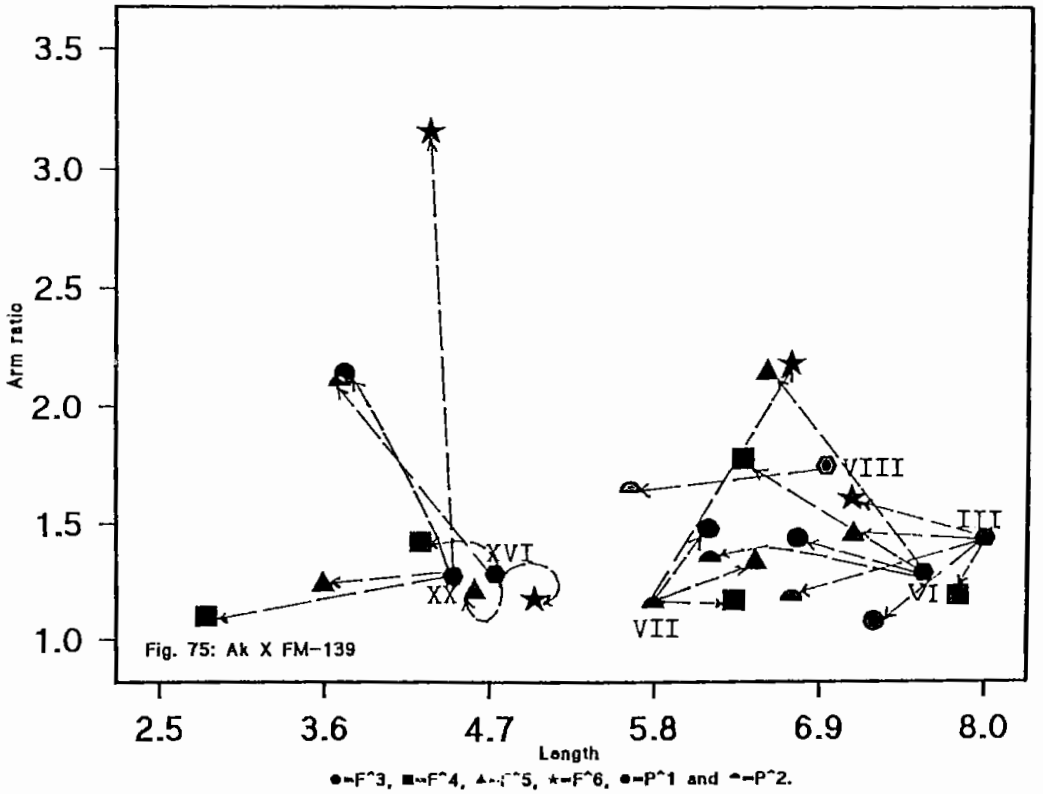
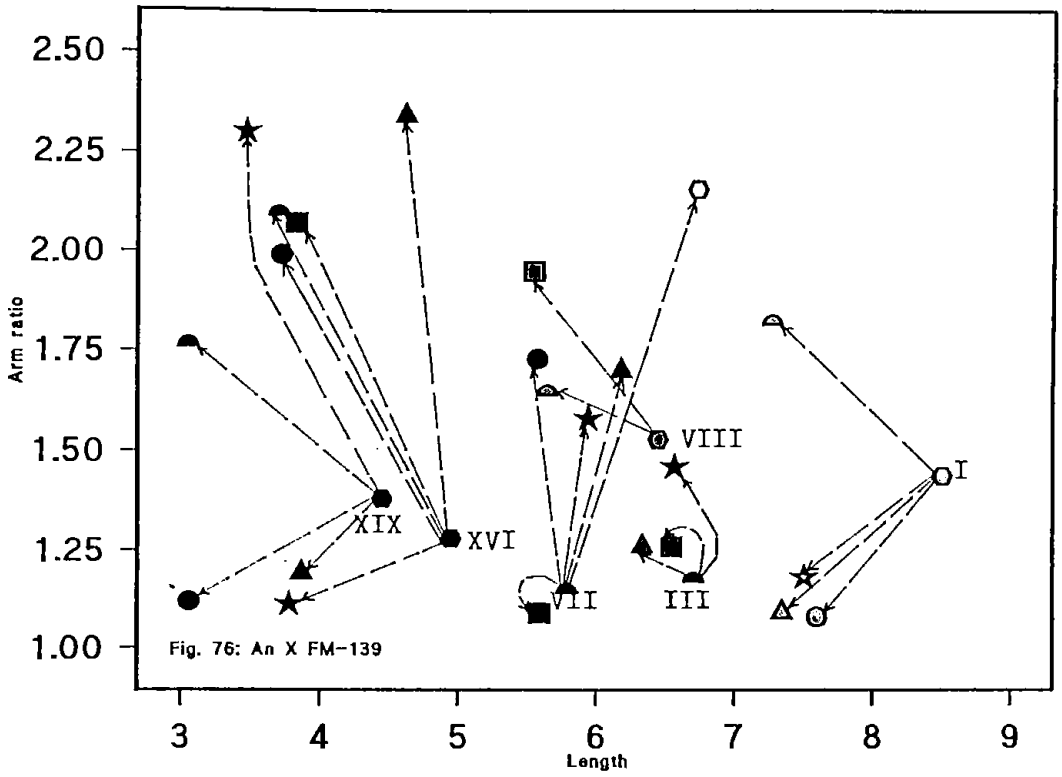
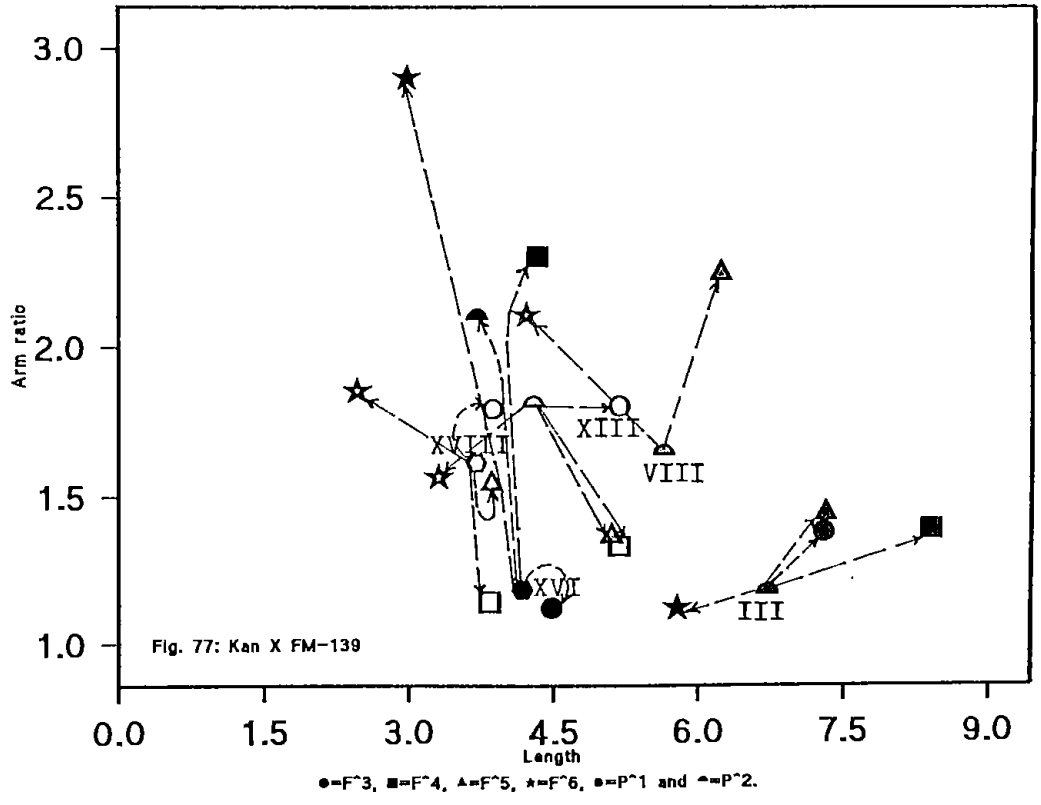


Fig. 75: Ak X FM-139

●=F^3, ■=F^4, ▲=F^5, ★=F^6, ●=P^1 and ^=P^2.

Figs. 74 & 75: Changes in the commonly identified chromosomes of Kan X FM-32 and Ak X FM-139 crosses.





Figs. 76 & 77: Changes in the commonly identified chromosomes of An X FM-139 and Kan X FM-139 crosses.

differed significantly due to changes in both the arms. Whereas, the long arm of chr.-X & XVI differed significantly but their total length remained as it was statistically. In case of FM-139, the total length and arm ratio of chr.- XVI was found to differ significantly due to change in it's short arm. The arm ratio, but not total length of chr.-I & X differed significantly for the change in their short arm. The chromosome-VII showed significant change only in long arm, while it's total length and arm ratio did not change statistically.

1. Ag X fm-32:

Five common chromosomes (*e.g.*, I, II, VI, VII & XXI) were identified individually in most of the generations of Ag X FM-32. The t-test indicated that F_3 generation did not show significant difference from their generation mean for any chromosome, in respect of both the arm lengths and ratios. It indicated the occurrence of non-structural changes in those chromosomes. The long arm of chr.-II in F_4 and chr.-VI in F_6 were found to differ significantly. The F_5 only differed significantly in respect of arm ratio of chr.-I & VI and for short arm of chr.-XXI. However, P_1 was found to differ significantly in respect of both arm and total lengths of chr.-I, short arm and total lengths, and arm ratios of chr.-II & VI and only in total length of chr.-VII. It indicated the occurrence of deletion in long and/or short arm of those chromosomes. The P_2 differed only in respect to arm ratio of chr.-I & VII and it indicated the occurrence of unequal translocation in those chromosomes.

2. Ak X FM-32:

Five common identifiable chromosomes (*e.g.*, I, IX, XVI, XX & XXI) were observed in most of the generations of Ak X FM-32. The test of significance indicated that the chromosome-I & XVI in P_1 (AK) and F_4, respectively differed significantly in respect of arm lengths and ratios from the generation mean. It might be due to deletion in both the arms of those chromosomes. Long arm length of the chromosome-IX in F_4 and P_1, total and long arm length of chromosome-XVI & XXI in F_3 and that of chromosome- XX in P_1 were found to differ significantly. Only the short arm length of chromosome-I in F_3 & P_2, that of chromosome-IX & XX in F_5 and that of chromosome-XVI in P_1 differed significantly. It might be due to deletion in one arm. Only the arm ratio of chromosome-XXI in p_2 (FM-32) differed significantly without modification of any length and it might be due to unequal translocation. However, the higher C.V. of arm length and ratio of chromosome-XVI & XXI indicated their poor reliability.

3. An X FM-32:

Four commonly identified chromosomes (*e.g.*, II, III, X & XXI) were observed in most of the generations of An X FM-32. The test of significance demonstrated that in F_3 none of these four chromosomes differed significantly from the generation mean in respect of both the length and arm ratio (Table 8). However, the chromosome-III in P_2 and chromosome-XXI in P_1 differed significantly in respect of the both arm length but not in arm ratio and it might be due to deletion of both arm. Whereas, in F_6 the chromosome-XXI differed significantly only in respect of arm ratio and it might be owe to the unequal translation. The

chromosome-III in F_4 and chromosome-X in F_6 were found to differ significantly in respect of arm ratio and length of one arm (S or L). It indicated that the deletion was occurred in one arm only.

4. Kan X FM-32:

In most of the generations of Kan X FM-32, four common identifiable chromosomes (*e.g.*, I, II & XXI) were observed . In F_6 none of these three chromosomes were found to differ significantly from the generation mean in respect of both the lengths and arm ratio. Here non-occurrence of true structural aberration was indicated. However, only the chromosome-XXI in P_1 were found to differ significantly in all lengths and arm ratio, whereas the chromosome-I of P_1 differed significantly in respect of one arm (S) length and ratio, which might be due to the occurrence of both/one arm(s). The long arm and total length but not arm ratio of chromosome-I & II in F_3 and the chromosome-XXI of F_4 differed significantly, whereas only the short arm length of chromosome-II in F_5 and chromosome-XXI in P_2 were found to differ significantly. It might be due to one arm deletion. In case of the chromosome-I of F_4, where only arm ratio was found to differ significantly because of the occurrence of unequal translocation.

5. Ak X FM-139:

Four identified chromosomes (*e.g.*, VI, VII, XVI & XX) were observed in most of the generations of Ak X FM-139. In F_3 none of these three chromosomes were found to differ significantly in respect of both the lengths and arm ratio.

Here, also non-occurrence of true structural aberration was indicated. However, only the chromosome-VII in F_6 was found to differ significantly in all lengths and arm ratio, while the chromosome-XVI in P_2 and chromosome-XX in F_6 were found to differ significantly in respect of one arm (S) and total length, and arm ratio. It might be due to the occurrence of deletion and/or duplication. Only one arm and/or total length but not the arm ratio of chromosome-XX in F_4, chromosome-XVI in F_6, chromosome-VI & XX in P_1 and chromosome-VI & VII in P_2 differed significantly. It might be due to the occurrence of deletion in one arm only. The chromosome-VI in F_5 was found to differ significantly in respect of arm ratio only and it might be due to the occurrence of unequal translocation.

6. An X FM-139:

Four common chromosomes (*e.g.*, I, VII, XVI & XIX) were identified in most of the generations of An X FM-139. The test of significance demonstrated that the chromosome-I in P_2, chromosome-VII in F_4 and P_2, and chromosome-XVI in F_5 and F_6 differed significantly from their mean values in respect to one arm length and arm ratio (Table 8). It might be due to the occurrence of deletion and/or duplication of their single arm. The chromosome-I and XIX in P_1 were found to differ only in respect of total length but not in arm length, which might be because of the deletion of both the arm. The chromosome-XIX in F_6 was found to differ significantly in respect of arm ratio only and it might be due to the occurrence of unequal translocation.

7. Kan X FM-139:

In Kan X FM-139 also four common identifiable chromosomes (*e.g.*, XIII, XVI & XVIII) were observed in most of the generations. In F_5, P_1 and P_2 none of these three chromosomes were found to differ significantly in respect of length and arm ratio from the generation mean. where non-occurrence of true structural aberration was indicated. However. the chromosome-III & XVI in F_6 were found to differ in respect of length and arm ratio. Deletion of one arm might be considered as the cause of such difference. The chromosome-XVI in F_3 & F_4 and chromosome-XIII & XVIII in F_6 differed significantly in respect of length but not in arm ratio. In this case. deletion of one and/or both arm(s) might be the cause of such difference. The chromosome-XVIII in F_4 was found to differ significantly in respect of arm ratio only and it might be due to the occurrence of unequal translocation.

I.5.2. Heterochromatin distribution and chromosome differentiation:

I.5.2.1. Heterochromatin distribution:

An effort was made to determine the heterochromatin distribution in metaphase chromosomes of common wheat by aceto-orecine and/or N-banding technique. The photomicrographs of banded chromosomes of six genotypes of wheat are shown in Figs. A-F.

The adopted technique yielded the heterochromatin differentially. Staining solution, however, greatly exceeding with buffer solution tended to inhibit the banding. More concentrated staining solution required a shorter staining time,

but the banding was not distinct. Geimsa diluted with 1/15 M Sorenson's phosphate buffer at pH 6.8 displayed somewhat recognizable bands with different classes of heterochromatin.

Nevertheless. the number and position of bands could be determined to identify the individual chromosome genomically. The size measurements were made from aceto-orecine stained chromosomes and then subjected to banding technique. Moreover, the haematoxylon staining technique and quantitative karyotypic analysis used in the preceding experiment, helped arranging the identified chromosomes in descending order within each genome.

To visualize the position and intensity of bands **Idiograms** were made for haploid complement of each genotype and these are shown in **Figs. G-L**.The position and number of bands for each chromosome pair of the six genotypes are also given in **Table 9**. All the chromosome pairs in most of the cases were found to be homomorphic. The maximum number of bands (175) were observed in **FM-32** and **FM-139**, and the minimum (168) in **Kanchan**. The remarkable feature was that both the exotic lines showed more number (175) of bands than the local varieties (168-170).

The maximum number of bands (15) was exhibited by the chromosome pair-VIII in Aghrani (Ag), Akbar (Ak), Kanchan (Kan) and FM-32; chromosome pair-III and VI in Ag; III in Kan, and V in Ananda (An) and Fm-139. The minimum number was 3 as revealed by the chromosome pair-XIII in all the genotypes. Along with this the chromosome pairs IX and XXI in Ag have had also the minimum number of bands (3). It is also mentionable that both the highest (15) and lowest (3) number of bands were observed in six different chromosome pairs in Ag.

Table 9. Genomic designation and positon & number of heterochromatic bands for each chromosome of the haploid complements of parental varieties/lines.

No. of chromo. pairs & Genomes		Aghrani (Ag)			Akbar (Ak)		
		Position of landmark bands		Total bands	Position of landmark bands		Total bands
		Short arm (S)	Long arm (L)		Short arm (S)	Long arm (L)	
I	1B	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	11	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	12
II	2B	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	10	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	10
III	3B	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	15	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	14
IV	1D	1.5(0.89)	–	8	1.5(0.89)	–	7
V	4B	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	11	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	12
VI	5B	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	15	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	14
VII	1A	–	–	5	–	–	6
VIII	6B	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	15	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	15
IX	2A	1.3(0.22)	–	3	1.3(0.22)	–	4
X	3A	1.3(0.72)	1.3(0.19),1.5(0.55)	5	1.3(0.72)	1.3(0.19),1.5(0.55)	5
XI	7B	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	11	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	11
XII	2D	1.3(0.79)	1.5(0.71)	9	1.3(0.79)	1.5(0.71)	8
XIII	4A	–	1.3(0.20)	3	–	1.3(0.20)	3
XIV	3D	–	–		1.3(0.32),	1.3(0.68),1.5(0.85)	6
XV	5A	1.3(0.29)	1.5(0.56)	6	1.3(0.29)	1.5(0.56)	6
XVI	4D	1.3(0.25),1.5(0.57)	1.5(0.83)	8	1.3(0.25),1.5(0.57)	1.5(0.83)	7
XVII	5D	–	–		1.3(0.22),	1.5(0.38),1.7(0.65)	8
XVIII	6D	1.5(0.56),	1.3(0.28),1.5(0.83)	8	–	1.3(0.28),1.5(0.83)	7
XIX	6A	–	1.3(0.16),1.5(0.55)	4	–	1.3(0.16),1.5(0.55)	4
XX	7D	1.5(0.44)	–	7	–	–	
XXI	7A	1.3(0.68)	1.3(0.34),1.5(0.68)	3	1.3(0.68)	1.3(0.34),1.5(0.68)	4
Total				170			169

Table : (Continued)

No. of chromo. pairs & Genomes	Ananda (An)			Kanchan (Kan)		
	Position of landmark bands		Total bands	Position of landmark bands		Total bands
	Short arm (S)	Long arm (L)		Short arm (S)	Long arm (L)	
I 1B	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	11	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	10
II 2B	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	11	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	12
III 3B	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	14	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	15
IV 1D	1.5(0.89)	1.3(0.25)	7	–	–	
V 4B	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	11	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	10
VI 5B	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	15	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	14
VII 1A	-	–	6	-	–	6
VIII 6B	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	14	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	15
IX 2A	1.3(0.22)	-	4	1.3(0.22)	-	4
X 3A	1.3(0.72)	1.3(0.19),1.5(0.55)	5	1.3(0.72)	1.3(0.19),1.5(0.55)	5
XI 7B	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	12	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	11
XII 2D	1.3(0.79)	1.5(0.71)	7	1.3(0.79)	1.5(0.71)	7
XIII 4A	-	1.3(0.20)	3	-	1.3(0.20)	3
XIV 3D	1.3(0.32),1.5(0.65)	1.3(0.68),1.5(0.85)	7	1.3(0.32),1.5(0.65)	1.3(0.68),1.5(0.85)	6
XV 5A	1.3(0.29)	1.5(0.56)	6	1.3(0.29)	1.5(0.56)	7
XVI 4D	–	–		1.3(0.25),1.5(0.57)	1.5(0.83)	8
XVII 5D	–	–		1.3(0.22),1.5(0.74)	1.5(0.38),1.7(0.65)	7
XVIII 6D	–	–	7	1.5(0.56),1.7(0.77)	1.3(0.28),1.5(0.83)	7
XIX 6A	-	1.3(0.16),1.5(0.55)	4	–	1.3(0.16),1.5(0.55)	4
XX 7D	1.5(0.44)		5	–	–	
XXI 7A	1.3(0.68)	1.3(0.34),1.5(0.68)	5	1.3(0.68)	1.3(0.34),1.5(0.68)	5
Total			169			168

Table : (Continued)

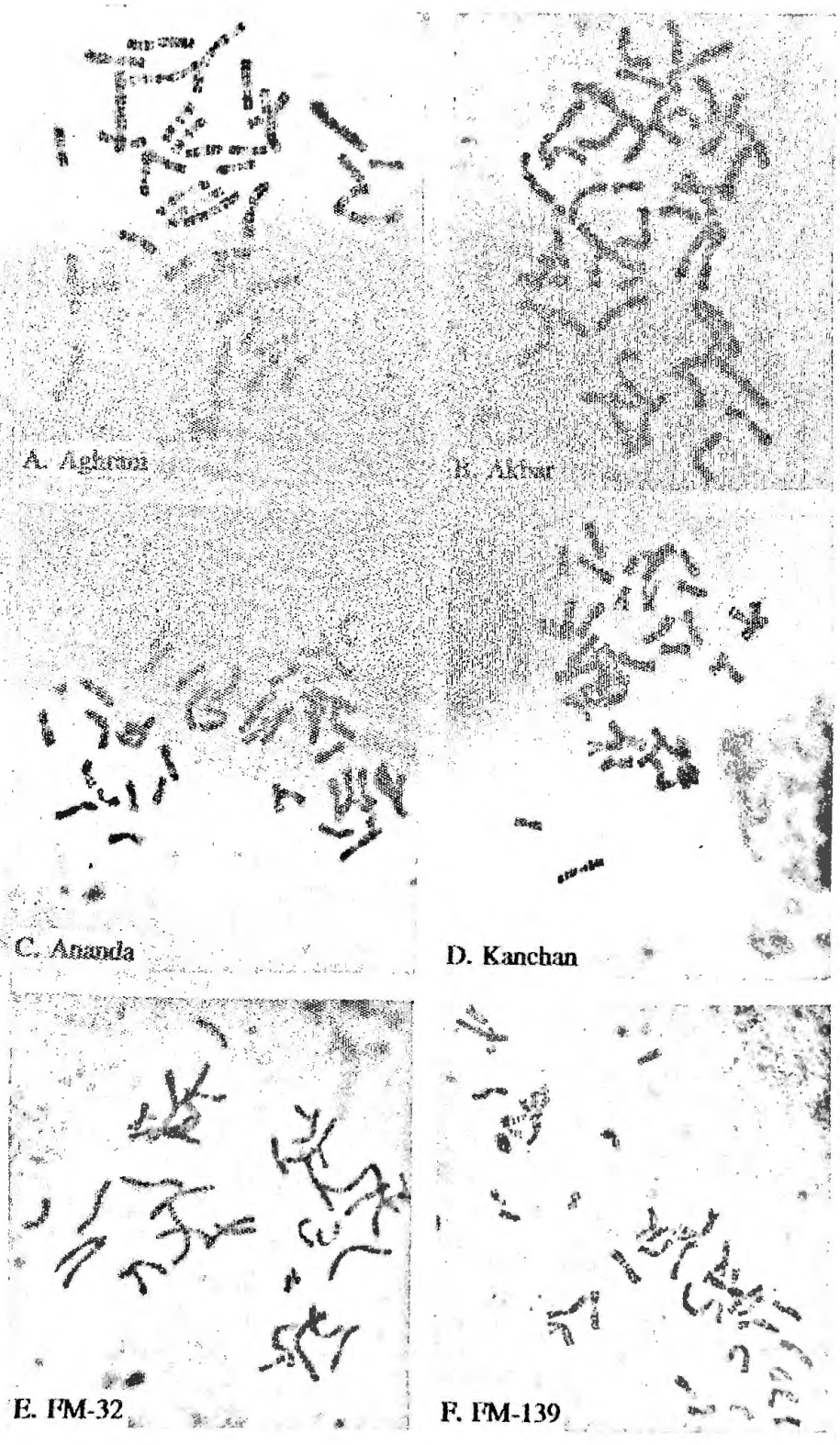
No. of chromo. pairs & Genomes		Fal/Max-32 (FM-32)			Fal/Max-139 (FM-139)		
		Position of landmark bands		Total bands	Position of landmark bands		Total bands
		Short arm (S)	Long arm (L)		Short arm (S)	Long arm (L)	
I	1B	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	11	1.3(0.24),1.5(0.36)	1.3(0.12),2.1(0.20)	12
II	2B	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	12	1.3(0.18),1.5(0.26)	1.3(0.11),2.1(0.50)	11
III	3B	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	13	1.3(0.11),1.4(0.22)	2.1(0.36),2.3(0.55)	13
IV	1D	-	-		1.5(0.89)	1.3(0.25)	7
V	4B	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	12	1.3(0.10),1.5(0.28)	2.1(0.37),2.5(0.61)	12
VI	5B	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	14	1.3(0.39),2.3(0.71)	2.1(0.49),2.5(0.65)	15
VII	2D	-	1.3(0.19),2.3(0.74)	7	-	-	
VIII	6B	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	15	1.3(0.10),1.5(0.21)	2.3(0.50),2.5(0.60)	14
IX	1A	-	-	6	-	-	5
X	2A	1.3(0.72)	1.3(0.19),1.5(0.55)	5	1.3(0.72)	1.3(0.19),1.5(0.55)	5
XI	7B	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	13	1.3(0.37),1.7(0.47)	2.1(0.42),2.3(0.61)	13
XII	3A	1.3(0.79)	1.5(0.71)	5	1.3(0.79)	1.5(0.71)	6
XIII	4A	-	1.3(0.20)	3	-	1.3(0.20)	3
XIV	5A	1.3(0.32),1.5(0.65)	1.3(0.68),1.5(0.85)	6	1.3(0.32),1.5(0.65)	1.3(0.68),1.5(0.85)	6
XV	3D	-	-		1.3(0.29)	1.5(0.56)	8
XVI	4D	1.3(0.25),1.5(0.57)	1.5(0.83)	8	1.3(0.25),1.5(0.57)	1.5(0.83)	7
XVII	5D	1.3(0.22),1.5(0.74)	1.5(0.38),1.7(0.65)	7	1.3(0.22),1.5(0.74)	1.5(0.38),1.7(0.65)	7
XVIII	6D	1.5(0.56),1.7(0.77)	1.3(0.28),1.5(0.83)	8	1.5(0.56),1.7(0.77)	1.3(0.28),1.5(0.83)	8
XIX	6A	-	1.3(0.16),1.5(0.55)	4	-	1.3(0.16),1.5(0.55)	4
XX	7D	1.5(0.44)	1.5(0.39),1.7(0.65)	7	1.5(0.44)	1.5(0.39),1.7(0.65)	7
XXI	7A	1.3(0.68)	1.3(0.34),1.5(0.68)	6	1.3(0.68)	1.3(0.34),1.5(0.68)	6
Total				175			175

Since some of the chromosome pairs in all the cases exhibited identical number of bands. the number of banding patterns become reduced to 9 in An, 10 in Ag and 11 in Ak. Kan. Fm-32 and FM-139. This , in turn, was assumed that the later genotypes were derived from a more advanced progenitor compared to that of the former two. However, the chromosome pairs XIV and XVIII in Ag, XX in Ak and Kan. XVI and XVII in Ananda, IV and XV in Fm-32 , and VII in Fm-139 did not show any distinctly dark or faint band; while their positions in the Idiogram of banded chromosomes have been shown as it was found in the 'standard karyotype'(Figs. 1-6.)

I.1.5.2. Chromosome differentiation:

Idiograms (Figs. G-L) of banded chromosomes of the haploid complement based on different genomes of the studied genotypes were constructed following few conditions as described bellow:

Centromeric heterochromatin was not observed in any of the chromosomes of a metaphase cell, but the first band in each chromosome belonged to centromeric heterochromatin. All dark bands were considered as landmark bands, whose number and position were used as diagnostic feature in the identification of individual chromosome. The B genome chromosomes were highly heterochromatic than the others, as they contained a series of proximal bands and their number of bands were 10 and above. D genome chromosomes were distinguished from A genome chromosomes by more distal landmark bands at the short arm (except 7D and 4A) and the number of bands were ranged from 6 to 9. Whereas the least



Figs. A-F. Representative plate for banded metaphase chromosomes in six varieties/lines of wheat (Ca 750X).

G. Aghrani

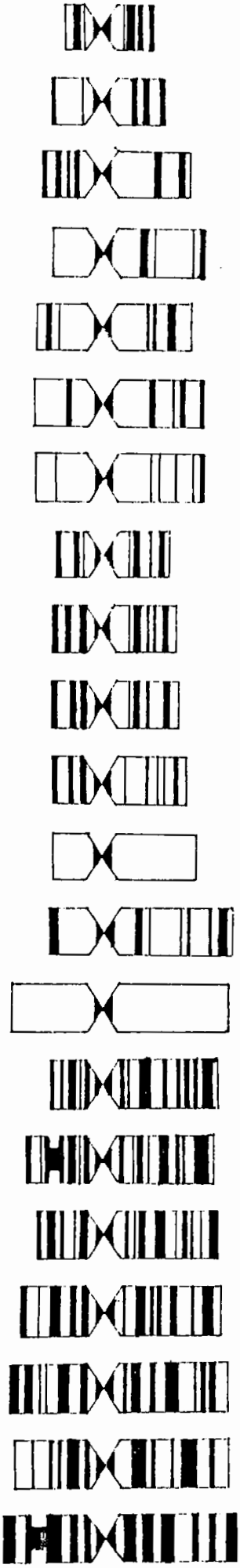
H. Akbar

Figs. G & H. Idiogram of banded chromosomes at metaphase in Aghrani and Akbar.

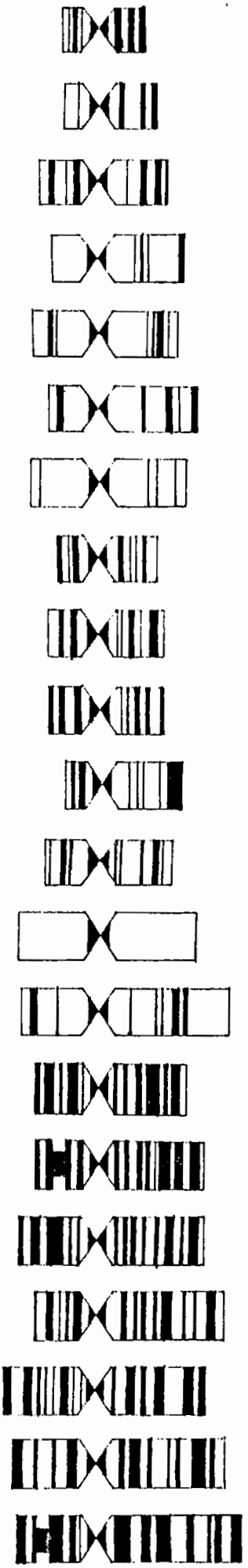
I. Ananda

J. Kanchan

Figs. I & J. Idiogram of banded chromosomes at metaphase in Ananda and Kanchan.



K. FM-32



L. FM-139

Figs. K & L. Idiogram of banded chromosomes at metaphase in FM-32 and FM-139.

number of bands (3 to 6) were found in the A genome chromosome. The individual chromosomes within each genome was distinguished and designated on the basis of previously proposed **standard karyotype.** Above all, in difficult situations, specially where landmark band was either indistinguishable or absent, the **'Description of individual chromosomes'** from Gill *et al.* (1991) were used for the identification of genome-based individual chromosome of the studied materials.

The overall banding patterns of the studied genotypes were mostly similar to the Chinese Spring as reported by Gill *et al.* (1991). The highly heterochromatic and mostly polymorphic but nearly identical in banding patterns of the B genome chromosomes corresponded individually in all the genotypes. In the D genome, 6D chromosome was identified individually and its banding pattern was almost identical in all the genotypes. 1D in FM-139, 3D in Ag and FM-32, 4D in An, 5D in Ag and An, and 7D in Ak and Kan were not found to be banded and remained as unidentifiable, although their position in Karyotype were determined on the basis of probabilistic inferences. In the A genome chromosomes, the banding pattern of 3A, 4A and 6A were quite similar in all the genotypes. However, the remaining chromosomes of A genome showed little difference in their heterochromatinization of different genotypes.

I.5.3. Chiasma frequency and chromosome association:

Genome analysis measures the total amount of chromosome pairing per cell. The determination of genomic homology becomes more difficult when the exact basic number of bivalent can not be found and multivalent become evident in

wheat. Therefore, the change in chiasma frequency and/or the distribution pattern of chiasmata in different genotypes of wheat were studied and the findings are described bellow:

I.5.3.1. Mean performances:

The mean values with standard error for different meiotic features in three types of plants of four different crosses are presented in Table 10. The t-test was used to compare the NILs with the check variety (Kanchan). There was a significant increase in bivalent frequency of all the semidwarf (N) populations except Kan X FM-32 with a corresponding significant decrease in quadrivalent frequency compared to that of check variety. However, significant increase in both the bivalent and quadrivalent frequencies were found in dwarf Type-III of An X FM-32. Significant decreased frequency of bivalent in all the types (N, II & III) of Kan X FM-32 and Type-II of An X FM-32 were observed.

A significantly increased disjunction index and proportion of regular tetrad were observed only in the N-population of Ak X FM-32. However, these two meiotic features were found to be decreased significantly in Type-II and Type-III populations of Kan X FM-32 compared to that of check variety. It is an important fact that no significant differences in pairing configurations were noticed in any of the population in comparison to that of the check variety.

Table 10: Mean performance of meiotic features in 12 Near Isogenic Lines (NILs) along with a check variety.

Meiotic features	Statistics	Check variety (Kan)	Cross 1: Ag X FM-32			Cross 2: Ak X FM-32			CRoss 3: An X FM-32			Cross 4: Kan X FM-32		
			N	II	III	N	II	III	N	II	III	N	II	III
Chiasma frequency	X	42.30	44.27*	40.93	42.87	44.97*	40.73	44.90*	44.13*	40.23*	43.10	39.93*	36.73*	39.53*
	S.E	±0.45	±0.29	±0.28	±0.37	±0.23	±0.48	±0.23	±0.34	±0.41	±0.36	±0.25	±0.27	±0.34
Bivalent frequqncy	X	18.90	20.40*	19.53	19.93	20.27*	19.23	20.00*	20.10*	19.17	20.37*	19.87	17.57*	19.53
	S.E	±0.29	±0.21	±0.29	±0.22	±0.20	±0.24	±0.21	±0.20	±0.27	±0.20	±0.20	±0.24	±0.22
Quadriva-lent freq	X	0.67	0.10	0.33	0.13	0.10	0.37	0.23	1.17	0.37	1.50	0.33	0.67	0.43
	S.E	±0.14	±0.07	±0.11	±0.07	±0.07	±0.10	±0.09	±0.06	±0.11	±0.11	±0.10	±0.10	±0.10
Trivalent frequency	X	0.37	0.20	0.33	0.40	0.23	0.47	0.27	0.20	0.50	0.23	0.23	1.03	0.27
	S.E	±0.10	±0.09	±0.10	±0.11	±0.09	±0.12	±0.10	±0.09	±0.13	±0.10	±0.10	±0.17	±0.11
Univalent frequency	X	0.43	0.20	0.60	0.40	0.23	0.67	0.27	0.27	0.50	0.16	0.23	1.00	0.40
	S.E	±0.11	±0.09	±0.14	±0.11	±0.09	±0.15	±0.10	±0.11	±0.13	±0.08	±0.10	±0.19	±0.13
Chr. No. in II+IV	X	40.47	41.20	40.40	40.40	40.80	39.93	40.93	41.00	39.67	41.13	41.13	37.80	40.80
	S.E	±0.36	±0.31	±0.34	±0.37	±0.35	±0.39	±0.30	±0.33	±0.48	±0.33	±0.30	±0.40	±0.31
Chr. No. in III+I	X	1.53	0.80	3.69	1.60	1.07	2.07	1.07	1.00	2.33	0.87	0.93	4.20	1.20
	S.E	±0.41	±0.35	±0.25	±0.42	±0.34	±0.45	±0.34	±0.38	±0.55	±0.38	±0.34	±0.46	±0.35
Disjuncti-on index	X	69.47	69.33	60.65*	67.31	76.57*	60.66*	67.61	70.36	59.39*	65.78	66.94	53.22*	58.41*
	S.E	±1.28	±0.76	±0.34	±0.39	±0.57	±0.70	±0.57	±0.45	±0.39	±0.55	±0.49	±0.37	±0.39
Regular tetrad	X	74.83	76.77	65.23*	73.06	83.79*	64.77*	71.79	77.88	64.76*	74.93	75.87	59.32*	66.31*
	S.E	±0.85	±0.65	±0.46	±0.55	±0.42	±0.73	±0.55	±0.46	±0.17	±0.72	±0.57	±0.41	±0.43

'*' indicating significant at 0.05 level of significance
N = Semidwarf. II = Dwarf type II and III = Dwarf type III

I.5.3.2. Regression coefficients of chiasma frequency:

The regression coefficients and lines of chiasma frequency on different meiotic features are shown in Table 11. and Figs. 78 - 109, respectively. Chiasma frequency exerted a significant positive influence on bivalent frequency in all the N-populations except the Ag X FM-32, in all Type II populations except Kan X FM-32, in all Type III populations except Ak X FM-32 and in check variety also. Thus, the direct influence of chiasma frequency on bivalent formation was noticed in most of the cases.

The inverse (negative) influence of chiasma frequency on univalent and multivalent formation were observed in most of the studied populations (Figs. 78-109). An interesting point is that all the N-populations of Kan X FM-32 and Type II population of An X FM-32 showed significant negative regression coefficients, which indicating the residual homology or translocation heterozygosity in those cases.

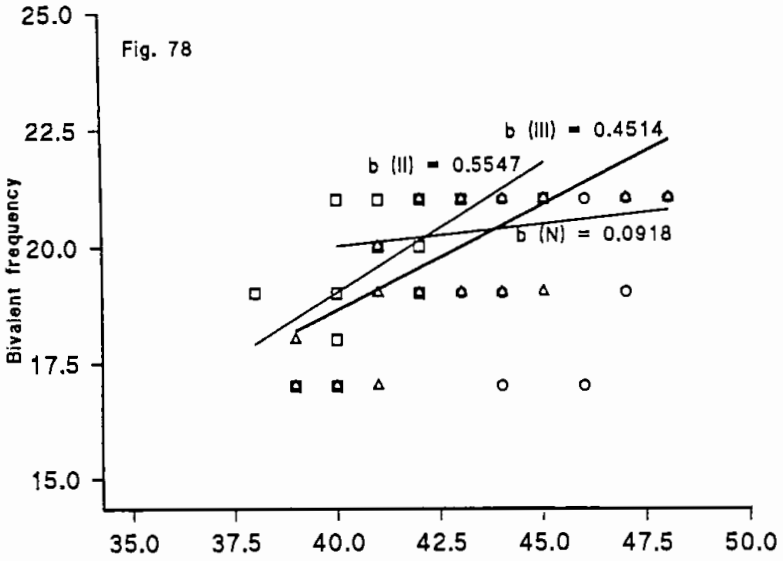
Both the quadrivalent and bivalent were found to produce balanced gametes by equal chromosomal disjunction at anaphase-I. The disjunction index gave an estimate of the proportion of balanced gametes, expected from the chromosome pairing configuration at meta-I. Moreover, the proportion of regular tetrad gave an idea about the fertility status of the populations. The regression coefficients of chiasma frequency on the number of chromosomes involved in bivalent and quadrivalent, and disjunction index appeared to be significant and positive in Type III populations of An X FM-32 and Kan X FM-32, and Type-II of Ak X FM-32 along with check variety. However, the Type-II of An X FM-32 and semidwarf (N)

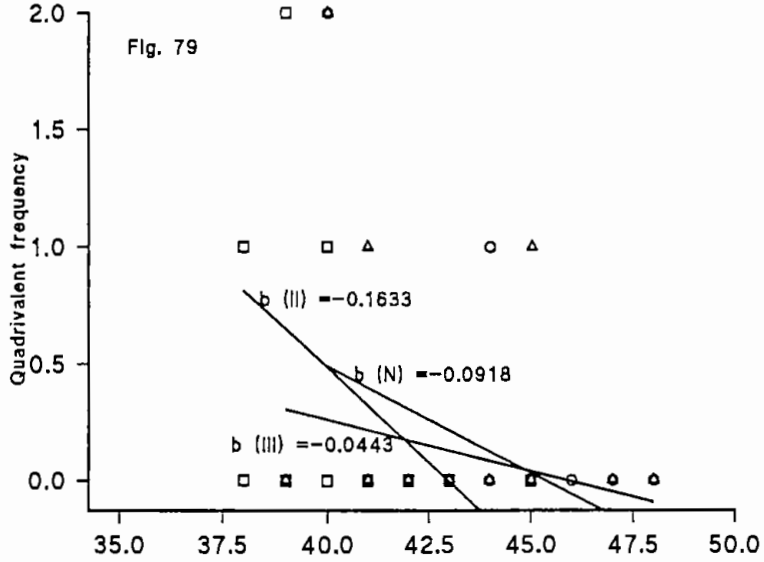
Table 11: Regression coefficients (b) and it's t-values for chiasma frequency on mitotic features of three types of plants from each of the four crosses, and the check variety.

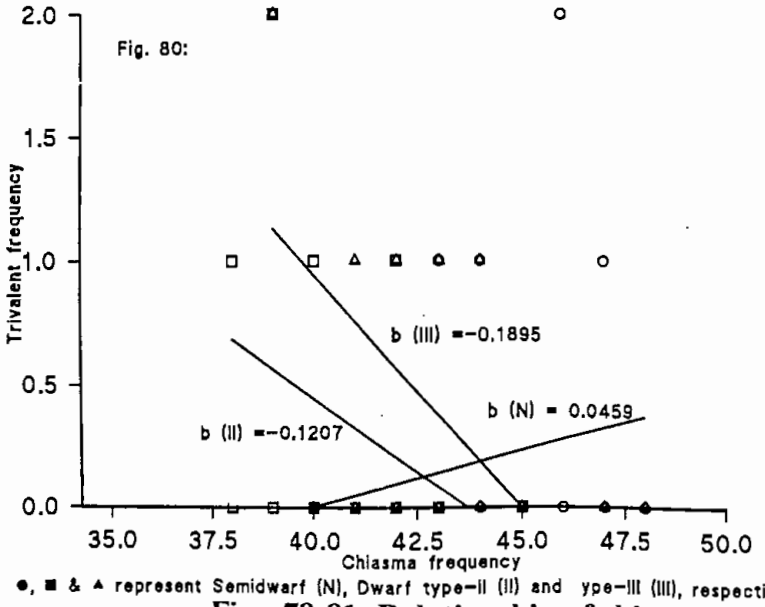
Meiotic feature	Statistics	Check variety Kanchan	Cross 1: Ag X FM-32			Cross 2: Ak X FM-32			Cross 3: An X FM-32			Cross 4: Kan X FM-32		
			N	II	III	N	II	III	N	II	III	N	II	III
Bivalent freq.	b	0.4058	0.0918	0.5547*	0.4514*	0.4250*	0.4681*	-0.0659	0.4166*	0.5939*	0.4151*	0.5807*	-0.0057	0.4731*
	t_b	4.2692*	0.6837	4.3578*	4.7890*	2.9657*	8.5222*	0.3777	5.2493*	10.306*	5.9972*	5.6523*	0.0338	5.7717*
Quadrivalent freq.	b	-0.0592	-0.0918*	-0.1634*	-0.0443	-0.0445	-0.1310*	0.0939	-0.1109*	-0.1167*	-0.0634	-0.1577*	0.0774	-0.1086*
	t_b	1.2099	2.4108*	2.9314*	1.1392	0.8572	4.5449*	1.4807	2.9849*	2.4419*	2.0042	2.6963*	1.2957	2.4205*
Trivalent freq.	b	-0.1071*	0.0459	-0.1207*	-0.1895*	-0.1203	-0.1049*	-0.0857	-0.0809	-0.1422*	-0.1547*	-0.1327*	-0.0456	-0.1329*
	t_b	3.4815*	0.9258	2.2889*	4.2838*	1.9465	2.4896*	1.2966	2.0316	2.7721*	4.0967*	2.0908*	0.4384	3.0225*
Univalent freq.	b	-0.1604*	0.0459	-0.0937	-0.1571*	-0.1811*	0.0977	0.0132	-0.0248	-0.1629*	-0.1125*	-0.1327*	-0.1710	-0.1193
	t_b	5.6720*	0.9258	1.1871	3.2353*	3.310*	1.8927	0.1941	0.4846	3.5065*	3.4713*	2.0908*	1.5047	2.0339
Chr. No. in II+IV	b	0.5747	-0.1836	0.4560*	0.7257*	0.7204*	0.4123*	0.2438	0.3896*	0.7878	0.5767*	0.4212	0.2980	0.5179*
	t_b	5.5312*	0.9258	2.2121*	4.4933*	2.9692*	2.7255*	1.0139	2.3162*	0.6243	4.2208*	2.0060	1.0649	3.7887*
Chr. No. in III+I	b	-0.5747*	0.1836	-0.4560*	-0.7257*	-0.5993*	-0.4123*	-0.2438	-0.3896*	-0.7878*	-0.5767*	-0.5306*	-0.2980	-0.4888*
	t_b	5.5312*	0.9258	2.2121*	4.4933*	2.8842*	2.7255*	1.0139	2.3162*	4.8195*	4.2167*	2.6243*	1.0649	3.4798*
Disjunction index	b	0.3167*	0.2149	-0.4194	-0.1031	0.5333	0.7203*	-0.1714	0.2724	0.4893*	0.7587*	0.8080*	0.1587	0.5297*
	t_b	3.0605*	0.4312	1.6204	0.4719	1.2035	2.679*	0.3676	1.1076	3.1535*	2.9468*	2.3924*	0.5988	2.8397*
Regular tetrad	b	0.0826	0.6624	-0.5811	0.0723	0.0553	0.7062*	-0.1238	-0.2671	0.2083*	0.7900*	0.2919	0.0388	0.7975*
	t_b	1.3495	1.6245	2.0287	0.2096	0.1661	2.4605*	0.2737	1.0357	3.0932*	2.2347*	0.6819	0.1356	4.3607*

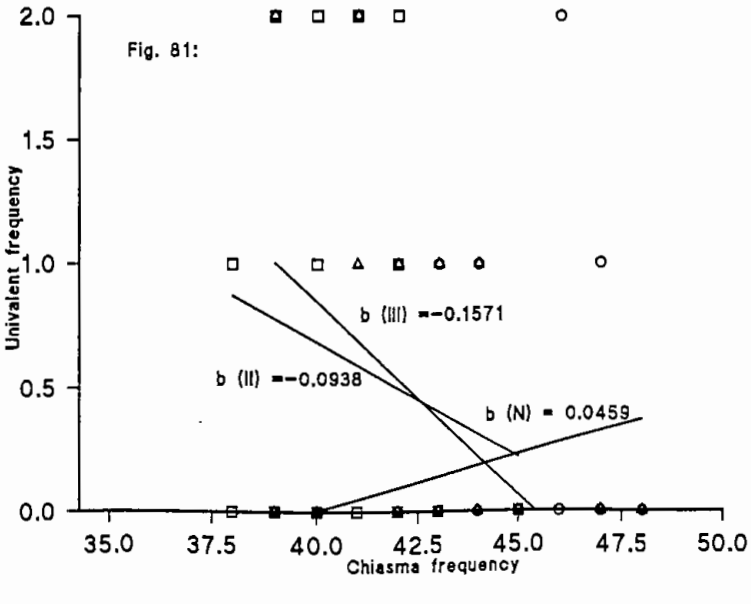
'*' indicating significant at 0.05 level of significance

N = Semidwarf, II = Dwarf type II and III = Dwarf type III



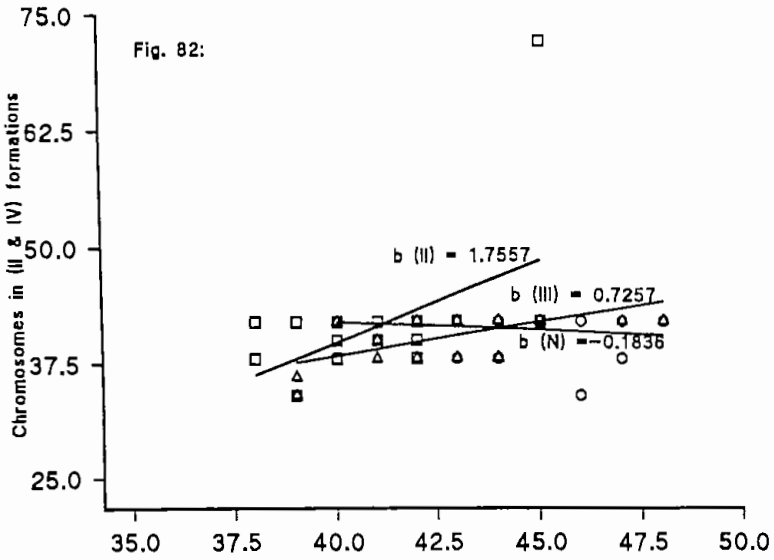


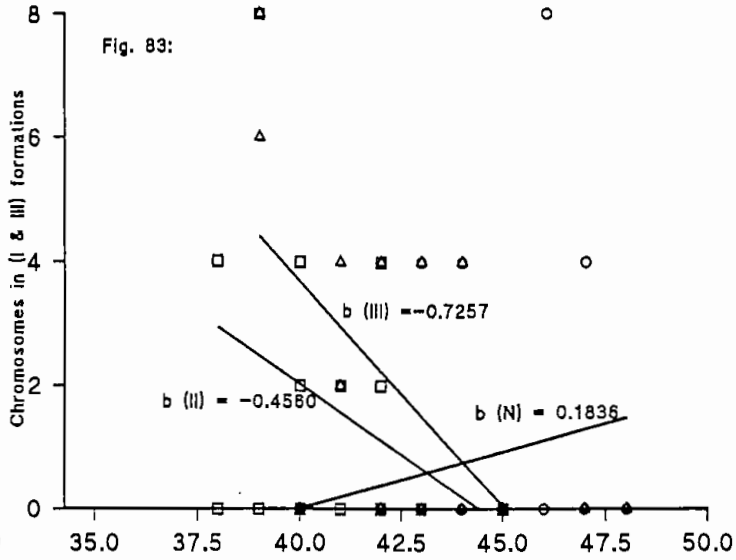


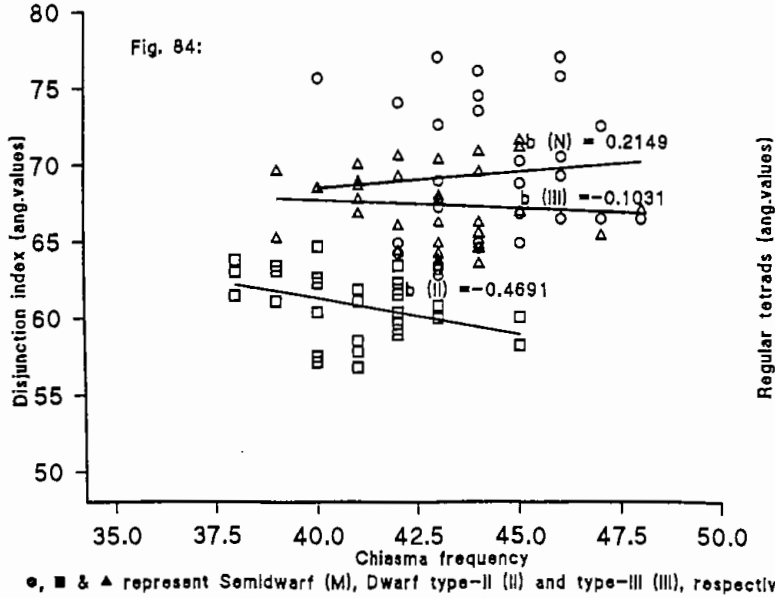


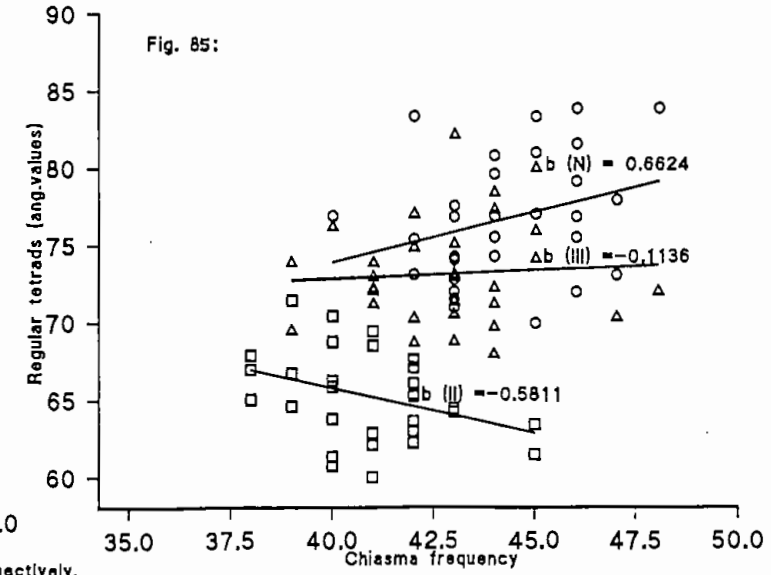
●, ■ & ▲ represent Semidwarf (N), Dwarf type-II (II) and ype-III (III), respectively.

Figs. 78-81: Relationship of chiasma frequency with pairing configurations in three selected populations (N, II & III) of Ag X FM-32.



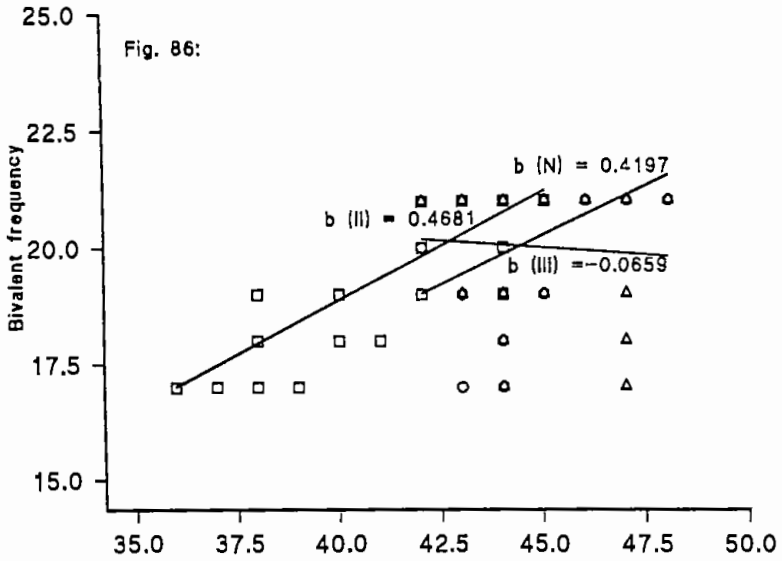


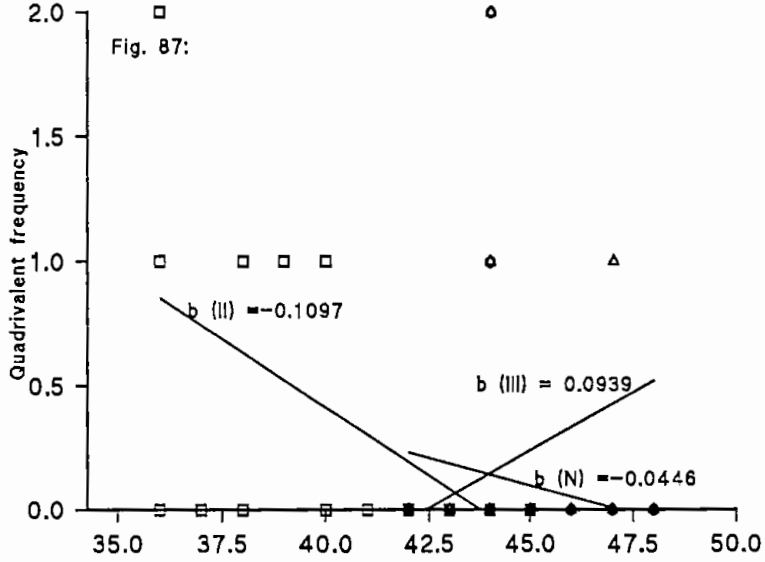


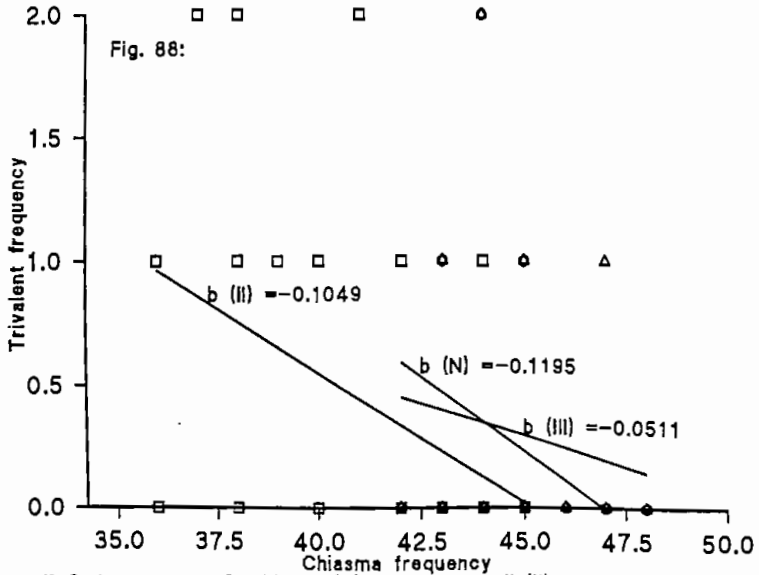


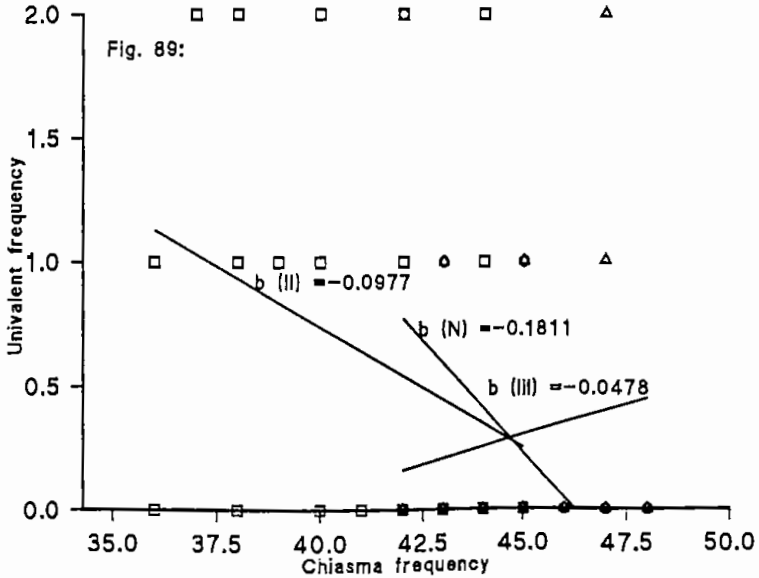
●, ■ & ▲ represent Semidwarf (M), Dwarf type-II (II) and type-III (III), respectively.

Figs. 82-85: Relationship of chiasma frequency with other meiotic features in three selected populations (N, II & III) of Ag X FM-32.



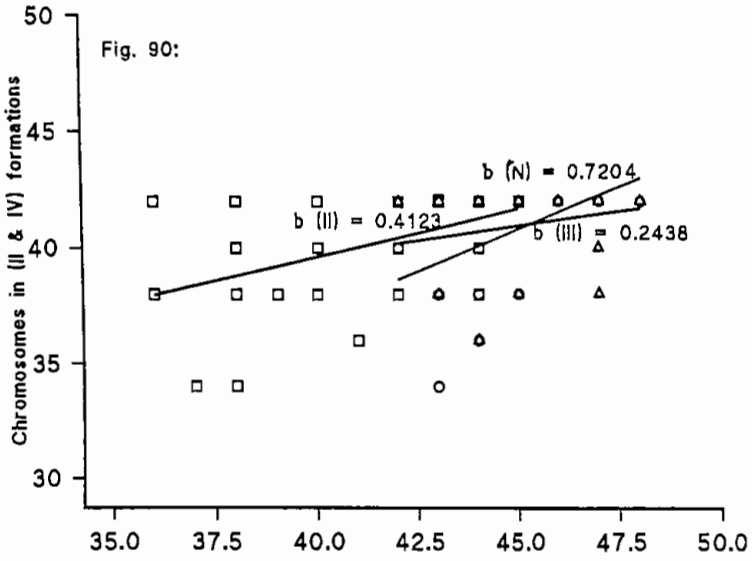


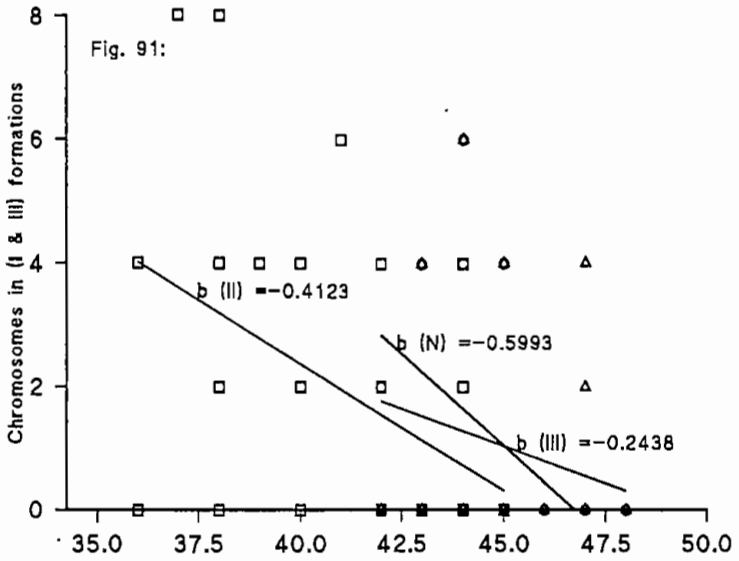


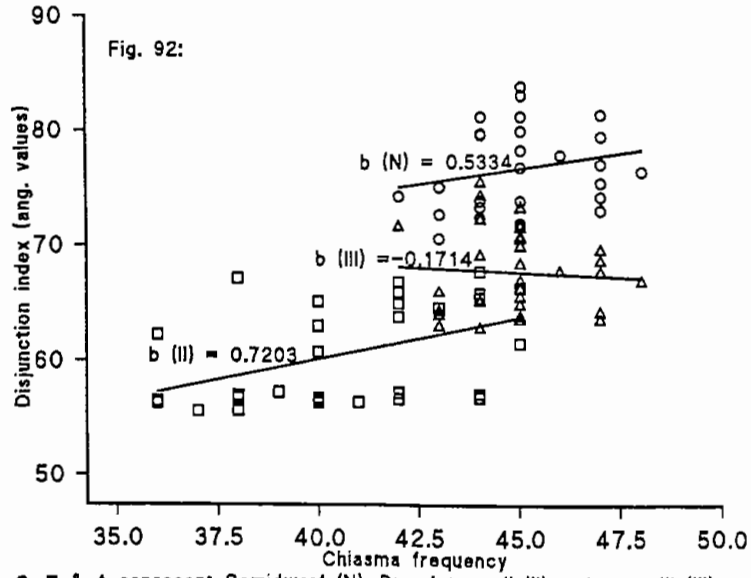


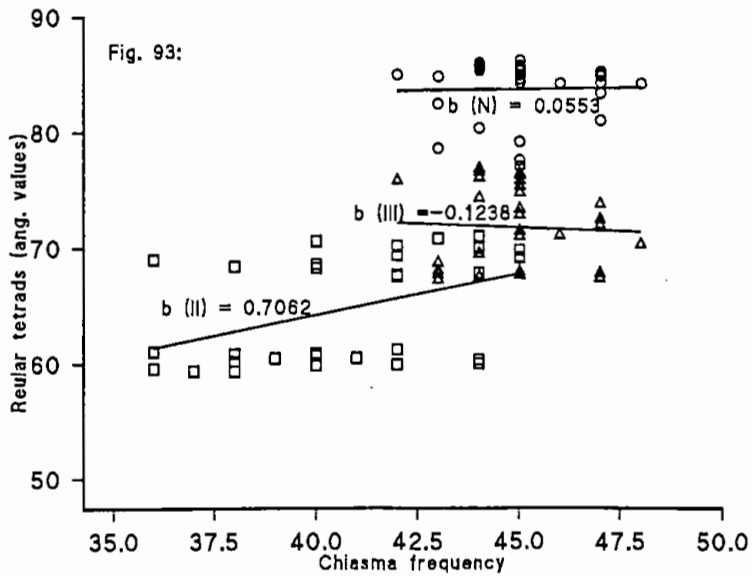
●, ■ & ▲ represent Semidwarf (N), Dwarf type-II (II) and type-III (III), respectively.

Figs. 86-89: Relationship of chiasma frequency with pairing configurations in three selected populations (N, II & III) of Ak X FM-32.



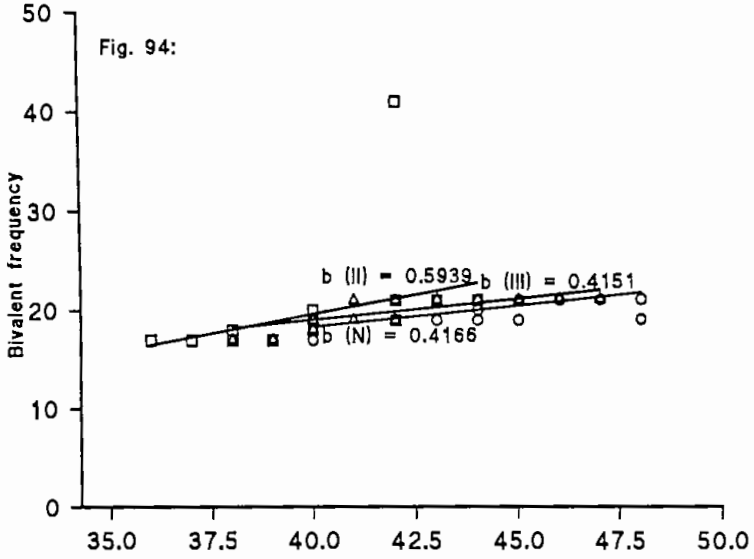


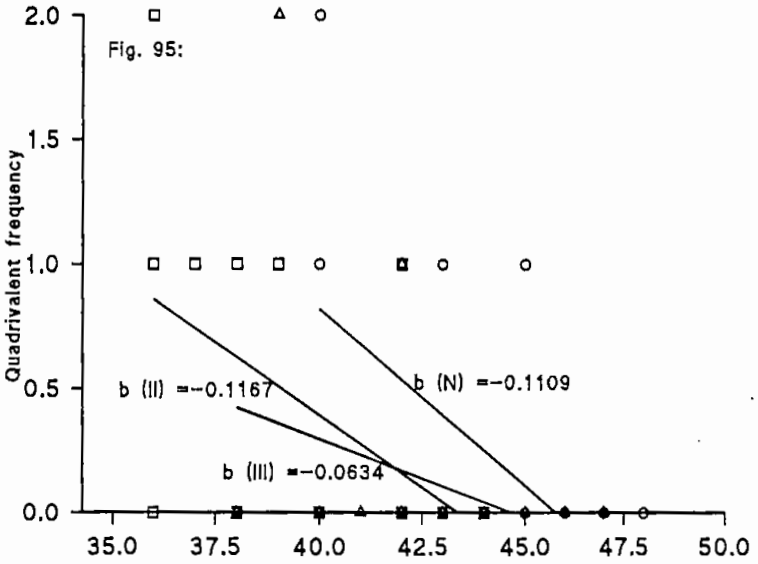


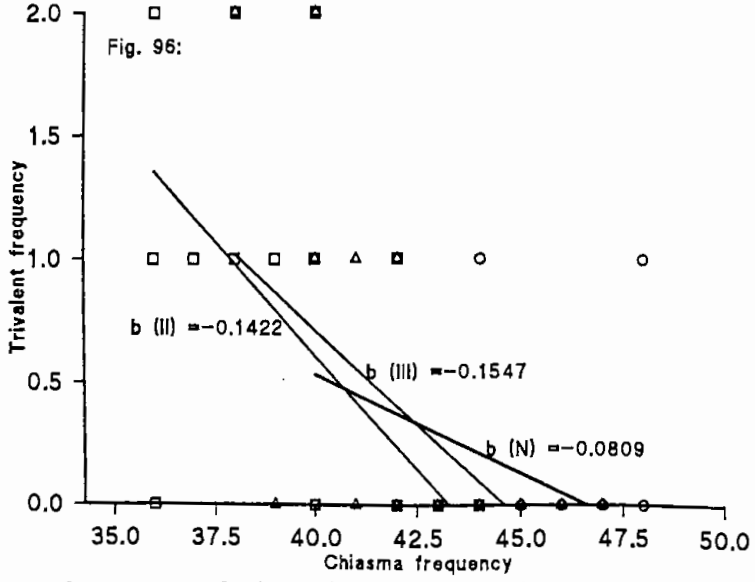


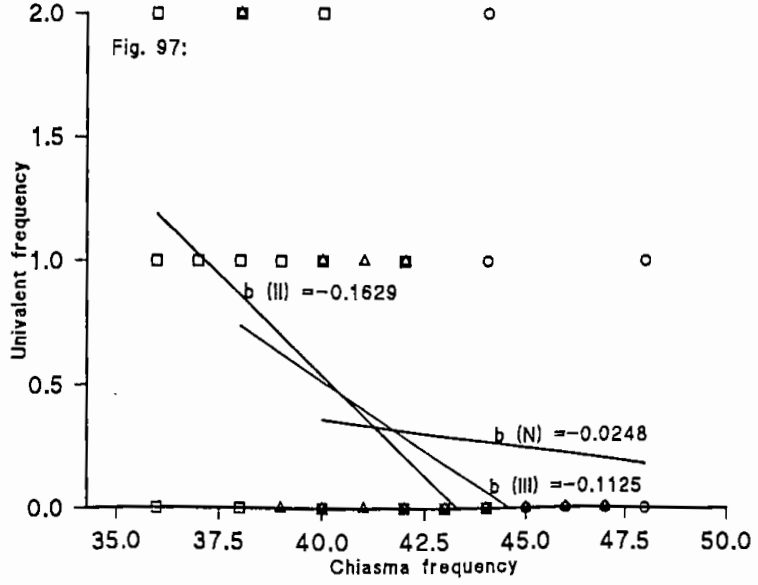
●, ■ & ▲ represent Semidwarf (N), Dwarf type-II (II) and type-III (III), respectively.

Figs. 90-93: Relationship of chiasma frequency with other meiotic features in three selected populations (N, II & III) of Ak X FM-32.



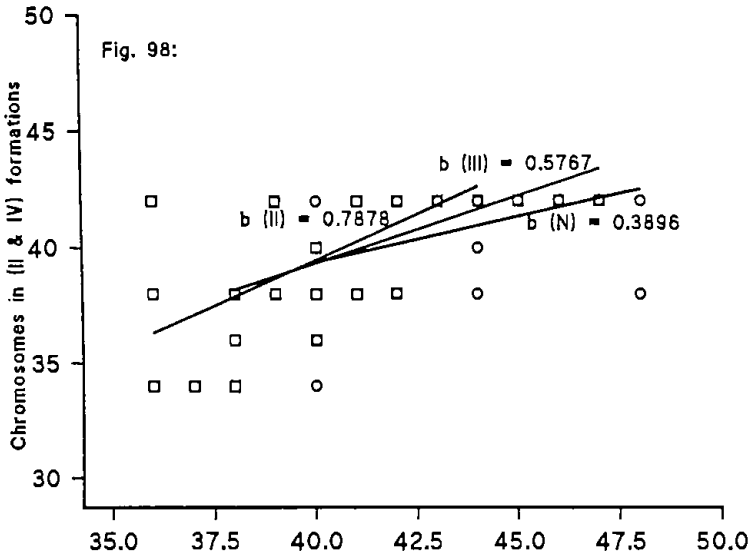


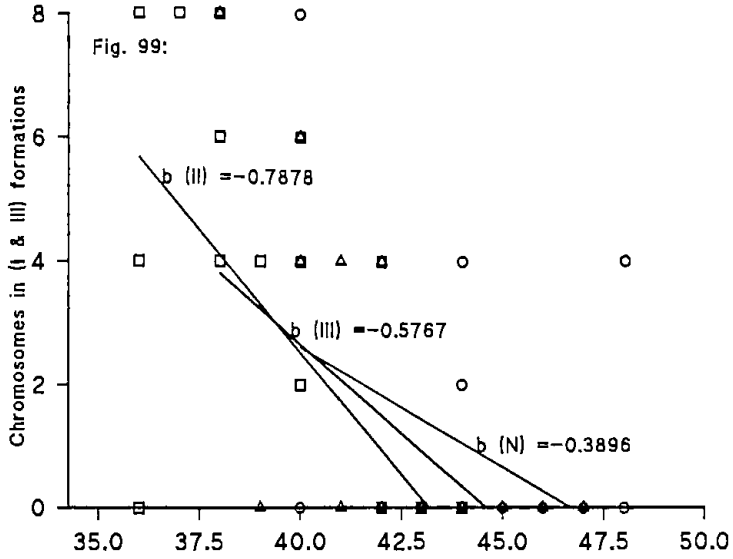


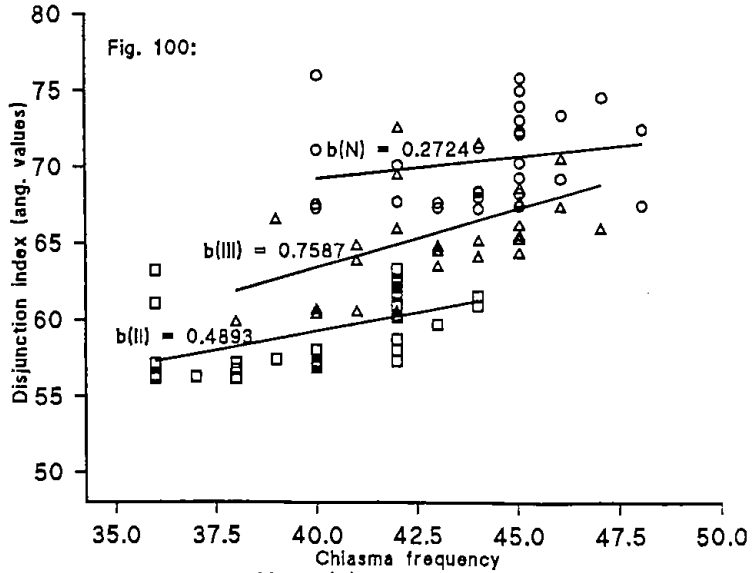


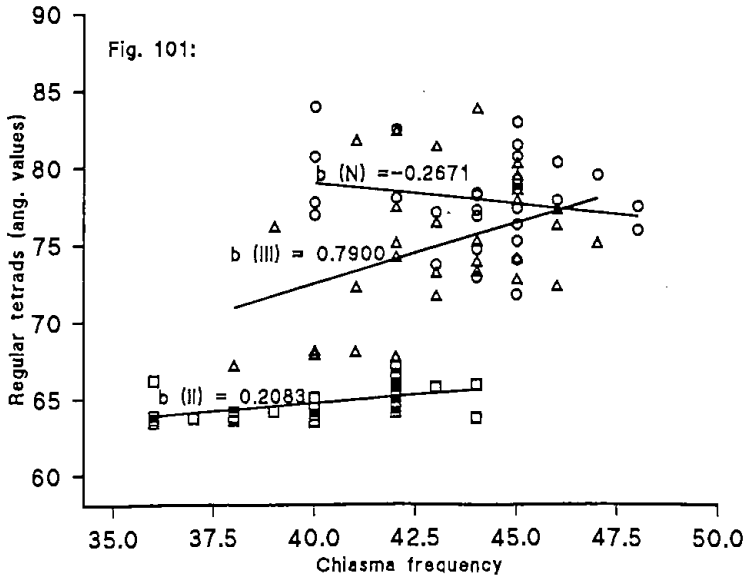
●, ■ & ▲ represent Semidwarf (N), Dwarf type–II (II) and type–III (III), respectively.

Figs. 94-97: Relationship of chiasma frequency with pairing configurations in three selected populations (N, II & III) of An X FM-32.



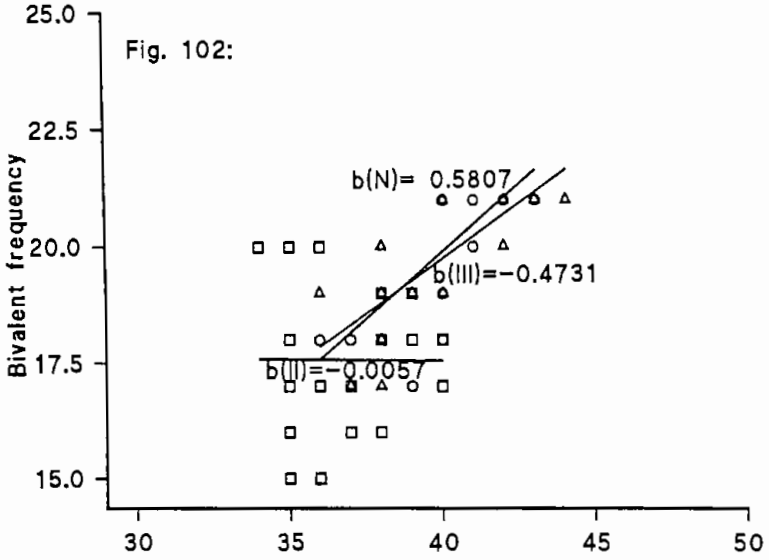


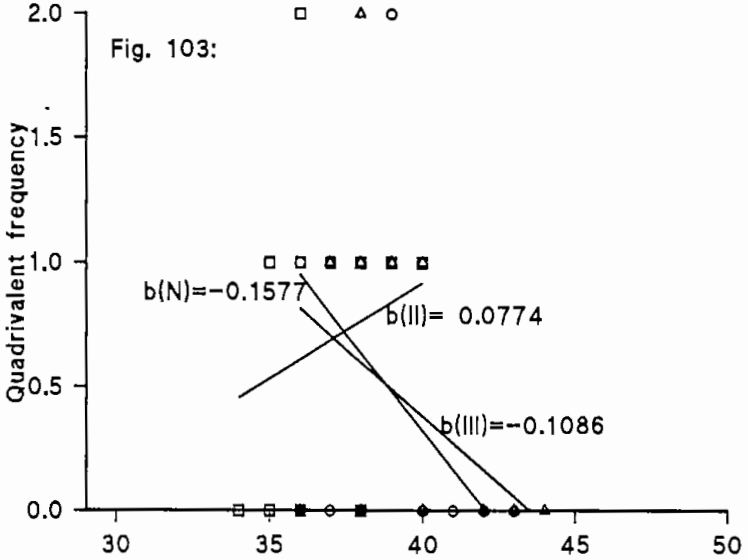


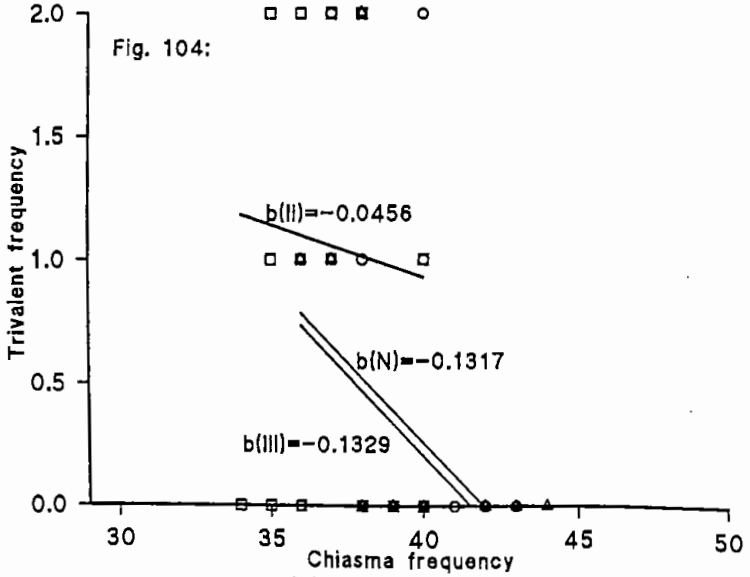


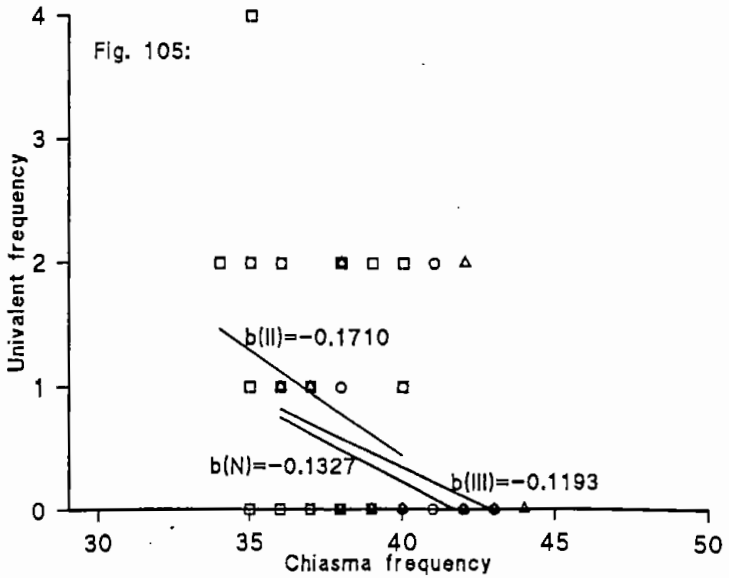
●, ■ & ▲ represent Semidwarf (N), Dwarf type-II (II) and type-III (III), respectively.

Figs. 98-101: Relationship of chiasma frequency with other meiotic features in three selected populations (N, II & III) of An X FM-32.



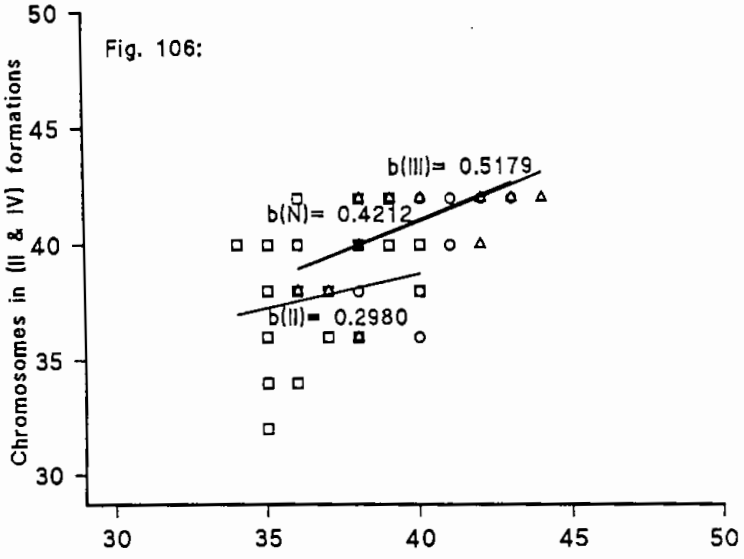


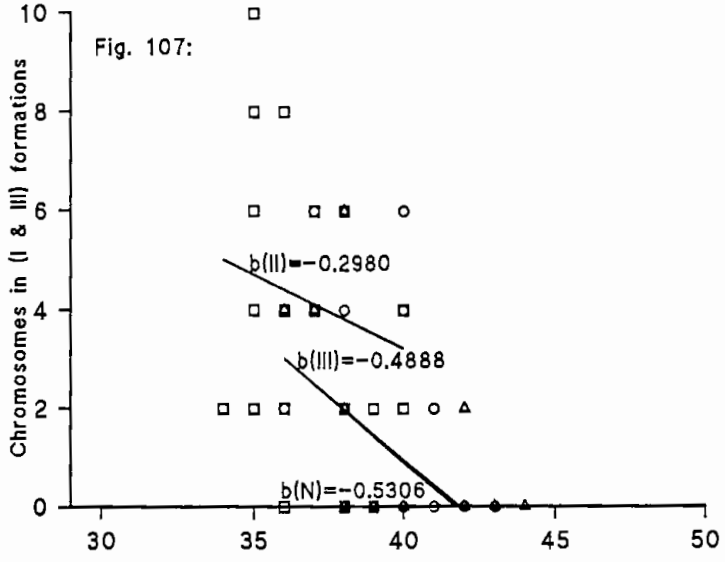


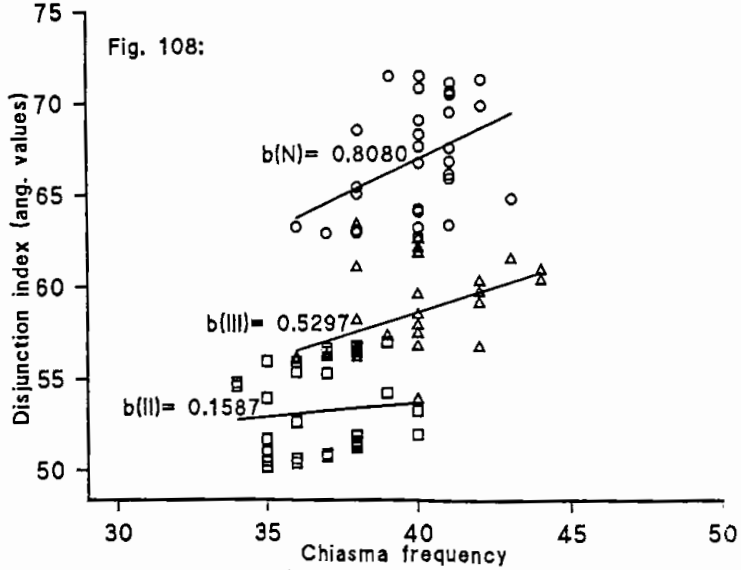


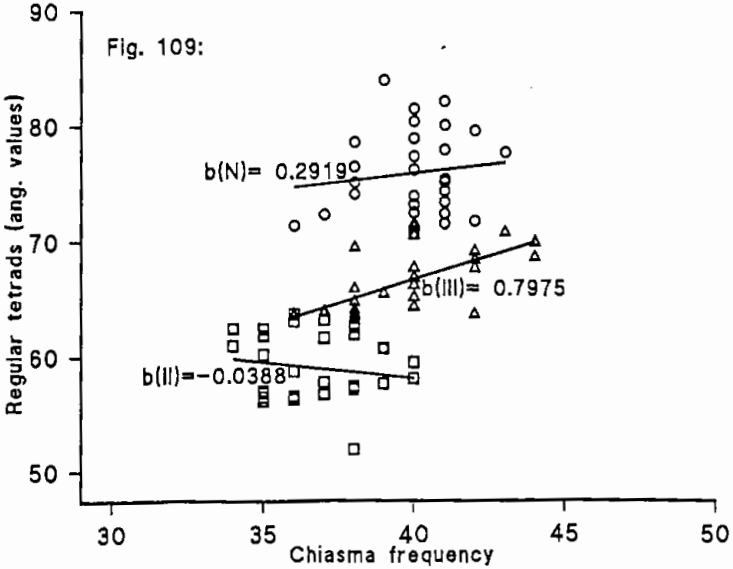
●, ■ & ▲ represent Semidwarf (N), Dwarf type-II (II) and type-III (III), respectively.

Figs. 102-105: Relationship of chiasma frequency with pairing configurations in three selected populations (N, II & III) of Kan X FM-32.









●, ■ & ▲ represent Semidwarf (N), Dwarf type–II (II) and type–III (III), respectively.

Figs. 106-109: Relationship of chiasma frequency with other meiotic features in three selected populations (N, II & III) of Kan X FM-32.

population of Kan X FM-32 showed the significant and positive regression on disjunction index, while on the number of chromosome in bivalent and quadrivalent formations it appeared to be nonsignificant but positive. On the other hand, significant positive regressions of chiasma frequency on the proportion of regular tetrad in the respective populations were in good agreement with the regressions on disjunction index.

I.5.3.3. Analysis of variance for regression and it's heterogeneity:

The analysis of variance for regressions between chiasma frequency and different meiotic features and their test of heterogeneity based on plant means are presented in Table 12 and 13., respectively.

A. Bivalent (II) and Quadrivalent (IV)

The variance for regressions (based on plant means) of chiasma frequency on bivalent formation appeared to be significant in all populations of An X FM-32, in N and II populations of Ak X FM-32, in N and III populations of Kan X FM-32, and in II and III populations of Ag X FM-32. However, the variance of regressions on quadrivalent formation was found to be significant in all II populations except Kan X FM-32, in all N populations except Ak X FM-32 and only in III population of Kan X FM-32. The heterogeneity between regressions of all the types in each cross became significant for both the bivalent and quadrivalent.

B. Trivalent (III) and Univalent (I)

Mean square of regressions on trivalent formation were significant in all II populations except Kan X FM-32, in N population of Kan X FM-32 and in III

Table 12: Variance analysis of regressions for chiasma frequency on different meiotic features of three types of plants (N, II & III) in four crosses.

Meiotic features	Items	df	Cross 1: Ag X FM-32						Cross 2: Ak X FM-32					
			N		II		III		N		II		III	
			MS	F	MS	F	MS	F	MS	F	MS	F	MS	F
Bivalent freq.	Regr.	1	0.8078	0.4674	28.8832	18.990**	25.1565	22.934**	10.9650	8.7959*	48.6214	72.614**	0.2636	0.1427
	Error	28	1.7283		1.5210		1.0969		1.2466		0.6696		1.8477	
Quadri. freq.	Regr.	1	0.8078	5.8113*	2.5049	8.590**	0.2423	1.2978	0.1202	0.7349	3.8082	20.657**	0.5352	2.1926
	Error	28	0.1390		0.2916		0.1867		0.1636		0.1844		0.2441	
Trivalent fre.	Regr.	1	0.2020	0.8572	1.3675	5.2434*	0.8246	1.4100	0.8782	3.7878	2.4410	6.1971*	0.4456	1.6802
	Error	28	0.2356		0.2608		0.5848		0.2319		0.3939		0.2652	
Univalent fre.	Regr.	1	0.2020	0.8572	0.8246	1.4100	3.0477	10.468**	2.1315	11.393**	2.1172	3.5814	0.0106	0.0378
	Error	28	0.2356		0.5848		0.2912		0.1871		0.5912		0.2807	
Chr. No. in II+IV	Regr.	1	3.2314	0.8571	19.5168	4.8930*	65.0227	20.190**	33.7147	72.143**	37.7131	7.4282*	3.6082	1.0282
	Error	28	3.7703		3.9887		3.2206		0.4673		5.0770		3.5093	
Chr. No. in I+III	Regr.	1	3.2314	0.8571	19.5168	4.8930*	65.0227	20.190**	23.3307	8.3176*	37.7131	7.4282*	3.6082	1.0282
	Error	28	3.7703		3.9887		3.2206		2.8050		5.0770		3.5093	
Disjunc. index	Regr.	1	4.4269	0.1859	16.5118	2.6257	1.3125	0.2227	18.4788	1.4485	115.111	7.1772*	1.7843	0.1352
	Error	28	23.809		6.2885		5.8946		12.7575		16.0385		13.1931	
Regular tetrad	Regr.	1	42.069	2.6529	31.6990	4.1156	0.6456	0.0439	0.1985	0.0276	110.640	6.0538*	0.9297	0.0749
	Error	28	15.858		7.7022		14.6966		7.1979		18.2761		12.4147	

'*' and '**' indicating significant at 0.05 and 0.01 level of significance, respectively.

Table 12: (Continued)

Meiotic features	Items	df	Cross 3: An X FM-32						Cross 4: Kan X FM-32					
			N		II		III		N		II		III	
			MS	F	MS	F	MS	F	MS	F	MS	F	MS	F
Bivalent freq.	Regr.	1	23.163	27.555**	68.1975	106.25**	25.2796	35.966**	24.2326	31.949**	0.0027	0.0012	31.2246	33.312**
	Error	28	0.8405		0.6419		0.7029		0.7585		2.3345		0.9373	
Quadri. freq.	Regr.	1	1.6423	8.9086**	2.6339	5.9638*	0.5896	4.0164	1.7867	7.2680*	0.4899	1.6769	1.6214	5.8590*
	Error	28	0.1842		0.4416		0.1468		0.2458		0.2921		0.2767	
Trivalent freq.	Regr.	1	0.8737	4.1280	3.9105	9.4477*	3.5117	16.784**	1.2646	4.3686*	0.1701	0.1921	2.4281	0.1095
	Error	28	0.2117		0.4139		0.2092		0.2895		0.8857		0.2658	
Univalent freq.	Regr.	1	0.0826	0.2363	5.13142	13.857**	1.8563	12.049**	1.2646	4.3686*	2.3940	2.2641	1.9565	4.1365
	Error	28	0.3496		0.3703		0.1541		0.2895		1.0574		0.4730	
Chr. No. in II+IV	Regr.	1	20.259	5.3646*	120.006	23.227**	48.7888	17.815**	12.7497	4.0238	7.2712	1.1340	36.8745	14.355**
	Error	28	3.7765		5.1666		2.7386		3.1686		6.4117		2.5688	
Chr. No. in I+III	Regr.	1	20.259	5.3646*	120.006	22.227**	48.7138	17.770**	20.2318	16.095**	7.2712	1.1340	32.8474	12.109**
	Error	28	3.7765		5.1666		2.7413		2.9153		6.4117		2.7126	
Disjunc. index	Regr.	1	9.9045	1.2269	46.2976	9.9448**	84.4433	8.6839**	46.9206	5.7705*	2.0615	0.3586	38.5675	8.0635*
	Error	28	8.0731		4.6554		9.7242		8.1311		5.7514		4.7829	
Regular tetrad	Regr.	1	9.5216	1.1142	8.3882	9.5663**	91.5531	4.9940*	6.1241	0.4698	0.1230	0.0183	87.4299	19.015**
	Error	28	8.5457		0.8768		18.3327		13.0356		6.7078		4.5979	

'*' and '**' indicating significant at 0.05 and 0.01 level of significance, respectively.

Table 13: Variance analyses of heterogeneity of regressions for chiasma frequency on different meiotic features.

Meiotic features	Items	df	Cross 1: Ag X FM-32		Cross 2: Ak X FM-32		Cross 3: An X FM-32		Cross 4: Kan X FM-32	
			MS	F	MS	F	MS	F	MS	F
Bivalent frequency	Between	2	64.3933	1244.54**	71.8613	1603.75**	31.3186	1203.85**	62.3866	1300.27**
	Within	84	0.0517		0.0448		0.0260		0.0480	
Quadrivalent frequency	Between	2	8.7127	1185.59**	9.2340	1310.01**	10.5639	1148.55**	12.2657	1264.82**
	Within	84	0.0073		0.0070		0.0092		0.0097	
Trivalent frquency	Between	2	11.3259	879.93**	12.0458	1135.63**	10.9197	1098.77**	19.6776	1147.06**
	Within	84	0.0129		0.0106		0.0099		0.0172	
Univalent frquency	Between	2	14.3314	1082.97**	12.8737	1021.14**	10.9001	1047.61**	24.6375	1137.18**
	Within	84	0.0132		0.0126		0.0104		0.0217	
No. of chr. in II+IV	Between	2	171.072	1308.79**	173.034	1605.43**	164.084	1179.88**	165.258	1142.61**
	Within	84	0.1307		0.1078		0.1391		0.1446	
No. of chr. in I+III	Between	2	171.072	1308.79**	155.778	1148.71**	164.162	1180.18**	163.740	1142.41**
	Within	84	0.1307		0.1356		0.1391		0.1433	
Disjunction index	Between	2	493.846	1152.56**	585.806	1171.92**	311.449	1164.67**	269.461	1212.65**
	Within	84	0.4285		0.4999		0.2674		0.2222	
Regular tetrad	Between	2	553.160	1214.57**	533.813	1183.47**	414.093	1253.24**	344.637	1189.32**
	Within	84	0.4554		0.4511		0.3304		0.2898	

'**' indicating significant at 0.01 level of significance

population of An X FM-32. However, the variance of regression on univalent was found to be significant in III populations of Ag X FM-32 and An X FM-32, and in N populations Ak X FM-32 and Kan X FM-32. Whereas the heterogeneity between regressions of three populations in all crosses was found to be significant for both the trivalent and univalent.

C. Number of chromosomes in II + IV and III + I formations

In a PMC, the number of chromosomes involved in IV + II formation was measured against the number of chromosomes in III + I. Therefore, the increase in the number of chromosomes in the former category (IV + II) was at the same rate as the decrease in number of chromosomes in the later configuration (III + I). Accordingly, it would be expected that the chiasma frequency might have the same regression coefficients with IV + II and III + I formations, except that the regression with the later it would be negative. That was evident from the regression slopes. However, the variance of these two regressions were corresponded in all respects and the heterogeneity between the populations in all crosses were found to be significant.

D. Disjunction index and regular tetrad

Like the number of chromosomes in II + IV formations both the disjunction index and regular tetrad were dependent on the frequencies of bivalent and quadrivalent. The later two, in turn, regressed positively with chiasma frequency, as already shown above. Therefore, it might be expected to regress with both the disjunction index and regular tetrad, and that was found in this study.

The variance of regression of them were found to be significant in Type II of Ak X FM-32 and An X FM-32, and in Type III populations of An x FM-32 and Kan X FM-32. However, their regression heterogeneity were found to be

significant in all the crosses. From these findings it might be stated that with an increase in chiasma frequency there were similar rate of increase in both the disjunction index and regular tetrad, and that was corresponded in all three populations of every crosses.

The above analysis of regressions were made on the basis of plant means. Therefore, it confirmed that an increase of chiasma frequency indicated the meiotic regularity and fertility status of the studied populations. The differences in chromosome association with increasing the chiasma frequency indicated the differences in chiasma distribution patterns. Such analyses would reveal that whether the pairing configurations were independent of chiasma frequency or such independence could be varied by selection pressure in the hybrid lines of wheat.

I.6. DISCUSSION

I.6.1. Somatic Karyotype:

General observation

The dearth of karyotypic information in the literature on wheat can be attributed to the difficulties encountered in spreading of chromosomes well apart into the same optical plane and getting true chromosome length and arm ratio, and thus making the complement analyzable for any detailed study. Identification of each chromosome of common wheat (*Triticum aestivum* L.) was made possible by an aneuploid series developed in a common wheat cultivar, and used as a powerful tool for recognizing individual chromosomes and chromosome arms and for studying their genetic effects. Further characterization of 21 individual chromosomes as to their size and arm ratio was carried out in monosomic at anaphase-II of meiosis (Morrison 1953, Sears 1954 and Gill *et al.* 1963). Endo and Gill (1987) postulated that chromosome size and arm ratio data from meiosis can not be reliably used for the identification of somatic chromosomes.

Schultz-Schaeffer and Haun (1961) and Zeller (1969) had been tried to construct the karyotype of somatic chromosome of common wheat by conventional procedure and found that many chromosomes appeared similar in length and arm ratio, and individual chromosome identification was difficult. Detail morphology of 16 and 14 somatic chromosomes of common wheat cv. Chinese spring and Wichita, respectively were described by Endo and Gill (1984) for the first time.

In this context, present findings may be compared with mitotic values reported in Chinese spring and Wichita (Endo and Gill, 1984), and the meiotic values reported in Chinese spring (Sears, 1954) and Wichita (Gill *et al.* 1963) (Table14). Discrepancies were appeared between the present and previously reported mitotic values and also between the mitotic and meiotic chromosomes of the same cultivar. Larsen and Kimber (1973) confirmed the occurrence of differential contraction of Chinese spring chromosome in mitosis and meiosis. Inconsistency between the

Table 14. Chromosome size variation between mitosis & meiosis and cultivars of *Triticum aestivum* L.

Chromosome number	Mitotic chromosome length (µm)			Meiotic chromosome length (µm)	
	Present study		Endo & Gill (1984)	Sears (1954)	Gill *et al.* (1963)
	Aghrani	FM-139	Chinese Spring	Chinese Spring	Wichita
I	9.05	7.28	13.8	12.3	13.1
II	8.51	7.01-7.5	12.9	11.3	12.8
III	8.01-9.0	6.71	12.7	10.9	12.4
IV	8.02	6.51-7.0	12.5	10.4	12.3
V	7.73	6.50	12.5	9.8	12.1
VI	7.29	6.17	12.1	9.1	11.8
VII	7.04	5.79	11.9	9.1	11.6
VIII	6.51-7.0	5.64	11.8	9.1	11.4
IX	6.51-7.0	5.21	11.5	9.0	11.4
X	6.27	5.21	11.5	8.8	11.4
XI	6.01-6.5	4.51-5.0	11.4	8.5	11.3
XII	5.81	4.51-5.0	11.3	8.2	10.6
XIII	5.15	4.29	10.1	8.1	10.2
XIV	4.51-5.0	4.01-4.5	10.1	7.9	10.1
XV	4.51-5.0	4.01-4.5	-	7.5	9.6
XVI	4.01-4.5	3.70	-	7.3	9.1
XVII	4.01-4.5	3.51-4.0	-	6.9	9.0
XVIII	4.01-4.5	3.51-4.0	9.8	6.3	8.6
XIX	3.86	3.05	-	5.9	8.3
XX	3.63	3.01-3.5	-	5.8	8.1
XXI	3.34	2.51-3.0	8.4	5.6	7.9
Total complement	129.97	108.99	-	177.80	223.10

present and previous mitotic values may be considered that the reported data appear to be on single cell observations and the cultivars have had different parentage.

Chromosome length and distribution

In this study, all the studied endogenous varieties except Kanchan has higher complement total length than the exotic lines. On the other hand, in the F_3, F_4, F_5 and F_6 progenies of Ag X FM-32, Ak X FM-32, An X FM-32 and Kan X FM-139 the complement total length have been reduced successively and become much lower than their both the parents. This suggests that during the course of selection pressure from a putative immediate progenitor, there had been a phylogenetic reduction in chromosome size to produce the present genomic status. Ahmad *et al.* (1983) postulated similar phylogenetic chromatin reduction in hybrid progenies of soybean.

Moreover, the coefficient of variation (C.V.) of complement total length indicated that the over all degree of chromosome contraction in different cells of all the studied genotypes was statistically identical, and it also reflects that the proper selection of studied cells for photomicrography and precision in taking chromosome measurements. Furthermore, the χ^2 -values and probability for chromosome distribution in respect to length classes of every haploid complement between the parents and their progenies indicated the independency.

Karyotypic composition

The centromeric formulae of all indigenous varieties except Akbar contains a greater number of median (m) chromosomes than the exotic line, particularly FM-139, which indicated that there had been either a phylogenetic reduction in chromosome size to produce the present Akbar and FM-139 karyotype or conversely a phylogenetic increase to produce other varieties/lines' karyotypes.

All the generations of Ag X FM-32 have had the similar centromeric formula (16m + 5sm) like their exotic parent, where stability of genomic transfer over successive generations indicated. The complement of F_6 progeny of Ak X FM-32, Kan x FM-32 and Ak X FM-139 have had similar centromeric composition (16m + 3sm + 2st), and which is the most advance than all other studied genotypes. This genomic advancement in intervarietal hybrids might be due to the simultaneous occurrence of deletion and duplication. Similar centromeric composition (11m + 9sm + 1st) of the complement was found in F_3 of Kan X FM-32 and in F_6 of Kan X FM-139, where the lowest number of median chromosome indicated the genomic advancement.

The Table 6 may provide the diagnostic features of the different chromosomes in haploid complement of parents and their progenies in seven crosses. These karyotypic formulae also indicated that the indigenous varieties/lines showed primitiveness compared to that of exotic lines, due to absence of short chromosome (< 3.0 μm). It was also clear that the F_3 progenies of Ag X FM-32, Ak X FM-32, Kan X FM-32 and Kan X FM-139, and the F_4 progenies of Ag X FM-32 and Ak X FM-32 have had no short chromosome like their indigenous parents. However, the F_6 progenies of Kan X FM-32 and An X FM-139

have no short chromosome, while they have possessed the large chromosome (> 7.01 μm) like their exotic dwarf parent. Therefore, in these genotypes the genome of dwarf parent did not transferred desirably.

However, the F_5 and F_6 progenies of almost all the crosses have showed the genomic transfer from their parent and thereby proved the efficiency of selection pressure toward the dwarfness. Above all the genome transfer from dwarf parent to the F_3 - F_6 progenies of An X FM-32 and Ak X FM-139 was found to occur most desirably and become stable. Moreover, the presence of more sub-metacentric (sm) and sub-telocentric (st) short chromosomes in them is another indicator of genomic advanceness. Thus, the formulated karyotype might be able to throw a light on the magnitude of genome transfer in the hybrid progenies from their respective parents and thereby useful in assessing the genomic stability of heterozygous populations.

Change in chromosome size

Ahmad *et al.* (1983) postulated that a reduction in chromosome size can result from either deletion or unequal translocation of chromosome segments. A translocation results in the change of size in the relevant chromosomes without affecting the complement length. If certain translocation have been fixed in a genotype, multivalent rings or chains would appear in the hybrid progeny. Such occurrence have been found in the present study. Similar evidence has been reported in case of soybean (Hadley and Hymowitz 1976, Palmer 1976). The deletion may change both the chromosome length and arm ratio and simultaneously reduced the total complement length.

In the present study, the unequal translocation was found to occur in chromosome-I of Kan X FM-32/F_4, in chromosome-VI of Ak X FM-139/F_5, in chromosome-XVIII of Kan X FM-139/F_4, in chromosome-XIX of An X FM-139/F_6 and chromosome-XXI of An X FM-32/F_6. Reduction of the rest commonly identified chromosomes might be due to deletion in one or both the arm/s. Ahmad *et al.* (1983) reported that the reduction in chromosome size of soybean species is due to deletion only.

Stebbins (1950) suggested that phylogenetic increase and decrease in chromosome size are almost equally common in higher plants. Karyotypic change is accomplished through the chromosomal aberrations, structural as well as numerical. Of the four structural changes in chromosomes, only deletion and duplication cause a net change in complement total length. Duplications are generally considered to be of greater significance in genomic change than deletions, since deletions commonly have a detrimental effect. However, Stebbins (1977) has argued that chromosomes of higher organisms carry many genes that are not duplicated. tandem-fashion along the chromosome, hundreds or even thousands of times. If a deletion removes one or a few copies of such highly duplicated or redundant genes, it can be tolerated. To produce a deletion, either one or two breakages must occur in the same chromosome. For a duplication, two chromosomes must be involved simultaneously, either with unequal cross over or involving three breakages. Thus, the probability of occurrence of deletion is likely to be greater than that for a duplication, and the difference in the probabilities is even greater where a series of such occurrences is conceived to be involved.

On these bases, Ahmad et al. (1984.) postulated an argument based on reduction in chromosome size through deletion is favoured to explain the phylogenetic relationships between *Glycine max* and *G. soja*. The chromosomal changes described here do not preclude other kinds of structural changes which might have occurred during the genome transfer in the progenies of the studied crosses. However, no indication of aneuploidy was found in this study.

This new approach to karyotype analysis was developed incorporating a scatter diagram technique with microscopic study. It has special bearing on wheat improvement work through chromosome manipulation. This technique should provide useful tool in identifying individual chromosomes involved in the loss or addition of chromosomes leading to aneuploidy of this and other species of wheat group.

I.6.2. Heterochromatin distribution and Chromosome differentiation:

Chromosome banding in plants did not have so great impact as it did in animal. This may be due to the fact that the proposed technique till today are not absolutely suitable for a range of higher plants, because of the variability in response to differential Giemsa staining.

The banding technique in the present study, however, yielded a reproducible result of heterochromatin in six genotypes of wheat. The schedule adopted by Endo and Gill (1984) was followed and the results obtained in this study were similar in some aspects. For the first time they identified 2A, 3A, 5A,

6A, 1D, 2D and 7D chromosomes of wheat. Prior to that in 1977, Gerlach's modified N-banding technique allowed to recognise nine wheat chromosomes. In the present study, chromosomes were identified on the basis of the position and number of landmark bands and proposed a standard karyotype.

In this study, the prolonged weak acid (45% AA) treatment of chromosome preparations at 60°C. and short duration (2 min.) of 1M NaH_2PO_4 buffer treatment at 94°C appeared to be critical in the detection of more banded chromosomes. The critical factor in this technique was the concentration of the **Sorenson's** buffer in Giemsa solution. The chromosomes stained quickly at higher concentration of buffer but banding was not distinct. The banding was brought out clearly when the chromosomes were stained with **4% Giemsa** diluted with **1/15M Sorenson's** buffer at pH 6.8.

In total chromosome length, B genome chromosomes were the longest, A genome chromosomes were of intermediate in length and D genome chromosomes were the shortest in the present studied genotypes, which is very much consistent with the findings of Endo and Gill (1984) observed in five wheat cultivars. This evidence generally corresponds with the DNA content of the respective genomes (Nishikawa and Furuta 1978). Although polymorphism in banding pattern was observed for many chromosomes, particularly the B genome chromosomes, among the studied genotypes. However, the overall banding patterns were similar among the homologous chromosomes. In this study, the heterogeneity of the heterochromatin distribution in the same chromosome of different genotypes might further be revealed by their differential DNA sequences and DNA-protein composition. Similar findings were reported in five cultivars of

common wheat by Endo and Gill (1984). Dvorak and McGuire (1981) reported the reduced level of chromosome pairing in intercultivar hybrids of hexaploid wheat and might be explained by heterochromatin band differences, as it exhibited in the present study.

The D genome chromosomes, in general, showed less number of heterochromatic bands and very little polymorphism, and corresponded well between the studied genotypes. Only in this genome one or more chromosome(s) remained indistinguishable due to lack of any bands in each of the studied genotypes, and it is consistent with the findings of Gill and Kimber (1974) and Gerlach (1977). In the A genome, chromosome 1A and 4A in Ananda, 2A in Aghrani and FM-139, 3A in Akbar and 6A in FM-32 showed little morphological changes in addition to differential heterochromatinization among the same chromosomes of different genotypes. It may be accounted for genomic diversity of the studied materials and also for the reduced pairing in intercultivar hybrids (as it was observed in the next experiment). Although a more detail analysis of the relationship between heterochromatin distribution and chromosome pairing is beyond the scope of this study, the effect of heterochromatin on chromosome pairing was considered firmly. This, in turn, established some biological significance for the extensive heterochromatinization in chromosomes of wheat cultivars/species during the course of isolation and finally evolution.

1.6.3. Chiasma frequency and chromosome association:

Three groups of factors that affect chromosome pairing could be identified. First, the homology - structural and chemical similarities between chromosomes; second, the genetic factors - such as the $5B^{l}$ system in wheat when present in recessive homozygous condition; and third, the cellular environment - during meiosis, which is also influenced by the external environment (Elliot 1955 & 1958, Wilson 1959, Rees and Naylor 1960, Law 1963, Bennett and Rees 1970, Mehra and Rai 1972, Fedak 1973).

The lowering of chiasma frequency was found to be associated with failure of zygotene chromosome pairing (asynapsis). The asynapsis might be due to a failure in the mechanism of chromosome pairing rather than the prealignment of homologues. In euploid wheat the sensitivity of chiasma frequency to temperature could influence the cytological stability (Bayliss and Riley 1972).

Plants of the studied populations were grown under the same environmental conditions and the frequency of univalent and multivalent did not differ significantly between the populations, whereas the chiasma frequency differed. Therefore, it was evidenced that the recessive genes affected the magnitude of chromosome pairing in the studied populations. The differences in chromosome association of the studied populations was thus assumed to be primarily due to either differences in chromosome homology or genetic diversity.

Depending on the regression slope between bivalent and chiasmata a related change in the slope between them would be expected. That was firstly, due to

bivalent formation at the expense of quadrivalent and secondly, due to an increase in chiasma frequency either with increasing bivalent or with increasing interstitial chiasmata of bivalent depending on the experimental materials (Hossain 1975). Such evidence was corresponded with the present studied materials.

The regression coefficients between bivalent and chiasmata of most of the isolated populations were greater and positive, in contrast to the smaller and negative regression between quadrivalent and chiasmata. This result was corresponded well with the findings of Hazarika and Riss (1967) in tetraploid rye. The heterogeneity between regression slopes of NILs of each cross were appeared to be significant for both the quadrivalent and bivalent. Thus, it was assumed that the studied populations might be regarded as directly different from one another with respect to their pairing pattern. In view of the short period of selection, the complex genetic basis of chromosome pairing behaviour (Rees and Thompson 1956, Jones 1969 & 1974), and the rather slow approach to homozygosity of the studied populations exhibited significant diverging tendencies. And that was consistent with the reports of Hossain and Moore (1975) in tetraploid rye.

As expected chiasma frequency was negatively regressed on both the trivalent and univalent frequency, and the regressions were significant in most of the cases. However, the regression heterogeneity for both were significant and it indicated that the rate of decrease in trivalent and univalent with increasing the chiasma frequency was not same between the isolated lines in all the crosses. That was also corresponded with the findings of Hossain and Moore (1975).

As the bivalent and quadrivalent lead to equal chromosomal separation, it results the formation of balanced gametes. Therefore, along with the number of chromosomes in bivalent and quadrivalent (II + IV), both disjunction index and regular tetrad would be dependent on the frequencies of bivalent and quadrivalent. Thus, it might be expected that chiasma frequency would be positively regressed with both the disjunction index and regular tetrad, and the present findings corresponded with this expectation. However, Hazarika and Riss (1967) reported that the increased quadrivalent frequency was accompanied by the decreased trivalent, bivalent and univalent in inbreed lines of autotetraploid rye. They also found that for the same or comparable chiasma frequency, the inbreed lines differed significantly for their average pairing configurations. That was inconsistent with the present findings due to amphidiploid nature of the genomic composition in hexaploid wheat.

The negative regression between multivalent and chiasmata in most of the studied populations was a feature of either genetic or chromosomal heterozygosity. On the other hand, the variance estimates of regression of chiasmata on other than bivalent configuration appeared to be significant in Type II populations of most crosses indicating that there exists a great influence of chromosome differentiation in the variability of 'pairs' in this population, which might provide the scope for increasing the frequency of bivalent.

The disjunction index and proportion of regular tetrad regressed positively in most of the populations, while they were found to be significant simultaneously in Type II populations of Ak X FM-32 and An X FM-32. Moreover, the significant influence of chiasma frequency in the variability of these two meiotic features,

i.e., fertility status of Type II populations in those two crosses indicated. Therefore, the poor fertility status of II populations might be improved by progressive selection pressure for higher disjunction index and regular tetrad.

Above all, the meiotic irregularity is lethal to semilethal which greatly limits the success of selection for the dwarf type II populations. It might be due to increased homozygosity of $5B^{I}$ population (II), which affected the chromosome pairing indiscriminately. The best result might be expected when the selected populations was comprised of the genetic heterozygosity and survived under normal growing conditions. In view of these difficulties, the complex genetical basis of chromosome pairing behaviour (Rees and Thompson 1956) and the short period of selection, the diverging tendency exhibited by the dwarf type II population would be nonetheless significant.

I.7. SUMMARY

It is difficult to manipulate the genomic make up of common wheat due to its numerous small chromosomes and allopolyploidy. The quantitative method of karyotypic analysis was adopted to determine the genomic composition of six cultivars/lines and their progenies (F_1 - F_6) in seven crosses of wheat. In this study, the data used from five cells with chromosomes having similar degree of contraction and were proved to be homogeneous statistically. To determine the homologous pairs of chromosomes and to derive their haploid values a scatter diagram was prepared on the basis of total length and arm ratio for every studied cell. The haploid complement values of five cells for each genotype were then plotted to identify as far as possible the individual chromosomes. Most of the chromosomes were identified and described individually, and the remaining unidentifiable chromosomes were characterized into classes based on probabilistic inferences of chromosome length and arm ratio.

The proposed 'centromeric formulae' comprised 19 m + 2 sm in Aghrani, 11 m + 10 sm in Akbar, 17 m + 4 sm in Ananda, 16 m + 5 sm in Kanchan, 16m + 5 sm FM-32 and 14 m + 7 sm chromosomes in FM-139. In karyotypic composition, more submedian chromosomes were observed in FM-lines compared to those in Bangladeshi varieties except Akbar.

In Ag X FM-32, the F_1 - F_6 progenies were found with 16m + 5sm chromosome to make their haploid complement. In Ak X FM-32, haploid complements were found with 13m + 8sm, 12m n+ 8sm + 1st, 13m + 6sm + 2st and 16m + 3sm + 2st chromosomes for F_1, F_4, F_5 and F_6 progenies, respectively. The

centromeric formula for F_3, F_4, F_5 and F_6 of An X FM-32 were found to comprise with 19m + 2sm, 14m + 6sm + 1st, 13m + 8sm and 14m + 6sm + 1st, chromosomes successively. For F_3, F_4, F_5 and F_6 progenies of Kan X FM-32 the centromeric formulae were consisted of 11m + 9sm + 1st, 16m + 4sm + 1st and 16m + 3sm + 2st chromosomes, respectively. The haploid complements of F_3, F_4, F_5 and F_6 progenies of Ak X FM-139 were found to consist of 12m + 9sm, 14m + 7sm, 12m + 9sm and 16m + 3sm + 2st chromosomes, successively. In An X FM-139 15m + 6sm, 16m + 5sm, 13m + 7sm + 1st and 15m + 5sm + 1st chromosomes comprised the haploid complement for F_3, F_4, F_5 and F_6 progenies, respectively. The F_3, F_4, F_5 and F_6 progenies of Kan X FM-139 comprised 13m + 8sm, 13m + 7sm + 1st, 14m + 6sm + 1st and 11m + 9sm + 1st, successively for their haploid complement.

It gives an idea about similarities and differences of the chromosomes of six varieties/lines and their progenies under study. One pair of short chromosome ($S_2^{\blacksquare}$) was invariably present in both the exotic dwarf lines, while it was absent in the indigenous lines. The occurrence of more than 5 pairs of long chromosome (L) were observed in all the indigenous varieties except Kanchan, whereas less than 5 pairs of long chromosome were found in exotic lines.

The F_3 progenies of most of the crosses and F_4 progenies of cross-1 & 2 did not posses any short chromosome (S_2) like their indigenous parent. However, the F_5 and F_6 progenies of most of the crosses have had at least one or more pair of S_2 chromosome/s like their exotic parent. All the progenies (F_3 - F_6) of cross-3 & 5 found to bear the S_2-chromosome. Moreover, the sub-terminal (st) chromosomes along with more sub-median chromosomes were frequently observed in the hybrid progenies of all crosses except Ag X FM-32, while it was fully absent in the parental genotypes.

Satellited chromosomes with a visible state were found occasionally. Usually two in parental genotypes and never more than four satellited chromosomes in hybrid progenies were found to be visible in any cell. The trabant was always found to bear by the short arm of the chromosome in all cases. From identified chromosomes of all the genotypes, it was confined that the chromosome III and VIII were confirmed with this character. Morphological features of the commonly identified chromosomes of parents and their hybrid progenies in all the cases were determined. The test of significance was also carried out by t-test for their morphological differences. The significant difference in chromosome size of the genomes might have occurred by deletion in most of the cases and by unequal translocation in few cases. A very limited case of increased chromosome length indicated that where duplication might be involved.

The chromosomal changes described here do not preclude other kind of structural changes which might have occurred during the genome transfer in the progenies of studied crosses. However, no indication of aneuploidy was found in this study. This new approach of karyotypic analysis has a special bearing on wheat improvement work through chromosome manipulation. This technique should provide a useful tool in identifying individual chromosomes involved in the loss or addition chromosome(s) leading to aneuploidy of any species of wheat group.

To determine the heterochromatin distribution in metaphase chromosomes of six parental genotypes of common wheat by adopting the banding technique. The size measurements were made from aceto-orecine stained chromosome and then subjected to banding technique. The number and position of heterochromatic bands were used to identify the individual chromosome genomically and quantitative karyotypic analysis were used to arrange the chromosomes in descending order within each genome.

The maximum number of bands (15) was exhibited by the chromosome pair-VIII in Aghrani (Ag), Akbar (Ak), Kanchan (Kan) and FM-32; chromosome pair-III and VI in Ag; III in Kan, and V in Ananda (An) and Fm-139. The minimum number was 3 as revealed by the chromosome pair-XIII in all the genotypes. Along with this the chromosome pairs IX and XXI in Ag have had also the minimum number of bands (3). It is also mentionable that both the highest (15) and lowest (3) number of bands were observed in six different chromosome pairs in Ag.

Since some of the chromosome pairs in all the cases exhibited identical number of bands, the number of banding patterns become reduced to 9 in An, 10 in Ag and 11 in Ak, Kan, Fm-32 and FM-139. This , in turn, was assumed that the later genotypes were derived from a more advanced progenitor compared to that of the former two. However, the chromosome pairs XIV and XVIII in Ag, XX in Ak and Kan, XVI and XVII in Ananda, IV and XV in Fm-32 , and VII in Fm-139 did not show any distinctly dark or faint band.

The highly heterochromatic and mostly polymorphic but nearly identical in banding patterns of the B genome chromosomes corresponded individually in all the genotypes. In the D genome, 6D chromosome was identified individually and its banding pattern was almost identical in all the genotypes. 1D in FM-139, 3D in Ag and FM-32, 4D in An, 5D in Ag and An, and 7D in Ak and Kan were not found to be banded and remained as unidentifiable, although their position in Karyotype were determined on the basis of probabilistic inferences. In the A genome chromosomes, the banding pattern of 3A, 4A and 6A were quite similar in all the genotypes. However, the remaining chromosomes of A genome showed little difference in their heterochromatinization of different genotypes.

The mean performance of different meiotic features of 12 NILs were compared with the check variety. Significantly increased bivalent frequency was noticed in all the semidwarf (N) populations except Kan X FM-32 with a concurrent significant decrease in multivalent frequency compared to that of check variety. However, significantly increased bivalent and quadrivalent frequencies were found in dwarf type III of An X FM-32. Significantly decreased bivalent frequency was observed in all the populations of Kan X FM-32 and in Type II of An X FM-32. The negative regression between multivalent and chiasmata in most of the studied populations was a feature of either genetic or chromosomal heterozygosity. On the other hand, the variance estimates of regression of chiasmata on other than bivalent configuration appeared to be significant in Type II populations of most crosses indicating that there exists a great influence of chromosome differentiation in the variability of 'pairs' in this population, which might provide the scope for increasing the frequency of bivalent. A significantly increased disjunction index and proportion of regular tetrads were regressed positively in most of the populations, while they were found to be significant simultaneously in Type II populations of Ak X FM-32 and An X FM-32. Moreover, the significant influence of chiasma frequency is detected in the variability of these meiotic features and thereby fertility status of the II populations. Therefore, their fertility status might be improved by progressive selection pressure for meiotic regularity in the advanced generations.

Part - II

GENE ACTION

II. GENE ACTION

II.1. INTRODUCTION:

Successful breeding programme for yield improvement in dwarf wheat (*Triticum aestivum* L.) requires information on (a) the fundamental nature of gene action and interactions involved in the inheritance of grain yield and its components, and (b) the efficacy of such genetic patterns in the selection process. The grain yield and its components are controlled by polygenic system. In this system both the additive and non-additive gene actions and interactions are found to be operative. Moreover, these characters are considerably influenced by both micro- and macroenvironments. Grain yield of wheat is a complex character, and it is the contribution of many morphological, physiological and developmental components. Grain yield/ plant is determined as the multiplicative function of morphological (primary yield) components, *viz.* , (a) No. of spikes (fertile tillers)/ plant, (b) No. of spikelets/ plant, (c) No. of grains/ spike and (d) Average grain weight. Like morphological yield components, physiological yield components *viz.*, (a) Biological yield (= active photosynthetic area) / plant and (b) Harvest index (= translocation strength of photosynthetates) / plant also determine the grain yield/ plant as the multiplicative function. In addition to the above mentioned characters, plant height and nature of reproductive development, *viz.*, (a) Days to booting, (b) Days to heading, (c) Days to flowering and (d) Days to maturity, as developmental characters might have important contribution to the yield.

Gene action is the magnitude of gene expression, causing heritable and non-heritable differences among individuals or populations. Fisher (1918) conceived that genetic variation in case of quantitative segregation may arise from three types of gene action, *viz.* additive, dominance and epistasis. Based on some genetic and statistic assumptions he separated the genetic components of total variation and then partitioned it into three sub-components. Mather (1949) and Hayman and Mather (1955) developed the scaling test and three-parameter model for estimation of the components of generation means. Adequacy of scale must satisfy the additivity of gene effects and independence of heritable components from non-heritable ones. Hayman (1958) and Jinks and Jones (1958) gave six-parameter model for estimation of various genetic components including non-allelic interactions. *viz.* additive-additive, additive-dominance and dominance-dominance.

A population with predominant additive gene action and additive X additive gene interaction is more responsive to selection than a population with predominantly non-additive gene action. In spring semidwarf wheat, additive, dominance and various types of epistasis have been reported for yield and its components (Jatassra and Paroda, 1978; Nanda *et al.* 1982 a, b and Singh *et al.* 1984 a, b). But the magnitude of these genetic parameters varied with the genotypes of the parents and the environments in which they studied their materials.

Heritability is a measure of the amount of genetic variability, excluding that expressed by heterozygote, and decreases with an increasing environmental component of variance for the character under observation. Estimates of heritability in relation to genetic interpretation is important in determining the

response to selection for the traits under observation. Heterosis is the phenotypic result of gene action and interaction in heterozygote and is, thus, confined to that state. It can be disrupted by inbreeding and restored by interbreeding of the inbred lines. In any crop improvement programme, exploitation of heterosis is directly related to the nature of gene effects. Additive gene effects provide information pertinent to pure line breeding, while dominant type of effects is important for development of hybrid variety. Heterosis is predominantly controlled by non-additive gene action. Dominance and epistasis influence the heterosis of grain yield in spring wheat (Shamsuddin, *et al.* 1982). Sharma and Ahmad (1978) proposed that in addition to non-additive gene action, additive gene action might be contributed to the heterosis. Presence of non-additive gene action and heterosis for yield and its components indicate the prospect of hybrid wheat. Development of hybrid dwarf wheat is getting increased importance to the breeders.

The dwarf wheats are much more sensitive to environment than the semidwarfs. Farrer (1898), McMillan (1937), Morrison (1957), Hermsen (1967) and Moore (1967), extensively studied the inheritance of dwarfness in hybrid wheat. While a poor studies have been made to verify the response for selection based on gene actions and thereby, heritability and heterosis in the hybrid dwarf population of wheat. But it is very important to study the inheritance of yield and its components along with dwarfness before starting any selection programme using a set of parental population and their progenies. In this context, the present investigation was under taken to study the gene action for determining the selection response of the yield traits and the estimates of heritability and heterosis, and their genetic interpretations were also taken up as a counterpart of this study.

I.2. REVIEW OF LITERATURE

For the study of gene action, heritability and heterosis there is a great need to review the literatures on the relevant subjects. The available literatures are reviewed here under different sub-heads.

II.2.1. Dwarfism:

The term 'hybrid dwarfness' or simply 'dwarfness' is used to distinguish it from 'semidwarfness' and to indicate that it is one of the forms of hybrid weakness in wheat. Hybrid weakness or inability is a term, used by Stebbins (1950) and Dobzhansky (1951) to indicate decreased vigour or lethality of hybrids from normal parents. The inheritance of hybrid dwarfness in wheat is far more complicated. Many hypothesis have been put forwarded to explain the occurrence and segregation of hybrid dwarfness in wheat as reviewed by Morrison (1957). Several authors were even unable to explain their data and confused about the genetics of dwarfness (Richardson, 1913, 1924; Stewart and Bischoff, 1931 and Morrison and Gfeller, 1957). The most profound and complete investigation on the occurrence and inheritance of dwarfness was carried out by McMillan (1937). He postulated an interaction of four pairs of genes (Gg, Ii, Aa and Bb) to explain the phenomena as follows:

1. Gg: the allele G is essential for occurrence of dwarfs.
2. Ii: the allele I, in the absence of the complementary genes A and B, inhibits the expression of G, resulting in normal.

3&4. Aa & Bb: when both A and B are present, they inhibit the action of I; so

that A. B. I. G-plants are dwarf. The gene pairs Bb and Ii are linked very closely in the repulsion series.

On the basis of this hypothesis the following genotypes are possible for:

dwarfs: ABIG, ABiG, AbiG, aBiG, abiG and

normal: ABig, AbIG, AbIg, aBig, abIG, abIg.

Owing to the possibility, absolute linkage between Bb and Ii (repulsion) the remaining five genotypes for normals (ABIg, Abig, aBIG, aBIg and abig) have not been obtained by McMillan (1937). Therefore, this hypothesis may be considered as the comprehensive and straight point to explain the genetics of hybrid dwarfness in bread wheat.

A new hypothesis have been made by Hermsen (1967) which is more easier and flexible to explain the genetics of hybrid dwarfness in wheat. He proposed that three gene pairs, D_1d_1 (=Gg), D_2d_2 (=BibI) and D_3d_3 (=Aa) are qualitatively similar in action (*ie.*, the production of 'antigibberellins', which suppress the length growth to different degrees, depends on the cross and environment), but different in expressivities and dominance relations among themself. Dwarfness may occur without D_3 being present, but D_1 and D_2 are indispensable. He postulated that it is dwarf, (1) if it carries D_1. D_2. D_3. either in homozygous or heterozygous condition, or (2) if, in the absence of D_3, the plant is homozygous for D_2 and either homozygous or heterozygous for D_1 (due to partial dominance of D_2 and complete dominance of D_1). Finally, he symbolised the genotypes for three hybrid dwarf types, *viz.* Type I-dwarf =D_1. D_2. D_3D_3. Type II-dwarf =D_1. D_2. D_3. and Type III-dwarf =D_1. D_2D_2 d_3d_3.

II.2.2. Gene action:

The fundamental nature of gene action and interaction involved in the inheritance of quantitative characters were not well understood, until the development of the biometrical methods and genetical assumptions. At first, Johansen (1909) published the theory of pure line selection, in which he clearly distinguished the heritable and non-heritable variance. Nilsson-Ehle (1909) stated his multiple factor hypothesis. East (1915) clearly showed that quantitative characters were inherited with the joint action of genetical and environmental factors. Fisher (1918 & 1946) suggested that several genes acted simultaneously on quantitative character producing the total variation. He was the first to provide statistical methods of partitioning the total variation into genetical and environmental components, and developed techniques for detecting the average additive and dominance effects of genes. Mather (1949) developed biometrical techniques and described how the additive and dominance variation could be estimated in wide variety of genetical experiments. He also determined the contributions of additive, dominance and non-allelic gene action to the total genetic variation and interaction components of continuous variation.

The work of Fisher *et al.* (1932) influenced several investigators, such as Castle and Wright (1921), Yates (1947), Comstock and Robinson (1948), Mather (1949), Cavalli (1952), Anderson (1953), Burton (1951), Kempthorne (1954), Jinks (1954), Jinks and Jones (1958) and Pe ter and Frey (1966) to work on the gene action and interactions in continuous variations and thus, most of the genetic models to study the continuous variation came into existence. Anderson and Kempthorne (1954) provided all the information about additive, dominance and

digenic epistatic variation through six-parameter model. Hayman (1958) successfully separated additive and dominance effects from epistasis by using three-parameter and six-parameter models. He suggested that means of generations were influenced by epistasis, which might be present in the form of interaction with additive effect, with dominant effect or with both additive and dominant effects.

Breeding for yield includes genetical manipulation of the components along with yield, which inherits polygenetically, exhibit additive and non-additive genetic variations, and their expression is influenced by environments. High proportion of additive genetic variation to non-additive genetic and environmental variations is very much important to get a good response for selecting a character. But the magnitude and proportion of the additive genetic variations for such characters vary among different populations (Law *et al.*, 1978; Bhular *et al.*, 1979 and Joarder *et al.*, 1982). Additive gene action was found to be predominant over non-additive gene action in spring wheat (Gill *et al.*, 1973) and in winter wheat (Schmidt *et al.*, 1980).The importance of non-additive gene action (dominance effect) for grain yield in spring wheat has been emphasized by others (Jatasra and Paroda, 1978 and Nanda *et al.*, 1982c). Sharma and Ahmad (1979) reported degree of dominance for grain yield at overdominance level. Singh *et al.* (1969) reported presence of complementary epistasis for grain yield in spring wheat. Both complementary and duplicate epistasis for grain yield were reported in different crosses of spring wheat varieties by Paroda and Joshi (1970a). Singh *et al.* (1984b) observed additive X additive, additive X dominance and dominance X dominance epistasis in wheat. Among these three types, additive X additive epistasis is preferred by the plant breeders as it can be fixed like additive gene action through the selection process.

Spikes (fertile tillers) per plant is one of the three primary (morphological) yield component of wheat controlled by both additive and non-additive gene actions (Tandon *et al.*, 1970 and Singh *et al.*, 1986). Verma and Yunus (1986) observed that this trait was controlled by all the types of epistasis. Inheritance of grains per spike has been found to be controlled under additive genetic system in spring wheat (Tandon *et al.*, 1970 and Gill *et al.*, 1972 & 1973). But Paroda and Joshi (1970b) reported predominance of non-additive gene action including complementary and duplicate epistasis in different wheat crosses. Verma and Yunus (1986) reported additive X dominance and dominance x dominance types of epistatic effects for this character. These informations indicated that considerable variations in the expression of gene actions for grains per spike were mostly due to different genetic materials of wheat grown in different environment. Average grain weight is controlled by additive gene action in spring wheat (Bhatt, 1972 and Sawant and Jain, 1985). Additive X additive type of epistasis in addition to additive and dominance gene actions was reported by Singh *et al.* (1984a).

Information on the inheritance of biological yield and harvest index is scanty. Between these two physiological yield components, biological yield is more complex, as it includes every parts of the plant. About 20 alleles have overdominance gene action for biological yield in spring wheat crosses (Sharma *et al.*, 1987). Biological yield was reported to be predominantly controlled by additive gene action (Thakral *et al.*, 1979) and non-additive gene action (Shamsuddin, 1982 and Sharma *et al.*, 1984). Harvest index is measured as the ratio of photosynthetates (= total plant dry weight) to the economic yield (= grain weight per plant) and is considered as one of the most important physiological yield components. Harvest index referred by Donald and Hamblin (1976) has also

been known as coefficient of effectiveness (Nichiporovich, 1960) and migration coefficients (Engledow and Wadham, 1923; Tsuneda, 1959). It is positively correlated with grain yield but negatively correlated with biological yield. An improved harvest index represents increased physiological capacity to translocate photosynthetase to the grain and it is useful measure of yield potential of crops. Vogel *et al.* (1963) reported that high yielding semidwarf wheat cultivars had an improved grain to straw ratio over tall varieties. Presence of both additive and dominance effects controlled this trait (Ali and El-Haddad, 1978 and Nanda *et al.*, 1982 c). However, Khalifa and Al-Shaheal (1984) reported the importance of dominance gene action, but additive gene action was reported by Thakral *et al.* (1979) and Sharma *et al.* (1984) for harvest index in wheat.

There are reports that two or three major genes along with some modifiers control plant height in semidwarf wheat (Romerio and Frey, 1973 and Yadav and Murty, 1979a). But cytological investigations by Sears (1954) and Allan and Vogel (1963) revealed that at least 11 to 16 of the 21 chromosomes of bread wheat carried the alleles for plant height. Pawar *et al.* (1985) studied generation means and found the presence of additive and non-additive gene actions for this character. Predominant additive gene action for the control of plant height was reported by Joarder *et al.* (1982). Nanda *et al.* (1982a) reported that it was controlled by additive X additive and dominance X dominance epistasis; but Singh *et al.* (1984b) reported duplicate type of epistasis. Sawant and Jain (1985) although reported additive X additive epistasis for plant height.

Van Dobben (1962) made comments on the fact that high temperature might shorten the period of development without giving sufficient compensation by faster growth, and this effect can be seen in kernel development of wheat if, for

example, temperatures are increased above $21/16^0$. Omar and El-Said (1963) reported that earliness in wheat was controlled by duplicate and complementary effects of four pairs of genes. Pokhryl *et al.* (1964) reported that the early and late varieties of wheat differed by additive gene effect at three loci, earliness being controlled by recessive genes. Walton (1972) found that dominance effect were evident in the inheritance of three developmental phases. Hanna (1973) reported that days to heading was controlled primarily by additive effects and secondarily by non-allelic interactions. Heading date was found to be controlled by genes with additive and dominance effects (Edward *et al.* 1976). The inheritance of days to heading in wheat was studied by Avey *et al.* 1980) in three crosses of winter wheat, where additive effects were found to be significant in cross 1, additive and dominance effects were significant in cross 2 and additive X additive effects were significant in cross 3.

II.2.3. Heritability:

Study of heritability of yield and its components is important in determining the response to selection for them. It has been observed that grain yield in bread wheat is a poorly heritable character. Both the broad and narrow sense heritability estimate of this character were very low (Kronstad and Foote, 1964; Paroda and Joshi, 1970b and Tanno *et al.* 1985). Various environmental effects on yield components finally influenced the expression of grain yield. Therefore, low heritability of grain yield is not unusual. In contrast to low heritability, high broad sense heritability for grain yield in spring wheat was reported by Sawant and Jain (1985). Bhatia *et al.* (1978) studied narrow sense heritability in spring wheat and reported 50.00%, 64.60%, 78.80% and 69.50%

heritability in F_1, F_2, F_3 and F_4 generations, respectively. The heritability values were considerably high and there was increasing tendency in later generations. Similar increasing tendency also reported by Bhular *et al.* (1974). Increase in heritability values in later generations was due to increase in additive genetic variance by fixation of the alleles.

Heritability studies on primary yield components of spring wheat indicated that spikes/ plant was a poorly heritable character (Paroda and Joshi, 1970b and Sayeed, 1978). But Sawant and Jain (1985) as well as Bhatia *et al.* (1978) obtained high broad sense and high narrow sense heritability for this character. Grains/ spikes was reported to be highly heritable by Bhular *et al.* (1974) and Sawant and Jain (1985). Medium heritability for this character was reported by Kronstad and Foote (1964) and Paroda and Joshi (1970b). Gill *et al.* (1973) estimated poor narrow sense heritability for grains per spike. Grain weight showed relatively high heritability in both broad and narrow sense (Sun *et al.* 1972; Bhatia *et al.* 1978; and Sawant and Jain, 1985). Sayeed (1978) estimated medium heritability for this character. High heritability for grain weight even when environment played a large role has been reported by Singh and Anand (1972).

Plant height is known to be a highly heritable character. Both broad and narrow sense heritability estimates for this character were reported to be considerably high. Joarder *et al.* (1982) and Sawant and Jain (1985) reported broad sense heritability values above 90% for plant height in spring wheat. Even narrow sense heritability was reported to be in the range of 90% by Bhatia *et al.* (1978) and Joarder *et al.* (1982).

Heritability of biological yield in spring wheat was studied by Shamsuddin (1982), who reported high broad sense heritability and low narrow sense heritability. Meidum to high heritability of harvest index was reported by Bhatt (1976 & 1977), Tanno *et al.* (1985) and Sharma and Smith (1986). But Borghi *et al.* (1983) reported poor heritability for this character. Harvest index was reported to be highly influenced by environments and genotype-environment interactions (Whan *et al.* 1981 and Latter and Ellison, 1983). Such environmental influences caused the poor heritability for harvest index when studied over wide range of environments.

II.2.4. Heterosis:

Development of hybrid dwarf wheat is getting importance now-a-days. In many cases, F_1 hybrids of wheat were found to outyield than their parents or local best varieties used as check. Ninety two percent heterosis was observed for grain yield in spring wheat (Yadav and Murty, 1976). Bhatti *et al.* (1985) reported 82% heterosis over mid parent for this character. Singh and Kandola (1969) observed that some of their F_1 hybrids outyielded the check variety, Kalyan 227. Singh and Anand (1971) also reported superiority of 6 F_1 hybrids over the best variety, Kalyansona.

In case of the heterosis of morphophysiological yield components, such as spikes per plant, Dudhat *et al.* (1986) reported 24.69% and 10.32% heterosis over mid and better parents, respectively. But singh and Singh (1978) observed significant negative heterosis for this character and significant positive heterosis for grains per spike. Dudhat *et al.* (1986) reported 19.68% heterosis for grains

per spike. For grain weight, Sun *et al.* (1972) reported significant heterosis up to 31.2% over mid parent. They noticed that distantly related parents gave higher heterosis.

Heterosis for biological yield and harvest index has been less studied. Singh and Singh (1978) reported maximum heterosis (6.30%) for harvest index over mid parent. Sharma *et al.* (1984) reported that average heterosis was significant for biological yield and specific heterosis was significant for harvest index. As dwarfism is a desirable character, so negative heterosis for plant height is preferred. Yadav and Marty (1976) observed negative heterosis up to -23.35% for plant height. Similarly, Sharma and Ahmad (1980) also reported negative heterosis (-4.26%) in semidwarf parents.

There is a close relationship between heterosis of grain yield and its primary components. Heterosis of yield was associated with heterosis of spikes per plant and grain weight (Singh and Singh, 1971). Sinha and Khanna (1975) reported that positive heterosis of yield is realised, if yield per spike is increased. It indicates that heterosis of grain yield is the cumulative effects of heterosis of yield components. And it causes higher estimates of heterosis for grain yield over its components.

Presence of non-additive gene action and heterosis for yield and its components indicate the prospect of hybrid wheat. But development of hybrid wheat is still some problem associated with sources of male sterility, restorer alleles, pollinators and pollination systems. Driscoll (1972, 1985) avoided cytoplasmic male sterility and developed a system of producing hybrid wheat using male sterility ,in monosomic and disomic addition lines. Gametocides, such

as 2-chloroethane phosphoric acid (Ethrel), Tribenzoic acid (tiba) and some other chemicals were used for producing hybrid wheat (Fairy and Stoskopf, 1975 and Dotlacil and Apltauerova, 1978). Sneep *et al.* (1979) suggested that use of gametocide is more promising than any other systems of producing hybrid wheat.

II.2.5. Selection:

Mather and Jinks (1971) showed that total genetic variance of F_3 generation is 3/4 D (additive) and 3/16 H (non-additive) as compared with 1/2 D and 1/4 H of F_2 generation. This indicates considerable increase in additive and decrease in non-additive genetic variance in F_3 from F_2 generation. Such increase in additive genetic variance facilitates good response for selection. O'Brien *et al.* (1978) evaluated response to selection for grain yield in four wheat crosses. They obtained significant response from F_3 to F_5 generations in two crosses, which had relatively higher genetic variation in F_3 populations. The other two had less genetic variation in F_3 and displayed non-significant response. This indicates that wider genetic variation in breeding population is necessary for obtaining a good response in selection. Therefore, selection for grain yield may be started from F_3 or onward generations.

Moreover, due to great genetic variability among the dwarfs from different crosses and high percentage of natural crossing tendency among the dwarfs, there are good prospect for selecting to find the best combinations of dwarfing genes and genetic background towards the production of hybrid dwarf varieties of wheat (Hermsen, 1967).

II.3. MATERIALS

The plant materials for this study was consisted of P_1, P_2, F_1, F_2, B_1 and B_2 generations of seven single crosses, viz. 1) Ag X FM-32, 2) Ak X FM-32, 3) An X FM-32, 4) Kan X FM-32, 5) Ak X FM-139, 6) An X FM-139 and 7) Kan X FM-139. Among the parental varieties/ lines, Aghrani (Ag), Akbar (Ak), Ananda (An) and Kanchan (Kan) are the registered varieties of Bangladesh, and FM-32 and FM-139 are the exotic selected dwarf lines of Falchetto X Maxicani cross. The seeds of different generations of all the seven crosses were supplied from a wheat breeding programme conducted by the Cytogenetics laboratory, Department of Botany, Rajshahi University. The parentage and source of six parents and their salient features are given in **Appendix 1 & 2**, respectively.

II.4. METHODS

II.4.1. Experimental design:

The experiment was conducted in the Rabi season of 1993-94 in the experimentation field of Rajshahi University. The size of the field was 14.5m X 13.7m. The field was divided into 3 blocks for three replications. The size of each block was 13.5m X 3.9m and was sub-divided into 7 plots for seven crosses. Each plot was consisted of 12 rows. There were single rowed P_1, P_2 and F_1 generations, two rowed B_1 and B_2 and five rowed F_2 generations of the same cross. The experimental materials were grown in Randomized Complete Block (RCB) design with three replications. The row and plant spacing were 30cm and 10cm, respectively. Each row contained 16 plants and 1.5 m in length. There was 0.5 m boundary space around the experimental field, between blocks and plots.

The experimentation field was well ploughed and moderately manured before sowing as per recommendation. The soil type of the experimental site was sandy clay loam with a pH of 8.2. Seeds were sown on December 2, 1993. After emergence of seedlings, common agronomic practices were made and irrigated twice at the time of tillering and heading. Chemical fertilizers were used in recommended doses. The weather records of the study period are shown in the Appendix 4.

II.4.2. Collection of data:

Data of the following characters were recorded from ten randomly selected individual plants of each population of all the blocks.

1) **Days to heading:** Number of days from the date of sowing to emergence of flower head.

2) **Days to maturity:** Number of days from sowing date to physiological maturity (determined by total loss of green colour).

3) **Plant height (cm):** Measured at maturity from the ground to the topmost spike (excluding awns).

4) **Fertile tillers/ plant:** Number of fertile tillers per plant.

5) **Spikelets/ ear:** Average number of spikelets per ear.

6) **Grains/ spike:** Average number of grains per spike (only primary ears were considered).

(7) **Hundred grains weight (gm):** Average dry weight of 100 seeds (sun dried bulk seeds).

8) **Biological yield (gm):** Total dry weight of the selected harvest-matured plants (excluding roots).

9) **Grain yield (gm):** Total dry weight of grains (obtained from the same plants used for biological yield).

10) **Harvest index:** Determined by dividing the grain yield by biological yield.

II.4.3. Analysis of data:

Breeding value of the experimental materials were estimated by analysing the data under different genetic parameters. Gene actions of yield and its components were studied through mean analysis, separation of components of generation means and variances, and estimation of heritability and heterosis analysis. The recorded data were transformed to logarithmic scale for converting the multiplicative intereffects of the characters into additive ones and subjected to scaling test of Mather (1949). The mean and variance of original data were subjected to joint scaling test of Cavalli (1952), analysed for different components of generation means based on six parameter model of Hayman (1958) and also used for estimation of components of variance and heritability based on Mather and Jinks (1977) model. The methods in detail are given bellow:

II.4.3.1. Mean analysis:

For preliminary determinatin of the nature of gene actions involved in controlling the studied characters, the observed and theoretical means were computed as follows:

(A) Observed mean and standard error: Mean, variance and standard error for each generation of the seven crosses were calculated pulling the data over replications. The formulae used for computation of these parameters are:

i) Mean, $\bar{X} = \Sigma X/n$

ii) Variance, $\sigma^2 = [\Sigma X^2 - (\Sigma X)^2/n]\ 1/(n-1)$

iii) Standard error, S.E. $= \sqrt{(\sigma^2/n)}$

Where, X = Value of individual observation, and

n = Total no. of observations per generation.

(B) Theoretical means: Theoretical arithmetic and geometric means were computed for F_1, F_2, B_1 and B_2 generations following Burton (1951). The formulae are given bellow:

i) Theoretical arithmetic means,

$\bar{F}_1 = \frac{1}{2}(\bar{P}_1 + \bar{P}_2)$,

$\bar{F}_2 = \frac{1}{4}(2\bar{F}_1 + \bar{P}_1 + \bar{P}_2)$,

$\bar{B}_1 = \frac{1}{2}(\bar{P}_1 + \bar{F}_1)$ and

$\bar{B}_2 = \frac{1}{2}\bar{P}_2 + \bar{F}_1)$.

ii) Theoretical geometric means,

$\bar{F}_1$ = Antilog $\frac{1}{2}$ [(log $\bar{P}_1$ + log $\bar{P}_2$)],

$\bar{F}_2$ = Antilog $\frac{1}{4}$ [(2 log $\bar{F}_1$ + log $\bar{P}_1$ + log $\bar{P}_2$)],

$\bar{B}_1$ = Antilog $\frac{1}{2}$ [(log $\bar{P}_1$ + log $\bar{F}_1$)] and

$\bar{B}_2$ = Antilog $\frac{1}{2}$ [(log $\bar{P}_2$ + log $\bar{F}_1$)].

The test statistics used by the following formula:

$$t = [\bar{X} - \mu_0] \div (S/\sqrt{n}), \text{ with } (n - 1) \text{ d.f.}$$

Where, $\bar{X}$ = observed mean, μ_0 = theoretical mean, and

$S/\sqrt{n}$ = standard error of observed mean.

II.4.3.2. Components of mean analysis:

A) Simple scaling test: For testing the presence or absence of epistasis, scaling test was done following Mather (1949) and Hayman and Mather (1955).

Altogether four scales (A, B, C & D) were used. Significance of any of these scales indicated the presence of epistasis. The test of significance was done with the use of respective standard errors of the scales. The four different scales and the formulae for the computation of its standard error are given bellow.

i) Scales:

$$A = 2\bar{B}_1 - \bar{P}_1 - \bar{F}_1,$$

$$B = 2\bar{B}_2 - \bar{P}_2 - \bar{F}_1,$$

$$C = 4\bar{F}_2 - 2\bar{F}_1 - \bar{P}_1 - \bar{P}_2 \text{ and}$$

$$D = 2\bar{F}_2 - \bar{B}_1 - \bar{B}_2.$$

ii) Standard error of scales:

$$\text{S.E. } A = [4V(\bar{B}_1) + V(\bar{P}_1) + V(\bar{F}_1)]^{\frac{1}{2}},$$

$$\text{S.E. } B = [4V(\bar{B}_2) + V(\bar{P}_2) + V(\bar{F}_1)]^{\frac{1}{2}},$$

$$\text{S.E. } C = [16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_1) + V(\bar{P}_2)]^{\frac{1}{2}} \text{ and}$$

$$\text{S.E. } D = [4V(\bar{F}_2) + V(\bar{B}_1) + V(\bar{B}_2)]^{\frac{1}{2}}.$$

Where, $V P_1$, $V P_2$, $V F_1$, $V F_2$, $V B_1$ and $V B_2$ are the variances of $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$, $\bar{B}_1$ and $\bar{B}_2$ populations, respectively.

B) Joint scaling test: Cavalli (1952) proposed a unique technique known as joint scaling test for estimating the genetic parameters using a number of generations at a time. This technique provides an advantage of using weight to different generation means. In the present investigation, joint scaling test was done based on 3-parameter model, as their expected components of means in six generations is given in Table 1. For testing the adequacy of additive-dominance model, a weighted χ^2 -test was done as proposed by Cavalli (1952).

Table 1: Expected components of means in different generations (Mather and Jinks, 1971).

Generations	Components of means		
	m	d	h
P_1	1	1	0
P_2	1	-1	0
F_1	1	0	1
F_2	1	0	0.5
B_1	1	0.5	0.5
B_2	1	-0.5	0.5

The goodness of fit were then tested by squaring the deviations of the observed from the expected values for each of the six families, multiplying by the corresponding weight and summing the product over all six types of families. The summed value obtained from six families gave a chi-square (χ^2) value for 3 d.f. If χ^2 is significant, it indicates that additive - dominance model is inadequate and the estimates of the 3-parameter were biased to an unknown extent by effects not attributable to the additive and dominant actions of the genes.

C). Estimation of genetic parameters: The data were analysed for computation of six genetic parameters *viz.* m, d, h, i, j and l following the analytical techniques of Hayman (1958) in order to separate epistatic gene effect.

These estimates are valid where the role of epistasis is indicated from the scaling test. In this model, **m** measures the mean effect, **d** and **h** measures the algebraic sum of additive and dominant effects, respectively and **i, j** and **l** measures algebraic sum of the epistatic effects additive X additive, additive X dominance and dominance X dominance types of gene interactions, respectively. These parameters were calculated using the following formulae.

$m = \bar{F}_2$,

$d = \bar{B}_1 - \bar{B}_2$,

$h = \bar{F}_1 + 2\bar{B}_1 + 2\bar{B}_2 - 4\bar{F}_2 - \frac{1}{2}\bar{P}_1 - \frac{1}{2}\bar{P}_2$,

$i = 2\bar{B}_1 + 2\bar{B}_2 - 4\bar{F}_2$,

$j = \bar{B}_1 - \bar{B}_2 + \frac{1}{2}\bar{P}_2 - \frac{1}{2}\bar{P}_1$ and

$l = \bar{P}_1 + \bar{P}_2 + 2\bar{F}_1 + 4\bar{F}_2 - 4\bar{B}_1 - 4\bar{B}_2$.

For the significance test of these parameters, their respective variances were calculated as follows:

$V_m = V(\bar{F}_2)$,

$V_d = V(\bar{B}_1) + V(\bar{B}_2)$,

$V_h = V(\bar{F}_1) + 4V(\bar{B}_1) + 4V(\bar{B}_2) + 16V(\bar{F}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2)$,

$V_i = 4V(\bar{B}_1) + 4V(\bar{B}_2) + 16V(\bar{F}_2)$,

$V_j = V(\bar{B}_1) + V(\bar{B}_2) + \frac{1}{4}V(\bar{P}_1) + \frac{1}{4}V(\bar{P}_2)$ and

$V_l = V(\bar{P}_1) + V(\bar{P}_2) + 4V(\bar{F}_1) + 16V(\bar{F}_2) + 16V(\bar{B}_1) + 16V(\bar{B}_2)$.

Standard errors of the estimates were calculated taking the square root of their respective variances. Thus,

$S.E.(m) = (V_m)^{\frac{1}{2}}$,

$S.E.(d) = (V_d)^{\frac{1}{2}}$,

$S.E.(h) = (V_h)^{\frac{1}{2}}$,

$S.E.(i) = (V_i)^{\frac{1}{2}}$,

S.E.(j) = $(V_j)^{\frac{1}{2}}$ and

S.E.(l) = $(V_l)^{\frac{1}{2}}$.

The 't'-values were calculated as bellow:

t (m) = m/ S.E.(m),

t (d) = d/ S.E.(d),

t (h) = h/ S.E.(h),

t (i) = i/ S.E.(i),

t (j) = j/ S.E.(j) and

t (l) = l/ S.E.(l).

When estimates of 't' exceeded 1.96, significant role of the concerned parameter was indicated.

II.4.3.3. Components of variance analysis:

The variance of non-segregating generations, *viz.* P_1, P_2 and F_1, are purely environmental, *ie.* non-heritable in nature. On the other hand, variances of segregating generations *viz.* F_2, B_1 and B_2 comprised both heritable and non-heritable components. The heritable components are constituted of fixable heritable (additive, D) and non-fixable heritable (dominance, H) type of variations. Based on this simple additive-dominance model, the expectations of the different generation's variances under study can be written following Mather and Jinks (1977).

$V\ F_2 = \frac{1}{2}D + \frac{1}{4}H + E_w$

$V\ B_1 + V\ B_2 = \frac{1}{2}D + \frac{1}{2}H + 2E_w$

$V\ P_1 = V\ P_2 = V\ F_1 = E_w$

Using these equations, the different components of variation, such as D, H and E_w were calculated. For estimation of E_w, non-segregating generations, *viz.* P_1, P_2 and F_1, variations were taken into consideration and thus E_w estimate was equal to $\frac{1}{4}V\ P_1 + \frac{1}{4}V\ P_2 + \frac{1}{2}V\ F_1$. Then D and H components along with F were calculated with the following formulae.

$D = 4V\ F_2 - 2\ (V\ B_1 + V\ B_2)$,

$H = 4\ [(V\ B_1 + V\ B_2) - (V\ F_2 + E_w)]$,

$F = V\ B_1 - V\ B_2$ and $F\ /\ \sqrt{D \times H}$ (= dominance deviation).

Where, F = weighted sum of the h's.

Positive F value indicate preponderance of P_1 over P_2 and negative F value indicate the preponderance of P_2 over P_1.

II.4.3.4. Heritability:

Heritability was calculated by two methods following Mather (1949) as bellow.

A). Broad sense heretability: It was expressed as the ratio of the genetic variance over the (expected) phenotypic variance of F_2 generations as follows.

$h^2_b = (\frac{1}{2}D + \frac{1}{4}H)/\ (\frac{1}{2}D + \frac{1}{4}H + E)$.

Where, D, H and E are the least square estimate of components of variation.

B). Narrow sense heritability: It was expressed as the ratio of fixable heritable variation (D) over the (expected) phenotypic variance of the F_2 generation as follow.

$h^2_n = \frac{1}{2}D/\ (\frac{1}{2}D + \frac{1}{4}H + E)$.

II.4.3.5. Heterosis:

As the role of epistasis is indicated from the scaling test, expected heterosis is measured based on six genetic parameters (Mather and Jinks, 1982) using the following formulae.

For positive heterosis,

Heterosis = $\bar{F}_1 - \bar{P}_1 = ([h] + [l]) - ([d] + [i])$;

and for negative heterosis,

Heterosis = $\bar{F}_1 - \bar{P}_2 = ([h] + [l]) - (-[d] + [i])$.

Where,

$\bar{F}_1 - \bar{P}_1$ and $\bar{F}_1 - \bar{P}_2$ are the observed positive and negative heterosis, respectively.

Percent heterosis was estimated as the percentage of the ratio of heterosis to its better parent.

II.5. RESULTS

The characters considered in this experiment vary continuously and are of polygenic control. Therefore, certain suitable biometrical techniques were used to determine the nature of gene action in the expression of those traits. The results obtained in this experiment are described bellow.

II.5.1. Analysis of generation means:

The standard errors were less than their corresponding mean values for most of the characters in all the generations of all crosses. Most of the mean values of F_1, F_2, B_1 and B_2 of each cross were not within the range of their parental values in almost all the cases (**Appendix 2 & 3**). This finding indicated the existence of sufficient genetic variability and showed the characteristics of normal distribution.

Theoretical arithmetic and geometric mean values along with their corresponding observed values for the F_1, F_2, B_1 and B_2 of seven crosses are given in Table 2. The results are described bellow.

In all the crosses, theoretical arithmetic and geometrical means were in close agreement for all characters in all the generations. The theoretical means differed significantly with corresponding observed means in case of days to heading (DH) and days to maturity (DM) for all the generations in all crosses,

Table 2. Means (Observed, arithmetic and geometric) of ten traits in hybrid progenies of seven crosses.

Traits	Popns.	Means	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
DH		OM	69.67	65.67	67.00	65.67	64.00	68.67	66.00
	F_1	AM	76.50**	75.50**	75.17**	75.17**	78.84**	78.84**	79.84**
		GM	75.87**	74.72**	74.33**	74.33**	77.55**	77.55**	78.74**
		OM	67.33	68.33	72.00	75.67	75.33	67.67	65.00
	F_2	AM	73.09**	70.59**	71.08	70.42**	71.42**	73.75*	72.92**
		GM	72.70**	70.05**	70.57	69.87**	70.45**	72.98*	72.09**
		OM	60.00	69.67	64.00	65.33	68.00	60.33	61.33
	B_1	AM	68.17**	65.17**	65.50	64.84	64.34**	66.67**	66.34**
		GM	68.15**	65.17**	65.48	64.83	64.33**	66.64**	66.34**
		OM	76.67	66.67	72.67	75.67	104.33	71.33	74.67
	B_2	AM	78.00**	76.00**	76.67*	76.00	78.50**	80.83**	79.50
		GM	77.55**	65.30**	76.05*	75.30	77.15**	79.91**	78.35
DM		OM	102.33	90.67	101.33	100.00	97.67	91.00	98.00
	F_1	AM	113.83**	111.50**	112.17*	112.17**	116.17**	116.17**	117.00**
		GM	113.52**	110.97**	111.70*	111.70**	115.13**	115.13**	116.08**
		OM	100.33	102.33	103.67	103.33	104.33	104.33	101.33
	F_2	AM	108.08**	101.09**	106.75**	106.08*	106.92**	103.59	107.50**
		GM	107.78**	100.30**	106.39**	105.69*	106.04**	102.36	106.66**
		OM	80.67	91.00	99.67	101.33	101.67	89.67	89.33
	B_1	AM	103.83**	95.67**	101.67	101.00	99.17**	95.84**	100.17**
		GM	103.82**	95.54**	101.66	101.00	99.16**	95.71**	100.14**
		OM	104.33	107.00	103.00	103.67	136.33	106.67	105.67
	B_2	AM	112.33**	106.50	111.83**	111.17**	114.67**	111.34	114.84**
		GM	111.88**	105.32*	111.34**	110.60**	113.40**	109.46	113.59**

OM = Observed mean, AM = Arithmatic mean, GM = Geometric mean, DH = Days to heading, DM=Days to maturity. * = P>0.05 and ** = P>0.01.

Table 2. (Continued)

Traits	Popns.	Means	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
PH(cm)		OM	66.13	63.10	61.17	66.87	80.68	69.18	74.40
	F_1	AM	66.98	65.92*	66.33	66.33	67.50**	67.50	69.02*
		GM	66.46	65.67*	66.05	66.05	67.38**	67.38	68.79*
		OM	51.20	53.73	57.53	77.37	70.83	77.38	75.29
	F_2	AM	66.56**	64.51**	63.75**	66.60*	74.09**	68.34*	71.71
		GM	66.38**	64.37**	63.56**	66.46*	73.73**	68.27*	71.54
		OM	70.00	71.80	73.10	76.70	86.82	78.32	73.18
	B_1	AM	69.93	67.35	66.80	69.65	76.14**	70.39	74.52
		GM	69.83	67.22	66.56	69.59	76.01**	70.38	74.52
		OM	58.73	56.97	53.60	75.97	61.44	44.80	69.20
	B_2	AM	61.18	61.67	60.70**	63.55	72.04**	66.29**	68.90
		GM	63.11	61.65	60.70**	63.46	71.52**	66.23**	68.68
BY(gm)		OM	161.17	132.33	158.70	187.17	124.87	126.10	147.00
	F_1	AM	216.22**	222.30**	192.62**	192.62	204.12**	204.12**	191.20**
		GM	215.87**	222.21**	189.25**	189.25	203.76**	203.76**	191.20**
		OM	379.83	333.50	308.00	359.93	432.10	334.73	357.97
	F_2	AM	191.70**	177.32**	175.66**	189.90	164.49**	165.11**	169.10**
		GM	189.97**	171.48**	173.31**	188.21	159.51**	160.23**	167.65**
		OM	297.93	346.27	266.90	374.17	315.13	210.77	211.93
	B_1	AM	185.57**	174.23**	157.74**	171.97**	170.50*	171.12*	168.65
		GM	184.66**	169.12**	157.73**	171.30**	164.28*	165.09*	167.26
		OM	488.40	251.10	310.50	433.87	338.63	295.90	298.13
	B_2	AM	197.82**	180.40*	193.59**	207.82	158.49**	159.10*	169.55*
		GM	195.43**	173.88*	190.42**	206.79	154.88**	155.64*	168.04*

PH= Plant height, BY= Biological yield.

Table 2. (Continued)

Traits	Popns.	Means	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
GY(gm)		OM	84.40	56.83	79.80	96.00	66.57	62.80	79.03
	F_1	AM	113.24**	115.42**	93.25**	93.25	115.42**	115.42**	109.44**
		GM	113.07**	115.12**	92.20**	92.20	115.12**	115.14**	109.41**
		OM	202.17	190.00	145.33	182.73	206.93	182.10	188.27
	F_2	AM	98.82**	86.12**	86.53**	94.63	90.99**	89.11*	94.23**
		GM	97.69**	80.89**	85.78**	94.08	87.54**	85.03*	92.99**
		OM	153.17	183.20	143.57	201.97	169.37	111.53	110.57
	B_1	AM	101.84**	90.23**	79.55**	87.65*	95.10*	93.22**	95.35
		GM	100.33**	83.82**	79.55**	87.25*	90.72*	88.11**	93.94
		OM	224.57	97.53	141.50	191.87	78.43	121.67	125.63
	B_2	AM	95.80**	82.02	93.50**	101.60	86.89	85.00	93.12
		GM	95.12**	78.05	92.49**	101.45	84.48	82.05*	92.04*
HI(%)		OM	50.67	43.03	50.27	51.23	53.30	50.20	53.97
	F_1	AM	53.04**	52.22**	48.39	49.07	51.54	51.54	52.39
		GM	52.74**	52.00**	49.04	49.04	51.25	51.25	52.01
		OM	53.43	56.93	48.97	49.73	48.63	54.07	52.37
	F_2	AM	51.85	47.63**	49.67	50.15	52.42	50.87	53.18
		GM	51.70	47.64**	49.29	50.13	52.26	50.72	52.98
		OM	51.47	52.47	53.73	53.50	54.13	53.30	53.33
	B_1	AM	54.64	50.00	50.47	50.95	55.14	53.59	56.32
		GM	54.49	49.51	50.47	50.95	55.10	53.48	56.27
		OM	45.67	38.77	45.67	43.60	23.40	41.40	44.80
	B_2	AM	49.07	45.25**	48.87	49.35**	49.70*	48.15**	50.04**
		GM	49.04	45.20**	48.85	49.31**	49.57*	48.11**	49.88**

GY = Grain yield (gm), HI = Harvest index (%)

Table 2. (Continued)

Traits	Popns.	Means	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
FT		OM	3.93	5.07	5.53	6.17	6.87	5.13	4.33
	F_1	AM	6.09**	6.00	5.09	5.09	5.35**	5.35	5.45*
		GM	6.08**	5.99	4.92	4.92	5.34**	5.34	5.44*
		OM	6.03	10.20	6.67	5.07	7.53	5.31	5.90
	F_2	AM	5.01	5.54**	5.31*	5.63	6.11	5.24	4.89
		GM	4.89	5.51**	5.22*	5.51	6.06	5.24	4.85
		OM	5.13	7.33	9.50	6.40	7.83	5.27	5.63
	B_1	AM	4.87	5.35	4.67	4.99	6.25*	5.38	5.08**
		GM	4.77	5.34	4.58	4.84	6.22*	5.37	5.02**
		OM	5.70	7.44	6.57	6.83	10.96	6.71	6.07
	B_2	AM	5.15	5.72*	5.95	6.27	5.97**	5.10	4.70*
		GM	5.00	5.68*	5.94	6.27	5.90**	5.10	4.69*
SE		OM	19.67	22.03	19.00	19.47	21.30	19.63	18.17
	F_1	AM	19.37	19.35**	19.08	19.08	19.74**	19.74	19.37**
		GM	19.36	19.34**	19.06	19.06	19.71**	19.71	19.32**
		OM	20.98	20.42	23.13	19.50	20.33	19.93	18.53
	F_2	AM	19.52	20.69	19.18**	19.28	20.52	19.68	18.77
		GM	19.51	20.64	19.03**	19.26	20.49	19.67	18.74
		OM	19.80	20.97	19.87	19.20	21.07	20.23	20.13
	B_1	AM	19.24	20.40	18.62	18.85	20.04	19.20**	18.10**
		GM	19.23	19.58	18.61	18.84	20.00	19.20**	18.10**
		OM	21.37	21.14	19.70	21.07	28.60	19.82	20.33
	B_2	AM	19.80	20.98	19.47	19.70*	21.00**	21.00*	19.44*
		GM	19.80	20.95	19.46	19.70*	21.00**	20.16	19.39*

FT = Fertile tillers/plant, SF = Spikelets/ear.

Table 2. (Continued)

Traits	Popns.	Means	Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
GE		OM	46.97	49.37	46.93	50.03	54.70	37.27	41.60
	F_1	AM	63.10	57.92**	61.15**	61.15	52.25	52.25**	47.97**
		GM	63.08	57.81**	61.15**	61.15	52.20	52.20**	47.92**
		OM	64.59	41.14	64.38	47.37	66.49	65.73	41.89
	F_2	AM	55.04	50.81**	55.02**	55.59*	53.48**	44.76**	44.78
		GM	54.43	53.43**	53.57**	55.31*	53.44**	44.11**	44.65
		OM	59.80	63.50	59.20	48.23	64.90	63.97	51.07
	B_1	AM	55.92	51.94**	53.95**	55.50**	54.60**	45.89**	43.77**
		GM	55.20	51.87**	53.49**	55.23**	54.60**	45.07**	43.71**
		OM	63.20	53.27	58.60	62.37	29.87	48.13	46.12
	B_2	AM	54.15	55.35	54.13**	55.68	52.35**	43.64	45.80
		GM	52.67	55.03	53.65**	55.39	52.30**	43.17	45.61
GW(gm)		OM	1.97	2.46	2.24	2.87	3.13	2.84	3.47
	F_1	AM	2.94	3.37**	3.12	3.12	3.64	3.64**	3.77
		GM	2.93	3.31**	3.10	3.10	3.63	3.63**	3.74
		OM	3.09	2.04	2.89	4.02	2.68	3.49	4.31
	F_2	AM	2.46*	3.05**	2.68	2.99*	3.39**	3.24**	3.62**
		GM	2.40*	2.85**	2.63	2.98*	3.37**	3.21**	3.60**
		OM	3.78	3.07	3.40	3.85	3.67	2.64	2.84
	B_1	AM	2.55**	3.22	2.86	3.17*	3.82	3.41**	3.85*
		GM	2.48**	3.13	2.79	3.16*	3.53	3.36**	3.83*
		OM	2.46	2.15	2.89	3.77	1.42	2.75	2.72
	B_2	AM	2.37	2.61**	2.50	2.82**	3.22**	3.08	3.39**
		GM	2.33	2.61**	2.49	2.81**	3.22**	3.07	3.39**

GE = Grains/ear, GW = 100-Grain weight (gm)

except B_1 of cross 3 and 4. But the plant height (PH) differed significantly in F_2 of all the crosses except cross 7, in F_1 of cross 2 and 7, in B_2 of cross 3 and 6. While in cross 5 it differed significantly in all the generations.

The observed mean of biological yield (BY) differed significantly from their theoretical means in all cases except in B_1 of cross 7 and in F_1, F_2 and B_2 of cross 4. The Harvest index (HI) differed significantly in B_2 for all crosses except cross 1 and 3, but only in F_1 and F_2 of cross 2. However, grain yield (GY) differed significantly in almost all cases except in cross 4.

In case of fertile tillers/ plant (FT), the differences between observed and theoretical means were significant in F_1 of cross 1, 5 and 7, in F_2 of cross 2 and 3 and in B_2 of cross 2, 5 and 7. The spikelets/ ear (SE) differed significantly only in F_1 of cross 2, 5 and 7, in F_2 of cross 3, and in B_2 of cross 4, 5 and 7. Number of grains/ ear (GE) and 100-grain weight (GW) differed significantly in most of the cases except cross 1 and 3, respectively.

II.5.2. Components of mean analysis:

Scaling test: One or more scales *viz.* A, B, C and D of the scaling test was/ were significant for all characters in Akbar X FM-32 (C_2) except the spikelets/ ear (SE) and in Akbar X FM-139 (C_5). But some of the characters in the rest five crosses were significant. However, χ^2 -value of the joint scaling test were significant for almost all of the characters in all crosses except in AghranixFM-32

(C_1) for harvest index (HI), fertile tillers/ plant (FT), spikelets/ ear (SE) and grains/ ear (GE). This indicated that simple additive-dominance model was inadequate to explain the nature of inheritance of those characters. Thus, the model was extended to six-parameter model (**Table 3**), which helped to arrive at perfect fit estimates of the six genetic parameters and to identify the types of gene action and interaction responsible for the departure from simple additive-dominance situation.

Genetic parameters: The magnitude of base population mean (m) for developmental yield components, *viz.* days to heading (DH), days to maturity (DM) and plant height (PH) were high, positive and significant in all the crosses. The former two characters in all crosses were mainly controlled by additive (d) gene action in addition to additive-additive (i) type of interaction along with dominance (h) except in C_2 for DH and in C_4 for DM, where dominant-dominant (l) type of interaction was involved. Plant height was controlled by d along with l in C_1 and C_2, but in C_3, C_4 and C_5 additive-dominant (j) type of interaction was significant in addition to d and in C_7 only i was significant. The absolute magnitude of h was higher than that of d for DM in all crosses, for PH in all crosses except C_3 and DH in C_2, C_3, C_4 and C_6. Dominance-dominance (l) type of digenic interaction was significant for DM in all crosses, for DH in all except C_7 and for PH in all except C_3 and C_4. On the other hand, h and l were significant, but had opposite sign (- / +) for DM in all crosses, for DH in all except C_5 and C_7, and for PH in C_1, C_2, C_5 and C_6. These indicated the involvement of duplicate type of gene action in those cases. However, in C_4 trigenic or higher order of interaction might be involved to control PH, because joint scaling test indicated the presence of epistasis, while none of the epistatic parameters were significant at digenic level.

Table 3. Gene action for ten characters in seven crosses of wheat

Test	Parameter	Days to heading (DH)						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	- 0.1106* ±0.0184	0.0580* ±0.0241	-0.0558 ±0.0484	-0.0108 ± 0.0287	0.0486 ±0.0381	-0.1172* ±0.0224	-0.0671 ±0.0461
	B	- 0.0091* ±0.0359	-0.1048* ±0.0392	-0.0386 ±0.0500	0.0053 ±0.0395	0.2958* ±0.0429	-0.0660 ±0.0526	-0.0088 ±0.0714
	C	- 0.1323* ±0.0495	-0.0684* ±0.0341	0.0356 ±0.0836	0.1221* ±0.0579	0.1502* ±0.0638	-0.1306 ±0.0975	-0.1449 ±0.0901
	D	- 0.0063 ±0.0173	0.0023 ±0.0105	-0.0473 ±0.0447	0.0638* ±0.0095	-0.0971* ±0.0212	0.0263 ±0.0192	-0.0345 ±0.0297
Joint Scaling (3-para. model)	$\hat{m}$	73.69* ±0.62	65.76* ±0.62	68.90* ± 1.46	86.70* ± 1.03	97.32* ± 0.59	75.35* ± 1.01	77.10* ± 1.13
	$\hat{d}$	-12.62 ±0.51	-0.12 ±0.58	-6.32* ± 1.47	-23.79* ± 0.82	-33.21* ± 0.53	-13.88* ± 0.98	-10.83* ± 0.89
	$\hat{h}$	- 7.18* ±1.11	4.98* ±1.06	1.28 ± 2.87	-22.82* ± 1.89	-23.69* ± 1.44	-13.00* ± 1.30	-21.13* ± 2.08
	$\chi^2_{(df\ 3)}$	123.15*	96.35*	20.33*	382.29*	471.66*	102.23*	25.47*
Genetic component of means (6-para model)	m	67.33* ±0.39	68.33* ± 0.19	72 00* ±1.00	75.67* ± 0.19	75.33* ± 0.51	67.67 ± 1.26	65.00* ± 0.33
	d	-16.67* ±0.55	3.00* ± 0.43	-8.67* ±1.43	-10.34* ± 0.43	-36.33* ± 0.39	-11.00* ± 1.09	-13.34* ± 1.51
	h	-2.81* ±2.10	-10.47* ± 1.68	-22.83* ± 5.17	-31.51* ± 1.81	-28.51* ± 2.55	-17.19* ± 5.57	-1.84 ± 3.78
	i	4.02* ±1.73	-0.64 ± 1.15	-14.66* ± 4.91	-20.68* ± 1.15	-43.34* ± 2.17	-7.36* ± 5.51	-12.00* ± 3.31
	j	-6.84* ±1.20	13.83* ± 1.19	2.50 ± 1.81	-0.51 ± 1.24	-22.17* ± 0.78	3.50* ± 1.29	-0.18 ± 1.69
	l	14.98* ±3.25	10.30* ± 3.09	25.65* ± 7.67	23.02* ± 3.36	-102.33* ± 3.70	38.38* ± 6.89	7.67 ± 7.16

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Days to maturity (DM)						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	-0.2239* ±0.1133	-0.0750* ±0.0016	-0.0511 ±0.0339	-0.0109 ±0.0266	0.0224 ±0.0285	-0.0623* ±0.0214	-0.0986* ±0.0310
	B	-0.0582* ±0.0170	-0.0164 ±0.0170	-0.0646 ±0.0329	-0.0536 ±0.0283	0.1607* ±0.0302	-0.0227 ±0.0338	-0.2135 ±0.1726
	C	-0.1219* ±0.0205	0.0308* ±0.0116	-0.0732 ±0.0535	-0.0503 ±0.0512	-0.0269 ±0.0612	0.0270 ±0.0704	-0.0877 ±0.0600
	D	0.0801 ±0.0571	0.0316* ±0.0089	0.0200 ±0.0161	0.0071 ±0.0164	-0.1050* ±0.0132	0.0560 ±0.0375	0.1122 ±0.0853
Joint Scaling (3-para. model)	$\hat{m}$	102.98* ± 0.53	111.84* ± 0.56	108.10* ± 1.44	108.61* ± 1.11	125.60* ± 1.17	128.52* ± 1.40	112.30* ± 1.04
	$\hat{d}$	0.22 ± 0.67	-14.48* ± 0.70	-3.12* ± 0.99	-5.67* ± 0.95	-32.80* ± 0.44	-52.66* ± 2.08	-11.47* ± 0.87
	$\hat{h}$	-1.40 ± 0.73	-21.26* ± 0.77	-10.10* ± 2.97	-9.23* ± 1.81	-15.07* ± 2.36	-37.41* ± 1.57	-90.35* ± 1.81
	$\chi^2_{(df\ 3)}$	118.10*	51.09*	29.90*	13.56*	451.53*	915.92*	177.17*
Genetic component of means (6-para model)	m	100.33* ± 0.19	102.33* ± 0.19	103.67* ± 0.19	103.33* ± 0.51	104.33* ± 0.51	104.33* ± 1.35	101.33* ± 0.19
	d	-23.66* ± 3.39	-16.00* ± 0.47	-3.33* ± 1.22	-2.34* ± 0.86	-34.66* ± 0.27	-17.00* ± 1.36	-16.34* ± 1.09
	h	-42.82* ± 6.89	-34.15* ± 1.56	-16.18* ± 3.48	-15.65* ± 3.03	40.18* ± 2.93	-50.48* ± 6.10	-34.32* ± 3.19
	i	-31.32* ± 6.83	-13.32* ± 1.22	-9.34* ± 2.55	-3.32 ± 2.66	58.68* ± 2.92	-24.64* ± 6.03	-15.32* ± 2.30
	j	-15.16* ± 3.51	-5.17* ± 1.06	6.84 ± 1.57	7.66* ± 1.24	-19.16* ± 0.81	2.17 ± 1.60	-1.67 ± 1.30
	l	93.64* ±13.71	21.66* ± 2.82	30.99* ± 6.83	17.98* ± 4.94	-107.00* ± 4.75	47.63* ± 7.87	55.32* ± 6.24

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Plant height (PH) in cm						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	-0.0017 ±0.1050	-0.0573 ±0.0648	0.0752 ±0.1992	0.0716 ±0.0995	0.1165* ±0.0480	0.0809 ±0.1422	-0.0174 ±0.0819
	B	-0.0770 ±0.2005	-0.0706 ±0.0860	-0.0905 ±0.1559	0.1519 ±0.1483	-0.1311* ±0.0412	-0.3403 ±0.0806	0.0062 ±0.0714
	C	-0.4225* ±0.1040	-0.3127* ±0.0608	-0.1377 ±0.3020	0.2491 ±0.2243	-0.0676 ±0.0593	0.2108 ±0.4719	0.0890 ±0.0970
	D	-0.1869 ±0.1225	-0.1497* ±0.0510	-0.0612 ±0.1327	0.0128 ±0.1241	-0.0265 ±0.0195	0.2351 ±0.2468	0.0501 ±0.0632
Joint Scaling (3-para. model)	$\hat{m}$	64.47* ± 1.01	56.97* ± 1.20	65.43* ± 1.03	67.80* ± 1.09	44.75* ± 1.14	10.84* ± 0.79	27.00* ± 1.11
	$\hat{d}$	6.95* ± 1.05	1.72 ± 1.48	13.03* ± 1.39	8.75* ± 1.09	11.50* ±0.69	4.90* ±0.86	7.24* ±1.72
	$\hat{h}$	-2.66 ± 1.73	2.78 ± 1.80	-14.39 ± 2.52	7.10 ± 3.96	9.03* ± 2.16	3.98* ± 1.41	5.36* ± 1.81
	$\chi^2_{(df\ 3)}$	70.81*	86.37*	49.74*	8.31*	4868.98*	9395.39*	2193.02*
Genetic component of means (6-para model)	m	51.20* ±0.93	53.73* ±0.43	57.53* ± 0.46	77.37* ±2.27	70.83* ± 0.21	77.38* ± 1.92	75.29* ± 1.21
	d	11.27* ± 5.14	14.83* ± 2.25	19.50* ± 6.60	0.73 ± 4.47	25.38* ± 1.02	33.52* ± 4.19	3.98 ± 2.68
	h	51.81* ±10.96	39.81* ± 4.96	18.12 ±15.24	-4.70 ± 14.53	26.38* ± 2.72	-62.02* ±11.47	-11.02 ± 7.35
	i	52.66 ±66.49	42.62* ± 4.81	23.28 ±13.33	-4.41 ±14.25	13.20* ± 2.22	-63.28* ±11.37	-16.40* ± 7.21
	j	4.52 ±5.16	9.15* ± 2.49	13.40* ± 6.62	-6.47 ± 4.52	21.43* ± 1.63	29.01* ± 4.27	-1.64 ± 2.83
	l	-43.93* ±20.96	-42.13* ±9.47	-21.68 ±30.33	-32.60 ±21.80	-13.36* ± 5.23	91.23* ±18.67	18.47 ±12.09

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Biological yield (BY) in gm						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.4290* ±0.1530	0.7063* ±0.1712	0.4542* ±0.1212	0.5748* ±0.2516	0.6124 ±0.4074	0.3574* ±0.1539	0.1844 ±0.2472
	B	0.8806* ±0.1536	0.4081 ±0.2396	0.4294 ±0.1304	0.5714 ±0.4970	0.6882* ±0.1942	0.5520 ±0.2941	0.4816 ±0.2961
	C	1.2208* ±0.2844	1.2412* ±0.4488	1.0058* ±0.1658	0.9092 ± 0.9336	1.7502* ±0.7163	1.3970* ±0.5713	1.3276* ±0.1772
	D	-0.0056 ±0.1149	0.1051 ±0.1453	0.0611 ±0.0917	-0.1185 ±0.5357	0.2248 ±0.3428	0.2438 ±0.2926	0.3308 ±0.1903
Joint Scaling (3-para. model)	$\hat{m}$	356.84* ±18.02	388.08* ±18.87	286.79* ±11.02	211.36* ±15.31	318.98* ±39.27	189.82* ±13.96	273.64* ±12.69
	$\hat{d}$	-13.59 ±17.63	124.61* ±15.92	-101.77* ±11.70	-16.99 ±15.25	79.88* ±39.03	-102.60* ±13.77	-88.39* ±13.43
	$\hat{h}$	-161.16* ±25.84	-212.90* ±35.76	-122.43* ±11.96	-25.05 ±18.57	-19.06* ±44.93	-152.77* ±21.44	-112.23* ±14.55
	$\chi^2_{(df\,3)}$	118.71*	24.45*	110.53*	18.20*	156.40*	209.20*	149.17*
Genetic component of means (6-para model)	m	379.83* ±15.21	333.50* ±13.97	308.00* ± 7.12	359.93* ±52.22	432.10* ±46.10	334.73* ±31.15	359.97* ± 8.04
	d	-190.47* ±17.51	95.17* ±16.67	-43.60* ±15.22	-59.70 ±76.11	-23.50 ±34.38	-85.13* ±28.82	-86.20* ±35.17
	h	4.29 ±71.88	-229.23* ±70.94	-111.12* ±42.69	-279.73 ±258.68	-500.13* ±198.59	-373.92* ±137.92	-455.96* ±77.86
	i	55.34 ±70.21	-139.26* ±65.06	-77.20 ±42.68	176.36 ±258.45	-420.88* ±196.81	-325.58* ±137.30	-411.76* ±77.34
	j	-178.22* ±22.01	101.34* ±30.35	-7.75 ±17.67	-40.62 ±76.65	-35.52 ±42.59	-67.47* ±30.00	-85.30* ±36.15
	l	-859.22* ±97.75	-346.22* ±103.77	-374.96* ±69.68	-999.33* ±369.85	-228.67 ±236.10	-86.69 ±171.75	68.04 ±145.43

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Grain yield (GY) in gm						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.3799* ±0.1389	0.7568* ±0.3277	0.5080* ±0.1463	0.5547 ±0.2998	0.5973 ±0.3876	0.4037* ±0.0980	0.1357 ±0.1526
	B	0.7442* ±0.1530	0.1922 ±0.2427	0.3698* ±0.1178	0.4666 ±0.5322	0.0316 ±0.1746	0.4218 ±0.2678	0.3899 ±0.2557
	C	1.2795* ±0.1962	1.5522* ±0.5291	0.9194* ±0.1565	0.8317 ±1.0629	1.6239* ±0.6190	1.5571* ±0.6155	1.3044* ±0.3226
	D	0.0777 ±0.0877	0.3016 ±0.2117	0.0208 ±0.1020	0.0534 ±0.6048	0.4975 ±0.2807	0.3658 ±0.3127	0.3894 ±0.2005
Joint Scaling (3-para. model)	$\hat{m}$	175.93* ± 6.31	200.05* ±10.17	118.29* ± 4.36	111.86* ± 5.90	165.87* ±17.34	104.83* ± 4.84	116.98* ± 5.53
	$\hat{d}$	39.61* ± 6.64	89.06* ± 9.89	-27.72* ± 4.59	2.38 ±5.90	61.32* ±17.06	-5.57 ± 4.76	1.62 ± 5.59
	$\hat{h}$	-76.57* ± 9.38	-133.39* ±16.01	-28.53* ± 5.75	-11.36 ±10.45	-98.06* ±19.92	-0.60 ± 7.65	-34.27* ± 5.65
	$\chi^2_{(df\ 3)}$	131.32*	19.51*	112.66*	12.21*	15.53*	77.14*	40.66*
Genetic component of means (6-para model)	m	202.17* ± 4.10	190.00* ±12.86	145.33* ± 3.22	182.73 ±29.70	206.93* ±18.13	182.10* ±19.95	188.27* ±10.95
	d	-71.40* ±11.93	85.67* ± 8.83	2.07 ±9.08	10.10 ±38.31	90.94* ±14.51	-10.14 ±10.02	-15.06 ±10.82
	h	-82.04* ±29.80	-257.13* ±56.53	-24.63 ±22.52	43.33 ±141.51	-380.97* ±79.60	-292.45* ±82.44	-311.09* ±48.97
	i	-53.20 ±28.95	-198.54* ±54.38	-11.18 ±22.25	56.76 ±141.38	-332.12* ±78.13	-262.00* ±82.29	-280.68* ±48.84
	j	-137.07* ±13.54	77.46* ±16.98	16.02 ± 9.54	7.87 ±38.46	82.73* ±20.51	3.81 ±10.44	-17.30 ±11.35
	l	-307.01* ±52.39	-18.43 ±69.65	-53.26 ±39.15	-433.57* ±194.28	200.49* ±97.77	107.70 ±89.85	185.21* ±61.96

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Harvest index (HI) in %						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	-0.0495 ±0.0480	0.0503 ±0.0656	0.0528 ±0.0671	-0.0199 ±0.0678	-0.0150 ±0.0510	0.0461 ±0.0837	-0.0487 ±0.1100
	B	-0.0621 ±0.0671	-0.1332 ±0.0735	-0.0605 ±0.0995	-0.1052 ±0.0671	-0.6589* ±0.1530	-0.1302 ±0.0755	-0.0918 ±0.0700
	C	0.0566 ±0.1233	0.3213* ±0.1439	-0.0243 ±0.1131	-0.0779 ±0.1863	-0.1259 ±0.1386	-0.1605 ±0.1473	-0.0225 ±0.1990
	D	0.0841 ±0.0663	0.2021* ±0.0748	-0.0083 ±0.0735	0.0236 ±0.0854	0.2740* ±0.0990	0.1223 ±0.0825	0.0590 ±0.1049
Joint Scaling (3-para. model)	$\hat{m}$	51.72* ± 1.17	52.06* ± 1.29	48.81* ± 1.61	51.81* ± 1.40	35.68* ± 1.15	29.35* ± 0.92	49.03* ± 1.46
	$\hat{d}$	5.36* ± 1.18	5.17* ± 1.26	-12.31* ± 1.20	7.54* ± 1.19	8.68* ± 1.16	2.49* ± 0.89	14.52* ± 1.40
	$\hat{h}$	-1.72 ± 1.67	-10.63* ± 2.14	-3.78* ±1.87	-5.38 ± 2.85	4.14* ± 1.61	1.12 ± 1.54	-0.43 ± 2.87
	$\chi^2_{(df\,3)}$	7.80	34.59*	198.55*	7.75	418.00*	661.93*	39.78*
Genetic component of means (6-para model)	m	53.43* ± 1.13	56.93* ± 1.39	48.97* ± 0.88	49.73 ± 1.54	48.63* ± 1.17	54.07* ± 1.36	52.37* ± 1.84
	d	5.80 ± 1.25	13.70* ± 1.39	8.06* ± 1.99	9.90* ± 1.10	30.73* ± 1.47	11.90* ± 1.85	8.53* ± 2.13
	h	-21.81* ± 5.25	-54.43* ± 6.32	4.12 ± 5.44	-6.56 ± 6.80	-37.70* ± 5.62	-25.07 ± 6.69	-11.64 ± 8.70
	i	-19.44* ± 5.15	-45.24* ± 6.20	2.92 ± 5.33	-4.72 ± 6.53	-39.46* ± 5.51	-26.88* ± 6.58	-13.22 ± 8.51
	j	0.24 ± 1.49	8.95* ±1.63	6.46* ± 2.13	4.30* ± 1.42	25.30* ± 1.64	9.62* ± 2.02	2.25 ± 2.33
	l	32.57* ± 7.02	53.26* ± 8.23	-3.04 ± 8.99	19.12* ± 8.47	94.07* ± 7.81	34.65* ± 9.48	29.67* ±11.82

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Fertile fillers / plant (FT)						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.0248 ±0.3292	0.3058 ±0.4051	0.5268* ±0.2354	0.0128 ±0.4442	0.2555 ±0.2907	0.0771 ±0.4874	0.1064 ±0.0989
	B	0.0369 ±0.4997	0.2370 ±0.1549	0.1058 ±0.1808	0.0573 ±0.3586	0.5313* ±0.1758	0.2123 ±0.3089	0.2255 ±0.1609
	C	0.2701 ±0.7819	1.1356* ±0.3526	0.4508 ±0.4110	-0.3537 ±0.6357	0.3714 ±0.6809	0.1666 ±0.4839	0.3295 ±0.3292
	D	0.1024 ±0.4863	0.2964 ±0.1803	-0.0909 ±0.1670	-0.2119 ±0.3861	-0.2077 ±0.3254	-0.0614 ±0.3701	-0.0012 ±0.1911
Joint Scaling (3-para. model)	$\hat{m}$	6.16* ± 0.37	9.92* ± 0.74	5.22* ± 0.35	6.07* ± 0.40	2.56* ± 0.34	3.80* ± 0.24	31.55* ± 0.27
	$\hat{d}$	-0.51 ± 0.37	2.34* ± 0.79	-1.31* ± 0.35	-0.23 ± 0.41	11.50* ± 0.34	0.58* ± 0.25	22.26* ± 0.25
	$\hat{h}$	-2.16* ± 0.56	-4.06* ± 0.94	1.43 ± 0.88	-0.18 ± 1.05	0.04 ± 0.36	0.66 ± 0.46	-0.92 ± 0.54
	$\chi^2_{(df\ 3)}$	1.07	36.08	4.00	1.48	1700.25*	15.14*	940.80*
Genetic component of means (6-para model)	m	6.03* ± 0.76	10.20* ± 0.32	6.67* ± 0.35	5.07* ± 0.53	7.53* ± 0.84	5.31* ± 0.44	5.90* ± 0.39
	d	-0.57 ± 1.04	-0.11 ± 0.86	2.93 ± 2.18	-0.43 ± 1.18	-3.13* ± 0.74	-1.44 ± 1.10	-0.44 ± 0.31
	h	-4.62 ± 3.69	-12.19* ± 2.26	-5.91 ± 4.61	6.25 ± 3.25	8.98* ± 3.72	3.42 ± 2.84	-1.32 ± 1.69
	i	-2.46 ± 3.69	-11.26* ± 2.15	5.46 ± 4.58	6.18 ± 3.18	7.46* ± 3.66	2.72 ± 2.82	-0.20 ± 1.66
	j	-0.29 ± 1.06	0.26 ± 1.08	4.22 ± 2.19	-0.16 ± 1.20	-3.41* ± 0.98	-0.81 ± 1.11	-0.82* ± 0.36
	l	0.83 ± 5.17	3.86 ± 3.93	-16.37 ± 8.92	-7.74 ± 5.37	-20.60* ± 4.65	-7.55 ± 4.77	-3.64 ± 2.07

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Spikelets / ear (SE)						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.0259 ±0.0656	0.0262 ±0.0436	0.0603 ±0.0959	0.0221 ±0.0469	0.0445 ±0.0557	0.0615 ±0.0636	0.0929* ±0.0418
	B	0.0601 ±0.1513	0.0079 ±0.0283	0.0144 ±0.0938	0.0586 ±0.0447	0.2670 ±0.0700	-0.0120 ±0.0755	0.0410 ±0.0349
	C	0.1226 ±0.1990	-0.0185 ±0.0405	0.3471 ±0.1817	0.0263 ±0.1058	0.0693 ±0.0860	0.0399 ±0.1533	-0.0197 ±0.1017
	D	-0.0183 ±0.1175	-0.0263 ±0.0257	0.1362* ±0.0574	-0.0272 ±0.0500	-0.1211* ±0.0583	-0.0048 ±0.0491	-0.0768 ±0.0514
Joint Scaling (3-para. model)	$\hat{m}$	19.41* ± 0.27	19.42* ± 0.27	19.16* ± 0.32	19.20* ± 0.36	16.22* ± 0.28	19.44* ± 0.33	20.55* ± 0.32
	$\hat{d}$	-0.57* ±0.27	-0.58* ± 0.27	-0.74* ± 0.30	-1.07* ± 0.33	1.05* ± 0.28	0.66* ± 0.27	0.57 ± 0.33
	$\hat{h}$	1.05 ± 0.87	2.70* ± 0.44	2.76* ± 0.93	0.86 ± 0.70	1.08* ± 0.35	2.29* ± 0.68	-2.36* ± 0.36
	$\chi^2_{(df\ 3)}$	1.62	1.36	21.19*	5.12	599.84*	10.82*	22.18*
Genetic component of means (6-para model)	m	20.98* ± 0.74	20.42* ± 0.10	23.13* ± 0.40	19.50* ± 0.33	21.33* ± 0.35	19.93* ± 0.35	18.58* ± 0.33
	d	-1.57 ± 1.19	-0.17 ± 0.38	0.17 ± 0.54	-1.87* ± 0.34	-7.53* ± 0.85	0.41 ± 0.29	-0.20 ± 0.30
	h	-1.28 ± 3.85	5.22* ± 0.90	-13.46* ± 2.23	3.03 ± 1.58	15.59* ± 2.20	0.55 ± 1.79	5.61* ± 1.49
	i	-1.58 ± 3.80	2.54* ± 0.86	-13.38* ± 1.95	2.54 ± 1.50	14.02* ± 2.19	0.38 ± 1.50	6.80* ± 1.47
	j	-1.01 ± 1.20	0.41 ± 0.42	1.02 ± 0.57	-0.92* ± 0.42	-6.57* ± 0.87	1.65* ± 0.35	1.14* ± 0.40
	l	-2.69 ± 5.75	-4.00* ± 1.66	10.40* ± 3.48	-6.18* ± 2.08	-31.29* ± 3.69	-2.29 ± 2.64	-12.65* ± 1.89

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	Grains / ear (GE)						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.1289 ±0.3369	0.1740 ±0 0876	0.0878* ±0.0130	0.0132 ±0.1025	0.0842 ±0.1164	0.2566 ±0.1625	0.1365 ±0.0843
	B	0.1903 ±0.3716	-0.0313 ±0.0958	-0.2982 ±0.1965	0.1045 ±0.1382	-0.4873* ±0.1926	-0.0179 ±0.1407	0.0009 ±0.1634
	C	0.4148 ±0.6657	-0.4547* ±0.0955	0.3210 ±0.1619	-0.1373 ±0.2366	0.3924 ±0.2657	0.6543* ±0.2263	-0.1202 ±0.2731
	D	0.0478 ±0.1606	- 0.2987* ±0.0748	0.2657* ±0.1237	-0.1275 ±0.0949	0.3605* ±0.1111	0.2078 ±0.1095	-0.1288 ±0.1565
Joint Scaling (3-para. model)	$\hat{m}$	62.65* ± 1.81	55.06* ± 0.96	53.49* ± 1.84	53.70* ± 1.56	52.88* ± 1.10	14.16* ± 1.47	18.07* ± 1.11
	$\hat{d}$	1.02 ± 1.80	-3.18* ± 1.03	-5.23* ± 1.86	-7.64* ± 1.46	1.42 ± 1.02	21.83* ± 0.79	0.72 ± 1.58
	$\hat{h}$	-3.08 ± 6.25	-6.67* ± 1.18	9.61* ± 3.28	-3.49 ± 4.15	15.81* ± 2.62	-55.50* ± 2.97	-3.19* ± 1.53
	$\chi^2_{(df\,3)}$	1.68	101.40*	79.90*	5.75	146.05*	3176.85*	1330.19*
Genetic component of means (6-para model)	m	64.59* ± 2.80	41.14* ± 0.72	64.38* ± 1.56	47.37* ± 1.43	66.49* ± 1.94	65.73* ± 1.69	41.89* ± 2.00
	d	-3.40 ± 5.22	10.23* ± 2.57	20.60* ± 3.51	-14.14* ± 2.53	65.03* ± 1.75	15.84* ± 3.65	4.95 ± 2.92
	h	-28.49 ±17.53	60.44* ± 5.94	-76.14* ± 9.60	28.12* ± 8.41	-73.97* ± 9.49	-56.94* ±10.31	20.46* ±10.00
	i	-12.36 ±15.32	68.98* ± 5.89	-61.92* ± 9.40	31.72* ± 7.64	-76.42* ± 8.51	-38.72* ± 9.94	26.82* ± 9.91
	j	-5.17 ± 5.36	13.65* ± 2.64	20.78* ± 3.71	-6.44* ± 2.74	32.78* ± 1.87	10.36* ± 3.85	-6.99* ± 3.11
	l	-13.50 ±29.21	-87.95* ±10.77	82.48* ±15.84	-45.60* ±13.58	100.78* ±13.40	0.03 ±17.00	42.07* ±14.39

* = significant at 5% probability level of significance

Table 3: (Continued)

Test	Parameter	100-Grain weight (GW) in gm						
		Cross-1	Cross-2	Cross-3	Cross-4	Cross-5	Cross-6	Cross-7
Simple Scaling	A	0.3954 ±0.2332	-0.0128 ±0.1371	0.3458 ±0.4012	0.0879 ±0.1382	0.0275 ±0.1649	0.0091 ±0.3137	-0.2588 ±0.2131
	B	0.0644 ±0.2910	-0.1638* ±0.0720	0.1664 ±0.2557	0.2574* ±0.0843	-0.7130* ±0.1952	-0.0880 ±0.1548	-0.1736 ±0.1732
	C	0.4912 ±0.4780	-0.5736* ±0.1758	0.3746 ±0.5807	0.4239 ±0.3429	-0.3861* ±0.1425	0.3581 ±0.3397	0.3378 ±0.2956
	D	0.0157 ±0.1549	-0.1985* ±0.0722	-0.0688 ±0.1149	0.0393 ±0.1700	0.1497 ±0.1140	0.2276* ±0.0762	0.3710* ±0.1237
Joint Scaling (3-para. model)	$\hat{m}$	3.11* ± 0.19	3.04* ± 0.17	3.16* ± 0.19	3.90* ± 0.19	2.29* ± 0.15	2.58* ± 0.14	4.15* ± 0.26
	$\hat{d}$	0.24* ± 0.18	0.71* ± 0.17	0.96* ± 0.17	0.36* ± 0.18	1.36* ± 0.18	0.17 ± 0.15	0.86* ± 0.22
	$\hat{h}$	-0.24* ±0.18	-0.95* ± 0.30	-0.25 ± 0.41	-0.45 ± 0.34	0.17 ± 0.32	-0.51* ± 0.22	0.56 ± 0.54
	$\chi^2_{(df\ 3)}$	14.70*	14.46*	14.85*	18.47*	60.14*	225.87*	60.18*
Genetic component of means (6-para model)	m	3.09* ± 0.13	2.04* ± 0.04	2.89* ± 0.09	4.02* ± 0.25	2.68* ± 0.03	3.49* ± 10.05	4.31* ± 0.13
	d	1.32* ± 0.24	0.92* ± 0.12	0.51* ± 0.20	0.08 ± 0.19	-2.25* ± 0.24	-0.11 ± 0.14	0.12 ± 0.20
	h	-0.85 ± 0.75	1.38* ± 0.33	0.15 ± 0.64	-1.47 ± 1.08	-1.05 ± 0.66	3.73* ± 0.39	-6.42* ± 0.74
	i	0.12 ± 0.69	2.28* ± 0.29	1.02 ± 0.54	-0.84 ± 1.06	0.54* ± 0.50	-3.18* ± 0.35	-0.02 ± 0.66
	j	-2.24* ± 0.24	0.32* ± 0.15	0.16 ± 0.21	-0.66* ± 0.21	1.92* ± 0.29	-0.19 ± 0.21	-0.34 ± 0.26
	l	-8.42* ± 1.21	-1.07 ± 0.60	-2.89* ± 1.11	-1.67 ± 1.29	3.90* ± 1.30	4.86* ± 0.69	9.48* ± 1.15

* = significant at 5% probability level of significance

The physiological yield components, *viz.* biological yield (BY), grain yield (GY) and harvest index (HI) were chiefly controlled by h in addition to i in all the crosses except in C_3 and C_4 for BY, GY and HI, and only for HI in C_7. Duplicate gene action was found to be involved in C_5 and C_6 for GY and HI, and only for HI in C_1 and C_2. The trigenic or higher order of interactions might be operative in C_3 for GY.

Morphological yield components, *viz.* fertile tillers/ plant (FT), spikelets/ ear (SE) and grains/ ear (GE) were controlled by one or more type(s) of digenic interaction(s) in all the crosses except C_1, where adequacy of additive-dominance model was indicated. However, 3-parameter model was adequate to explain the nature of inheritance of FT in C_1, C_3 and C_4, and of SE and GE in C_1. On the other hand, duplicate gene action was involved in case of SE and GE in C_2, C_3 and C_5, of FT in C_5 and of GW in C_7. Inheritance of grain weight(GW) was mainly controlled by d in addition to different types of epistasis in C_1, C_2, C_3 and C_5. However, trigenic or higher order of interaction might be involved in C_6 for FT.

II.5.3. Components of variation analysis:

The estimates of variance components along with F and F/ $\sqrt{D.H}$ are presented in Table 4. Having only four parameters (D, H, F and E_1) a perfect fit of solution was possible and thus neither the standard deviations of the estimates or test of the goodness of fit could be done. The results are described below.

Table 4. Estimates of components of genetic variation (D, H, F, F/√D.H and E_w) for ten traits in seven crosses.

Cross No.	Heterosis	Characters									
		DH	DM	PH	BY	GY	HI	FT	SE	GE	GW
1.	D	00.30	-22.89	-49.10	312.74	-217.39	1.94	0.18	-0.65	-23.20	-0.82
	H	-05.48	42.77	93.00	-530.12	320.59	-2.09	1.77	2.60	-70.92	0.01
	F	00.08	11.22	-11.83	-190.35	-125.43	-0.45	-0.45	-1.12	-13.90	-0.02
	F/√D.H	-00.06	-00.36	00.18	00.47	00.48	0.22	-0.80	0.66	-00.34	0.70
	E_w	01.37	00.79	00.53	207.60	45.35	0.82	0.50	0.22	37.14	0.04
2.	D	-0.23	-0.30	-9.37	224.12	505.21	3.81	-1.05	-0.25	-11.12	-0.02
	H	-4.88	-2.92	14.14	-2553.95	-1248.48	4.40	0.65	0.35	22.60	-0.03
	F	-0.11	0.00	-0.71	-275.30	-26.64	0.40	0.50	0.08	-0.40	0.01
	F/√D.H	-0.10	0.00	0.06	00.36	00.03	0.10	0.61	-0.27	0.03	0.41
	E_w	1.37	0.92	1.33	721.48	224.84	1.12	0.47	0.05	0.43	0.02
3.	D	-0.08	-2.83	-86.34	-260.62	-123.47	-4.83	-9.00	0.06	-14.80	-0.04
	H	3.53	-7.28	63.63	393.94	246.86	9.31	17.62	-1.91	28.96	-0.12
	F	0.63	1.26	42.30	34.21	29.73	-1.06	4.68	0.02	-2.87	0.01
	F/√D.H	1.19	0.28	-0.57	-0.11	-0.17	0.16	0.37	-0.06	0.14	0.14
	E_w	1.92	3.27	27.47	82.50	10.36	0.87	0.22	0.61	2.61	0.06
4.	D	-0.23	-0.44	-9.30	-680.98	594.19	7.01	-1.66	0.22	-4.62	0.18
	H	-5.96	-3.92	32.41	11870.01	2244.66	-13.46	3.33	-0.47	-9.28	-0.19
	F	-0.11	-0.66	-9.29	-3465.66	-581.42	0.41	0.25	-0.05	-6.26	0.03
	F/√D.H	-0.09	-0.50	0.54	1.22	-0.50	0.04	0.11	0.16	0.96	0.16
	E_w	1.64	1.46	4.23	99.45	24.11	2.22	0.28	0.12	6.68	0.02
5.	D	0.74	0.89	-1.91	6137.23	894.43	1.14	1.71	-0.95	2.98	-0.11
	H	-4.92	-10.66	-4.17	-6449.42	-1354.13	-0.91	-2.30	2.23	-38.78	-0.17
	F	0.08	0.00	0.73	588.85	192.27	-1.19	-0.32	-0.34	-2.85	0.15
	F/√D.H	-0.04	0.00	0.33	-0.09	-0.17	1.17	0.16	0.23	0.27	1.10
	E_w	1.12	2.48	2.04	669.08	221.23	1.02	0.42	0.04	9.00	0.10
6.	D	4.02	3.52	-20.32	2221.22	1391.69	0.61	-1.61	0.31	-15.31	-0.03
	H	-4.04	-2.21	49.79	-1038.92	-1445.58	2.09	3.78	-2.11	24.00	-0.05
	F	-1.12	-1.34	14.56	-687.62	-96.58	1.60	0.26	-0.08	5.31	0.001
	F/√D.H	0.28	0.48	-0.46	0.45	0.07	1.42	-0.11	0.10	-0.28	0.03
	E_w	0.60	0.76	1.41	119.68	16.27	1.03	0.06	0.49	4.50	0.03
7.	D	-4.13	-2.22	-8.49	-2215.30	245.09	4.50	0.41	0.26	-0.96	-0.009
	h	0.87	-6.18	16.89	4385.15	-58.39	-3.63	-0.50	-0.36	12.21	-4.03
	F	-2.22	-0.88	2.12	-372.35	-37.32	3.35	-0.09	-0.01	-5.79	0.03
	F/D.H	1.17	0.24	0.18	0.12	0.31	.0.83	0.20	0.03	1.69	0.16
	E_w	1.96	2.69	1.48	75.95	11.88	2.05	0.07	0.07	1.44	1.03

The developmental yield components, days to heading (DH), days to maturity (DM) and plant height (PH) of all the crosses were found to possess higher dominant genetic variance (H) compared to that of additive component (D) except for DH in C_7, for DM in C_6 and for PH in C_3. F-value was positive for DH in C_1, C_3 and C_5; for DM in C_1, C_2, C_3 and C_5; and for PH in C_3, C_5, C_6 and C_7. The ratio of $F/\sqrt{D.H}$ was high for DH in C_3 and C_7, for DM in C_4 and for PH in C_3 and C_4. However, in general, the analysis revealed that the dominance component of genetic variation was greater in magnitude and played a predominant role in genetic variation of the developmental yield traits. Moreover, in most of those cases, both the parents had equal share in the genetic variation and the dominance deviation at different loci were particularly consistent in sign and magnitude.

In case of physiological yield components, *viz.* biological yield (BY), grain yield (GY) and harvest index (HI) the absolute magnitude of dominant genetic variation (H) was, in general, higher than the additive (D) counterpart in all the cases except for BY in C_6, for GY in C_7 and for HI in C_5 and C_7, and indicated the predominant role of dominance in the genetic variation of those traits. The value of $F/\sqrt{D.H}$ gave an idea of the consistency of sign/ magnitude of dominance deviation at different loci, as it was low in all the cases except for BY and GY in C_4 and for HI in C_5, C_6 and C_7.

The morphological yield components, *viz.* fertile tillers/ plant (FT), spikelets/ ear (SE), grains/ ear (GE) and 100-grain weight (GW) were found to control their variability chiefly by dominance gene effect in all the crosses except for GW in C_1 and for FT in C_2. In general, H values were higher than the

D. On the other hand, consistency in dominance deviation at different loci indicated in all those cases except for FT in C_1 and C_2, for SE in C_1, for GE in C_4 and C_7, and for GW in C_1 and C_5, where the value of F/ $\sqrt{D.H}$ was high.

II.5.4. Heritability:

Heritability estimates, both in broad (h^2_b) and narrow sense (h^2_n) based on components of variation are shown in **Table 5.** The major part of total phenotypic variation of the developmental yield components, *viz.* DH, DM and PH were of non-genetic in nature, as the estimates of broad sense heritability were found to be very low to moderately high in all the crosses. On the other hand, the estimates of narrow sense heritability were also low to moderate in most of the cases; but high in C_1, C_5 and C_6 for DH, and in C_5 for DM, where major part of the total phenotypic variation were of genetic in nature.

In the physiological yield components, *viz.* BY, GY and HI, estimates of H^2_b were low to moderately high in all the cases. However, the h^2_n estimates were high only in C_5 and C_6 for BY, in C_2, C_5, C_6 and C_7 for GY and in C_4 for PH, which indicated the presence of heritable variation.

In case of morphological yield components, *viz.* FT, SE, GE and GW, the estimates of h^2_b were low to moderate; whereas, h^2_n estimates were only high in C_5 and C_7 for FT, in C_6 and C_7 for SE, in C_5 for GE and in C_4 for GW indicating the involvement of genetic variability.

Table 5. Heritability estimates (in percentage) for ten traits in seven crosses.

Cross No.	Heritability	Characters									
		DH	DM	PH	BY	GY	HI	PT	SB	GB	GW
AgX32	h^2_b	00.00	00.00	00.00	10.30	00.00	35.31	91.42	54.50	00.00	00.00
	h^2_n	100.00	00.00	00.00	67.56	00.00	76.53	15.45	00.00	00.00	00.00
AkX32	h^2_b	00.00	00.00	00.00	00.00	00.00	41.82	00.00	00.00	17.31	00.00
	h^2_n	00.00	00.00	00.00	57.45	100.00	98.96	00.00	00.00	00.00	00.00
AnX32	h^2_b	00.00	00.00	00.00	00.00	00.00	00.00	00.00	00.00	00.00	00.00
	h^2_n	00.00	00.00	00.00	00.00	00.00	00.00	00.00	36.92	00.00	00.00
KanX32	h^2_b	00.00	00.00	44.94	00.00	97.27	05.93	00.88	00.00	00.00	68.00
	h^2_n	00.00	00.00	00.00	96.35	33.67	100.00	00.00	97.78	00.00	100.00
AkX139	h^2_b	00.00	00.00	00.00	68.52	32.94	25.14	40.00	67.35	00.00	00.00
	h^2_n	100.00	100.00	00.00	100.00	100.00	41.83	100.00	00.00	100.00	00.00
AnX139	h^2_b	62.50	61.37	61.87	87.67	95.36	44.55	70.00	00.00	00.00	00.00
	h^2_n	100.00	89.45	00.00	100.00	100.00	16.42	00.00	100.00	00.00	00.00
KanX139	h^2_b	00.00	00.00	00.00	00.00	90.09	39.57	53.33	36.36	64.11	00.00
	h^2_n	00.00	00.00	00.00	00.00	100.00	66.32	100.00	100.00	00.00	00.00

h^2_b = Heritability in broad sense and h^2_n = Heritability in narrow sense

II. 5. 5. Heterosis:

The estimates of expected, observed and percent heterosis are presented in Table 6. Results manifested the significant positive better parent heterosis for plant height in all crosses except C_2, for days to heading in C_1,C_2, C_3 and C_6, for fertile tillers per plant in C_5 and C_6, for spikelets per ear in C_2 and C_5 and for grains per ear in C_5. Significant negative heterotic performance were found for most of the characters in all crosses except above mentioned cases. Non-significant heterosis was observed only in C_2 for plant height, fertile tillers, biological and grain yield, in C_4 for grains per ear and in C_6 for biological yield. The studied crosses having dispersion of genes might produce sufficient heterosis for almost all the characters.

Table 6. Estimation of heterosis over better parent for ten traits in seven crosses.

Cross	Heterosis	Characters									
		DH	DM	PH	BY	GY	HI	PT	SE	GE	GW
	EX	24.79	105.80	-56.05	-719.80	-264.45	24.40	-00.76	-00.82	-26.23	-10.71
1.	OB	03.00*	-03.00*	05.90*	-67.30*	-34.87*	-07.93*	-02.44*	-00.26*	-17.90*	-01.15*
	%	04.45	-02.85	09.80	-29.46	-29.24	-13.53	-38.30	-01.31	-27.59	-36.86
	EX	-02.53	16.83	-02.32	-531.36	-162.69	30.37	03.04	-01.15	-106.72	-02.89
2.	OB	01.00*	-10.00*	02.87	-96.14	-66.80	-13.94*	-01.30	02.10*	-11.96*	-01.51*
	%	01.55	-09.93	04.77	-42.08	-54.03	-24.47	-20.41	10.54	-19.50	-03.80
	EX	26.15	27.48	-46.34	-365.28	-68.78	-09.90	-30.67	10.15	47.66	-04.27
3.	OB	03.00*	-00.67*	00.94*	-69.77*	-27.40*	-00.40*	-00.84*	-00.93*	-14.40*	-01.23*
	%	04.69	-00.66	01.56	-30.54	-25.56	-00.79	-13.19	-04.67	-23.48	-35.45
	EX	22.53	07.99	-33.89	-1395.72	-457.10	12.56	-01.49	-03.82	-17.48	-02.38
4.	OB	-01.00*	-20.33*	06.64*	-41.30*	-15.67*	-07.44*	-00.20*	-00.46*	-11.30	-01.36*
	%	-01.50	-16.90	11.02	-18.08	-14.03	-12.68	-03.14	-02.31	-18.43	-32.15
	EX	-51.17	-90.84	-25.56	-284.42	60.70	65.10	-15.95	-23.19	38.20	02.85
5.	OB	-00.67*	-03.00*	17.28*	-91.26*	-57.06	-03.67*	01.24*	00.60*	00.20*	-00.84*
	%	01.04	-02.98	27.26	-42.25	-46.15	-06.44	22.02	02.90	00.37	-21.16
	EX	39.55	38.79	58.97	-49.90	87.39	24.56	-05.41	-02.53	-34.03	11.88
6.	OB	04.67*	-11.00*	05.78*	-66.00	-44.40*	-00.47*	00.06*	-01.07*	-17.23*	-00.63*
	%	07.30	-10.78	09.12	-34.36	-41.42	-00.93	01.18	-05.17	-31.62	-18.16
	EX	31.17	52.66	19.87	110.04	169.86	22.72	-04.32	-13.64	30.73	02.96
7.	OB	-00.67*	-22.33*	11.00*	-45.10*	-32.64*	-04.70*	-01.50*	-02.53*	-08.40*	-00.76*
	%	-01.01	-18.57	17.35	-23.48	-29.23	-08.01	-25.73	-12.22	-16.80	-17.97

EX = Expected heterosis, OB = Observed heterosis,

% = Percentnge of heterosis and * = P>0.05

II.6. DISCUSSIONS

Hybrid dwarf genotypes of wheat are very much suitable for the low land and semi-arid areas of Bangladesh because of their better adaptation to delayed planting. The dwarfing genes (D_1 and D_2) in these genotypes are linked to the photoperiod sensitive genes (Ppd_1 and Ppd_2) on the chromosomes 2D and 2B, respectively (Law, 1978). The major weakness of hybrid dwarf genotypes is their poor grain yield associated with long photoperiod and high thermal sensitivity for their reproductive development. Long photoperiod (>8 hrs) and high temperature (>16°C) are responsible for flowering and they, in turn, have important influence on final grain yield in the field condition at spring. Steeply raising spring temperature was the cause of reduction in grain yield when anthesis was delayed (Beech and Norman, 1966).

To unify thermotolerance and improved yield condition, the crosses were made between dwarf and semidwarf genotypes of wheat. There are many reports on the flowering response of the hybrid dwarf wheat plant to long photoperiod and high temperature, but very little is known on the effect of dwarf genes as well as photoperiod sensitive genes on the expression of plant's characters useful for developing the hybrid dwarf wheat.

It is obvious that genetic improvement of this crop with respect to thermotolerance and yield will be helpful to increase the total wheat production in Bangladesh. In this endeavour, utilization and exploitation of yield and its nine component characters require a clear cut understanding about the genetic mechanisms involved in their inheritance in seven single crosses of four indigenous and two exotic genotypes. All the characters showed continuous

variations and followed normal distribution in each case. Hence, biometrical techniques were found to be suitable to study the inheritance of those traits.

The genetic analysis was done following the biometrical model of single cross analysis which considers some basic assumptions, *viz.* i) absence of multiple alleles, ii) absence of linkage, iii) absence of lethal genes, iv) constant viability of all genotypes and v) environmental effects. There will be no serious expected predisposition in the estimates of the parameters from assumptions (i) and (iii), as the parental lines were homozygous. The viability was expected to be constant for all the genotypes. Presence of linkage among the genes may cause some prejudice in the estimates. Only the first backcross and F_2 generations of the crosses were considered in this study and as equilibrium of linkage relation was improbable (Comstock and Rabinson, 1952 and Mather, 1949), the epistatic predisposition due to linkage relation would be present in the estimates of the gene effects (Kempthorne, 1957). The most serious bias would be expected to occur in the estimates of additive X additive (i) and dominance X dominance (l) interaction effects. However, apparent linkage bias might be due to trigenic or higher order of epistasis (Gamble 1962, Hill 1966, Mather and Jinks 1971 and Joarder *et al.* 1980). Ketata *et al.* (1976a) reported that discrepancy in their study on the detection of epistasis might have resulted from environmental influence. More definitive data on the presence of epistatic effects would be needed to estimate the masking effects of genotype-environment interactions.

In most of the cases, mean values of the F_1, B_1, B_2 and F_2 generations were not within their respective parental rage, though the standard errors were less than their corresponding mean values. However, observed means of those

generations deviated significantly from their theoretical arithmetic and geometric means in most of the traits. Similar results were observed by Bhatt (1971), Azam (1981), Hassan (1981) and Rahman (1982). It means that in addition to additive effect, dominance and non-allelic gene interactions including linkage among the genes controlling those characters were involved. Thus, it indicated that the inheritance of studied traits were not simple and straight forward.

As revealed by Mather's (1949) A, B, C and D scaling test, residual effects may cause a significant deviation of observed mean values from their expectations in many cases. Log transformation usually removes those effects from data and thus the estimates of A, B, C and D becomes statistically zero in those case. The result of simple scaling test indicated the inadequacy of additive-dominance model in most of the cases in the present study. Since each test has its own expectation in terms of type and magnitude of epistatic effects, agreement should not necessarily be expected among these tests. Cavalli's (1952) joint scaling test is more effective than any other test in detecting epistasis, since it uses information from all the six populations of each cross at a time.

However, χ^2 -values of the joint scaling test were significant for almost all the characters in the all crosses except Aghrani X FM-32 (C_1) for harvest index, fertile tillers/ plant, spikelets/ ear and grains/ ear, where 3-parameter model was satisfactory to explain the genetic differences. This indicated that simple additive-dominance model was inadequate to explain the nature of inheritance of those traits in most crosses. Thus, the model was extended to six parameter model, which helped to arrive at perfect fit estimates of the six genetic

parameters and to identify the types of gene action and interaction responsible for the departure from simple additive-dominance situation.

Large contribution of epistasis was reported by Ketata *et al.* (1976 a,b) and Avey *et al.* (1980) for days to heading and maturity. The present findings are in close agreement with their observation. Plant height was reported to be controlled by additive gene action (Bhatt, 1972). But, Chapman and McNeal (1971) reported the involvement of dominance and epistasis along with additive effect for this character. The same result was reported by Shamsuddin (1990) in some crosses of spring wheat, which agreed well with the present investigation except C_4 and C_7, where neither d nor **h** were significant. It might be due to the differential effects of environment on the genes responsible for expression of this trait. Joarder *et al.* (1981) reported similar estimates of **d** and **h** in spring wheat. Epistasis, predominantly of duplicate type was reported for this character by Law *et al.* (1978).

Duplicate type of epistasis was noticed mainly for spikelets/ear and grains/ear of C_2, C_3 and C_5 in this investigation. Spikes per plant was reported to be mainly controlled by non-additive gene action (Sayeed, 1978 and Nanda *et al.*, 1982 a, b). Additive gene action for grains per ear, and dominance effect and epistasis for grain weight have been reported by Bhatt (1972), Ketata *et al.* (1976a), Gill *et al.* (1979). Johanson *et al.* (1966), Singh and Anand (1971, 1972), Gill *et al.* (1979) and Guenzi and Lucken (1980) detected both additive and dominance gene effects for spikelets per ear. Sawant and Jain (1985) and Islam *et al.* (1985) reported additive, dominance and epistasis for this primary yield components in spring wheat crosses. The present findings are consistent with

those reports except fertile tillers/plant. Chapman and McNeal (1971) found no significant epistatic effect for spikelets per ear, grains per ear and grain weight in spring wheat crosses. This contrasting result might be due to the difference in genotype and environments they have studied.

For harvest index and biological yield, predominance of additive gene action was reported by Thakral *et al.* (1979). But Nanda *et al.* (1982a) and Khalifa and Al-Shaheal (1984) reported that harvest index was controlled by dominant gene action. In the present study, significant 'd' and 'i' was found to control this character in all the crosses. Paroda and Joshi (1970a), Ketata *et al.* (1976a) and Gill *et al.* (1979) reported both complementary and duplicate epistasis for grain yield in different crosses of wheat. Law *et al.* (1978) detected mainly duplicate epistasis for this character in winter wheat. The present findings revealed that grain yield was mainly controlled by additive-dominant epistasis in addition to additive and dominance gene effect in C_1, C_2, C_4 and C_7, and duplicate gene action was involved in C_5 and C_6. But in C_3 higher order of interactions might be involved, which is not consistent with them.

The non-significant interaction components under six-parameter analysis appeared to be contradictory to the indication given by Cavalli's joint scaling test that non-allelic interaction was involved in the inheritance of grain yield and its components. This apparent contradiction may be due to relatively large standard errors of the interaction items. Similar findings were reported by Burton (1968) and he thought that manifestation of different epistasis was determined to some extent by the genotypes and the environments where they grown.

The components of yield are sequentially developed and have independent genetic system for expression and are controlled by additive and epistatic gene actions. Thomas *et al.*(1971) pointed out that yield components finally projected their genetic controls through yield. In the present study, Aghrani X FM-32 (C_1) and Akbar X FM-139 (C_5) showed epistatic control for all characters (except fertile tillers/ plant in C_1) and there were also appreciable amount of additive gene action. Therefore, these two crosses might give best response to selection for yield. Kanchan X FM-32 showed the significant additive gene action along with epistatic action for all the characters except fertile tillers and grain weight, which revealed better response to selection. In Akbar X FM-32 (C_2)and Ananda x FM-32 (C_3), Ananda X FM-139 (C_6) and Kanchan X FM-139 (C_7) lack of significant additive effect and presence of duplicate epistasis for grain yield and some yield components indicated that selection for them would not be effective in early segregating generation as in F_2.

Components of variance were computed on the basis of simple additive-dominance model. Having only four equations of four parameters, *viz.* D, H, E and F, a perfect fit solution to them was obtained. Therefore, standard deviations of the estimates or the test of goodness of fit of additive-dominance model could not be done. However, the analysis revealed that dominance component of genetic variation was, in general, greater in magnitude. Thus, the predominant role of dominance gene action in major cases was further proved and the result of the components of variance analysis somewhat agreed with those of generation mean analysis.

The estimates of H component were negative in a number of cases and the D was also negative in some cases. Negative estimates of components of variation, however, might arise from sampling errors (Mather, 1949) and/or genotype-environment interaction (Hill, 1966). These values are to be considered either as zero or as very small but positive (Mather, 1949). Negative estimates of D and H have been reported by in *Solidago sempervirens* L. (Goodwin 1944), in *Nicotiana rustica* L. (Mather 1949), in *Brassica campestris* L. (Joarder *et al.* 1977), in rice (Khaleque *et al.* 1978), in jute (Paul *et al.* 1978), in egg plant (Joarder *et al.*1980) and in wheat (Rahman 1982). Walton (1972) and Rahman (1982) reported the importance of additive and dominance genetic variance for grain yield and its component traits in wheat. The results of the present investigation agreed well with those reports for yield and some yield components.

Furthermore, in most of the cases the estimates of $F/\sqrt{D.H}$ ratio was low, which provided little evidence that the dominance deviation at different loci were particularly consistent in sign and magnitude. This estimate, of course, was found high in a very limited cases, *viz.* in C_1 for FT, SE and GW, in C_3 for DH and PH, in C_4 for DM, PH, BY, GE and GY, in C_5 for HI and GW, and in C_7 for DH, HI and GE. Thus, in these cases dominance deviations at different loci were particularly consistent in sign or magnitude. This situation was observed by Rahman (1982) in wheat and Anonym (1984) in mungbean.

Heritability estimates from the components of variations could give considerable upward bias (specially in those cases where high estimates were obtained) and the estimates so obtained should be considered as maximum heritabilities. Moreover, heritability estimates should be considered as zero or

very much low, where negative D estimates were observed. Estimates of heritability in the narrow sense are considered generally to give more accurate predictive values than the estimates in broad sense in the case of self pollinated crops with little opportunity for utilization of interallelic dominance relationship. Since selfing results increase of homozygous genotypes inter allelic or epistatic combination should be favoured. Epistatic combinations with phenotypic appeal eventually would be fixed in those populations where selection could be practiced. Non-additive gene effects may account for some of the differences between narrow sense and broad sense heritability estimates in this study, but it is somewhat difficult to interpret due to the fact that some of the narrow sense estimates are larger than the broad sense estimates. However, genotype-environment interaction was not evaluated in this study and it might be stated that the GE interaction biased the estimates of heritability.

The estimates of both the broad and narrow sense heritability were low to moderate in most of the cases. High narrow sense heritability was observed in C_1, C_5 and C_6 for DH in C_2, C_5, C_6 and C_7 for GY and in C_5, C_6 and C_7 for FT and SE. Stuber *et al.* (1962) reported that flowering dates were highly heritable, whereas grain yield and no. of fertile tillers were less heritable and plant height was least heritable. Their results agreed well with the present findings. More or less similar results were observed by Ketata *et al.* (1976a). They reported that heritability estimates were high for heading dates, moderately high for kernel weight, moderate for plant height and tiller number, and low for spikelets per ear and grains per ear. However, contrasting reports were also given by many authors. Paroda and Joshi (1970a) estimated poor narrow sense heritability for spikelets per plant. Gill *et al.* (1977) showed grains per ear as a poorly heritable

character. Plant height and 100-grain weight were also reported to be highly heritable (Singh and Anand 1972, Bhatia *et al.* 1978 and Joarder *et al.* 1982). Biological yield was considered as poorly heritable trait by Paroda and Joshi (1970a) and Shamsuddin (1982). As it is known that this trait is controlled by large number of polygene and thus cumulated environmental effects showed its poor heritability. Heritability of harvest index was reported to be medium to high (Bhatt 1976, and Sharma and Smith 1986), which is similar to the present findings.

The inheritance of the grain yield and its components were predominantly of dominance nature in most of the cases determined on the basis of components of variance analysis. Moreover, these characters were low to moderately heritable. Therefore, selection for them would be effective in F_3 or later generations. Although grain yield, harvest index and days to heading in C_4, C_5 and C_6 were controlled predominantly by additive gene action and they were highly heritable indicating selection for them might be effective in early segregating generations.

Presence of significant heterotic performance for yield and its components in this study indicated the prospect of hybrid wheat. Development of hybrid wheat is getting increased importance. To investigate the cause of heterosis in a particular cross it requires the appropriate model, *i.e.* digenic or higher order interactions or linkage of interacting genes for its specification.

In the presence of digenic interactions, there are many ways in which heterosis could arise. Nevertheless, it is more likely to arise with a greater magnitude when one or more of the following conditions are satisfied.

In presence of duplicate interaction heterosis probably arise due to the dispersion of genes so that their contribution to the measure of the degree of association of genes of like effect (r_d) is very small or zero, and hence, the contribution of positive effect of like gene (d) is negligible. Such situations were observed in cross 1 for DH, PH and HI, in cross 2 for DM, HI SE and GE, in cross 3 for DM, SE and GE, in cross 5 for all except BY, GY and GW, in cross 6 for DM, PH, GY and HI, and in cross 7 for DH, DM, and GW. Few heterotic crosses for some traits showed greater h than d, while interaction was absent and h was not significant, which indicated that the genes were dispersed in those cases.

Since there is very indication that heterosis was not due to over dominance, it might be possible to fix such heterosis in homozygous condition of dwarf wheat if selection is practiced in successive segregating generations. Sinha and Khanna (1975) reported that positive significant heterosis of yield was released when yield per spike was increased in wheat. It indicates that heterosis of grain yield is the cumulative effects due to heterotic nature of yield components.

i) [h] and [l] have the same sign, *i.e.*, interaction is of predominantly complementary kind.

ii) The genes are so dispersed that their contribution to r_d is very small or zero and hence, the contribution of [d] is negligible.

iii) There are many more dispersed associated pairs of interacting genes so that their contribution to r_i is very small or negative thus, making the contribution of [i] negligible or the opposite sign to s_i. For classical interactions the latter would make the contribution of [i] and [l] to the heterosis for same sign.

Since linkage, even of interacting pairs of genes, does not affect the specification of the parental and F_1 means, the specification of heterosis is independent of linkage. But gene interaction prejudices the estimates of three of the four components of heterosis. So it will distort the relative magnitudes of these components and affect the interpretation of the cause of heterosis.

It is interesting to note that the C_4 for PH, C_3, C_4 and C_6 for FT, C_1 for SE and GE and C_3 for GY showed significant heterosis over better parent even when dominance (h) and other non-allelic interaction components were found to be non-significant. Such desirable and fixable heterosis probably occurred due to the dispersion of the incompletely dominant genes. Mather and Jinks (1982) observed in *Nicotiana rustica* that heterosis were more frequent in crosses which consistently failed to fit a additive-dominance model and it is more likely to arise when h and i have the same sign, *i.e.* interaction is of predominantly complementary kind. Present findings closely agreed with their results.

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II.7. SUMMARY

This part of investigation was undertaken to know the nature of gene actions involved in the inheritance of grain yield and it's components in seven single crosses of wheat. The crosses are Aghrani X FM-32 (C_1), Akbar X FM-32 (C_2), Ananda X FM-32 (C_3). Kanchan X FM-32 (C_4), Akbar X FM-139 (C_5), Ananda X FM-139 (C_6) and Kanchan X FM-139 (C_7). The four indigenous parental varieties were Aghrani, Akbar, Ananda and Kanchan. The two exotic dwarf lines (near isogeneic) of Falchetto X Maxicani were FM-32 and FM-139. The estimates of gene actions were taken to determine the selection response of those crosses. Estimates of heritability and heterosis, and their genetic interpretations were also taken as counterpart of this breeding programme.

The technique of generation mean analysis was used for the study of inheritance pattern. Simple scaling tests were applied for testing the presence or absence of epistasis and the joint scaling test was used for testing the adequacy of additive-dominance model. Genetic parameters were estimated based on six-parameter model in order to separate and identify different epistatic gene effect. Estimates of the fixable and non-fixable heritable components of variation were used to determine the nature of heritability. An attempt was made to estimate the magnitude of heterosis in relation to gene effects.

The standard errors were less than their corresponding mean values for most of the characters in all generations of all the crosses. The mean values of segregating and F_1 generations were not within their parental range in most of the cases. Thus, it indicated the existence of sufficient genetic variability and showed the characteristics of normal distribution.

Theoretical arithmetic and geometrical means were in close agreement for all traits of all the generations in all crosses. The theoretical means differed significantly with corresponding observed means in most of the cases. It indicated that the inheritance of those traits were not simple and straight forward. This suggested that non-additivity of genes were involved in most of the characters.

Scaling tests revealed that epistasis was operative in almost all the cases and indicated the inadequacy of additive-dominance model. Additive-dominance model was found to be adequate to explain the gene action for spikelets/ear, grains/ear and fertile tillers/plants only in C_1. Genetic components of means were analysed based on six-parameter model which displayed the preponderance of additive gene effect along with epistasis for most of the cases except fertile tillers/plant in C_1, C_3 and C_4, and biological yield in C_5. In C_6 and C_7 grain yield and some component traits were controlled by dominance and epistasis. The involvement of duplicate type of gene action was found in case of spikelets/ear in C_2, C_3 and C_7, grains/ear and grain weight in C_6 and C_7, and plant height and days to heading in C_6. Plant height in C_4, grain yield in C_3 and fertile tillers/ plant in C_6 indicated the involvement of trigenic or higher order of interaction.

In this research programme, Aghrani X FM-32 (C_1) and Akbar X FM-139 (C_5) showed epistatic control for all characters (except fertile tillers/plant in C_1) and there were also appreciable amount of additive gene action. Therefore, these crosses might give best response to selection for yield. Kanchan X FM-32 (C_4) showed the significant additive gene action along with epistatic action for all the characters except fertile tillers and grains weight, which revealed better response to selection. In Akbar X FM-32 (C_2) and Ananda X FM-32 (C_3), Ananda

X FM-139 (C_6) and Kanchan X FM-139 (C_7) lack of significant additive effect and presence of duplicate epistasis for Grain yield and some yield components suggested that selection for them would not be effective in early segregating generation as in F_2.

Components of variance were computed on the basis of simple additive-dominance model. Having only four equations of four parameters, viz. D, H, E and F, a perfect fit solution to them was obtained. Therefore, standard deviations of the estimates or the test of goodness of fit of additive-dominance model could not be done. However, the analysis revealed that dominance component of genetic variation was, in general, greater in magnitude. Thus, the predominant role of dominance gene action in major cases was proved. The result of the components of variance analysis agreed somewhat with those of generation mean analysis.

The estimates of H component were negative in a number of cases and the D were also negative in some cases. Negative estimates of components of variation, however, might arise from sampling errors and/or genotype-environment interaction. These values are to be considered either as zero or as very small but positive. Furthermore, in most of the cases the estimates of $F/\sqrt{D.H}$ ratio was low, which provided little evidence that the dominance deviation at different loci were particularly consistent in sign and magnitude. This estimate, of course, was found to be high in a very limited cases, viz. in C_1 for FT, SE and GW; in C_3 for DH and PH; in C_4 for DM, PH, BY, GE and GY; in C_5 for HI and GW; and in C_7 for DH, HI and GE. Thus, in these cases, dominance deviations at different loci were particularly consistent in sign or magnitude.

Heritability, estimated from the components of variation could give considerable upward bias (specially in those cases where high estimates were obtained) and the estimates so obtained should be considered as maximum heritabilities. Moreover, heritability estimate should be considered as zero or very much low, where negative D estimates were observed. However, the estimates of both the broad and narrow sense heritability were low to moderate in most of the cases, but high narrow sense heritability were observed in C_1, C_5 and C_6 for DH, in C_2, C_5, C_6 and C_7 for GY and in C_5, C_6 and C_7 for FT and SE.

The inheritance of the grain yield and its components were of predominantly dominant nature in most of the cases based on the components of variance analysis. Moreover, these characters were low to moderately heritable. Therefore, selection for them would be effective in F_3 or later generations. Although grain yield, harvest index and days to heading in C_4, C_5 and C_6 were controlled predominantly by additive gene action and highly heritable which indicated that selection for them might be effective in early segregating generations.

Significant heterotic performance in most of the traits in all crosses indicated good prospect of hybrid wheat. Significant positive better parent heterotic performances were observed for plant height in all crosses except C_2, for days to heading in C_1, C_2, C_3 and C_6,for fertile tillers in C_5 and C_6, for spikelets per ear in C_2 and C_5,and for grains per ear in C_5.

PART - III

GENOTYPE-ENVIRONMENT INTERACTION

III. GENOTYPE–ENVIRONMENT INTERACTION

III. 1. INTRODUCTION

All living things are the products of both *nature* and *nurture*. The hereditary material provides the organism with its *nature* (or biological potentialities and limitations), while the environment provides the *nurture*, which interacts with the genes to give the organism its distinctive anatomical, biochemical, physiological and behavioural characteristics. The additive-dominance-epistasis model assumes that genetic and environmental differences contribute independently of one another to the variation in phenotype. In turn, considering the interaction of gene and environmental differences, the variance contributed by GE interaction may be estimated when the environmental factor is applied as a treatment to different genotypes.

Selection of superior genotypes over environments may be possible by stratification of environments. Such technique has been used effectively to reduce the GE interaction. In presence of significant GE interactions, estimates of stability parameters are used to determine the superiority of individual genotype across the range of environments. Although plant breeders are very much aware of the importance of genotypic difference in adaptability, they have been unable to exploit them fully in breeding programmes due to lack of suitable methods of defining and measuring them.

Two main approaches have been made for detecting and estimating the interaction between genotypes and environments. The first one is purely

statistical method proposed by Yates and Cochran (1938). This method was used by Finlay and Wilkinson (1963) to detect and measure the magnitude of genotype-environment interactions in barley and considered linear regression slopes as a measure of stability. Eberhart and Russell (1966) emphasized the need of considering both the linear (b) and non-linear (S^2_d) components of genotype-environment interactions in judging the phenotypic stability of a genotype.

The second approach involves the fitting models, which specify the contributions of genetic and environmental actions and genotype-environment interactions to the generation means and variances. It also determines the contribution of additive, dominance and non-allelic gene action to the total genotype-environment interaction components. Following second approach Bucio-Alanis and Hill (1966) provided more informative conclusions and that can be used to predict across generations as well as environments.

Perkins and Jinks (1968a) formed a bridge over the gap between two alternative analyses. Later, Breese (1969), and Paroda and Hayes (1971) advocated that the linear regression (b) could simply be regarded as a measure of response of a particular genotype, whereas the deviations around the regression lines (S^2_d) were considered as a better measure of stability; genotypes with the lowest deviations being the most stable and *vice versa*. Using the above definition of the term stability, it was possible to judge the phenotypic stability and due consideration was also given to the mean performance and linear response of the individual genotype.

The stability of agronomic characters is important to the plant breeders. Inheritance of genotype may show low genotype-environment interaction for

desired characters, while other characters may show the high GE interaction. Such genotypes are said to be 'well bufferred' as these can adjust their genotypic and phenotypic states in response to the changing of environmental conditions. This is called genetic homeostasis (Lerner, 1954). Coefficient of variability for the inbreeds were larger than those for the hybrids (Adams 1982). Allard and Harding (1963) reported that the hybrid had a greater advantage over the homozygotes under unfavourable environments in self pollinated crops.

In wheat (*Triticum aestivum* L.) extensive studies has been made on this aspect. Most of the studies were of varietal performance. The information on stability parameters of segregating generations is mostly lacking. Genotype-environment interactions have been studied by Jatasra and Paroda (1981) in parental, F_1, F_2 and F_3 generations of four crosses between Indian and Mexican varieties of wheat. They found that the mean performance appeared to be associated with linear component of genotype-environment interactions, whereas no such relationship of non-linear component with mean performance as well as regression coefficient was evident.

In Bangladesh the soil, climate and cropping pattern are such that wheat can not be sown at the same time all over the country. Generally, wheat are sown after aman rice harvest which is delayed mostly due to late rain. Thus, it's seeding time varies from mid november to early january at different regions of this country. All Bangladeshi cultivars of wheat are semidwarf spring type and they give poor stand, reduced crop yield and grain quality at late seeding. In this situation it is essential to identify the suitable genotypes which could perform consistently well over a wide range of environments. In this regard, dwarf wheat genotypes might be deserved for sustainable wheat production in

the adverse environment of Bangladesh, especially the areas which suffer from the stresses of late planting.

Dwarfs are obtained after crossing of normal genotypes having diverse origin. Dwarf wheat is normally distinguished from semidwarf by it's characteristic tufted growth habit, short and do not become reproductive under 8 hours photoperiod and 16°C temperature (Moore 1966). Since dwarfing genes are expressed differentially in different environments and because of the great genetic variability among the dwarfs, there are good prospects for selection and to find the best genotypes along with their phenotypic stability under different environments.

There are different methods available for estimating the magnitude of GE interactions and stability parameters. However, the model proposed by Eberhart and Russell (1966) is relatively simple and most widely used for this purpose. Accordingly, in this investigation an attempt has been made to determine the magnitude of GE interactions *vis-a-vis* stability parameters, and to find the superior genotypes from the nearly isogeneic lines (NILs) of hybrid dwarf wheat, after making trials at different seeding times.

III.2. REVIEW OF LITERATURE

Most of the genotype-environment (GE) interaction studies in wheat deals with the variety x fertilizer or variety x location. The variety x seeding date/rate trials were carried out mostly for the evaluation of mean performance. The available literatures on this context are reviewed and described below:

The statistical method proposed by Yates and Cochran (1938) is applicable to any number of varieties/lines grown in any number of environments for detecting and estimating the GE interaction. This method was used by Finlay and Wilkinson (1963) and Eberhart and Russell (1966) to detect the magnitude of GE interactions in barley and maize, respectively. But they did not try to show any relationship between the components of variance analyses with the genetic parameters.

The fitting models specify the contributions of genetic and environmental actions and GE interactions to the generation means and the variances. It also determines the contributions of additive, dominance and non-allelic gene action to the total genetic action and GE interaction components. Following the fitting model Bucio Alanis (1966) and Bucio Alanis and Hill (1966) studied a pair of inbreed lines and the generations derived from an initial cross between them. Their methods of analysis provided more informative conclusions and could be used to predict the performance and stability of the genotypes across generations as well as environments.

Dracea and Saulescu (1967) analyzed yield variability of five winter wheat varieties over six years in Rommania. They reported that the best measure of stability was obtained by determining the total yield variance of each variety and estimated the yield regression against average yield of the experiment.

Anand (1968) reported the estimates of GE interaction from a trial involving twelve varieties of wheat at four sites grown for three years in India. He found that the variety x site and the variety x site x year interactions were significant, and indicated that the performance of varieties varied with the change of environments. Perkins (1974) and Perkins and Jinks (1968a & b) observed the environmental and genotype-environmental components of variability in multiple lines and crosses of wheat for metrical traits and showed that both the linear and non-linear component of GE interaction might be operative in most of the characters studied.

From the experiments of Breese (1969) in grasses, Reich and Atkins (1970) in sorghum and Paroda and Hayes (1971) in barley it becomes clear that the linear regression could simply be regarded as response of a particular genotype. A genotype with higher and lower regression coefficient will indicate above and below average response, respectively. The genotype with near unity b_i (1.00) and low S^2_{di} (near to zero) would be the most stable one.

The performance and stability of 28 cultivars grown in an international winter wheat performance nursery in 1969 and 1970 was studied by Stroike and Johnson (1972). Cultivars mean performance ($\bar{X}$), regression coefficient (b_i) and regression deviation mean square ($\bar{S}^2_{di}$) were computed for yield, agronomic traits

and seed protein. Stability parameters for most traits indicated wide cultivar difference in response to environment. Regression coefficient and deviation mean square values for these traits also differentiated the cultivar performance potential.

Eagles and Frey (1977) postulated that the yield of crop plant is a quantitative character and highly influenced by environmental variation. Such variation confounds the selection of superior cultivars by altering their relative productivity in different environments. Langer *et al.* (1979) advocated that the genotype with near to zero deviation mean square, near to unity regression coefficient and high mean performance would be the most stable and suitable one with the change of environments.

Jatasra and Paroda (1979) studied the stability for synchrony traits in wheat and concluded that the nonsignificant correlations of $\bar{S}^2_{di}$ with the mean performance and regression coefficient were indicative of the fact that non-linear component of GE interaction of a genotype was independent of its mean performance and linear response. Accordingly, stability parameters appeared to be governed by different genes or gene combinations.

Joarder and Eunus (1980) reported a significant variety x fertilizer and variety x year interaction in their studies on wheat. Significant effects of fertilizers were also noted for grain yield and several other agronomic traits. Chabi and Sapra (1980)studied the GE interaction in triticale genotypes. The genotype, environment and GE interaction variance of fourteen triticale genotypes

were estimated for yield and its components in six environments. They found that the genotype, environment and GE interaction were highly significant for all the characters. Some genotypes showed weaker stability due to deviations from regression significantly different form zero.

Jatasra and Paroda (1981) studied the genotype-environment interaction in parental, F_1, F_2 and F_3 generations of four crosses between Indian and Mexican varieties of wheat. They observed that the mean performance appeared to be associated with linear component of GE interaction, while the non-linear component was not related with mean performance as well as regression coefficient. Parh and Khan (1985 and 1986) evaluated some most stable wheat genotypes over all the sowing dates based on three parameters, *e.g.* phenotypic index (p) greater than zero, regression coefficient (b_i) around unity and least deviation from regression ($\bar{S}^2_{di}$). They recommended those genotypes for using in hybridization programme due to their suitability to transmit high mean yields with increased stability. In another experiment, they observed independent behavior of $\bar{S}^2_{di}$ in relation to other stability parameters for tillers/plant, spike length and grains/spike. They suggested that independent genetic mechanism and the characters could be reviewed cautiously in a wheat breeding programme to attain greater stability to the ultimate trait, the yield.

Hossain and Farid (1987) reported that the date of sowing had significant influence on the grain yield and yield contributing characters. High grain yield were obtained from the sowing between the November 5 and December 5. Hossain *et al.* (1987) observed that all the entries showed decreasing trend in grain yield

due to late seeding. The maturity also showed a significant response as yield against the seeding dates. The late sown crop took at least 15 to 20 days less time to mature because of forced maturity due to rise of temperature in March. Islam *et al.* (1987) reported that the varieties interacted significantly with the environments and these interactions were accounted mainly for the linear function of the environmental means.

III. 3. MATERIALS

The materials used in this experiment were seven trios of near isogeneic lines (NILs) of F_6 populations. Those were isolated from the seven crosses of wheat *viz.*. 1). Ag x FM-32, 2). Ak x FM-32, 3). An x FM-32, 4). Kn x FM-32, 5). Ak x FM-139, 6). An x FM-139 and 7). Kn x FM-139, during the growing season of 1993-94. Germplasm of these materials were developed by selfing plants heterozygous for the dwarfing genes from F_2 to F_5 generations in the department of Botany of Rajshahi University and were supplied for this study. The dwarf lines were mainly three types and their phenotypic performance are shown in Table 1. The designation, quality and parentage of the studied materials are given in Table 2.

Table 1: Phenotypic performance of three dwarf types.

Type	Seedling stage	Tillering stage	Shooting stage	Heading stage
– I	Stiff dark green leaves and delayed growth.	Growth stunted, dark green grass-clump with small and erect leaves	No growth, gradually died within 2–3 months	None produced ear.
II	Like normal.	Numerous tillers but dwarf with dark green leaves	Complete or partial lack of growth.	Produced ears one or few weeks later than normal, delayed maturity.
III	Like normal.	Profuse tillering, remain dwarfs up to 1–2 weeks after tillering.	Shooting started sometimes later than normal.	Like normal.

All the type-I dwarfs died as vegetative within 2-3 months of emergence of seedling. In type-II and III dwarfs showed clear variations regarding size, shape and colour of the leaves, tillering capacity, height at maturity, number of ears/plant and seeds/ear.

Table 2: Designation, quality and parentage of 21 wheat genotypes (NILs)

Sl.no.	Designation	Quality	Parentage
1.	AgFM32903-1-6-3-5	Normal	Ag x FM32851-4-8-4-2
2.	AkFM32906-2-1-6-4	,,	Ak x FM32857-2-6-1-3
3.	AnFM32907-1-3-2-9	,,	An x FM32858-4-1-6-2
4.	KnFM32908-2-4-5-3	,,	Kn x FM32859-1-4-3-5
5.	AkFM139904-3-5-7-1	,,	Ak x FM139863-3-5-4-2
6.	AnFM139902-4-2-4-6	,,	An x FM139864-5-2-7-1
7.	KnFM139905-3-7-1-2	,,	Kn x FM139865-6-7-2-4
8.	AgFM32903-1-6-3-7	Dwarf-III	Ag x FM32851-4-8-4-2
9.	AkFM32906-2-1-6-6	,,	Ak x FM32857-2-6-1-3
10.	AnFM32907-1-3-2-8	,,	An x FM32858-4-1-6-2
11.	KnFM32908-2-4-5-5	,,	Kn x FM32859-1-4-3-5
12.	AkFM139904-3-5-7-3	,,	Ak x FM139863-3-5-4-2
13.	AnFM139902-4-2-4-4	,,	An x FM139864-5-2-7-1
14.	KnFM139905-3-7-1-1	,,	Kn x FM139865-6-7-2-4
15.	AgFM32903-1-6-3-3	Dwarf-II	Ag x FM32851-4-8-4-2
16.	AkFM32906-2-1-6-2	,,	Ak x FM32857-2-6-1-3
17.	AnFM32907-1-3-2-7	,,	An x FM32858-4-1-6-2
18.	KnFM32908-2-4-5-8	,,	Kn x FM32859-1-4-3-5
19.	AkFM139904-3-5-7-5	,,	Ak x FM139863-3-5-4-2
20.	AnFM139902-4-2-4-9	,,	An x FM139864-5-2-7-1
21.	KnFM139905-3-7-1-4	,,	Kn x FM139865-6-7-2-4

III. 4. METHODS

III. 4. 1. Experimental design:

Selected twenty one Near Isogeneic Lines (NILs) were isolated on the basis of their developmental performance during the growing season of 1993-94. Those were raised and evaluated at the following six seeding dates, S_1 = 10th November'93, S_2 = 30th November '93, S_3 = 20th December '93, S_4 = 15th November'94, S_5 = 5th December '94 and S_6 = 25th December '94. These seeding dates were considered as different environments and the NILs as genotype. The experimentation field was laid out in a Randomized Complete Block (RCB) design with three replications for each of the seedings. Each block was of 6.6 m X 1.5 m with 0.5m space between and around the blocks. Every block was consisted of 23 rows, one for each of the 21 NILs and rest two boundary rows were of non-experimental plants. An uniform row to row space was 30 cm and plant to plant space was 10 cm for all the trials.

Fertilizers were applied @ 60 kg urea, 40 kg TSP, 40 kg MP and 1 ton cowdung per hectare. Fifty percent of urea and all other fertilizers in full were applied as basal. The rest 50% of urea was top dressed in two equal splits during tillering and heading stage of the crop. Uniform and standard intercultural operations were done as and when necessary for all trials to raise the good crop. The weather records of the growing season of 1993-94 and 1994-95 are given in Appendix 4.

III.4.2. Collection of Data:

Ten plants were randomly selected from each row of every block of all the trials and data were recorded on grain yield/plant along with five developmental four primary yield traits, *viz.* 1) Days to booting (DB), 2) Days to heading (DH), 3) Days to flowering (DF), 4) Days to maturity (DM), 5) Plant height (PH), 6) Fertile tillers/plant (FT), 7) Spikelets/ear (SE), 8) Grains/ear (GE), 9) 100-grains weight (GW) and 10) Grain yield/plant (GY).

III. 4. 3. Analysis of Data:

When the variance due to genotype-environment (GE) interaction was found to be significant, then Eberhart and Russell model was used to measure the stability of genotypes as follows:

$Y_{ij} = m + B_i.I_j + \sigma_{ij}$ (i = 1, 2, ...t and j = 1, 2, ...s).

Where,

Y_{ij} = Mean of i th genotype in j th environment,

m = Mean of all the genotypes over all environments (grand mean),

B_j = Regression coefficient of the i th genotype on the environmental index, which measures the response of this genotype to the varying environments,

I_j = The environmental index is defined as the deviation of the mean of all genotypes at a given environment from the over all mean,

Mathematically,

$$I_j = \Sigma_i Y_{ij}/t - \Sigma_i \Sigma_j Y_{ij}/ts$$

where,

$\Sigma_j I_j$ = 0 and

σ_{ij} = The deviation from regression of the i th genotype at j the environment.

III.4.3.1 : Stability Parameters :

Two parameters of stability were calculated as follows :

a) Regression coefficient (b_i), which was the regression of the performance (response) of each genotype under different environments on the environmental means over all the genotypes. This was estimated as follows :

$$\bar{b}_i = \Sigma_j Y_{ij} I_j / \Sigma_j I^2_j,$$

where,

$\Sigma_j Y_{ij} I_j$ was the sum of products of environmental index and mean of genotypes at each environment, and

$\Sigma_j I^2_j$ was the sum of squares of environmental index.

b) Mean square deviation ($\bar{S}^2_{di}$) from linear regression, which was stability or non-linearity of each genotype under different environments. This was estimated as follows :

$$\bar{S}^2_{di} = [\Sigma_j \sigma^2_{ij}/S-2] - S^2e/r.$$

Where,

$\Sigma_j \sigma^2_{ij} = [\Sigma_j Y_{ij} - (\Sigma Y^2_i)/t] - (\Sigma_j Y_{ij} I_j)^2/\Sigma_j I^2_j$, and

S^2e = the estimate of pooled error.

The various computational steps were involved in the estimation of stability parameters. Those were as follows :

I) Computation of environmental index (I_j) :

$$I_j = \Sigma_j Y_{ij}/t - \Sigma_i \Sigma_j Y_{ij}/ts,$$

Thus, the sum of environmental index (ΣI_j) for all environments was

$$I_1+I_2+I_3+I_4+I_5+I_6 = 0.$$

II) Computation of regression coefficient (b_i) : For each genotype,

$$\bar{b}_i = \Sigma_j Y_{ij} I_j / \Sigma_j I^2{}_j,$$

where,

a) $\Sigma_j I^2{}_j$ was common and equal for each value of regression coefficient.

b) $\Sigma_j Y_{ij}$ for each genotype was the sum product of environmental index ((I_j) with corresponding mean (X) of that genotype at each environment. These values may be obtained in the following manner,

$$[X]\ [I_j] = [\Sigma_j Y_{ij} I_j] = [S].$$

Where,

[X] = Matrix of means,

[I_j]= Vector for environmental index, and

[S] = Vector for sum of products, *i.e.* $\Sigma_j Y_{ij} I_j$.

c) Now, b_i value for each variety was calculated as dividing the $\Sigma_j Y_{ij}$ for each genotype (as calculated above in b) by $\Sigma_j I^2{}_j$ (as obtained above under a).

Thus,

$$\bar{b}_i = \Sigma_i b_i/N = \Sigma(b_1+b_2+b_3+b_4+b_5+b_6)/N.$$

Where,

Σb_i= regression coefficient of all genotypes, and

N = Total number of genotypes.

III : Computation of $\bar{S}^2_{di}$(Stability):

In a regression analysis, the variance of the dependent variable (Y) may be expressed symbolically as,

$\sigma^2 Y = \sigma^2$regression + σ^2deviation from regression.

Obviously, by subtracting the variance due to regression (σ^2reg.) form $\sigma^2 Y$ to getting the variance due to deviations from regression (σ^2dev.), which in turn can be used for estimating S^2_{di} values. The variance of means over different environments with regard to individual genotype may be obtained in the following way :

$$\sigma^2 v_i = \Sigma_j Y^2_{ij} - (\Sigma Y_i)^2/t.$$

Where,

$\sigma^2 v_i$ = the variance due to dependent variable (genotype),

$\Sigma_j Y^2_{ij}$= sum of square of i th genotype from all environments,

$(\Sigma Y_i)^2$= square of total of i th genotype of all environments, and

t = number of environments.

Now, the variance due to deviations from regression for a genotype being,

$$\Sigma_j \sigma^2_{ij} = [\Sigma_j Y^2_{ij} - (\Sigma Y_i)^2/t] - (\Sigma Y_{ij} I_j)^2/\Sigma_j I^2_j.$$

Where,

$\Sigma Y^2_{ij} - (\Sigma Y_i)^2/t$ = variance due to dependent variable, and

$(\Sigma_j Y_{ij} I_j)^2/(\Sigma I^2_j)$ = variance due to regression.

Then, the stability parameter, S^2_{di} for each genotype was computed as follows:

$$\bar{S}^2_{di} = [\Sigma_j \sigma^2_{ij}/S-2] - (S^2e/r).$$

Where,

$\Sigma_j \sigma^2_{ij}$ = individual deviation, and

S^2e = mean square for pooled error.

Hence, the pooled deviation computed as,

$$\Sigma_i(\Sigma_j \sigma^2_{ij} = \Sigma_j \sigma^2 v_i - (b_i \Sigma Y_{ij} I_j).$$

III.4.3.2: Analysis of Variance:

At first, factorial ANOVA was carried out based on "One Factor (genotypes) Randomised Complete Block Design Combined Over Environments", and error-I was found to be nonsignificant against error-II in all the cases. Thus, error-I and error-II were added up to compute the pooled error.

Then, the total sum of squares was partitioned into four main parts, those are,

i) sum of squares due to genotypes,

ii) sum of squares due to genotype-environment (GE) interaction,

iii) sum of squares due to environment + EG interaction, and

iv) sum of squares due to pooled error.

Lastly, the sum of squares due to GE interaction was further partitioned into three parts, *e.g.*,

i) S.S. due to $GE_{(linear)}$ which was in fact S.S. due to regression,

ii) S.S. due to deviation of i th genotype from linearity of response,

iii) S.S. due to pooled deviations from linearity of response.

These S.S. were computed by the following formulae:

Source of variation	d.f.	Sum of squares
1. Total	n-1	$\Sigma X^2 - (\Sigma X_i)/n$
2. Genotypes (G)	g-1	$1/18\ \Sigma G^2$ - C.F.
3. Environments (E)	e-1	$1/63\ \Sigma E^2$ - C.F.
4. GE interaction	(g-1)(e-1)	$[\ 1/3\ \Sigma(G \times E)^2]$ - C.F. - ESS - GSS
5. E + GE	g (e-1)	ESS + (G x E) SS
6. $E_{(linear)}$	1	$\Sigma_i \Sigma Y_{ij} I_j$
7. $GE_{(linear)}$	1 (g-1)	$\Sigma_j [b_i . \Sigma Y_{ij}] - ESS_{(linear)}$
8. Pooled deviation	g (e-2)	$\Sigma_i \Sigma \sigma^2_{ij}$
9. i th deviation	e-2	$\Sigma \sigma^2_{ij}$
10. Pooled error	g.e (r-1)	1/3 [Total SS - GSS - ESS - (G xE)SS]

Where,

X = Values of 10 individual plants/replication,

G = Values of genotypes over environments and replications,

E = Values of environments over genotypes and replications,

GxE = Values of genotypes and environments over replications,

$\Sigma_i \Sigma_j Y_{ij} I_j$ = Sum products of j th environmental index and mean

values of genotypes form j th environments,

$b_i.\Sigma Y_{ij}I_j$ = Variance due to regression,

$\Sigma\sigma^2_{ij}$ = Deviation from regression,

n = number of observations(378),

r = number of replications(3),

g = number of genotypes(21) and

e = number of environments(6).

Test of significance (F-test):

a) In order to test the significance of the differences among the genotype means, *i.e.* $H_0 = \mu_1 = \mu_2 = \mu_3 \ldots \ldots \mu_{21}$, the appropriate F-test was defined as F = Genotype MS/ Pooled deviation MS.

b) To test the genotypes which did not differ from their linear component of regression on the environmental index, then

F = $E_{(linear)}$ MS/ Pooled deviation MS.

c) To test that genotypes which did not differ from their non-linear component of regression on the environmental index, then

F = G x $E_{(linear)}$ MS/ Pooled deviation MS.

d) Individual deviation from linear regression was tested as

F = Pooled deviation of i th genotype MS/ Pooled error MS.

III.4.3.3: Stable genotype :

A genotype with unit regression coefficient ($\bar{b}_i$=1) and the deviation not significantly different from zero ($\bar{S}^2d$=0) was said to be the stable one. For the test of significance of regression coefficient (b_i) the t-values were calculated as follows,

$t_{(bi)}$ = $b_i/\sqrt{}$(MS due to pooled deviation of i th genotype/ΣI^2_j)

The estimated t-values were compared with the tabulated t-value at 0.05 and 0.01 probability level of significance and at the degrees of freedom, e-2.

For the test of significance of non-linearity of each genotype under different environments (*i.e.* mean square deviation, S^2d), the F-values were computed as follows,

F = Mean square deviation of i th genotype ($\bar{S}^2d$)/ pooled deviation MS.

III.5. RESULTS

Five developmental and four primary yield traits along with grain yield per plant were studied. The response of these characters of wheat genotypes to environments is genetically controlled. Therefore, to exploit GE interaction the stability of those genotypes were determined and thereby screened. The results obtained in this experiment are described bellow.

III.5.1. Developmental yield component characters:

III.5.1.1. Pooled ANOVA:

The combined ANOVA for developmental yield traits, *viz.* days to booting (DB), days to heading (DH), days to flowering (DF), days to maturity (DM) and plant height (PH) of 21 genotypes over six environments are shown in Table 3, 5, 7, 9, and 11. It revealed significant differences among the genotypes and environments. The significant genotype-environment (GE) interaction indicated that the data might be extended for estimating stability parameters. The significant E + GE component indicated that the genotypes reacted differentially in different environments. The GE interaction and their linear components were highly significant for all the traits except DM. Therefore, prediction of the genotypes in the environments appeared feasible for all the characters except DM. The significant non-linear component (pooled deviation) for all the characters suggested that the genotypes differed considerably with respect to their stability. However, the genotypes 2, 7, 14–16 and 18 for DB, the 2, 7, 12, 14, 18

and 19 for DH, the 2, 3, 5, 7, 8, 11, 12, 14 and 17-20 for DF, the 4 and 11 for DM and the 4, 5 and 12 for PH appeared to be significant in respect to the magnitude of their individual non-linear component indicating non-linear relationship between the genotypes and the environmental effects. Thus, prediction of these genotypes for the specified characters on environmental indices would apparently be feasible.

III.5.1.2. Mean performance, response and stability:

The average DB, DH, DF, DM and PH of the genotypes under different environments and over all environments along with their response (regression coefficients, b_i) and stability (deviation from regression, S^2_{di}) are presented in Table 4, 6, 8, 10 and 12. It was observed that the lowest developmental durations (*i.e.* DB, DH, DF and DM) appeared from S_3 (December 20, 1993) and that was followed by S_6, S_2, S_1, S_5 and S_4. However, S_6 showed lowest PH and that was followed by S_3, S_1, S_4, S_5 and S_2. Positive environmental index at S_1, S_4 and S_5 indicated the highest developmental potential of these three seedings. December 20, 1993 was the most favourable seeding day and most of all the genotypes had the potentiality for exploiting this environment to confer lowest growth and developmental durations. The differences in developmental characters among the genotypes indicated their differential developmental abilities under different environments.

From the analyses of two stability parameters, the significant linear sensitivity (b_i) was found to appear for DB, DH, DF, DM and PH in eighteen, nineteen, seventeen, twenty one and eleven genotypes, respectively. Whereas,

three, two, four and two lines showed non-linear (S^2_{di}) sensitivity for DB, DH, DF and PH, respectively. Combined b_i and S^2_{di} sensitivity were observed in DB, DH, DF, DM and PH for three, four, six, two and two genotypes, respectively. These indicating that both the linear and non-linear components were responsible for their GE interaction. None of the genotypes showed both nonsignificant linear and non-linear components of GE interaction in all the developmental traits except plant height.

The NILs having near unity b_i values with nonsignificant deviations and mean performance of the developmental characters were lower than the grand mean appeared in the genotype nos. 1 and 5 for DB, 1, 3, 5, 10 and 13 for DH, 1, 5, 10 and 13 for DF and 1-3, 5-7, 9, 10 and 12-14 for DM. Considering stability parameters (Eberhart and Russell 1966), these genotypes were considered as the most stable with the change of environments for the characters studied. The near unity b_i values with nonsignificant deviations were also considered as stable in case of the genotype nos. 8, 10, 17 and 21 for DB, 8, 15-17, 20 and 21 for DH, 15-17 and 21 for DF, 8, 15, 16 and 18-21 for DM and 1, 2, 8, 10, 11 and 13 for PH. But they were not acceptable because of their higher mean performance (higher than the experimental average). The NIL nos. 3, 4, 6, 11 and 13 for DB, 3, 4, 6, 11 and 13 for DH, 4 and 6 for DF, 15-19 and 21 for PH having significant but lower b_i values with nonsignificant S^2_{di} were found to be suitable for unfavorable environments because of their lower mean performance than the grand mean. The genotype nos. 2, 7, 14-16 and 18 for DB, 2, 7, 12, 14, 18 and 19 for DH, 2, 3, 7, 8, 11, 12,, 14 and 18-20 for DF, 4 and 11 for DM and 4, 5, 12 and 20 for PH were found to be unstable because of significant S^2_{di} values.

Table 3 : Analysis of variance for days to booting in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum ofsquares	F-values
Total		377	28821.791	76.450	
Environment (E)		5	13034.839	2606.968 *	
Genotype (G)		20	10456.402	522.820	65.141 **
G x E		100	4931.884	49.319 **	
E + (G x E)		105	17966.723	171.112 **	
E (linear)		1	4328.344	4328.344 **	
G x E (linear)		20	982.439	49.122	6.120 **
Pooled deviation		84	674.219	8.026 **	
Genotype	1	4	17.920	4.480	2.832
	2	4	39.378	9.845	6.223 *
	3	4	8.727	2.182	1.379
	4	4	11.289	2.822	1.784
	5	4	23.852	5.963	3.769
	6	4	8.358	2.090	1.321
	7	4	86.624	21.656	13.689 **
	8	4	17.091	4.273	2.701
	9	4	9.878	2.470	1.561
	10	4	15.308	3.827	2.419
	11	4	12.546	3.137	1.983
	12	4	28.012	7.003	4.427
	13	4	3.498	0.875	0.553
	14	4	119.003	29.751	18.806 **
	15	4	67.593	16.898	10.682 *
	16	4	39.593	9.898	6.257 *
	17	4	9.160	2.290	1.448
	18	4	89.310	22.328	14.113 **
	19	4	21.492	5.373	3.396
	20	4	21.443	5.361	3.389
	21	4	14.144	3.536	2.235
Pooled error		252	398.666	1.582	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 4 : Mean days to booting and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	61	60	58	73	69	59	63.33	0.913 **	3.953
2	58	60	56	62	68	56	60.00	0.560	9.317 *
3	60	58	54	63	64	53	58.67	0.678 **	1.655
4	55	52	52	59	60	51	54.83	0.556 **	2.295
5	58	54	52	66	67	53	58.33	0.980 **	5.436
6	58	57	55	62	62	52	57.67	0.579 **	1.563
7	55	51	50	52	63	50	53.50	0.434	21.129 *
8	66	68	58	74	73	63	67.00	0.901 **	3.746
9	64	65	63	73	70	61	66.00	0.676 **	1.943
10	64	60	58	74	68	60	64.00	0.906 **	3.300
11	62	61	55	62	62	58	60.00	0.378 *	2.609
12	68	61	56	86	78	58	67.83	1.832 **	6.476
13	63	64	58	67	67	56	62.50	0.669 **	2.848
14	64	65	53	57	64	54	59.50	0.384	29.224 **
15	75	76	59	84	76	60	71.67	1.447 **	16.371 *
16	74	69	62	87	74	61	71.17	1.429 **	9.371
17	68	64	57	82	73	59	67.17	1.440 **	1.763
18	68	64	53	87	69	60	66.83	1.666 **	21.800 **
19	70	69	57	91	78	60	70.83	1.911 **	4.846
20	69	67	59	86	74	59	69.00	1.555 **	4.834
21	64	65	58	78	70	60	65.83	1.105 **	3.009
Env. Mean	64.00	62.38	56.33	72.62	69.00	57.29	63.60		
Env. Index	0.40	-1.23	-7.27	9.02	5.40	-6.31			
CV%	2.72	2.04	1.56	1.87	1.71	1.48			
LSD at 0.05	2.872	2.099	1.453	2.238	1.948	1.392			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 5 : Analysis of variance for Days to heading in wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	26312.934	69.796	
Environment (E)		5	12662.140	2532.428 *	
Genotype (G)		20	9699.767	484.988	67.145
GxE		100	3706.360	37.064 **	
E + (G x E)		105	16368.500	155.890 **	
E (linear)		1	4242.862	4242.862 **	
G x E (linear)		20	542.459	27.123	3.755 **
Pooled deviation		84	606.700	7.223 **	
Genotype	1	4	8.789	2.197	2.263
	2	4	38.941	9.735	10.026 *
	3	4	18.365	4.591	4.728
	4	4	11.319	2.830	2.914
	5	4	20.934	5.234	5.390
	6	4	11.369	2.842	2.927
	7	4	27.007	6.752	6.953 *
	8	4	17.451	4.363	4.493
	9	4	3.183	0.796	0.820
	10	4	9.833	2.458	2.532
	11	4	18.670	4.668	4.807
	12	4	34.593	8.648	8.907 *
	13	4	14.498	3.625	3.733
	14	4	113.465	28.366	29.213 **
	15	4	14.975	3.744	3.856
	16	4	17.552	4.388	4.519
	17	4	20.565	5.141	5.295
	18	4	61.371	15.343	15.801 **
	19	4	110.291	27.573	28.396 **
	20	4	18.046	4.512	4.646
	21	4	15.483	3.871	3.986
Pooled error		252	244.667	0.971	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 6 : Mean days to heading and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	68	65	62	77	73	63	68.00	0.947 **	1.873
2	70	64	60	66	70	61	65.17	0.517	9.411 *
3	68	63	58	68	68	57	63.67	0.755 **	4.267
4	61	57	55	63	64	54	59.00	0.625 **	2.506
5	64	59	56	70	70	58	62.83	0.913 **	4.910
6	63	61	59	67	67	56	62.17	0.651 **	2.518
7	59	56	54	66	67	54	59.33	0.847 **	6.428 *
8	73	71	61	78	76	67	71.00	0.936 **	4.039
9	71	69	66	76	72	64	69.67	0.669 **	0.472
10	69	65	60	79	73	63	68.17	1.081 **	2.134
11	68	66	59	67	68	62	65.00	0.494 *	4.344
12	73	76	60	89	83	63	74.00	1.718 **	8.324 *
13	69	69	61	72	72	61	67.33	0.755 **	3.301
14	71	69	56	64	68	58	64.33	0.613	28.042 **
15	79	79	66	89	81	68	77.00	1.328 **	3.420
16	77	72	67	89	78	65	74.67	1.345 **	4.064
17	73	69	66	86	77	64	72.50	1.239 **	4.817
18	73	69	63	90	73	64	72.00	1.443 **	15.019 **
19	75	72	66	94	73	65	74.17	1.480 *	27.249 **
20	74	73	63	90	78	64	73.67	1.557 **	4.187
21	75	69	62	83	74	66	71.50	1.141 **	3.547
Env. Mean	70.14	67.29	60.95	77.29	72.62	61.76	68.34		
Env. Index	1.80	-1.05	-7.39	8.95	4.28	-6.58			
CV%	1.91	2.24	1.48	0.96	0.92	1.68			
LSD at 0.05	2.205	2.480	1.487	1.228	1.106	1.713			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 7 : Analysis of variance for days to flowering in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	25573.608	67.835	
Environment (E)		5	12711.735	2542.347 **	
Genotype (G)		20	9368.942	468.447	59.395 **
G x E		100	3304.931	33.049 **	
E + (G x E)		105	16016.666	152.540 **	
E (linear)		1	4173.151	4173.151 **	
G x E (linear)		20	641.679	32.084	4.068 **
Pooled deviation		84	662.527	7.887 *	
Genotype	1	4	6.459	1.615	2.164
	2	4	51.609	12.902	17.295 **
	3	4	103.988	25.997	34.847 **
	4	4	3.423	0.856	1.147
	5	4	17.375	4.344	5.822 *
	6	4	5.755	1.439	1.929
	7	4	27.093	6.773	9.079 *
	8	4	23.071	5.768	7.731 *
	9	4	4.316	1.079	1.446
	10	4	9.164	2.291	3.071
	11	4	28.020	7.005	9.390 *
	12	4	42.307	10.577	14.177 **
	13	4	12.924	3.231	4.331
	14	4	101.282	25.321	33.940 **
	15	4	14.017	3.504	4.697
	16	4	14.451	3.613	4.843
	17	4	19.611	4.903	6.572 *
	18	4	60.577	15.144	20.300 **
	19	4	84.918	21.230	28.457 **
	20	4	22.241	5.560	7.453 *
	21	4	9.926	2.482	3.326
Pooled error		252	188.000	0.746	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 8 : Mean days to flowering and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	71	70	65	81	75	66	71.33	0.926 **	1.366
2	75	68	63	70	73	64	68.83	0.564	12.635 **
3	72	76	63	72	71	60	69.00	0.650	25.748 **
4	65	61	58	69	67	58	63.00	0.731 **	0.607
5	70	62	59	74	72	61	66.33	0.971 **	4.095
6	67	63	61	72	70	60	65.50	0.762 **	1.190
7	62	59	57	70	70	58	62.67	0.862 **	6.524 *
8	76	74	65	81	80	71	74.50	0.880 **	5.519 *
9	73	71	69	80	76	68	72.83	0.703 **	0.830
10	73	68	65	82	76	67	71.83	0.996 **	2.042
11	74	70	64	71	71	66	69.33	0.445	6.756 *
12	76	71	63	93	86	69	76.33	1.717 **	10.328 **
13	73	71	64	76	75	64	70.50	0.803 **	2.982
14	74	72	60	68	72	62	68.00	0.597	25.072 **
15	81	80	73	93	84	71	80.33	1.229 **	3.255
16	81	74	70	93	82	69	78.17	1.409 **	3.364
17	75	71	67	90	80	67	75.00	1.370 **	4.654
18	76	71	67	94	77	68	75.50	1.473 **	14.895 **
19	79	75	68	96	76	70	77.33	1.441 *	20.980 **
20	77	76	71	93	82	67	77.67	1.568 **	5.311 *
21	78	71	67	86	78	69	74.83	1.108 **	2.232
Env. Mean	73.71	70.19	64.71	81.14	75.86	65.48	71.85		
Env. Index	1.86	-1.66	-7.14	9.29	4.01	-6.37			
CV%	1.80	1.08	1.16	1.12	0.75	1.02			
LSD at 0.05	2.189	1.247	1.234	1.500	0.935	1.100			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 9 : Analysis of variance for days to maturity in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	41927.124	111.213	
Environment (E)		5	28495.981	5699.196 *	
Genotype (G)		20	11536.291	576.815	125.613
G x E		100	1413.519	14.135 **	
E + (G x E)		105	29909.500	284.852 **	
E (linear)		1	9664.170	9664.170 **	
G x E (linear)		20	124.390	6.220	1.354
Pooled deviation		84	385.760	4.592 **	
Genotype	1	4	16.676	4.169	2.183
	2	4	7.193	1.798	0.941
	3	4	9.845	2.461	1.289
	4	4	58.019	14.505	7.594 *
	5	4	5.801	1.450	0.759
	6	4	10.506	2.627	1.375
	7	4	8.220	2.055	1.076
	8	4	25.410	6.353	3.326
	9	4	7.956	1.989	1.041
	10	4	13.171	3.293	1.724
	11	4	57.820	14.455	7.568 *
	12	4	8.535	2.134	1.117
	13	4	4.767	1.192	0.624
	14	4	16.922	4.231	2.215
	15	4	12.957	3.239	1.696
	16	4	31.444	7.861	4.116
	17	4	10.136	2.534	1.327
	18	4	6.244	1.561	0.817
	19	4	35.751	8.938	4.679
	20	4	21.097	5.274	2.761
	21	4	17.290	4.323	2.263
Pooled error		252	481.333	1.910	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 10: Mean days to maturity and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	106	93	82	111	106	86	97.33	1.236 **	3.532
2	105	92	82	102	100	84	94.17	1.002 **	1.161
3	105	92	82	102	100	86	94.50	0.957 **	1.824
4	106	84	80	101	98	84	92.17	1.070 **	13.868 *
5	105	90	81	104	98	82	93.33	1.101 **	0.813
6	104	91	82	102	97	81	92.83	1.018 **	1.989
7	101	86	80	101	97	80	90.83	1.037 **	1.418
8	106	97	88	113	108	89	100.17	1.061 **	5.715
9	106	95	89	109	105	89	98.83	0.924 **	1.352
10	107	94	87	107	103	92	98.33	0.868 *	2.656
11	105	90	89	106	102	81	95.50	1.008 **	13.818 *
12	107	96	86	109	103	91	98.67	0.947 **	1.497
13	106	95	86	105	100	87	96.50	0.900 **	0.555
14	106	97	86	107	101	84	96.83	1.011 **	3.594
15	118	110	96	121	115	99	109.83	1.057 **	2.603
16	116	108	92	114	114	96	106.67	1.036 *	7.224
17	108	103	94	109	108	94	102.67	0.718 *	1.897
18	110	102	91	112	108	95	103.00	0.882 *	0.924
19	115	111	97	116	111	97	107.83	0.856 **	8.301
20	115	98	93	117	110	94	104.50	1.104 **	4.637
21	117	107	91	120	115	97	107.83	1.205 **	3.685
Env. Mean	108.29	96.71	87.33	108.95	104.71	88.95	99.16		
Env. Index	9.133	-2.447	-11.827	9.793	5.553	-10.207			
CV%	1.64	1.65	1.19	1.14	1.18	1.51			
LSD at 0.05	2.931	2.641	1.711	2.047	2.043	2.221			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 11 : Analysis of variance for plant height (cm) in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	27321.307	72.470	
Environment (E)		5	3748.644	749.729 **	
Genotype (G)		20	18820.178	941.009	98.257
G x E		100	4007.520	40.075 **	
E + (G x E)		105	7756.164	73.868 **	
E (linear)		1	1172.213	1172.213 **	
G x E (linear)		20	608.247	30.412	3.175 **
Pooled deviation		84	804.493	9.577 *	
Genotype	1	4	30.522	7.631	2.581
	2	4	10.893	2.723	0.921
	3	4	28.967	7.242	2.450
	4	4	78.958	19.740	6.677 *
	5	4	82.936	20.734	7.014 *
	6	4	19.322	4.831	1.634
	7	4	22.223	5.556	1.879
	8	4	9.048	2.262	0.765
	9	4	46.281	11.570	3.914
	10	4	36.210	9.053	3.062
	11	4	22.511	5.628	1.904
	12	4	70.779	17.695	5.986 *
	13	4	15.564	3.891	1.316
	14	4	35.052	8.763	2.964
	15	4	29.142	7.286	2.464
	16	4	37.737	9.434	3.191
	17	4	30.641	7.660	2.591
	18	4	36.875	9.219	3.118
	19	4	27.103	6.776	2.292
	20	4	82.736	20.684	6.997 *
	21	4	50.993	12.748	4.312
Pooled error		252	744.965	2.956	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 12 : Mean plant height (cm) and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	68.02	65.00	56.70	68.23	63.67	55.57	62.87	1.445 *	6.646
2	67.58	67.52	60.55	69.13	65.67	58.20	64.78	1.215 **	1.738
3	74.83	74.05	63.40	76.33	70.70	61.17	70.08	1.723 **	6.257
4	67.40	66.25	66.95	69.67	65.40	53.73	64.90	1.185	18.755 *
5	71.67	65.70	57.83	76.00	69.50	54.90	65.93	2.074 *	19.749 *
6	65.79	66.82	58.37	67.33	63.70	51.80	62.30	1.688 **	3.846
7	67.06	66.30	55.54	70.03	67.47	55.80	63.70	1.752 **	4.571
8	66.52	68.71	59.22	66.10	68.13	59.97	64.78	1.151 **	1.277
9	59.70	68.12	63.24	61.17	65.00	58.30	62.59	0.586	10.585
10	66.88	62.72	55.82	67.60	64.45	57.80	62.55	1.173 *	8.067
11	70.30	72.62	63.71	66.97	68.20	59.80	66.93	1.206 *	4.643
12	85.68	83.91	67.27	78.13	79.10	62.80	76.15	2.446 *	16.710 *
13	62.96	67.10	58.41	64.97	67.63	60.13	63.53	0.971 *	2.906
14	66.15	68.67	67.13	66.40	65.11	58.43	65.32	0.713	7.778
15	47.36	53.75	52.22	49.03	52.03	49.10	50.58	0.119	6.301
16	52.62	49.13	46.73	49.84	55.15	51.10	50.76	0.299	8.449
17	48.88	49.17	43.63	49.43	52.30	49.57	48.83	0.412	6.675
18	48.75	55.05	55.39	53.43	56.25	52.55	53.57	0.057	8.234
19	53.19	55.99	50.46	57.24	58.20	55.03	55.02	0.482	5.791
20	46.53	57.08	50.62	48.07	55.57	51.90	51.63	0.209	19.699 *
21	48.27	57.08	55.48	54.00	56.50	53.27	54.10	0.103	11.763
Env. Mean	62.20	63.84	57.56	63.29	63.32	55.76	60.99		
Env. Index	1.20	2.84	-3.44	2.29	2.32	-5.24			
CV%	3.77	2.96	2.68	2.35	1.79	2.92			
LSD at 0.05	3.866	3.119	2.543	2.453	1.874	2.689			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

III.5.2. Morphological yield component characters:

III.5.2.1. Pooled ANOVA:

Combined analysis of variance (Table 13, 15, 17, 19 and 21) for morphological yield traits of 21 genotypes at six seeding dates (environments) showed considerable variation among the genotypes and environments. The genotype-environment (GE) interaction was found to be significant in all the cases and suggested for estimating the stability parameters. The significant E + (G x E) indicated the differential reaction of genotypes upon the environments. Both the significant linear and non-linear (pooled deviation) components of GE interaction in most of the cases indicated that the genotypes differed significantly with respect to their response (b_i) and stability (S^2_{di}). The highly significant GE interaction along with their significant linear component in all the cases except grains per ear and grain yield per predicted the feasibility of the genotypes under different environments. However, the prediction of the genotypes in the changes of environments appeared to be difficult for grains per ear and grain yield per plant due to their nonsignificant linear component of GE interaction. The genotype nos. 10, 11, 14, 16 and 19 for FT, 15 for SE, 6, 15, 17 and 20 for GE, 12 and 15 for GW and 6, 12 and 15-20 for GY showed their non-linear relationship with the environments, as their mean square deviation appeared to be significant.

III.5.2.2. Mean performance, response and stability:

Stability parameters (b_i and S^2_{di}) and the mean performance of morphological yield traits under different environments and over all environments

for 21 NILs are presented in Table 14, 16, 18, 20 and 22. Highest mean performances were obtained from S_4 seeding for FT, S_2 for SE, S_5 for GE, S_1 for GW and S_2 for GY. These seeding days were most favorable and most of the genotypes had potentiality for exploiting these environments to confer highest performances for specified characters. Highest performing potentialities were observed at S_1, S_2, S_4 and S_5 for FT, at S_2, S_3, S_5 and S_6 for SE, at S_2 and S_5 for GE, at S_1, S_2 S_4 and S_5 for GW and GY as their environmental indices were positive. The genotype no. 20 for FT, 19 for SE, 8 for GE, 5 GW and 9 for GY showed the highest mean performance over all environments, and performed well in most of the specific environments. Differential performing ability under different environments was found to be appear among the genotypes.

The significant regression coefficient (b_i) appeared in eight, twelve, fourteen, seventeen and fifteen genotypes for FT, SE, GE, GW and GY, respectively and indicated their linear sensitivity. Mean square deviation (S^2_{di}) was found to be significant in four, four, one and two genotypes for FT, GE, GW and GY indicating their linear sensitivity, respectively. Both the linear and non-linear components were responsible for GE interaction in case of the genotype no. 11 for FT, 15 for SE, and 12 for GW, as they showed combined b_i and S^2_{di} sensitivity. Many genotypes showed nonsignificant b_i and S^2_{di} combinedly, which indicated that the non-existence of genotype-environment interaction in these cases.

The genotype nos. 10-12 and 16 for SE, 1-3 and 8-12 for GE, 3, 10 and 11 for GW and 8-14 for GY, and none for FT had near unity b_i values with nonsignificant deviations and their mean performances were higher than the over all mean. These genotypes might be considered as most stable with the change

Table 13 : Analysis of variance for fertile tillers/plant in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum ofsquares	F-values
Total		377	2474.802	6.564	
Environment (E)		5	49.821	9.964	
Genotype (G)		20	2137.281	106.864	203.550
G x E		100	250.289	2.503 *	
E + (G x E)		105	300.110	2.858	
E (linear)		1	15.725	15.725 **	
G x E (linear)		20	40.360	2.018	3.843 **
Pooled deviation		84	44.113	0.525 **	
Genotype	1	4	0.542	0.136	0.916
	2	4	1.023	0.256	1.728
	3	4	0.713	0.178	1.204
	4	4	1.988	0.497	3.358
	5	4	0.668	0.167	1.128
	6	4	0.492	0.123	0.831
	7	4	0.500	0.125	0.845
	8	4	0.083	0.021	0.140
	9	4	0.619	0.155	1.046
	10	4	3.755	0.939	6.343 *
	11	4	6.308	1.577	10.655 *
	12	4	1.455	0.364	2.458
	13	4	0.438	0.110	0.740
	14	4	6.441	1.610	10.880 *
	15	4	0.211	0.053	0.356
	16	4	8.940	2.235	15.101 **
	17	4	0.600	0.150	1.014
	18	4	1.778	0.445	3.003
	19	4	6.233	1.558	10.529 *
	20	4	0.680	0.170	1.149
	21	4	0.646	0.162	1.091
Pooled error		252	37.411	0.148	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 14: Mean fertile tillers/plant and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	4.30	5.40	3.77	4.83	5.13	4.13	4.59	1.363 *	0.087
2	4.50	6.03	3.80	5.07	5.47	4.10	4.83	1.830 *	0.207
3	4.87	5.70	3.27	4.77	4.83	3.23	4.45	2.317 **	0.129
4	4.07	5.83	3.93	4.23	5.00	3.60	4.44	1.350	0.448
5	5.83	6.70	3.87	5.77	6.03	4.37	5.43	2.578 **	0.118
6	5.03	5.83	4.03	5.07	5.07	3.90	4.82	1.676 *	0.074
7	4.80	5.17	3.43	4.80	5.43	3.40	4.51	2.081 **	0.076
8	6.83	7.13	5.83	6.90	6.83	5.93	6.58	1.366 *	0.034
9	6.13	6.77	7.03	6.43	6.70	6.17	6.54	-0.137	0.106
10	9.27	7.17	6.80	9.33	7.80	7.23	7.93	1.753	0.890 *
11	11.23	8.77	5.83	10.57	9.53	7.90	8.97	4.056 *	1.528 *
12	8.63	7.43	7.03	8.80	7.90	6.80	7.77	1.600	0.315
13	7.40	8.10	6.57	7.83	7.27	6.23	7.23	1.670 *	0.060
14	10.67	7.93	6.87	10.73	9.23	8.23	8.94	2.707	1.561 *
15	6.80	6.53	7.20	7.13	6.93	7.20	6.97	-0.423	0.004
16	7.07	10.17	11.93	6.97	9.13	10.20	9.25	-3.567	2.186 *
17	8.20	8.57	8.37	8.17	8.87	9.07	8.54	-0.294	0.101
18	5.33	6.07	5.80	5.10	5.80	5.60	5.62	-0.247	0.395
19	10.73	9.73	11.23	13.13	10.80	11.20	11.14	0.133	1.509 *
20	11.73	11.23	12.20	12.30	11.83	12.43	11.95	-0.623	0.121
21	11.25	11.80	11.53	11.63	11.07	12.17	11.58	-0.385	0.113
Env. Mean	7.37	7.53	6.68	7.60	7.46	6.81	7.24		
Env. Index	0.128	0.288	-0.562	0.358	0.218	-0.432			
CV%	6.130	6.010	5.740	4.090	4.300	4.360			
LSD at 0.05	0.745	0.747	0.633	0.511	0.532	0.490			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 15 : Analysis of variance for spikelets/ear in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	1208.972	3.207	
Environment (E)		5	287.107	57.421	
Genotype (G)		20	630.201	31.510	73.279 **
G x E		100	235.601	2.356 **	
E + (G x E)		105	522.708	4.978 **	
E (linear)		1	93.874	93.874 **	
G x E (linear)		20	38.196	1.910	4.442 **
Pooled deviation		84	36.115	0.430 **	
Genotype	1	4	0.917	0.229	1.030
	2	4	0.719	0.180	0.808
	3	4	0.289	0.072	0.325
	4	4	0.592	0.148	0.665
	5	4	3.391	0.848	3.811
	6	4	4.102	1.026	4.610
	7	4	0.046	0.012	0.052
	8	4	1.130	0.283	1.270
	9	4	1.207	0.302	1.356
	10	4	1.313	0.328	1.475
	11	4	0.740	0.185	0.832
	12	4	1.815	0.454	2.040
	13	4	1.206	0.302	1.355
	14	4	0.171	0.043	0.192
	15	4	6.583	1.646	7.398 *
	16	4	2.971	0.743	3.339
	17	4	1.418	0.355	1.593
	18	4	2.967	0.742	3.334
	19	4	0.407	0.102	0.457
	20	4	0.916	0.229	1.029
	21	4	3.215	0.804	3.613
Pooled error		252	56.063	0.222	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 16: Mean spikelets/ear and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	21.20	22.90	21.80	21.07	21.83	21.43	21.71	0.533	0.155
2	21.07	22.97	21.80	21.27	22.73	21.63	21.91	0.715 *	0.106
3	21.57	21.57	21.87	21.90	21.87	22.23	21.84	0.057	-0.002
4	18.23	20.17	19.93	18.80	20.10	19.20	19.41	0.754 *	0.074
5	23.87	23.87	21.90	23.77	24.17	23.73	23.55	-0.018	0.774
6	20.67	23.67	20.87	20.80	23.27	21.07	21.73	1.078	0.952
7	21.13	21.17	21.00	21.17	21.23	21.00	21.12	-0.004	-0.063
8	21.97	23.20	23.70	21.77	23.07	22.50	22.70	0.616	0.209
9	22.10	22.67	23.73	22.20	22.87	23.33	22.82	0.425	0.228
10	21.07	23.80	23.40	22.27	23.77	22.53	22.81	0.985 *	0.254
11	20.47	23.70	23.27	21.80	23.77	23.53	22.76	1.353 **	0.111
12	22.82	26.93	24.07	22.87	26.83	25.63	24.86	1.873 **	0.379
13	20.73	23.87	22.17	20.83	23.90	22.17	22.28	1.377 *	0.227
14	20.00	20.90	20.43	20.29	21.17	20.97	20.63	0.439 *	-0.031
15	20.17	23.70	25.17	20.30	24.10	25.27	23.12	2.125 *	1.572 *
16	22.30	23.54	24.83	22.20	23.93	24.90	23.62	0.945	0.669
17	21.23	22.93	23.30	21.10	22.87	23.73	22.53	1.017 *	0.280
18	20.88	25.90	24.80	20.70	23.90	24.77	23.49	2.165 *	0.668
19	24.70	26.18	25.07	24.87	26.17	25.47	25.41	0.613 *	0.028
20	20.27	23.87	21.83	20.17	23.90	23.57	22.27	1.807 **	0.155
21	20.25	24.73	22.12	20.43	24.30	24.87	22.78	1.976 **	0.730
Env. Mean	21.27	23.44	22.72	21.46	23.32	23.03	22.54		
Env. Index	-1.27	0.90	0.18	-1.08	0.78	0.49			
CV%	2.69	2.17	2.05	1.70	1.60	2.13			
LSD at 0.05	0.944	0.838	0.769	0.600	0.617	0.808			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 17 : Analysis of variance for grains/ear in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	25282.317	67.062	
Environment (E)		5	9389.595	1877.919	
Genotype (G)		20	10994.608	549.730	45.023
G x E		100	4198.410	41.984 **	
E + (G x E)		105	13588.005	129.410 **	
E (linear)		1	3094.500	3094.500	
G x E (linear)		20	445.650	22.283	1.825
Pooled deviation		84	1025.652	12.210	
Genotype	1	4	24.375	6.094	2.195
	2	4	60.059	15.015	5.408
	3	4	39.767	9.942	3.581
	4	4	6.134	1.534	0.552
	5	4	3.033	0.758	0.273
	6	4	209.830	52.458	18.893 **
	7	4	15.850	3.963	1.427
	8	4	9.154	2.289	0.824
	9	4	59.803	14.951	5.385
	10	4	13.275	3.319	1.195
	11	4	41.186	10.297	3.708
	12	4	19.265	4.816	1.735
	13	4	57.539	14.385	5.181
	14	4	25.490	6.373	2.295
	15	4	127.832	31.958	11.510 *
	16	4	47.054	11.764	4.237
	17	4	119.440	29.860	10.754 *
	18	4	17.028	4.257	1.533
	19	4	54.898	13.725	4.943
	20	4	69.440	17.360	6.252 *
	21	4	5.200	1.300	0.468
Pooled error		252	699.704	2.777	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 18 : Mean grains/ear and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability S^2di
1	54.77	63.23	48.33	55.53	61.83	43.83	54.59	1.319 **	5.400
2	55.88	61.17	42.80	56.00	61.77	41.17	53.13	1.523 **	14.321
3	44.43	57.50	48.43	48.63	58.17	46.17	50.56	0.941 *	9.248
4	38.90	41.57	35.57	40.07	44.83	35.83	39.46	0.616 **	0.839
5	44.60	55.77	36.87	45.17	58.17	37.87	46.41	1.622 **	0.064
6	55.50	47.06	39.57	55.50	50.17	39.50	47.88	0.590	51.763 **
7	33.00	43.87	27.40	37.83	46.50	30.17	36.46	1.360 **	3.268
8	57.40	62.60	50.17	58.03	64.83	50.83	57.31	1.067 **	1.594
9	46.58	66.76	48.43	49.97	66.17	46.10	54.00	1.672 **	14.257
10	48.87	59.40	47.17	50.50	60.17	48.83	52.49	1.013 **	2.625
11	52.67	65.73	47.97	48.83	61.50	49.17	54.31	1.272 **	9.603
12	54.43	61.87	50.27	50.17	60.93	50.17	54.64	0.943 **	4.122
13	49.60	48.35	40.90	51.83	50.50	41.60	47.13	0.598	13.691
14	47.43	46.33	39.17	45.17	48.27	39.50	44.31	0.606 *	5.678
15	45.20	64.03	53.77	48.83	62.17	50.83	54.14	1.018	31.264 *
16	59.87	58.67	50.43	59.37	58.83	50.83	56.33	0.591	11.070
17	40.30	52.40	46.10	40.93	54.17	49.50	47.23	0.579	29.166 *
18	45.63	59.30	43.43	45.93	60.27	41.93	49.42	1.460 *	3.563
19	47.20	57.40	49.50	45.17	58.27	48.83	51.06	0.798	13.030
20	51.73	50.23	39.60	50.50	50.93	40.27	47.21	0.783	6.666 *
21	54.40	60.50	52.83	53.83	60.27	53.27	55.85	0.626 **	0.606
Env. Mean	48.97	56.37	44.70	49.42	57.08	44.58	50.19		
Env. Index	-1.22	6.18	-5.49	-0.77	6.89	-5.61			
CV%	3.69	3.03	3.73	3.29	2.80	3.63			
LSD at 0.05	2.989	2.822	2.748	2.682	2.633	2.673			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 19 : Analysis of variance for 100 grain weight (g) in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	79.771	0.212	
Environment (E)		5	35.164	7.033	
Genotype (G)		20	23.136	1.157	37.323
G x E		100	15.602	0.156 **	
E + (G x E)		105	50.766	0.483 **	
E (linear)		1	11.718	11.718	
G x E (linear)		20	2.113	0.106	3.419
Pooled deviation		84	2.613	0.031	
Genotype	1	4	0.179	0.045	1.921
	2	4	0.088	0.022	0.945
	3	4	0.008	0.002	0.086
	4	4	0.101	0.025	1.084
	5	4	0.021	0.005	0.225
	6	4	0.010	0.003	0.107
	7	4	0.012	0.003	0.129
	8	4	0.037	0.009	0.397
	9	4	0.053	0.013	0.569
	10	4	0.058	0.015	0.623
	11	4	0.017	0.004	0.182
	12	4	1.136	0.284	12.194 *
	13	4	0.001	0.000	0.011
	14	4	0.063	0.016	0.676
	15	4	0.551	0.138	5.915 *
	16	4	0.005	0.001	0.054
	17	4	0.017	0.004	0.182
	18	4	0.048	0.012	0.515
	19	4	0.043	0.011	0.462
	20	4	0.053	0.013	0.569
	21	4	0.112	0.028	1.202
Pooled error		252	5.869	0.023	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 20: Mean 100 grain weight (g) and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean ($\bar{X}$)	Response (bi)	Stability $\bar{S^2}di$
1	2.33	2.52	1.89	2.33	2.65	1.93	2.28	0.688	0.039
2	2.97	2.28	2.05	2.90	2.37	2.03	2.43	1.120 *	0.016
3	3.13	2.92	2.25	3.05	2.79	2.15	2.72	1.242 **	-0.016
4	2.99	2.47	2.32	2.95	2.35	2.18	2.54	0.892 *	0.019
5	3.47	3.35	3.02	3.25	3.08	2.95	3.19	0.523 *	-0.001
6	3.07	2.96	2.73	3.18	2.98	2.68	2.93	0.565 **	-0.016
7	2.67	2.61	2.07	2.75	2.52	2.02	2.44	0.933 **	-0.015
8	2.63	2.26	1.87	2.55	2.22	1.97	2.25	0.869 **	-0.009
9	2.86	2.43	2.24	2.87	2.35	2.20	2.49	0.801	0.007
10	3.10	2.64	2.13	3.02	2.48	2.08	2.58	1.250 **	-0.003
11	2.98	2.90	2.43	2.92	2.85	2.32	2.73	0.828 **	-0.014
12	3.97	2.28	2.01	3.95	2.38	1.92	2.75	2.415 *	0.278 *
13	3.20	3.05	2.77	3.18	3.05	2.75	3.00	0.587 **	-0.018
14	2.70	2.77	2.23	2.68	2.75	2.18	2.55	0.738 *	-0.002
15	2.23	2.84	1.90	2.22	2.75	1.92	2.31	0.641	0.132 *
16	2.53	2.33	2.10	2.45	2.38	2.05	2.31	0.568 *	-0.017
17	2.97	2.63	2.13	2.98	2.55	2.05	2.55	1.181 **	-0.014
18	2.55	2.60	1.85	2.52	2.57	1.85	2.32	1.020 **	0.006
19	2.83	2.77	1.90	2.82	2.58	1.78	2.45	1.410 **	-0.007
20	2.87	2.67	1.93	2.92	2.73	1.78	2.48	1.474 **	-0.005
21	2.60	2.67	1.73	2.58	2.68	1.72	2.33	1.293 **	0.022
Env. Mean	2.89	2.66	2.17	2.86	2.62	2.12	2.55		
Env. Index	0.34	0.11	-0.38	0.31	0.07	-0.43			
CV%	5.81	5.72	6.22	5.34	5.41	7.35			
LSD at 0.05	0.276	0.250	0.221	0.250	0.233	0.256			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

Table 21 : Analysis of variance for grain yield/plant (g) in 21 wheat genotypes

Source of variation		Degrees of freedom	Sum of squares	Mean sum of squares	F-values
Total		377	588.076	1.560	
Environment (E)		5	172.657	34.531	
Genotype (G)		20	263.451	13.173	37.637
GxE		100	113.950	1 140 **	
E + (G x E)		105	286.607	2.730 **	
E (linear)		1	57.971	57.971	
G x E (linear)		20	9.270	0.464	1.325
Pooled deviation		84	29.388	0.350	
Genotype	1	4	0.405	0.101	0.671
	2	4	0.215	0.054	0.356
	3	4	0.403	0.101	0.668
	4	4	0.686	0.172	1.137
	5	4	0.402	0.101	0.666
	6	4	3.369	0.842	5.583 **
	7	4	0.258	0.065	0.428
	8	4	0.117	0.029	0.194
	9	4	0.578	0.145	0.958
	10	4	0.450	0.113	0.746
	11	4	0.578	0.145	0.958
	12	4	1.762	0.441	2.920 *
	13	4	0.545	0.136	0.903
	14	4	1.307	0.327	2.166
	15	4	1.980	0.495	3.281 *
	16	4	4.345	1.086	7.200 **
	17	4	2.396	0.599	3.970 **
	18	4	3.050	0.763	5.054 **
	19	4	2.204	0.551	3.652 **
	20	4	3.854	0.964	6.387 **
	21	4	0.484	0.121	0.802
Pooled error		252	38.018	0.151	

* and ** = Significant at 0.05 and 0.01 probability level, respectively.

Table 22: Mean grain yield/plant (g) and estimated stability parameters for 21 wheat genotypes.

Genotype	Env. 1	Env. 2	Env. 3	Env. 4	Env. 5	Env. 6	Mean $\bar{X}$	Response (bi)	Stability $\bar{S^2di}$
1	4.14	3.52	2.13	4.12	3.72	2.18	3.30	1.180 **	0.051
2	4.31	3.94	3.28	4.22	3.82	3.12	3.78	0.601 *	0.004
3	4.95	4.73	2.68	4.92	4.28	2.55	4.02	1.457 **	0.051
4	4.24	3.41	2.91	3.95	3.28	2.78	3.43	0.595 *	0.122
5	5.49	4.98	2.75	5.18	4.92	2.35	4.28	1.797 **	0.051
6	5.40	3.58	2.14	5.25	3.62	2.23	3.70	1.546 **	0.792
7	4.31	3.96	2.17	3.87	3.88	2.46	3.44	1.167 **	0.015
8	5.24	5.08	3.74	5.22	4.97	3.75	4.67	0.956 **	-0.021
9	7.14	6.68	4.68	6.81	6.24	4.74	6.05	1.385 **	0.094
10	6.42	5.86	4.11	6.17	5.77	4.34	5.45	1.259 **	0.063
11	6.84	6.06	4.69	6.74	6.37	4.45	5.86	1.331 **	0.094
12	7.21	5.89	4.46	6.92	5.84	4.58	5.82	1.326 **	0.390
13	6.41	6.12	4.92	6.55	5.84	4.35	5.70	1.105 **	0.086
14	6.00	4.88	3.94	5.94	4.94	3.88	4.93	1.042 *	0.277
15	3.93	5.36	4.32	4.37	5.67	4.38	4.67	0.360	0.445
16	3.67	6.28	5.42	4.82	5.72	4.44	5.06	0.182	1.036 *
17	4.14	5.73	4.10	4.32	5.85	4.21	4.73	0.623	0.549
18	3.93	5.72	3.44	4.02	5.78	3.63	4.42	0.955	0.713
19	3.17	5.01	3.17	3.68	4.75	3.25	3.84	0.684	0.501
20	3.81	5.85	4.07	3.92	5.85	3.85	4.56	0.665	0.913 *
21	4.37	4.04	3.13	4.28	4.85	3.53	4.03	0.726 *	0.071
Env. Mean	5.01	5.08	3.63	5.01	5.05	3.57	4.56		
Env. Index	0.45	0.52	-0.93	0.45	0.49	-0.99			
CV%	8.71	8.47	10.86	7.23	6.79	10.51			
LSD at 0.05	0.719	0.710	0.652	0.597	0.565	0.620			

* / ** bi and S^2di are significantly different from 1.0 and 0.0 respectively at 0.05 / 0.01 probability level.

of environments. The genotype nos. 6, 13 and 17 for SE, 7 and 18 for GE, 2, 4, 7, 8 and 17 -21 for GW and 1, 3, 7 and 18 for GY had also the near unity b_i values with nonsignificant S^2_{di}. Their mean performance were lower than the grand mean. which indicated that they are stable but unacceptable. Due to significant lower regression coefficients with nonsignificant mean square deviations and higher mean performances the genotype no. 19 for SE, 21 for GE, 5 6, 13 and 14 for GW might be considered as suitable for unfavorable environments. The genotype nos. 10, 11, 14, 16 and 19 for FT, 15 for SE, 6, 15, 17 and 20 for GE, 12 and 15 for GW and the 16 and 20 for GY were proved to be unstable, as their mean square deviations were significant.

III.6. DISCUSSION

The yield and its contributing traits in crop plants are the quantitative characters and highly influenced by environmental variation. Such variation confounds the selection of superior cultivars/lines by altering their relative productivity in different environments (Eagles and Fray 1977). Selection of suitable genotypes over environments may be possible by stratification of environments. The hybrid dwarf lines of wheat show higher photothermal sensitivity and better performance than the normal ones under adverse environments. On this regard, different environments were established by planting experimental materials at six different dates of sowing over two years, to evaluate the magnitude of GE interaction *vis-a-vis* stability parameters in 21 near isogeneic lines (NILs) of hybrid wheat.

Estimate of population means varied within and between environments. High or low mean performance was not confined to any particular genotype. The variation of mean performance between genotypes was an indication of genetic diversity of the genotypes. Estimate of environmental means indicated that different environments had differential effects on different characters of the genotypes considered. The combined ANOVA revealed that both the genotype and environment differed significantly for all the yield traits. In all the cases, the significant E + (GxE) component indicated that the genotypes responded differentially in different environments.

The information on different types of GE interaction in wheat was given by several authors (Dracea and Saulescu 1967, Anand 1968, Stroike and Johnson 1972, Joarder and Eunus 1980, Joarder *et al.* 1980, Islam et al. 1987, Hossain and Farid 1987, Hossain *et al.* 1987, *etc.*). Their findings agreed well with the results of present investigation. The present results indicated that genetic effect was effective like the environment in all cases. Thus, it suggested that both the genotype and environmental components were of major significance, and considerable emphasis should be given on both in case of the evaluation of breeding materials.

The results of pooled analysis indicated that both the linear and non-linear components of GE interaction were operative in most of the cases. However, non-linear component was found to be significantly greater than the linear component in cases of DM, GE and GY, which indicated that these three characters of the genotypes had less environmental influence. The linear and non-linear relationship with environments have been reported by many investigators (Finlay and Wilkinson 1963, Eberhart and Russell 1966, Bucio Alanis 1966, Perkins and Jinks 1968a & b, Perkins 1974, Khaleque 1975, Joarder *et al.* 1980, Jatasra and Paroda 1979 and 1981, Mahajan and Khehra 1992, Manget 1992, *etc.*).

Finlay and Wilkinson (1963) considered the linear regression (b_i) as a measure of stability. But Eberhart and Russell (1966) pointed out that the criteria for stability should be a regression coefficient (b_i) and deviation from regression (S^2_{di}) to judge the stability of a genotype. Breese (1969), Reich and Atkins (1970), Paroda and Hayes 1971), Stroike and Johnson (1972) and Langer *et al.* (1979) observed that the linear regression could simply be regarded as response of a

particular genotype. Average response is indicated by regression coefficient of unity (b_i=1). A genotype with $b_i > 1$ and $b_i < 1$ would indicate above average and bellow average response to the changing environments, respectively. The genotype with low (near to zero) deviation mean square (S^2_{di}) and with near unity (1.00) b_i would be the most stable one. Apparently a genotype that failed to meet these qualifications would be classed as unstable to the changing environments. Hence, a desired genotype should be with high performance, a near unity regression coefficient (b_i=1) and nonsignificant (low) deviation from regression (S^2_{di}) irrespective of sign.

In this respect, the desired genotypes were 1 and 5 for all the developmental yield traits. In addition to that the genotype 10 and 13 for DH, DF and DM were also found to be stable and suitable with any change of environment. Moreover, in case of the primary yield contributing characters the genotype nos. 10-12 and 16 for SE, 1-3 and 8-12 for GE and 3, 10 and 11 for GY had near unity b_i values with nonsignificant deviations and higher mean performance than the over all means. Thus, these genotypes might be considered as most stable with the change of environments and could be used preferably for the future breeding programme. These results are consistent with the findings of Paroda and Hayes (1971).

Many different combinations of stability parameters are possible and each requires somewhat different interpretations. Stroike and Johnson (1972) considered that a genotype having low mean performance, high b_i value and low S^2_{di} value could be described as particularly well suited to unfavourable environments in relation to other genotypes. In this investigation, such stability

parameters were found in the genotype nos. 8, 10, 17 and 21 for DB, 8, 15-17, 20 and 21 for DH, 15-17 and 21 for DF, 8, 15 16 and 18-21 for DM, 1, 2, 8, 10, 11 and 13 for PH, 6, 13 and 17 for SE, the 7 and 18 for GE, 2, 4, 7, 8 and 17-21 for GW and 1, 3, 7 and 18 for GY. These genotypes might be stable and suitable for unfavourable environments, and the results agreed well with the findings of Stroike and Johnson (1972).

In this investigation, certain genotypes showed the combined linear and non-linear sensitivity for some characters. This fact indicated that the non-linear component of GE interaction of a genotype was independent of its linear response. Accordingly, stability parameters appeared to be governed by different genes or gene combinations. Thus, the present findings were very much consistent with the concluding remarks of Jatasra and Paroda (1979). Moreover, some genotypes of this study were found to be unstable due to their deviations from regression significantly different from zero. It was consistent with the findings obtained by Chabi and Sapra (1980) in certain Triticale genotypes.

Mahajan and Khehra (1992) evaluated twenty eight single cross hybrids of maize over eight environments for grain yield and its component characters. They observed stable ear length and grain yield but unstable kernel weight. The deviation (S^2_{di}) appeared to be more important than the regression (b_i) for measuring their stability. This is contrasting with the present findings. After evaluating forty seven rice genotypes under four low land environments De *et al.* (1992) reported that the linear component was predominant for fertile tillers per hill and non-linear component for grain yield, while both were equally important for panicle length and weight. This is somewhat consistent with the present findings.

The stability parameters as studied in this investigation for developmental yield traits, four genotypes (1, 5, 10 and 13) become proved to be stable and suitable with any change of environments. And for the morphological yield traits, other four genotypes (3 and 10-12) were found to be stable and suitable for any environments. Because of their high average performance, they responded well to the changing environments and predictable in specified environment(s). Such comparative evaluation would greatly simplify the task of breeder in developing either specific or generally adopted genotypes. As GE interaction is under genetic control, breeders would be able to select suitable genotypes in advanced generations by growing them under different environmental conditions. The present study also revealed that the yield potentiality can be increased by increasing the performance of the yield components in appropriate environment, since these characters are associated with the yield.

III.7. SUMMARY

The magnitude of genotype-environment interaction and the stability parameters of twenty one near isogeneic lines (NILs) of hybrid wheat (F_6), which developed from four indigenous inbreed lines and two exotic selected lines, were estimated over six seeding dates for the grain yield and its component traits. The NILs were isolated on the basis of their photothermal sensitivity and developmental characteristics. The twenty one NILs were considered as different genotypes and the six seeding dates over two years were treated as different environments. Five developmental yield traits, (days to booting, DB; days to heading, DH; days to flowering, DF; days to maturity, DM and plant height, PH) and four morphological yield traits, (fertile tillers per plant, FT; spikelets per ear, SE; grains per ear, GE and grains weight, GW) along with grain yield were studied in this investigation.

The experiment was conducted in Randomized Complete Block (RCB) design for each seeding in the experimentation field of Rajshahi University in the growing seasons of 1993-94 and 1994-95. Combined one factorial analysis of variance was used to estimate the magnitude of GE interactions and the stability parameters, (performance, $\bar{\bar{X}}$; response, $\bar{b}i$ and stability $\bar{S}^2_{di}$) were computed following the model of Eberhart and Russell (1966).

Combined analysis of variance for all the developmental and morphological yield traits showed considerable variation among the genotypes and environments. The genotype-environment (GE) interaction was found to be significant in all the cases and suggested for estimating the stability parameters. The significant E + (G x E) indicated the differential reaction of genotypes with the change of environments. Both the linear and non-linear (pooled deviation) components of GE

interaction in most of the cases indicated that the genotypes differed significantly with respect to their response (b_i) and stability (S^2_{di}). The highly significant GE interaction along with their significant linear component for all the traits except the days to maturity, grains per ear and grain yield per plant predicted the feasibility of the genotypes under different environments. However, the prediction of the genotypes with the changing environments appeared to be difficult for DM, GE and GY. The linear relationship with the environment was found predominant for most of the characters studied, compared to that of non-linear relationship.

From the estimation of stability parameters the genotype nos. 1, 5, 10 and 13 for almost all the developmental yield traits were found to be most stable and suitable with the change of environments. In case of morphological yield traits the genotype nos. 10-12 and 16 for SE and 3, 10 and 11 for GE and GY were proved to be most stable and suitable performer in any environment and could be used for the future breeding programme. On the other hand, the genotype nos. 8, 15-17 and 21 for developmental yield traits and the genotype nos. 7, 17 and 18 for most of the morphological yield traits might be stable and suitable performer under the unfavourable environments.

Such comparative evaluation would be able to simplify the task of breeders in developing the stable and good performer with either specific or general photothermal adaptation. The present study also revealed that the yield potentiality can be increased by increasing the performance of the yield component traits in appropriate environment.

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* Original literature not seen.

Appendix 1: Parentage and source of Bangladeshi varieties and grass dwarf lines

Varities/ selected lines	Parentage	Source	Type
Akbar (Ak)	RON/TOB'S CM7705-3M-1Y-2M-2Y-OY-OJA	RARS* Ishurdi, Bangladesh	Semi dwarf
Ananda (An)	KAL/BB CM26992-3OM-3OOY-3OOM-5OOM-OY-OJA	Do	Do
Aghrani (Ag)	INIA/3/SON64/P4060E//SON64. PK6841-2A-1A-OA	Do	Do
Kanchan (Kan)	UP301/C306 1187-1-1P-5P-5JA-OJA.	Do	Do
FM - 32	Falchetto x Mexicani	Dept. of Agric. and Env. Sciences; University of New Castle Upon Tyne U. K.	Grass dwarf
FM - 139	Falchetto x Mexicani	Do	Do

* RARS = Regional Agricultural Research Station

Appendix 2. Mean performance of ten traits* in six parental varieties/lines

Traits	Aghrani	Akbar	Ananda	Kanchan	FM-32	FM-139
Days to heading	66.67 ±00.88	64.67 ±00.33	64.00 ±00.58	66.67 ±01.20	86.33 ±03.84	93.00 ±02.31
Days to maturity	105.33 ±00.67	100.67 ±01.45	102.00 ±01.73	120.33 ±00.88	122.33 ±02.96	131.67 ±02.33
Plant height (cm)	73.73 ±01.47	71.60 ±03.40	72.43 ±01.35	74.63 ±01.60	60.23 ±01.53	63.40 ±02.79
Biological yield (gm)	203.97 ±35.82	216.13 ±82.86	156.77 ±10.54	190.30 ±10.95	228.47 ±29.22	192.10 ±26.85
Grain yield (gm)	119.27 ±20.28	123.63 ±49.43	79.30 ±04.80	111.67 ±07.73	107.20 ±08.98	107.25 ±08.99
Harvest index (%)	58.60 ±01.83	56.97 ±02.04	50.67 ±01.45	58.67 ±02.22	47.47 ±02.14	46.10 ±02.42
Fertile tillers/plant	05.80 ±00.38	05.63 ±02.19	03.80 ±00.42	05.83 ±00.50	06.37 ±00.65	05.07 ±00.44
Spikelets/ear	18.80 ±00.26	18.77 ±00.38	18.23 ±00.43	18.03 ±00.73	19.93 ±00.48	20.70 ±00.53
Grains/ear	64.87 ±03.97	54.50 ±01.63	60.97 ±03.97	45.93 ±03.40	61.33 ±01.35	50.00 ±01.51
100-grain weight (gm)	03.12 ±00.29	03.97 ±00.30	03.47 ±00.27	04.23 ±00.35	02.76 ±00.27	03.31 ±00.46

* Recorded in the year of 1993-94 by the author

Appendix 3. Mean and Standard error (X ± S.E.) of ten yield component traits in four generations (F_1 , F_2 , B_1 & B_2) of seven crosses of wheat.

Crosses/ Generations	Characters									
	DH	DM	BY	GY	HI	PH	FT	SE	GE	GW
Ag × FM-32/										
F_1 :	69.67	102.33	167.17	84.40	50.67	66.13	3.93	19.67	46.97	1.97
	± 0.67	± 0.33	± 13.31	± 5.11	± 0.98	± 1.39	± 0.41	± 1.09	±14.63	± 0.47
F_2:	67.33	100.33	379.83	202.17	53.43	51.20	6.03	20.98	64.59	3.09
	± 0.67	± 0.33	± 26.35	± 7.10	± 1.95	± 1.61	± 1.32	± 1.28	± 4.85	± 0.22
B_1:	60.00	80.67	297.93	153.17	51.47	70.00	5.13	19.80	59.80	3.78
	± 0.58	± 5.84	± 13.20	± 5.03	± 1.29	± 4.67	± 0.97	± 0.67	± 4.48	± 0.23
B_2:	76.67	104.33	488.40	224.57	45.67	58.73	5.70	21.37	63.20	2.46
	± 0.33	± 0.67	± 27.30	± 20.04	± 1.74	± 7.57	± 1.51	± 1.95	± 7.86	± 0.34
Ak × FM-32/										
F_1 :	65.67	90.67	132.33	56.83	43.03	63.10	5.07	22.03	49.37	2.46
	± 0.88	± 0.33	± 21.66	± 9.33	± 1.53	± 1.01	± 0.43	± 0.32	± 0.60	± 0.22
F_2:	68.33	102.33	333.50	190.00	56.93	53.73	10.20	20.42	41.14	2.04
	± 0.33	± 0.33	± 24.19	± 22.27	± 2.40	± 0.74	± 0.56	± 0.52	± 1.25	± 0.18
B_1:	69.67	91.00	348.93	183.20	52.47	71.80	7.33	20.97	63.50	3.07
	± 0.33	± 0.58	± 6.19	± 8.78	± 1.87	± 2.55	± 1.36	± 0.58	± 3.05	± 0.21
B_2:	66.67	107.00	251.10	97.53	38.77	56.97	7.44	21.14	53.27	2.15
	± 0.67	± 0.58	± 28.81	± 12.53	± 1.52	± 2.94	± 0.60	± 0.32	± 3.24	± 0.17
An × FM-32/										
F_1 :	67.00	101.33	158.70	79.80	50.27	61.17	5.53	19.00	46.93	2.24
	± 2.00	± 3.71	± 3.54	± 3.21	± 1.36	±12.79	± 1.04	± 1.86	± 2.62	± 0.58
F_2:	72.00	103.67	308.00	145.33	48.97	57.53	6.67	23.13	64.38	2.89
	± 1.73	± 0.33	± 12.33	± 5.57	± 1.53	± 0.79	± 0.61	± 0.70	± 2.71	± 0.16
B_1:	64.00	99.67	266.90	143.57	53.73	73.10	9.50	19.87	59.20	3.40
	± 2.00	± 2.03	± 19.97	± 12.97	± 2.09	±11.35	± 3.76	± 0.67	± 3.76	± 0.28
B_2:	72.67	103.00	310.50	141.50	45.67	53.60	6.57	19.70	38.60	2.89
	± 1.45	± 0.58	± 17.21	± 8.89	± 2.75	± 1.39	± 0.33	± 0.64	± 4.77	± 0.19
Kan × FM-32/										
F_1 :	65.67	100.00	187.17	96.00	51.23	66.87	6.17	19.47	50.03	2.87
	± 1.33	± 2.00	± 10.48	± 8.63	± 2.93	± 4.79	± 1.16	± 0.58	± 5.78	± 0.25
F_2:	75.67	103.33	359.93	182.73	49.73	77.37	5.07	19.50	47.37	4.02
	± 0.33	± 0.88	± 90.44	± 51.45	± 2.66	± 4.80	± 0.92	± 0.58	± 2.48	± 0.43
B_1:	65.33	101.33	374.17	201.97	53.50	76.70	6.40	19.20	48.23	3.85
	± 0.33	± 0.33	± 59.09	± 36.46	± 1.56	± 4.01	± 1.57	± 0.32	± 0.47	± 0.30
B_2:	75.67	103.67	433.87	191.87	43.60	75.97	6.83	21.07	62.37	3.77
	± 0.67	± 1.45	±117.8	± 55.44	± 1.10	± 6.63	± 1.31	± 0.49	± 4.36	± 0.12

Appendix 3. Mean and Standard error (X ± S.E.) of ten yield component traits in four generations (F_1, F_2, B_1 & B_2) of seven crosses of wheat.

Crosses/ Generations	Characters									
	DH	DM	BY	GY	HI	PH	FT	SE	GE	GW
Ag × FM-32/										
F_1 :	69.67 ± 0.67	102.33 ± 0.33	167.17 ± 13.31	84.40 ± 5.11	50.67 ± 0.98	66.13 ± 1.39	3.93 ± 0.41	19.67 ± 1.09	46.97 ±14.63	1.97 ± 0.47
F_2:	67.33 ± 0.67	100.33 ± 0.33	379.83 ± 26.35	202.17 ± 7.10	53.43 ± 1.95	51.20 ± 1.61	6.03 ± 1.32	20.98 ± 1.28	64.59 ± 4.85	3.09 ± 0.22
B_1:	60.00 ± 0.58	80.67 ± 5.84	297.93 ± 13.20	153.17 ± 5.03	51.47 ± 1.29	70.00 ± 4.67	5.13 ± 0.97	19.80 ± 0.67	59.80 ± 4.48	3.78 ± 0.23
B_2:	76.67 ± 0.33	104.33 ± 0.67	488.40 ± 27.30	224.57 ± 20.04	45.67 ± 1.74	58.73 ± 7.57	5.70 ± 1.51	21.37 ± 1.95	63.20 ± 7.86	2.46 ± 0.34
Ak × FM-32/										
F_1 :	65.67 ± 0.88	90.67 ± 0.33	132.33 ± 21.66	56.83 ± 9.33	43.03 ± 1.53	63.10 ± 1.01	5.07 ± 0.43	22.03 ± 0.32	49.37 ± 0.60	2.46 ± 0.22
F_2:	68.33 ± 0.33	102.33 ± 0.33	333.50 ± 24.19	190.00 ± 22.27	56.93 ± 2.40	53.73 ± 0.74	10.20 ± 0.56	20.42 ± 0.52	41.14 ± 1.25	2.04 ± 0.18
B_1:	69.67 ± 0.33	91.00 ± 0.58	348.93 ± 6.19	183.20 ± 8.78	52.47 ± 1.87	71.80 ± 2.55	7.33 ± 1.36	20.97 ± 0.58	63.50 ± 3.05	3.07 ± 0.21
B_2:	66.67 ± 0.67	107.00 ± 0.58	251.10 ± 28.81	97.53 ± 12.53	38.77 ± 1.52	56.97 ± 2.94	7.44 ± 0.60	21.14 ± 0.32	53.27 ± 3.24	2.15 ± 0.17
An × FM-32/										
F_1 :	67.00 ± 2.00	101.33 ± 3.71	158.70 ± 3.54	79.80 ± 3.21	50.27 ± 1.36	61.17 ±12.79	5.53 ± 1.04	19.00 ± 1.86	46.93 ± 2.62	2.24 ± 0.58
F_2:	72.00 ± 1.73	103.67 ± 0.33	308.00 ± 12.33	145.33 ± 5.57	48.97 ± 1.53	57.53 ± 0.79	6.67 ± 0.61	23.13 ± 0.70	64.38 ± 2.71	2.89 ± 0.16
B_1:	64.00 ± 2.00	99.67 ± 2.03	266.90 ± 19.97	143.57 ± 12.97	53.73 ± 2.09	73.10 ±11.35	9.50 ± 3.76	19.87 ± 0.67	59.20 ± 3.76	3.40 ± 0.28
B_2:	72.67 ± 1.45	103.00 ± 0.58	310.50 ± 17.21	141.50 ± 8.89	45.67 ± 2.75	53.60 ± 1.39	6.57 ± 0.33	19.70 ± 0.64	38.60 ± 4.77	2.89 ± 0.19
Kan × FM-32/										
F_1 :	65.67 ± 1.33	100.00 ± 2.00	187.17 ± 10.48	96.00 ± 8.63	51.23 ± 2.93	66.87 ± 4.79	6.17 ± 1.16	19.47 ± 0.58	50.03 ± 5.78	2.87 ± 0.25
F_2:	75.67 ± 0.33	103.33 ± 0.88	359.93 ± 90.44	182.73 ± 51.45	49.73 ± 2.66	77.37 ± 4.80	5.07 ± 0.92	19.50 ± 0.58	47.37 ± 2.48	4.02 ± 0.43
B_1:	65.33 ± 0.33	101.33 ± 0.33	374.17 ± 59.09	201.97 ± 36.46	53.50 ± 1.56	76.70 ± 4.01	6.40 ± 1.57	19.20 ± 0.32	48.23 ± 0.47	3.85 ± 0.30
B_2:	75.67 ± 0.67	103.67 ± 1.45	433.87 ±117.8	191.87 ± 55.44	43.60 ± 1.10	75.97 ± 6.63	6.83 ± 1.31	21.07 ± 0.49	62.37 ± 4.36	3.77 ± 0.12

Appendix 3 (Continued).

Crosses/ Generations	Characters									
	DH	DM	BY	GY	HI	PH	FT	SE	GE	GW
Ak × FM-139/										
F_1 :	64.00 ± 2.00	97.67 ± 3.33	124.87 ± 14.87	66.57 ± 8.08	53.30 ± 1.04	80.68 ± 1.61	6.87 ± 0.15	21.30 ± 0.23	54.70 ± 7.18	3.13 ± 0.69
F_2:	75.33 ± 0.88	104.33 ± 0.88	432.10 ± 79.85	206.93 ± 31.41	48.63 ± 2.02	70.83 ± 0.37	7.53 ± 1.45	21.33 ± 0.60	66.49 ± 3.36	2.68 ± 0.06
B_1:	68.00 ± 0.58	101.67 ± 0.33	315.13 ± 51.54	169.37 ± 24.58	54.13 ± 1.20	86.82 ± 1.63	7.83 ± 0.58	21.07 ± 0.75	64.90 ± 0.57	3.67 ± 0.39
B_2:	104.33 ± 0.33	136.33 ± 0.33	338.63 ± 29.83	78.43 ± 5.23	23.40 ± 2.24	61.44 ± 0.69	10.96 ± 1.14	28.60 ± 1.26	29.87 ± 2.98	1.42 ± 0.15
An × FM-139/										
F_1 :	68.67 ± 0.88	91.00 ± 0.58	126.10 ± 17.38	62.80 ± 6.76	50.20 ± 1.48	69.18 ± 2.12	5.13 ± 0.43	19.63 ± 1.64	37.27 ± 4.24	2.84 ± 0.14
F_2:	67.67 ± 2.19	104.33 ± 2.33	334.73 ± 53.96	182.10 ± 34.56	54.07 ± 2.36	77.38 ± 3.33	5.31 ± 0.77	19.93 ± 0.60	65.73 ± 2.92	3.49 ± 0.09
B_1:	60.33 ± 0.33	89.67 ± 0.88	210.77 ± 14.64	111.53 ± 2.40	53.30 ± 2.74	78.32 ± 6.94	5.27 ± 1.48	20.23 ± 0.09	63.97 ± 5.29	2.64 ± 0.14
B_2:	71.33 ± 1.86	106.67 ± 2.19	295.90 ± 47.72	121.67 ± 17.19	41.40 ± 1.65	44.80 ± 2.12	6.71 ± 1.19	19.82 ± 0.49	48.13 ± 3.47	2.75 ± 0.20
Kan ×FM-139/										
F_1 :	66.00 ± 2.89	98.00 ± 3.61	147.00 ± 5.94	79.03 ± 1.01	53.97 ± 2.63	74.40 ± 1.93	4.33 ± 0.44	18.17 ± 0.12	41.60 ± 1.31	3.47 ± 0.47
F_2:	65.00 ± 0.58	101.33 ± 0.33	357.97 ± 13.92	188.27 ± 18.96	52.37 ± 3.19	75.29 ± 2.09	5.90 ± 0.67	18.53 ± 0.58	41.89 ± 3.47	4.31 ± 0.23
B_1:	61.33 ± 0.33	89.33 ± 0.67	211.93 ± 36.01	110.57 ± 10.94	53.33 ± 3.44	73.18 ± 3.73	5.63 ± 0.03	20.13 ± 0.34	51.07 ± 2.02	2.84 ± 0.32
B_2:	74.67 ± 2.60	105.67 ± 1.76	298.13 ± 49.13	125.63 ± 15.22	44.80 ± 1.33	69.20 ± 2.75	6.07 ± 0.53	20.33 ± 0.40	46.12 ± 4.63	2.72 ± 0.13

Appendix 4. Mean weekly temperature and photoperiod during the reproductive developmental phase of wheat at the experimental field (R.U.) for 1994 & 1995.

Period		Temperature (0^0 C)			Photoperiod (hr)		
Month	Days	Max. T.	Min. T.	Day degrees	Sun rise (A.M)	Sun set (P.M)	Day length
Jan.'94	17-23	24.90	12.00	08.45	6.48	5.39	10.51
	24-31	24.15	11.70	07.93	6.45	5.43	10.58
Feb.'94	01-07	26.29	15.75	11.02	6.39	5.47	11.08
	08-14	26.00	16.07	11.04	6.34	5.51	11.17
	15-21	29.43	17.43	13.43	6.30	5.55	11.25
	22-28	27.50	16.50	12.00	6.24	5.59	11.52
March '94	01-08	30.56	19.19	14.88	6.17	6.03	11.46
	09-16	33.13	20.50	16.82	6.10	6.07	11.57
	17-24	36.25	20.44	18.35	6.03	6.10	12.07
	25-31	32.36	20.43	16.40	5.55	6.12	12.17
April '94	01-08	31.21	20.58	15.90	5.48	6.15	12.27
	09-16	34.33	23.13	18.73	5.42	6.19	12.37
Jan.'95	17-23	22.98	11.62	07.30	6.47	5.40	10.53
	24-31	23.12	11.93	07.53	6.48	5.45	10.59
Feb.'95	01-07	25.68	14.36	10.02	6.44	5.48	11.04
	08-14	26.18	15.08	10.63	6.41	5.50	11.09
	15-21	28.33	16.72	12.53	6.37	5.53	11.16
	22-28	29.05	17.10	13.08	6.31	5.57	11.26
March '95	01-08	30.46	18.89	14.68	6.24	6.01	11.37
	09-16	32.59	19.73	16.16	6.19	6.04	11.45
	17-24	30.12	18.56	14.34	6.12	6.09	11.57
	25-31	35.72	20.33	18.03	6.05	6.12	12.07
April '95	01-08	37.12	22.36	19.74	5.58	6.15	12.17
	09-16	36.47	21.85	19.16	5.50	6.18	12.28

* Day degrees = $\frac{\text{Max. T.} + \text{Min. T.}}{2} - 10^0$ C.