FACTORS INFLUENCING GRAIN YIELD IN PEARL MILLET *PENNISETUM glaucum* (L.) R. Br.

by

ABALO WIDI TCHALA

B.S. Université du Bénin Lomé Togo, 1974

M.S. Université de Paris Sud,

Orsay France, 1977

A Dissertation Submitted to the Graduate Faculty

of the University of Georgia in Partial Fulfillment

of the

Requirements for the Degree

DOCTOR OF PHILOSOPHY

ATHENS, GEORGIA

1989

significant on tillering, total head seed weight and grain yield, were not agronomically important.

The analysis of data from the plant breeding /genetic study showed that mean heterosis was low (-11 to 8%) for maturity, head length and seed size in the material studied and that plot mean broad sense heritability was 65%, 58%, and 74%, respectively, for these traits. The frequency distribution was continuous for head length and seed size but varied for maturity. Large seed was dominant over small seed. The direction of dominance varied for maturity and head length. Overdominance was recorded for head length and seed size. The minmum gene number controlling each trait as suggested by the study, was 1 or 2 loci for seed size, at least 2 loci for head length, and 1 to 3 genes for maturity.

INDEX WORDS: Pearl Millet, Planting Date, Earliness,
Dwarfness, Density, Leaf Spot Diseases,
Head Length, Seed Size, Gene Number

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(I) INTRODUCTION

Pearl millet, Pennisetum glaucum, is the sixth most important cereal crop in the world and the most important cereal in the semi-arid tropics, where according to Burton (1983) it will grow, produce and mature seeds on sandy or rocky soils too acid, too dry and too infertile for sorghum (Sorgum bicolor(L.) moench) and maize (Zea mays (L.)). It has great yield potential and can produce more forage than either sorghum or maize. Grain production of the best sorghum or maize hybrids outyielded the top pearl millet hybrids under optimum growing conditions (Burton, 1983). Frere (1982) showed that the world average yield of maize, sorghum and pearl millet were 4500, 3000 and 1250 kg/ha under high inputs and 1000, 875 and 600 kg/ha under low intputs, respectively. This low grain yield of pearl millet, as compared to maize and sorghum, needs to be corrected by developing more productive cultivars or hybrids because pearl millet is irreplaceable in some parts of the semi-arid tropics and increased grain yields would have significant impact on supplying people living there with sufficient amounts of the only cereal they can grow. Grain yield increase in pearl millet would also stimulate more interest in the crop and speed up its extension.

Frere (1982) noted an increase in sorghum and millet production by region from 1960 to 1980 in Africa (66%), Asia

(100%) and Latin America (560%). Hanna (1985, personal communication) indicated that there was also an increased interest in pearl millet as a grain crop in the U.S.(to date it is cultivated in this region as a forage crop) because of its drought tolerance and its ability to produce grain under minimal inputs, but that more information was needed to successfully grow the crop in the U.S. "The possible use of pearl millet as a grain crop in the U.S. awaits the development of short early-maturing hybrids that can be planted and harvested with the same equipment used for sorghum and wheat" Burton (1983).

Increased pearl millet yields are a necessity to provide more food especially in tropical areas with rapid population growth and extreme climatic conditions. Such increases can be attained by developing pearl millet cultivars with longer heads, larger seeds, resistance to drought, pests and diseases and with earliness allowing two or more crops per year. One can also increase grain yield by optimizing plant density and/or providing the best field conditions and cultural methods which will maximize grain production.

Rachie and Majmudar (1980) reported on pearl millet cultivars having good grain yield characteristics in India and Africa such as 'Bajra' large-seeded in India; 'Sanio' large-seeded, drought resistant but late-maturing in Senegal; 'Zongo' with very long heads (up to 100cm) in Niger; and 'Maiwa' resistant to downy mildew (Sclerospora graminicola (Sacc.) Schroet) or green ear disease but late-maturing in Nigeria. One can also add large-seeded and very early-

maturing 'Missi' and 'Gnari' in Togo. From these examples, characteristics for increasing grain yield appear to exist in pearl millet but so far they are not well associated in a good cultivar, even though some attempts are reported from India. This needs to be done especially in the U.S. where economical conditions allow the growth of high-yielding lines and hybrids. Some progress has been made at Tifton, Ga. (Hash, 1986) in developing early large-seeded lines.

The objectives of this dissertation were to study the agronomic effects of genes controlling early maturity, large seeds, long heads, dwarf (combine height) growth, rust (Puccinia substriata var indica Zimm.) resistance, and leaf blast (Pyricularia grisea (Cke) Salc.) resistance. Two projects were designed to reach these objectives.

1. Management/Genetic studies

The objective was to determine the effects of planting date, dwarfness and earliness in inbreds, and foliar diseases (leaf blast and rust) on pearl millet grain yield and its components.

2. Plant breeding/Genetic studies

The objectives were:

(a) to determine the genetics of head length and seed size, and

(b) to determine the feasibility of developing long-headed, large-seeded, early and dwarf (combine height) inbreds.

(II) LITERATURE REVIEW

A. INTRODUCTION

Tremendous progress has been made in agriculture and plant breeding in many parts of the world and yet there is still a great need for high quality food to feed a rapidly growing population and to avert severe famines such as occurred in Ethiopia in 1985. To increase the world food supply, damage from insects and diseases needs to be minimized; yields of established crops, increased; new cultivars developed and new crops introduced into areas, where, because of geographical limitations and cultural traditions, they are not cultivated. Such is the case for pearl millet which is easily grown for forage in the southern U.S. (Burton, 1951, 1980, 1981 and 1983; Hanna and Burton, 1985a) but its grain is not used as human food or for animal feed. Recently, Smith (1987) showed that pearl millet and grain sorghum can replace corn in chick rations without adversely affecting chick body weight or efficiency. This may interest farmers to grow early-maturing pearl millet cultivars in the future. Successful cultivation of pearl millet as a grain crop in the U.S. requires economical grain yields, cultivars adapted to machine harvesting, and guidelines on production and management. The development of dwarf, early inbreds and hybrids, with long heads and large seeds, coupled with a good management program are needed to increase pearl millet grain production in the U.S. Furthermore, such lines and hybrids could be grown elsewhere in the world to increase food production.

Although pearl millet has gone through a number of taxonomic name changes throughout its history (Chase, 1921; Terrel, 1976; Brunken et al., 1977 and Jauhar, 1981), this dissertation will utilize the latest published scientific name which is Pennisetum glaucum (L.) R. Br. (Terrel et al., 1986).

B. BIOLOGY AND MORPHOLOGY OF PEARL MILLET

Pearl millet plant is a robust annual grass ranging in height from 30 cm to more than 4 m. The inflorescence (false spike) may be stiff and compact , cylindrical, conical, spindle-shaped or candle-like, 2-3 cm or more in width, and its length can range from 6 cm to more than 100 cm. The rachis is straight, cylindrical, solid and unbranched.

In pearl millet, the female flowers (pistils and their stigmas) emerge and mature 2 to 3 days before the male flowers (stamen) of the same inflorescence. This is called protogyny and accounts for the fact that pearl millet is a cross-pollinated crop in which pollen can be carried by both wind and insects (Rachie and Majmudar, 1980; Jauhar, 1981). The genus Pennisetum has four basic chromosome numbers: x = 5; x = 7; x = 8 and x = 9. Pearl millet (P. glaucum) has the basic chromosome number of x = 7, and is a diploid plant with 2n = 2x = 14.

C. MANAGEMENT / GENETIC STUDY

The increasing world food demand can be satisfied through the development and use of more productive crop cultivars combined with good management to maximize the growth and yield of improved cultivars.

Through soil and plant management, growth conditions such as soil moisture, soil aeration, plant density and weed population can be maintained at levels that permit optimum plant growth for better yield.

Plant characters such as maturity, tillering ability, height, head length and head thickness have been found to affect yield in pearl millet (Burton, 1951; Shanker et al., 1963 and Gupta and Atwal, 1966). Most of these characters are quantitatively controlled and thus are affected by environmental factors and cultural practices.

Attempts are being made throughout the world (Gupta and Nanda, 1971; Khadr and Oyinloye, 1978 and Bramel-Cox et al., 1986) to develop more productive pearl millet cultivars. More information is needed on crop management of these improved cultivars.

Burton (1951) showed that plant forage yield was positively correlated with culm number, culm diameter, plant height and leaf width. After studying four groups of germplasm collections, Gupta and Nanda (1971) found head weight, tiller number, earliness, grain size and grain density to be important components of grain yield. They concluded that single head weight was closely related to grain yield. Tillering, grain size and grain density were also important in India and American inbreds while earliness and head thickness were important in West and East African cultivars.

Burton (1951) found earliness to show some partial dominance over late maturity. Ram and Singh (1975) showed that earliness is primarily due to dominant genes in Indian lines. Later research showed that there are also recessive genes controlling early maturity in pearl millet (Burton, 1981 and Hanna and Burton, 1985a). Studies by Burton and

ABALO WIDI TCHALA
Factors influencing grain yield in Pearl millet Pennisetum glaucum (L.) R. Br.
(Under the direction of WAYNE W. HANNA)

There is a need to increase pearl millet grain yield to provide more food of this highly palatable and nutritious crop to the growing world human population. Management and plant breeding projects were conducted at the Coastal Plain Experiment Station in Tifton, Georgia, to study factors that influence pearl millet grain yield and its components. The objective of the management study was to determine the agronomic effects of planting date, density, dwarfness, earliness, and foliar diseases (leaf blast caused by Pyricularia grisea (Cke) Salc., and rust caused by Puccinia substriata var indica) on plant and seed characteristics. The plant breeding project was conducted to determine the genetics of pearl millet maturity, head length and seed size, and also to determine the possibilities of developing early, dwarf (combine height), long-headed, and large-seeded pearl millet cultivars.

Four near-isogenic inbred lines were grown for two consecutive years in a split plot design in which two density levels (444000 plants/ha, and 66000 plants/ha) were main plots while the inbred lines were subplots. The experimental design was a completely randomized block design with 8 replications in 1985 and 5 replications in 1986. Two planting dates each year made possible a study of both date of planting and disease effects.

Three Tift inbreds lines and three introduced cultivars were used to make crosses and study parental, F_1, F_2 and backcross (BC) generations in the plant breeding project.

The results of the management study showed that earliness increased disease ratings, tillering, seed size, and grain yield, but decreased plant height. Dwarfness increased tillering but decreased total head seed weight and grain yield. Higher plant populations matured earlier, had higher disease ratings, and were taller, but tillered less and had lower total head seed weight than low plant populations. Late planting reduced maturity, tillering, total head seed weight, and grain yield, but increased plant height. Disease effects even though statistically

Fortson (1966) showed dwarfness in the D_1 and D_2 lines to be controlled by single recessive genes $\underline{d}_1$ and $\underline{d}_2$.

Burton et al. (1969) reported that the $\underline{d}_2$ gene in pearl millet reduced the rate of growth, internode length, plant height and dry matter yields, and increased leaf percentage, in vitro dry matter digestibility (IVDMD) and crude protein content of the culms in spaced plants (0.9 m spacing between plants). Yield reduction was 91% to 69% in a dense stand (planted without thinning) but only 78% in 0.9 m spaced rows for $\underline{d}_2$ dwarfs as compared to tall pearl millet. Extending maturity date in pearl millet increased
leaf percentage and leaf yield, but decreased dry matter percentages (Burton, Primo and Lowry, 1986).

Similar studies have been found useful in crop plants other than pearl millet. Sorghum in particular has been subject to these types of management studies. Francis et al. (1984) concluded that some sorghum hybrids were stable in early planting whereas others were stable only in late plantings and that yield stability seemed mainly a property of inbred parents. Duncan and Moss (1986), evaluating 47 sorghum hybrids in ratoon cropping, reported that at a Coastal Plain (Georgia) location the medium and late maturity groups produced more grain weight per hectare than the early maturity group. Kalmbacher and Martin (1986) found grain sorghum to decrease by about 310 kg/ha with each cm increase in spacing. Adjei-Twum (1987) did not find marked differences in the effects of plant density on sorghum growth and grain yield in any season under dryland conditions in Ethiopia.

A study of 'FARZ 23' and 'FARZ 25' cultivars of maize (Zea mays (L.)) grown at plant populations of 37000, 53000 and 80000 plants/ha for 2 years in Nigeria showed that optimum total dry matter yield and grain yield were reached at 80000 plant/ha and 53000 plants/ha, respectively (Lucas and Remison, 1984). Bauer and Carter (1986) found that delayed planting , high plant densities and low applied N, increased kernel breakage susceptibility in corn. Pfeiffer and Pilcher (1987) reported a 9% decrease in soybean (Glycine max (L.)) yield due to delayed planting.

The importance of management and the use of various plant characteristics to increase yield cannot be overemphasized and to date there are only a few studies on pearl millet in the USA where the crop is gaining more and more attention.

Early maturity can be a desirable plant characteristic in crops used for grain production to facilitate double cropping and escape adverse environmental conditions such as drought, diseases and pests. Pyricularia spp. (leaf blast) attacks millet in July in the Georgia Coastal Plain, followed by rust (Puccinia substriata var indica) which becomes serious in August (Hanna and Burton, 1985a). Planting early and/or using early maturing cultivars could reduce the losses in grain yield from diseases.

Wells et al. (1973) first observed an outbreak of rust in 1972 that appeared to be potentially destructive, especially in pearl millet late plantings. Later, Hanna, Wells and Burton (1985) developed rust resistant pearl millet

lines controlled by a dominant gene. The dominant nature of the resistance made it possible to have resistance in only one of the parents to produce rust resistant hybrids. Independently, Andrews, Rai and Singh (1985) also found rust to be controlled by a single dominant gene in India where rust (Puccinia pennisitum, timme) occurs in July, where increase in rust severity is directly correlated with temperature and relative humidity. Unless several sprays of Dithane M-45 are applied, rust can cause heavy losses under favorable disease conditions (Sokhi et al. 1978). According to Andrews et al. (1985) "pearl millet rust can reduce yield in hybrid seed production fields, quality in forage, and occasionally grain yields". Monson et al. (1986) studied the effects of rust on yield and quality of pearl millet forage and reported a 51% reduction (for rust susceptible plants as compared to resistant plants) in digestible dry matter yield due to rust infection. Their "results demonstrated the benefits to be derived from incorporation of rust resistance into existing or new cultivars of pearl millet". Singh and Sokhi (1983) found that rust incidence and severity were higher in fast-rusting lines than in slow-rusting ones, due to lower receptivity and less sporulation per uredium in the latter. The authors also indicated that as disease increased, grain size and number per plant decreased.

Leaf and stem rust impact on crop production has been also investigated in other economically important plants, especially wheat (Triticum aestivum (L.) em Thell). Kapoor and Joshi in 1986 studied components of slow rusting in

wheat. Reduced pustule density, smaller pustule size, longer latent period and reduced spore production were recorded. The authors found that pustule size and spore amount were controlled by additive gene action. Heritability estimate was fairly high for pustule size (1 to 3.39 mm^2 pustule area) and latent period (10 to 12.60 days), low for pustule density (3.62 to 6.56 pustules/cm^2) and moderately high for spore production amount (0.020 to 0.080 spore amount/pustule (µg)). Sharma, Kang and Bhullar (1986) found the components of slow rusting in wheat to positively correlate with each other, producing cumulative effects. Whether the cumulation was additive or multiplicative was not stated in the report. Kapoor, Pande and Joshi (1986) found rust severity and infection rates to vary among six susceptible wheat cultivars.

According to Rachie and Majmudar (1980) the principal and most widespread pearl millet diseases in both India and Africa are downy mildew or green ear disease caused by Sclerospora graminicola Sacc. Shroet, ergot (Claviceps microcephala etc.), smut (Tolyposporium penicillariae etc.), rust, and phanerogamic parasite witchweed (Striga spp.). In the United States, even though rust appeared to be potentially destructive as shown earlier, attention has been given to diseases affecting the seedling stage such as leaf and seedling blights (Helminthosporium spp.), top rot or twisted top (Fusarium moniliforme) and smut. Rachie and Majmudar (1980) gave an extensive literature review on these major millet diseases.

D) PLANT BREEDING / GENETIC STUDIES

(1) Introduction

Genetic and breeding improvements are long term ways of improving grain yields. In pearl millet, characteristics such as large seed, long heads, tillering ability, pest and disease resistance, and earliness favor high yields.

Pearl millet breeding behaviour and strategy have been summarized by Rachie and Majmudar (1980) and Jauhar (1981). The major breeding objectives in the past have been: increasing grain yield and quality, incorporating resistance to disease and pests (mainly birds), increasing stress tolerance, and raising the response to better management (particularly higher fertility levels and higher plant populations). These authors added that grain yields can be improved by selecting for head length and diameter, head weight or compactness, head-bearing culms, and size of seeds. Jauhar (1981) emphazised the need to maximize hybrid vigor and improve nutritional quality. Also, modern hybrid cultivars must be genetically broadbased in order to provide some insurance against genetic vulnerability to disease. Burton (1983) stated that pearl millet is equal to maize and sorghum in genetic diversity and has excellent cytoplasmic male sterility (cms) that facilitates commercial hybrid production. To produce such hybrids,
genetic information is needed on yield and its components such as seed size and head length.

(2) Seed size

In grasses the seeds are termed grains , caryopses, or kernels. A grain is a fruit consisting of an embryo - the actual seed developed from the ovule - and the endosperm both surrounded by purely maternal tissue forming the pericarp and the seed coat. The seed coat or testa derived from the ovule, together with the pericarp derived from the ovary wall, protects the seed against moisture loss, attacks of organisms and injuries from fungicides and insecticides. Both envelopes adhere to the seed very closely making it difficult to distinguish the seed from this very special grass fruit called a grain. The embryo (or germ) and the endosperm (foodstore for the germ) inherit identical genetic information through meiosis and double fertilization but in different quantities. In a diploid plant, the diploid embryo inherits n chromosomes from the seed or maternal parent and n chromosomes from the pollen or paternal parent. The triploid endosperm gets 2n chromosomes from the seed parent and n chromosomes from the pollen parent. According to Kiesselbach (1960), the growth rate of the endosperm greatly exceeds that of the embryo in early developmental stages following fertilization in maize. He stated that the ratio of embryo to endosperm weight is influenced genetically and also by the favorableness of growth conditions which affect their food supply. He defined the xenia effect as any immediate effect of a foreign pollen parent on non-maternal tissue (embryo and endosperm) of the kernel and listed three causes of the effects: (1) change in hybrid vigor of the non-

maternal tissues, which may be related to the action of either chromosomal dosage of specific genes; (2) change from recessive to dominant endosperm with its accompanying physiological effects; and (3) (less important) quantitative (size) inheritance. Citing several authors Kiesselbach (1960) further indicated that certain inbred lines and hybrids used as pollinators may increase the kernel weight and others may reduce it, and that a change in endosperm type from recessive to dominant as an immediate effect of crossing is accompanied by increased weight of mature kernels. He also found that xenia effects due to primary endosperm change bring about materially increased yield of grain per plant or per acre, whereas mere changes in the hybrid vigor of kernels may or may not have such yield effects. Therefore, the information on the xenia effects of a crop can be very important in its improvement.

According to Hutchinson (1984), larger seeds produce larger seedlings than do smaller seeds of the same species, and within-species grain-size differences derive from variation in the maternal contribution and not from varying embryo sizes. The author also reported that only the genotype and external environment, and not differing maternal contributions of seed foodstores, contribute to the expression of quantitative characters during the latter half of the life cycle of Avena barbata plants in nature.
Agyanger et. al. 1983, (cited by Voigt et. al. 1966), found that the weight of sorghum seed is highly correlated with seed size, so that weight is a reliable index for the size of

seed. Voigt et. al. (1966) studied the genetics of seed size in sorghum and the possibility of increasing the trait through selection. Using 300 seed weight for a seed size index, the authors combined methods outlined by Mather (1949), Powers and Lyon (1941), Powers (1942) and Hayman (1958, 1960) to calculate expected means for the F_1, F_2, backcross one (BC_1) and backcross two (BC_2) from observed parental means estimated by the least squares method. They also analyzed the means of all populations to provide information on the nature of gene action involved in determining seed size. Their study showed seed size gene action to be almost entirely additive with a heritability of about 60% making it possible to increase seed size by selecting and recombining large seeded F_2s. Using the formula outlined by Sinnott et. al. (1950), Voigt et al. found n = 4 loci or chromosome segments involved in seed size expression. But using a different formula, taking into account all the generation means, they obtained n = 3 loci. Both equations for estimating the number of genes expressing a quantitative trait like seed size were based on the assumption that the genes are additive, equal in their effects, independently inherited and all alleles for largest expression (here large seed size) are in one parent. This seemed to be the case for sorghum lines studied by Voigt et al. (1966).

If dominance exists, another formula, attributed to Sewell Wright by Burton (1951), can be used to estimate the minimum number of genes controlling a single quantitative

character. According to Burton (1951), that formula will give an unbïased estimate of the gene number if the following assumptions apply :

1) No linkage exists between pertinent genes.
2) One parent supplies only "+" factors and the other only "-" factors among those which differ.
3) All genes are equally important.
4) The degree of dominance of all "+" factors is the same for all of them.
5) No interactions (epistasis) between pertinent non-allelic genes.

The formula gives a value of n that may be much smaller than the true gene number when these assumptions do not apply.

Kiniry (1988), using shading prior to anthesis to reduce the number of kernels per panicle in sorghum reported a 31% increase in kernel weight in response to decreased kernel number as compared to seed weight in non-shaded plants. In Avena barbata, Hutchinson (1984) found larger seeds to produce larger seedlings than did smaller seeds but larger seeds did not produce plants that were larger at later stages when the seed-size difference was determined by floret position within the same genotype (as it was the case in that species). Larger seeds did not produce plants that were larger at later stages when the seed-size difference characterized populations having different genotypes at many loci.

In pearl millet, Phul and Athwal 1969, studied seven generations (P_1, P_2, F_1, F_2, F_3, BC_1 (F_1 x P_1) and B_C2 (F_1 x P_2)) and found grain size to be: 1) mainly controlled by additive plus additive by dominant gene actions, 2) correlated positively with grain hardness, 3) correlated negatively low with protein content, and 4) greatly influenced by environmental factors.They also reported grain hardness to be highly and negatively correlated with protein content, to be mainly controlled by additive and dominant gene effects, and greatly influenced by environmental conditions . Hash (1986) found millet seed size quantitatively inherited but heritability was relatively low. He also found 100-seed weight more reproductible than harvestable culm number, head seed weight and grain number per head. He reported the plot mean grain size to be positively ($p<0.01$) correlated with plot mean plant height, head diameter and grain weight per head but negatively ($p<0.05$) correlated with mean heading date and grain number per cm^2 of head surface area. He remarked "none of these correlations was so strong as to make selection of desirable combinations of plant characteristics unusually difficult".

(3) Earliness and plant improvement

Earliness can be useful in plant management but it can also affect plant improvement. Van Dat and Peterson (1983) compared two near-isogenic rice cultivars and reported that the early maturing 'ED7' yielded significantly more than

the late 'Calrose 76' in both early (May 11) and later (May 21) plantings. 'ED7' also had significantly higher 100-grain weights and fewer sterile florets than 'Calrose 76' for the later sowing and in general performed better in the cool environment used in the experiment.

Heterosis has been found of less magnitude for heading date than for yield in Durum wheat (Triticum durum (L.) (Amaya et al., 1972), and to be -8% in grain sorghum for earliness against 66% for yield (Kulkarni and Shinde, 1985). Saeed and Francis (1986), found a highly significant and positive correlation between grain yield and days to flowering in sorghum in environments with relatively high night temperatures but the correlation was low in cool night temperature environments. Rana et. al.(1984) reported nonlinear relationships among plant height, flowering time, and grain yield but found early flowering and low leaf number correlated with higher yield in sorghum. Sandhu and Phul (1984) reported high heritability estimates for pearl millet head length, days to 50 percent flowering and plant height in two environments. For the same crop, Sagar et. al. (1985) found the gene effects for heading and maturity similar with non-additive variance predominant over additive variance and concluded that days to heading would therefore be used for the development of early-maturing types in pearl millet.

(4) Head Length

Burton (1951), in a study of quantitative inheritance in pearl millet, reported that heterosis was operating in the

expression of head length but his results showed an unusually large h^2 of 0.98 for head length. But as mentioned earlier, Sandhu and Phul (1984) also found pearl millet head length highly heritable. Upadhyay and Murty (1971) studied 20 genetic stocks of pearl millet in a complete diallel minus reciprocal F_1s and found that no single genetic stock was a good combiner for all the characters studied nor was a specific cross combination good for all characters. The gene action was non-additive in general but the additive component was substantial for flowering, tiller number, ear length, bristle length, and yield. As one would expect, they found high heterosis in crosses between divergent parents for most characters while progeny of least divergent parents did not show marked heterosis. Another diallel also excluding reciprocals but involving only 10 inbred parents was conducted by Tyagi et al. (1975) who found limited heterosis for head length, ear diameter, grain weight, and days to head emergence, but maximum heterosis and SCA (specific combining ability) effects for grain yield and head number per plant. After studying F_2 and F_3 generations of five crosses in sorghum, Fanous et. al. (1971) reported relatively large estimates of heritability and expected genetic advance in each cross, for panicle length and rachis branch length which were positively correlated to each other. They therefore concluded that "rapid progress should result from early generation selection for either character, which should also result in simultaneous improvement in the other character as well". In wheat, the additive, dominance and

dominance by dominance types of gene action have been found significant for spike length, peduncle length and spikelets per spike but the correlations were negative between dominant (h) and epistasic (I) parameters for all measured characters. The authors suggested the use of population improvement coupled with recurrent selection and multiple breeding techniques for making rapid advances in the development of improved lines . (Singh, Bhullar and Gill, 1984)

(III) MATERIALS AND METHODS

Two projects were conducted for this dissertation. One was to provide information on agronomic effects of plant height, maturity, and plant spacing on (a) grain yield and its components and (b) effect of foliar disease complex (Pyricularia and rust) on grain yield. The second project was designed to determine the genetics of head length and seed size and to study the feasibility of developing dwarf, early maturing, long-headed and large-seeded pearl millet parental lines and hybrids.

Both projects were conducted at the Coastal Plain Experimental Station, Tifton, Georgia in the field and the greenhouse.

A. MANAGEMENT / GENETIC STUDY

(1) Materials

Four near-isogenic pearl millet lines were used in this project.

1. Tift 23B, released on 1 July , 1963 (Burton, 1965a), was described as follows: " 1.8 to 2.4 m tall with bluish grey seeds borne in heads 12.5 to 20 cm long. Planted on May 1, it will flower in 90 days and mature seeds 3 to 4 weeks later, but planted on 15 August, it will flower in only 70

days. It is highly self fertile and the sterility maintainer for the cytoplasmic male sterile line Tift 23A ".

2. Tift 23BE was developed "by selecting an early maturing plant from a selfed population of BC_2 plants developed by back-crossing Tift $23B_1$, to an early maturing mutant induced with ethyl methane sulfonate in Tift $23B_1$" (Hanna and Burton, 1985a, 1985b). Compared to Tift $23B_1$, Tift $23B_1E_1$ has shorter mature plant height (1.4 vs 1.9 m), shorter heads (17.8 vs 20.0 cm), narrower culm diameter (15 vs 20 mm), shorter peduncles (21.8 vs. 24.5 cm) and fewer internodes (6 vs. 9). Planted in late May or early June, "Tift $23B_1E_1$ will flower in 45 to 50 days after planting, and mature seeds in 70 to 75 days (from planting to harvest) compared to Tift $23B_1$ which will flower 75 to 80 days after planting and mature seeds in 100 to 105 days".

3. Tift 23DB was developed by transferring the $\underline{d}_2$ dwarf gene from Tift inbred 239 to Tift 23B, and appears to be identical to Tift 23B except for height, 0.90 to 1.35 m for the dwarf compared to 1.8 to 2.4 m for the tall. The $\underline{d}_2$ gene reduces the length of all internodes without altering the length of the peduncle and seedhead (Burton, 1967).

4. Tift 23DBE was developed by transferring the recessive early maturing e_1 gene from a 'Katherine' pearl millet, a cultivar of African origin, to the dwarf late inbred Tift 23DB. Tift 23DBE is photoperiod insensitive and flowers in 45 to 55 days regardless of the summer planting date unlike Tift 23DB which matures earlier when summer

planting is delayed (Burton, 1981).

Some characters of these four inbreds recorded from this two-year study are given in the following table:

Inbred	Earliness* (50% heading)	Plant* Height	Head* Length
1.Tall-late Tift 23B	71 to 81 days	2.30 m	18 - 28 cm
2.Tall-early Tift 23BE	54 days	1.60 m	16 - 23 cm
3.Dwarf-late Tift 23DB	76 to 83 days	1.30 m	16 - 20 cm
4.Dwarf-early Tift 23DBE	51 days	0.90 - 1 m	15 - 24 cm

* Two year summary

(2)Methods

Two plantings per year of the four near-isogenic lines were made in 1985 and 1986. The two plantings were necessary to study the plants'ability to escape grain yield reduction due to diseases, early planting (13 May, 1985 and 13 June, 1986) being disease free and late planting (09 July, 1985 and 18 July, 1986) being affected by the diseases.

In each season, the four near-isogenic inbred lines were planted at the Coastal Plain Experimental Station in a split plot design with 8 replications in 1985 and 5 replications in 1986. Two levels of plant spacing (2.5 cm between plants on the same row, i.e. 40 plants per meter row, and 17.0 cm

between plants on the same row, i.e. 6 plants per meter row) were main plots and near-isogenic lines were subplots. Each subplot was a six-row plot 4.8 m long and 0.9 m between rows. A two-row border surrounded the entire test.

Plots were planted with cone planters that placed 50 to 60 seeds per meter of row. Plants were thinned to one plant every 2.5 cm (high plant population density: 444 000 plants /ha) or one plant every 17 cm (low plant population density: 66 000 plants /ha) at about 15 to 20 days after planting, and 0.80 m wide alleys were cleared to mark plot limits.

To increase the effectiveness of disease infection in the late plantings, diseased plant materials from infested nurseries were harvested with a silage chopper and spread between rows on the test at about 40 days after planting.

After seed set, insecticide-treated kraft bags were used to protect harvestable open-pollinated heads from insect and bird damage. The Tifton, fine-loamy, siliceous, thermic, Plinthic, Kandiudult, soil received 5-10-50 fertilizer at the rate of 280 kg/ha applied in the row just before planting. A preemergence application of propazine (Milogard), or 2 - chloro - 4, 6 - bis (isopropylamino) - s - triazine, at 2.24 kg/ha was made immediately after planting to control weeds. Weed control was further achieved by mechanical tillage two to three weeks after planting (immediately after plant thinning) or as needed. Whenever necessary, the field was sprayed with monocrotophos (Azodrin), or dimethyl, cis-1-methyl-2-methylcarbamoylvinyl phosphate (McEwen et al.,1979),

at recommended rates to control insects.

Data was recorded for ten characteristics as follows:

(1) Plant number per plot: Immediately after thinning to one plant per hill (before tillering started), plants of the center two rows were counted and the average plant number per row recorded for each replication.

(2) Heading date: Days to 50% stigma exertion on the center two rows.

(3) Head number per plot: Mean of the center two rows, after heads flowered.

(4) Plant height (cm): Mean height (tip of head to soil surface) of the plants in the center two rows of each plot at maturity.

(5) Disease rating: Ratings were made on a scale of 0 to 5 based on disease severity, that is the area of plant tissue (leaf area in this study) affected by disease and expressed as a percentage of the total area. Rating # 0 corresponded to 0% and rating # 5 to 80-100% disease severity; ratings # 1, 2, 3, and 4 corresponded to 1-20%, 20-40%, 40-60%, and 60-80% disease severity, respectively. The ratings were made when disease symptoms were first noticeable. There was one rating on 16 September for the late planting in 1985 (early inbreds were maturing seeds and late inbreds were at fecondation stage). Also, there was one rating on 10 September for both early and late plantings in 1986 (in the early planting early inbreds were maturing seeds and late inbreds were at fecondation stage, while in the late planting early inbreds

were at milk stage and late inbreds between boot and half bloom stages). A second rating was performed on 23 September for the late planting in 1986 (early inbreds were at hard dough stage and late inbreds were between fecondation and early milk stages).

At maturity, ten bagged heads were harvested on the center two rows of each treatment plot, tied in a bundle, tagged by the inbred name and the replication number and allowed to dry for several weeks in a greenhouse. A day or two prior to threshing, the bundles were transferred to forced air ovens at 38 - 40^{0}C. The information on each bundle was transferred to 10 number 1 coin storage brown kraft envelopes. The length of head was measured and written on the envelope that would contain the seed from that head. Heads were individually machine threshed and clean seeds kept in envelopes and weighed to the nearest 0.01g on a digital scale.

(6) Head length (cm): Average of ten measurements for each replication.

(7) Total head seed weight (g): Average of ten measurements for each replication.

(8) Weight of 100 seeds (g): Mean of 10 measurements. Whenever there was enough seeds, four 100-seed counts were made for each envelope using a COUNT-A-PACK seedcounter in Athens. Each 100-seed package was weighed to the nearest 0.01 g and the weight recorded.

(9) Average head number per plant: Head number per plot

divided by plant number per plot.

(10) Yield (kg/ha):

$$\frac{1\ kg \times \text{mean head seed weight (g)} \times \text{head/plot} \times 10000\ m^2}{0.9\ m \times 4\ m \times 1000g}$$

or mean head seed weight x head number /plot x $(0.36)^{-1}$

Method of Analysis

The experimental design was a completely randomized bloc design and the treatment design was a split plot design with inbred lines as fixed effects and replications as random effects. The analysis of variance relative to a split plot design along with Duncan's new multiple range test was used to interpret the data .

B. PLANT BREEDING/GENETIC STUDY

(1) Materials

The objective of this project was to study the genetics of seed size and head length and the feasibility of developing a dwarf, early, large-seeded (1.2 g/100 seeds) and long-headed millet. Six millet cultivars were used in this study.

(1) Tift 23DBE : Dwarf, early small seeded (0.51 g /100 seeds) and small-headed inbred line, (Burton, 1969).

(2) Tift 23B : Tall, late, small-seeded (0.44 g/100 seeds) and small-headed inbred line near-isogenic to Tift 23DBE. Both inbreds were already described in the management study.

(3) Tift 18BE : It is an early mutation of the late Tift 18B released on 01 May , 1965 (Burton, 1965b) as the sterility maintainer of the male-sterile Tift 18A and described as daylength insensitive that flowers in 90 days in spring planting and in 70 days in 15 August planting. Tift 18B produces white seeds borne in heads 45 to 90 cm long. Tift 18BE is a mid size plant with long heads but matures in about half the time required for 18B.

(4) 'Gero', long head cultivar : It is a daylength insensitive millet introduced in 1962 by Dr. Glenn Burton. Its heads are as long as or longer than those of Tift 18BE but thicker and more robust. Plants also are taller. Although described as an early-maturing millet in Nigeria as compared to photoperiod-sensitive 'maiwa' (Rachie and Majmudar, 1980), Gero is a late maturing cultivar in Tifton, 70 to 90 days to flowering depending on planting date. Seeds from these two long-headed cultivars are mid size to small, weighing on average 0.76 g/ 100 seeds.

(5) 'Togo' : It is mid-size plant, short head, early large-seeded cultivar originally from Togo but given to Dr. W. W. Hanna by Dr. Anand Kumar from Niger under the number 15198 and reported to flower in 36 days in Niger. In Tifton it is as early as Tift 23DBE and is highly male-sterile. It has short, thick heads which bears very large seeds (1.18 g /100 seeds).

(6) 'Walor Kassens' cultivar : It is a plant introduction

(PI) cultivar called Walor Kassens from Ghana and registered under the number PI 316666, 30 September , 1966, as an early pearl millet from the Institute of Technology and Science Academy. It flowers about 45 days after planting and has small heads bearing large seeds (1.26 g /100 seeds).

(2) Methods

To accomplish the objectives of this project, crosses were made in all combinations allowed by manageable plant characteristics such as maturity and fertility. It was for example possible to store pollen from early-maturing cultivars and use it later to fertilize late-maturing cultivars (Hanna et al., 1983). However, pollen could not be stored for the highly male-sterile early Togo cultivar, so, the Togo (early) x Gero (late) crosses were very difficult to make.

Backcrosses were made by growing F_1 plants and parents together and crossing the hybrids with their respective parents. Parents, F_1, F_2 and backcrosses were grown in replicated plots under the same conditions and relevant traits were recorded and analyzed. All crossings and plot tests were conducted in the Coastal Plain Experimental Station fields and greenhouse in Tifton, Georgia. In summer 1985, the first crosses were made in the field. In the winter 1985 to 1986, backcrosses (BC) were made in the greenhouse along with selfing F_1 plants to produce F_2 seeds. In summer 1986, F_2 and BC seeds from the greenhouse were grown in replication in the field and more BCs were made. In summer

1987, parents and F_1s were grown in a completely randomized block design (CRBD) with 5 replications, and F_2s and BCs were grown in replication in the field.

Plots for parents and F_1s were 4.45 m long, and plots were 28.45 m and 62 m long for F_2s and BCs in 1986 and 1987, respectively. In both years and for all families, plots were 0.9 m wide .

Two to three weeks after planting, plants were thinnned to a single plant per hill, 17 - 20 cm spacing between plants within the row. The soil conditions and cultural practices were similar to that outlined for the management study.

Selfing and crossing

Selfing was achieved by protecting pearl millet inflorescences from outside pollen with insecticide-treated 7.5 x 35 cm kraft bags prior to stigma receptivity. Self-pollination was made under the stappled bags.

To make crosses, 7.5 x 35 cm glassine bags were put on seed plant inflorescences and stapled prior to stigma receptivity. A day before crossing, insecticide-treated kraft bags were put on male plant inflorescences starting to shed pollen. On the day of the crossing (when stigmas on seed plant inflorescences were receptive) pollen was collected by carefully shaking and removing the kraft bags from the male plants. The cross was made by replacing the glassine bag on the seed plant with a pollen-containing kraft bag which was shaken to spread the pollen on the receptive stigmas. The

kraft bag was stapled to avoid its removal by the wind.

Since some heads were longer than 35 cm (Gero and Tift 18BE), controlled pollination (selfing or crossing) only affected the top 35 cm of the long heads. However, sometimes the head could be bent and up to 50 cm of the head could therefore be enclosed in the Kraft bag.

Data collection

(1) Heading date : This was recorded only for selfed plants and corresponded to the date the Kraft bag was placed on the head ; that is when the head was partly or entirely out of the boot but prior to stigma exertion. This date was marked on the bag and transferred to the seed storage envelope at threshing.

(2) Head length (cm) : Some heads were longer than the kraft bags, so, the entire head length (Head L) was recorded and used to study the genetics of the heads. The head covered by the bag (or seed head length) was also recorded and used in the formula that estimated the seed weight of the entire head.

(3) Total head seed weight (THSW in g) : After measuring the head length, the part of the head that was outside the kraft bag was cut off and only the controlled pollination part of the head was threshed. For most heads, HSW was the weight of the seeds directly collected from threshing and represented the seeds from the entire head. For other heads, collected seeds were from only part of the head and the following

formula was used to estimate the seed weight of the entire head:

$$THSW = \frac{\text{Seed weight x Head length}}{\text{Seed head length}}$$

(4) Weight of 100 seeds (g) : 100 seeds from each head were counted and weighed to the nearest 0.01 g to get 100-seed weight.

Method of analyses

Mean analyses were conducted on original data to study families and replications means and their variances. The analyses showed that family variances were proportional to the means and the coefficients of variation were high for the total head seed weight and ranged from 21% (F_1 family 87-10142) to 158% (Parent family 87-10080, Table A2).

In such a situation, data transformation was needed as suggested by Hoyle (1973) to satisfy at least one of the following three basic assumptions of the standard statistical techniques associated with the linear model:

1. Additivity: According to this assumption, the main effects combine linearly or add up to 'explain' the observations. "This assumption is necessary to ensure identification of the parameters in most cases and is therefore important in the interpretation of the data" (Hoyle, 1973).
2. Constancy of variance: The observations are assumed to have a constant variance about their varying means, that is, the variance is assumed to be independent of both the expected values of the observations and the sample size. This

assumption "is usually made because it simplifies the estimation technique. With it, least squares estimators are also minimum variance unbiased linear estimators (LSE = MVULE). Without it, a weighted least squares analysis gives the MVULE's" (Hoyle, 1973).

3. Normality: The observations are assumed to have a normal distribution. This "assumption is critically important in the testing of hypotheses, for the normality of the observations leads to comparatively simple and standard testing procedures which have been thoroughly investigated,
and more importantly, leads to distributions which have been tabulated" (Hoyle, 1973).

Using the above knowledge and suggested transformation methods, square root, and both natural and decimal logarithm transformations were attempted on the original data.

Only the decimal logarithm transformation stabilised the variances, and reduced the coefficients of variation (CV's). After the transformation, the CV's for the total head seed weight ranged from 2.7% (F_1 family 87-10142) to 29% (Parent family 87-10080). To avoid negative values associated with the logarithm of small numbers, total head seed weight and hundred seed weight were multiplied by 100 during the transformation. For days to flowering and head length the transformation was $x = \log_{10}(X_0)$ and for both total head and hundred seed weights it was $x = \log_{10}(100 \times X_0)$. In each case X_0 was the data in original units. Even though this logarithm transformation was found necessary, it was more convenient

(easier to follow through), in some cases, to analyse the data in original units.

The univariate analysis was conducted along with the frequency distributions per family and per replication observations. This helped to detect and eliminate extreme values (outliers) in some parent and F_1 families.

The analysis of variance was performed over the data of the parents and hybrids grown in a completely randomized block design (CRBD) with 5 replications in 1987. The results (Tables A4 & A5) showed within variations in some cultivars. The various causes of these variations may be the susceptibility of the inbred lines to environmental sources of variation, uncontrolled outcrossing, or a mixture of genotypes in cultivars.

Data in Table 1 showed those within-cultivar variations, computed from Table A5, and translated into the original units. All differences in the table were significant ($p < 0.004$) except for the hundred seed weight difference between T23B and T23DBE. The reason why a 39% difference between the two near-isogenic inbreds was not detected as significant was probably because T23DBE had only one observation for head and hundred seed weights (Table A3C) creating a negative degree of freedom for reps x family interaction. The two-year management study showed that T23B was on the average ($p = 0.002$) 13% lower in hundred seed weight than T23DBE. This significant difference would have been confirmed here if it were not for the high sterility of T23DBE in 1987. The 3%

difference in head length between the two near-isogenic inbreds was not significant in the management study.

For true inbred lines the within-cultivar variation should be due to environmental effects mainly. Since Tift 18BE, with 6 families, is an established inbred, its within-cultivar variance can be assumed to be mainly of environmental origin and can be used as a reference to test other within-cultivar variances as shown in Table 2.

Table 1:Difference between extreme values within-cultivars and their percentage to the minimum value.

Cultivar	Maturity (days) Range	Diff.	Head length Range	Diff.	Seed size Range	Diff.
Gero f = 9 n = 45 - 72	60.3 to 67.5	7.2 12%	31.8 cm to 51.1 cm	19.3 cm 61%	0.56 g to 0.99 g	0.43 g 78%
T18BE f = 6 n = 46 - 84	43.6 to 44.7	1.1 3%	39.3 cm to 42.1 cm	2.8 cm 7%	0.74 g to 0.84 g	0.10 g 14%
Walor f = 15 n = 1; 22 - 59	43.8 to 49.4	5.7 13%	14.1 cm to 24.4 cm	9.3 cm 66%	0.93 g to 1.7 g	0.73 g 79%
Togo f = 9 n = 25 - 64	41.8 to 47.5	5.8 14%	17.9 cm to 19.5 cm	1.6 cm 9%	1.0 g to 1.2 g	0.2 g 17%
T23B n = 60 vs T23DBE n = 62	70.0 vs 47.0	23.0 49%	17.3 cm vs 17.7	0.4 cm 2%	0.4 g vs 0.6 g	0.2 g 39% ns

Diff. = difference between extreme values;
f = number of families grown for the cultivar;
n = number of plants studied per family;
Seed size was meazured by the weight (g) of 100 seeds.

T23B and T23DBE are near-isogenic inbreds but only one family of each was grown and their individual within-cultivar variances could not be estimated.

From data in Table 2, within-cultivar variances for all three traits under study were too high in late long-headed Gero and early large-seeded Walor to be considered due to environmental effects only. Within-cultivar variance of head length and hundred seed weight in the early large-seeded Togo can be assumed to be due to mainly environmental effects. But this cultivar's maturity variance happened to be large. Taking into account the management study, it appears that T23B and T23DBE are very
different in their maturity (as expected), but they also differ in their seed size.

One conclusion that can be drawn from this, (Table 2), is that environment effects alone cannot account for the large within-cultivar variances found in Gero, Walor, and to some extent in Togo materials. Another important source of variation could be of genetic origin. The choice of the parents for quantitative traits can be a very delicate step. It is possible that Gero, Walor and Togo cultivars are mixtures of genotypes instead of each having a single genotype. This may explain part of the within-cultivar variance found in Gero and Walor for head length and seed size, both traits being reported to have dominant effects and expected to be controlled by a few genes. Burton (1951) found maturity to be controlled by several genes but later studies

(Burton, 1981; Hanna and Burton, 1985a) showed earliness to be recessive and controlled by a single gene.

It is possible that maturity in Gero, Togo and Walor is controlled by several genes and the genetic variance among different families of the same cultivar could explain part of the within cultivar variance found in these materials.

For each single cross between inbred lines, the hierarchy of variances of the parents (P), hybrids (F_1),

Table 2: Evaluation of within-cultivar variances using Tift 18BE as reference with the within-cultivar variance set to 100%.

Cultivar	Maturity	Head length	Seed size
Gero f = 9 n = 45 - 72	466%	847%	567%
T18BE f = 6 n = 46 - 84	100%	100%	100%
Walor f = 15 n = 1; 22 - 59	505%	920%	566%
Togo f = 9 n = 25 - 64	535%	124%	125%
T23B n = 60 vs T23DBE n = 62	1904%	32%	282%

f = number of families grown per cultivar;
n = number of plants studied per family.

and segregating families (F_2) and backcrosses (BC) is as following: $F_2 > BC > F_1 = P_1 = P_2$. This expected hierarchy of variances across generations was observed only in some crosses for each character studied. No explaination is speculated for why in other crosses one parent would show more variability than an F_2 or why an F2 would be less variable than an F_1. Similar deviations, however, were recorded by Burton (1951).

These deviations and the variations within the cultivars limited the number of crosses to study and also the choice of analyses that could be conducted on the data. For example, finding crosses that were logical and could make up a diallel without reciprocals was not possible so that general and specific combining abilities were not studied. Only crosses that showed the expected hierarchy of variances (crosses 3, 7, and 15 in 1987 for maturity ; crosses 1, 3, 4, and 7 in 1987 and crosses 1, 2, and 3 in 1986 for headlength ; and crosses 9, and 13 in 1987 for seed size, Tables A1 & A2) were retained for further analyses, and only heterosis, broad sense heritability, frequency distribution, and a tentative determination of the number of genes in maturity, head length and seed size were attempted. However, the analysis of the whole data is available in Appendix Tables A11 to A14.

Heterosis was computed using the formulas given by Fehr (1987, p. 175) and Jinks (Frankel, 1983 p. 4).

Mid-parent (MP) heterosis and high-parent (HP) heterosis are defined as following :

Mid-parent heterosis (%) = $(\bar{F}_1 - \overline{MP}) \times 100 / \overline{MP}$

High-parent heterosis (%) = $(\bar{F}_1 - \overline{HP}) \times 100 / \overline{HP}$

where $\bar{F}_1$ and $\overline{HP}$ are mean performances of the hybrid and high-parent respectively and $\overline{MP} = 0.5(\bar{P}_1 + \bar{P}_2)$ with $\bar{P}_1$ and $\bar{P}_2$ being the mean performances of the parents, (Fehr, 1987).

According to Jinks (Frankel, 1983), heterosis (H) is equal to $H = \bar{F}_1 - \bar{P}_2 = h + d$ for traits like maturity where the better parent has a lower value than the other parent and $H = \bar{F}_1 - \bar{P}_1 = h - d$ for traits like head length where the better parent has a higher value than the other parent. In these formulas, d represents the sum of additive effects of independent loci and is equal to $0.5(\bar{P}_1 - \bar{P}_2)$, and h, the sum of dominant effects is equal to $\bar{F}_1 - 0.5(\bar{P}_1 + \bar{P}_2)$.

The broad sense heritability (H^2) was computed using the formulas outlined by Allard (1960):

$V_E = (V_{P1} + V_{P2} + V_{F1})/3$; $V_G = V_{F2} - V_E$; and

$H^2 = V_G / V_{F2}$. V is the variance of environment (E), parents (P_1 & P_2), hybrid (F_1), F_2, and genotype (G).

Since the selected crosses only had one backcross data (instead of data of both backcrosses), the narrow sense heritability could not be estimated.

The frequency distribution figures were plotted using the scientific graph system SIGMAPLOT.

Since headlength, seed size, and maturity involved some kind of dominance in a cross pollinated crop like pearl millet, the number of genes was determined using the formula attributed to Sewell Wright by Burton (1951), that is :

$n = 0.25(0.75 - h + h^2)D^2/(\tilde{O}^2_{F2} - \tilde{O}^2_{F1})$ where $D = P_2 - \bar{P}_1$ and $\bar{h} = (\bar{F}_1 - P_1)/D$ with P_2 being the largest parent, D the additive effect, and h the dominant effect.

The number of genes controlling each trait again was estimated using the chisquare test outlined by Hanna et al., in 1978. To do this, each F2 distribution was divided into two classes: the recessive class and the dominant class. The level of dominance was determined by comparing the means of both parents to that of the hybrid F_1. The mean of the hybrid is supposed to be closer to that of the dominant parent than to the mean of the recessive parent.

The next step was to locate the mean of the recessive parent in the F_2 distribution. The frequency of the recessive F_2 class was the frequency of the individuals with values going from the mean of the recessive parent (or one to two units higher or lower than the mean, according to the situation), to the nearest end of the distribution.

The linkage chisquare test also proposed by Hanna et al., 1978, was used to check for linkage between any two of the three traits under consideration, that is, maturity, head length and seed size.

(IV) RESULTS AND DISCUSSION

(A) Management / Genetic Study

A1. Results

The results of this management study are presented in Tabbles 3 through 12. Data in Tables 3 through 8 include analyses of variances (ANOVA) tables and data in Tables 9 through 12 summarize the findings per season and per year for easier interpretation. The analyses per growing season are available in Appendix Tables 33 to 36.

The interaction between years (Y), inbreds (I) and plant population density (D), (Tables 5 and 6), was non-significant at p = 0.05 for head number per plot, head length, total head seed weight, 100-seed weight and yield in early plantings (Table 5) but was highly significant for plant height (p=0.0044), days to 50% heading or maturity (p = 0.0001) and significant for head number per plant or plant tillering ability (p = 0.0311). The YxIxD interaction was highly significant for head number per plot (p = 0.0089), significant for total head seed weight (p = 0.0279) and non-significant for all other traits at p = 0.05, in late plantings (Table 6). Whenever non-significant, the YxIxD was used as a more accurate error term in computing F -Tests for main effects and lower levels of interaction.

Table 3: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings in two seasons 13 May, and 09 July, 1985

Treatment	Plant # per plot	Plant height*	Maturity (days)	Head no. per plot	Head no. per plant	Head length	Head seed wt (g.)	100 seeds weight (g)	Yield kg/ha
SEASONS (S)[1]									
Early	27b	58b	64.9a	118b	5.2a	19.2a	6.2a	0.55a	1950a
Late	63a	136a	55.2b	130a	3.2b	19.1a	2.6b	0.53a	930b
INBRED(I)[1]									
T23B	51a	146a	68.9b	105c	3.0c	21.2a	7.0a	0.54b	1960a
T23BE	49a	93b	50.7c	154a	4.6b	18.4c	4.1b	0.60a	1960a
T23DB	49a	84c	72.3a	99d	3.0c	17.8d	3.3c	0.30c	860b
T23DBE	32b	64d	48.4d	139b	6.2a	19.2b	2.5d	0.53b	990b
DENSITY(D)[1]									
High	69a	98a	58.8b	134a	2.7b	18.8b	4.1b	0.49a	1470a
Low	21b	96b	61.3a	114b	5.7a	19.5a	4.7a	0.49a	1440a
				A	N O V A				
(S)	0.0001	0.0001	0.0001	0.0026	0.0001	0.2354	0.0001	0.0001	0.0001
(I)	0.0001	0.0001	0.0001	0.0003	0.0001	0.0001	0.0004	0.0030	0.0001
(D)	0.0001	0.0001	0.0001	0.0010	0.0001	0.0001	0.0118	0.8167	0.38
(SxI)	0.0001	0.0001	0.0001	0.0269	0.0001	0.0001	0.0248	0.0284	0.20
(SxD)	0.0001	0.0001	0.0001	0.0465	0.0005	0.8953	0.0608	0.0469	0.42
(IxD)	0.0001	0.0237	0.0001	0.4670	0.0001	0.0110	0.6389	0.0200	0.04
S x I x D	0.0001	0.0001	0.0001	0.6386	0.0065	0.0219	0.7484	0.0756	0.08
CV	11	3	2	9	4	4	24	12	26
Overall Mean	45	97	60.1	124	14.7	19.1	4.4	0.54	1200

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for p > 0.05. * : Plant height and head length are in cm .

Table 4: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings in two seasons: 13 June, and 18 July, 1986

Treatment	Plant # per plot	Plant height*	Maturity (days)	Head no. per plot	Head no. per plant	Head length	Head seed weight(g)	100 seeds weight(g)	Yield kg/ha
SEASONS (S)[1]									
Early	37b	133a	60.3a	100a	3.5a	18.6a	6.4a	0.63a	1770a
Late	48a	134a	56.4b	99a	2.9b	18.0b	3.6b	0.52b	990b
INBRED(I)[1]									
T23B	40b	187a	68.4a	95c	3.2b	18.1b	5.6a	0.50d	1470b
T23BE	46a	139b	48.8b	119a	3.6a	18.9a	5.4a	0.61b	1780a
T23DB	41b	113c	68.1a	79d	2.7c	17.3c	4.1c	0.55c	870c
T23DBE	49b	96d	48.0c	105b	3.4b	19.1a	4.9b	0.64a	1390b
DENSITY(D)[1]									
High	65a	139a	56.9b	109a	1.7b	18.0b	4.5b	0.58a	1340a
Low	19b	128b	59.8a	90b	4.7a	18.7a	5.6a	0.57a	1410a
				A N O V A					
(S)	0.0001	0.7691	0.0001	0.7910	0.0001	0.0015	0.0001	0.0001	0.0001
(I)	0.0003	0.0001	0.0001	0.0011	0.0321	0.0004	0.0904	0.0001	0.0001
(D)	0.0001	0.0013	0.0010	0.0011	0.0001	0.1020	0.0263	0.5849	0.3300
(SxI)	0.0757	0.0215	0.0005	0.0475	0.1834	0.0262	0.0621	0.0001	0.0020
(SxD)	0.0001	0.0305	0.0288	0.3117	0.6654	0.4094	0.8981	0.5000	0.1700
(IxD)	0.0111	0.0256	0.0297	0.0002	0.0302	0.0028	0.0001	0.5726	0.0000
S x I x D	0.0222	0.4724	0.4061	0.6129	0.1851	0.0040	0.1343	0.0001	0.0200
CV	10	4	2	9	11	5	17	6	24
Overall Mean	42	134	58.3	99	3.2	18.3	5.0	0.6	1150

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for p > 0.05 ; * : Plant height and head length are in cm .

Table 5: Plant and seed characteristics of four near-isogenic pearl millet inbred lines planted at two spacings in 13 May, 1985 and 13 June, 1986 (early plantings)

Treatment	Plant # per plot	Plant height*	Maturity (days)	Head no. per plot	Head no. per plant	Head length	Head seed weight(g)	100 seeds weight(g)	Yield kg/ha
YEAR (Y)[1]									
1985	28b	59b	64.5a	122a	5.2a	19.3a	6.4a	0.55b	2070a
1986	37a	133a	60.3b	100b	3.5b	18.6b	6.4a	0.64a	1770b
INBRED(I)[1]									
T23B	33a	139a	74.4b	97c	3.4c	20.2a	8.0a	0.54b	2140b
T23BE	36a	95b	51.0c	136a	4.7b	18.6b	6.8b	0.62a	2510a
T23DB	33a	83c	75.5a	86d	3.2c	18.1c	5.8c	0.51c	1350d
T23DBE	28b	67d	48.8d	125b	6.0a	19.0b	5.1c	0.63a	1680c
DENSITY(D)[1]									
High	47a	101a	60.4b	123a	2.9b	18.7b	5.8b	0.56b	1960a
Low	18b	91b	64.4a	99b	5.8a	19.2a	7.0a	0.59a	1890a
				A N O V A					
(Y)	0.0001	0.0001	0.0001	0.0001	0.0001	0.0048	0.9375	0.0001	0.0023
(I)	0.0001	0.0001	0.0001	0.0650	0.0001	0.6287	0.5864	0.4657	0.0001
(D)	0.0001	0.0001	0.0001	0.0972	0.0001	0.2422	0.0392	0.5938	0.4600
(YxI)	0.0001	0.0001	0.0001	0.0529	0.0001	0.0174	0.0240	0.0030	0.0108
(YxD)	0.0467	0.1662	0.0001	0.2856	0.0001	0.4795	0.8590	0.0131	0.4900
(IxD)	0.0001	0.0001	0.4432	0.2778	0.8566	0.1918	0.2699	0.0282	0.0155
Y x I x D	0.0003	0.0044	0.0001	0.2174	0.0311	0.0514	0.1375	0.6256	0.8200
CV	14	4	2	9	16	4	18	7	22
Overall Mean	32	96	62.4	111	4.3	19.0	6.4	0.6	1600

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for p > 0.05 ; * : Plant height and head length are in cm .

Table 6: Plant and seed characteristics of four near-isogenic pearl millet inbred lines planted at two spacings in 9 July, 1985 and 18 July, 1986 (late plantings)

Treatment	Plant # per plot	Plant height*	Maturity (days)	Head no. per plot	Head no. per plant	Head length	Head seed weight(g)	100 seeds weight(g)	Yield kg/ha
YEAR (Y) [1]									
1985	62a	97b	55.1b	133a	3.3a	19.0a	2.6b	0.45b	950a
1986	48b	134a	56.4a	99b	2.9b	18.0b	3.6a	0.53a	990a
INBRED(I)[1]									
T23B	58a	194a	62.4b	105c	2.8b	19.2a	5.0a	0.50b	1450a
T23BE	59a	137b	48.5c	142a	3.6a	18.9a	3.4b	0.60a	1300b
T23DB	58a	114c	64.6a	97d	2.6b	17.0b	1.5d	0.30c	390d
T23DBE	47b	93d	47.6d	121b	3.5a	19.1a	2.4c	0.50b	740c
DENSITY(D)[1]									
High	88a	137a	55.1b	123a	1.4b	18.2b	2.8b	0.49a	950a
Low	23b	133b	56.4a	108b	4.8a	19.0a	3.4a	0.47a	990a
				A N O V A					
(Y)	0.0001	0.6628	0.0010	0.0001	0.0004	0.0001	0.0001	0.0025	0.4300
(I)	0.0001	0.0073	0.0019	0.0483	0.0001	0.4253	0.0001	0.3781	0.0472
(D)	0.0001	0.5687	0.3000	0.0668	0.0001	0.4028	0.0001	0.5146	0.7600
(YxI)	0.0001	0.0062	0.0234	0.0250	0.0001	0.0001	0.0006	0.0175	0.0480
(YxD)	0.0001	0.0307	0.3874	0.1491	0.0001	0.0009	0.0001	0.3214	0.0930
(IxD)	0.0001	0.4048	0.0622	0.4029	0.0001	0.2238	0.0006	0.6238	0.2100
(Y x I x D)	0.0001	0.1538	0.1017	0.6675	0.0089	0.9879	0.0279	0.1108	0.4270
CV	7	3	1	9	9	10	20	12	24
Overall Mean	55	135	55.7	116	3.1	18.7	3.1	0.5	810

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for p > 0.05 ; * : Plant height and head length are in cm .

Table 7. Disease rating[1] for four near-isogenic pearl millet inbreds planted at two spacings in late planting 1985

Treatment	Pyricularia[2]	Rust[2]
INBRED(I)		
T23B	2.7 b	2.7 a
T23BE	3.5 a	2.8 a
T23DB	2.5 c	2.9 a
T23DBE	3.6 a	2.9 a
DENSITY(D)		
HIGH	3.5 a	3.0 a
LOW	2.7 b	2.6 b
A N O V A		
INBRED(I)	0.0001 **	0.1316 NS
DENSITY(D)	0.0001 **	0.0185 *
I x D	0.0914 NS	0.5046 NS
CV	8%	12%
Overall Mean	2.8	2.8

1 : Rating on a 0 to 5 scale: 0 = disease free, and 5 = severely affected.
2 : Duncan's new multiple range test at 5%
NS : non-significant
* : significant at 1 to 5% level
** : significant at p < 1% level

Table 8. Disease rating[1] for four near-isogenic pearl millet inbreds planted at two spacings in early and late plantings in 1986

Treatment	Foliar Disease Late planting	Pyricularia Early Planting	Pyricularia Late Planting
INBRED(I)[2]			
T23B	2.0 b	2.0 b	1.4 ab
T23BE	4.3 a	3.5 a	1.6 a
T23DB	2.1 b	2.3 b	1.3 b
T23DBE	4.2 a	3.3 a	1.6 a
DENSITY(D)[2]			
HIGH	3.5 a	3.4 a	1.9 a
LOW	2.8 b	2.2 b	1.1 b
	A N O V A		
INBRED(I)	0.0001 **	0.0001**	0.1998 NS
DENSITY(D)	0.0249 *	0.0025 **	0.0132 *
I x D	0.5885 NS	0.1898 NS	0.0220 *
CV	16%	13%	17%
Overall Mean	3.2	2.8	1.5

1 : Rating on a 0 to 5 scale: 0 = disease free and 5 = severely affected.
2 : Duncan's new multiple range test at 5%
NS : non significant
* : significant at 1 to 5% level
** : significant at p < 1% level

Table 9. Plant and seed characteristics of the lines[1]

Treat.	Maturity (days)	Plant height (cm)	Head/ Plant (no.)	Head Length (cm)	Head-seed weight (g/head)	100-seed Weight (g/100)	Yield kg/ha
Maturity in Inbreds							
Early	49b*	98b	4.5a	18.9a	4.4b	0.6a	1530a
Late	70a	132a	3.0b	18.6b	5.0a	0.5b	1290b
Plant height in Inbreds							
Dwarf	59a	89b	3.9a	18.3b	5.7a	0.6a	1030b
Tall	60a	141a	3.6b	19.2a	3.7b	0.5b	1800a
Plant population density							
High	58b*	119a	2.2b	18.4b	4.3b	0.53a	1410a
Low	61a	112b	5.2a	19.1a	5.1a	0.53a	1410a

[1] : Overall means over both seasons and years.
* : Duncan's multiple range test at 5% level.

Table 10. Plant and seed characteristics of the lines[1]

Treat.	Maturity (days)	Plant height (cm)	Head/ Plant (no.)	Head Length (cm)	Head-seed weight (g/head)	100 seed Weight (g/100)	Yield kg/ha
Season[1]			(Overall Average)[1]				
Early	63a*	96b	4.4a	18.9a	6.3a	0.58a	1380a
Late	56b	135a	3.1b	18.6b	3.1b	0.59b	940b
Year[2]							
1985	60a*	97b	4.3a	19.2a	4.5b	0.48b	1440a
1986	58b	134a	3.2b	18.3b	5.0a	0.58a	1380b

[1] : Two year summary;
[2] : Means of both seasons of the year.
* : Duncan's multiple range test at 5% level.

Table 11. Disease rating* for the four lines (Summary of Tables 7 & 8)

Treatment	Pyricularia[1] Late Plantings 1985, 1986	Rust Late Plant. 1985	Foliar Diseases Early and Late Plantings 1986
Maturity in Inbreds			
Early	2.6 a**	2.9 a	3.9 a
Late	2.0 b	2.8 a	2.1 b
Plant height in Inbreds			
Dwarf	2.3 a	2.9 a	3.0 a
Tall	2.4 a	2.8 a	3.0 a
Density			
High	2.7 a**	3.0 a	3.5 a
Low	1.9 b	2.6 a	2.5 b

[1] : Two year summary ;
* : Rating from 0 = disease free
to 5 = severely affected.
** : Duncan's multiple range test at 5% level.

Table 12: Yield means*

Treatment	1985 Early	1985 Late	1986 Early	1986 Late	Early/Late 1985	Early/Late 1986	1985/1986 Early	1985/1986 Late	Overall 1985	Overall 1986
Inbred										
Early	2020a	930a	2090a	1080a	1470a	1590a	2100a	1020a	1470a	1590a
Late	1890a	930a	1450b	900a	1410a	1170b	1750b	920a	1410a	1170b
Dwarf	1430b	410b	1550b	710b	920b	1130b	1520b	570b	920b	1130b
Tall	2480a	1450a	1990a	1260a	1960a	1630a	2330a	1370a	1960a	1630a
Density										
High	2090a	940a	1780a	900b	1470a	1340a	1960a	950a	1470a	1340b
Low	1900a	930a	1760a	1020a	1410a	1410a	1890a	990a	1410a	1410a

* Duncan's new multiple range test at 5% level.

Table 13: Average rainfall per day (mm. of water/day) from planting to heading.

Early planting 1985		Late Plant. 1985		Early plant. 1986		Late plant. 1986	
Early Inbreds	Late Inbreds	Early Inbreds	Late Inbreds	Early Inbreds	Late Inbreds	Early Inbreds	Late Inbreds
1.9	1.98	8.5	3.78	2.73	2.88	3.65	3.2*
Season Average** 6.26/79 = 0.08		Season Average** 9.96/66 = 0.15		Season Average** 8.61/75 = 0.12		Season Average** 8.18/64 = 0.13	

* Note : The late heading (T223B & 23DB) in the late planting in 1985 occured in the middle of a 13 day period of drought. A 0.25 mm rain on September 20 and a 0.50 mm rain on September 21 after 6 dry days initiated flowering of the late inbreds in late planting in 1986 and then followed 12 dry days before it rained again. In both cases it was necessary to water the field to avoid too much plant stress. The conditions were wetter in the other six flowering situations.
** : From planting to late inbreds'heading.

The YxI interaction was significant ($p < 0.03$) for all traits in both planting dates (Tables 5 and 6) except for head number per plot in early plantings (Table 5). This seems to indicate that at least some of the inbreds show a differential phenotypic response due to environment.

The IxD interaction (Tables 5 and 6) was only significant for plant height ($p = 0.0001$), 100-seed weight ($p = 0.03$) and yield ($p = 0.016$) in early plantings (Table 5) and for head number per plot ($p = 0.0001$) and total head seed weight ($p = 0.0006$) in late plantings (Table 6). The main effect showed the same tendency:

The inbred (I) effect was significant for 4 out of 8 traits in early plantings (Table 5) and for 6 out of 8 traits in late plantings (Table 6), the plant number per plot was not considered.

The density (D) effect was significant for 4 traits in early plantings and for only 2 traits in late plantings (Tables 5 and 6, respectively).

Three traits were dependent on plant population density (Tables 3 through 6):

(1) Days to 50% heading: Plants spaced 2.5 cm apart flowered earlier than plants spaced 17 cm apart ($p < 0.006$ for all analyses except for the late plantings across the years), probably because of higher competition in the high population density condition.

(2) Head number per plant: plants in low density produced more heads per plant or more tillers than plants in high density level ($p = 0.0001$ for all analyses), suggesting that tiller number in pearl millet could be controlled through plant spacing. The closeness between plants in high density conditions probably did not allow plants to produce as much tillers as they could otherwise.

(3) Total head seed weight: plants in low density conditions produced higher total head seed weight than plants in high density (more competitive conditions), ($p < 0.04$ for 7 out of 8 analyses). This shows that total head seed weight also could be manipulated through plant spacing.

The density effect (Tables 3 to 6) was significant in only 4 out of 8 analyses ($p = 0.005$) for head length. This is rather surprising because one would expect head length to follow the same pattern as total head seed weight.

The interaction between planting date or season (S), inbred (I), and plant population density (D), SxIxD interaction, (Tables 3 & 4), was not significant at $p = 0.05$ for head number per plot, total head seed weight, 100-seed weight, and yield in 1985 (Table 3) and for plant height, days to 50% heading, head number per plant and total head seed weight in 1986 (Table 4). When non-significant, the SxIxD interaction was used as an error term in F-tests for main effects and lower level interactions.

The SxI interaction (Tables 5 & 6) was significant for all traits ($p < 0.03$) except for yield ($p = 0.20$) in 1985 and significant for plant height ($p < 0.022$), days to 50% heading ($p = 0.0005$), head number per plot ($p < 0.048$), head length ($p < 0.03$), 100-seed weight ($p = 0.0001$) and yield ($p = 0.002$) in 1986.

Plant population density tended to buffer the season effects and the SxD interaction (Tables 3 & 4) was not significant for head length ($p = 0.89$), total head seed weight ($p = 0.06$) and yield ($p = 0.42$) in 1985 and for head number per plot ($p = 0.31$), head number per plant ($p = 0.66$), head length ($p = 0.41$), total head seed weight ($p = 0.90$), 100-seed weight ($p = 0.50$) and yield ($p = 0.17$) in 1986.

The IxD interaction (Tables 3 & 4) was significant ($p < 0.03$) for all traits in 1985 except for head number per plot ($p = 0.47$) and total head seed weight ($p = 0.64$), and in 1986 except for 100-seed weight ($p = 0.57$, Table 4).

The consistency of significant interactions between inbreds and plant population density (IxD), Tables 3 to 6, for the head number per plant, except for the combined analyses over years in late plantings, shows that the tillering ability of the inbreds is a trait that depends on the plant population density to express itself. Whenever the distance between two plants exceeded a certain limit, the plants tended to fill in the blank space with tillers. If the distance was smaller than the limit, very few or no

tillers were produced. Early maturing inbreds (Tift 23BE and Tift 23DBE) produced 50% more tillers than late inbreds (T23B and T23DB), Table 9 . Dwarf inbreds (T23DBE and T23DB) produced 8% more tillers than tall inbreds (T23B and T23BE), Table 9. The low plant population density produced 136% more tillers than the high plant population density, Table 9. Early plantings produced 41% more tillers than late plantings, Table 10 and plants had 34% more tillers in 1985 than in 1986, Table 10.

The head length varied from a mean of 16.4 cm for Tift 23DB in the 1986 late planting to a mean value of 21.90 cm for Tift 23B in the 1985 early planting . The means were statistically different but the variation (2 to 5% between inbreds) was not agronomically important (Tables 9 & 10).

The late maturing inbreds produced 14% more total head seed weight on the average than early inbreds. The dwarf inbreds produced 54% more total head seed weight than the tall inbreds. For the same trait, plants in low density conditions were 19% higher than those in high density level. The trait (total head seed weight) was 103% higher in early than in late planting, and 11% higher in 1986 than in 1985 (Tables 9 & 10).

The hundred seed weight was not dependent on plant population density on the average, but it was 20% higher in early inbreds than in late inbreds and 20% higher in dwarf than in tall inbreds. The trait was 21% higher in 1986

than in 1985 and only 2 % higher in the late plantings than in early plantings (Tables 9 & 10).

Yield, like 100-seed weight, was independent of the plant population density and 20% higher for early lines than for late maturing ones. But, unlike 100-seed weight, yield was 70% higher for tall inbreds versus dwarfs, 99% higher in the early plantings than in late plantings and 5% higher in 1985 than in 1986 (Tables 9, 10, and 12).

Disease effects on plants

The inbred (I) and plant population density (D) interaction was significant in late planting in 1986 ($p = 0.022$, Appendix Table 37) but not in 1985 (Table 7) for pyricularia rating . For the same trait, plant population density was significant ($p < 0.013$) in both late plantings and the inbred effect was significant in late planting 1985 ($p = 0.0001$) but not in late planting 1986. Only the plant population density effect was significant ($p = 0.0185$) for the only rust rating taken in the 1985 late planting (Table 7). In the 1986 late planting it was more difficult to separate rust effect from pyricularia effect and only a general leaf spot disease rating was taken in late September. The IxD interaction was not significant for leaf spot disease rating in both plantings in 1986 (Table 8). The inbred effect and plant density effect were significant ($p = 0.0001$ and $p < 0.025$ respectively) for leaf spot disease in both plantings

in 1986 (Table 8). Data in this table also showed that the season (S) and inbred (I) interaction and the DxS interaction were not significant.

On the average, early inbreds were more affected by pyricularia and leaf spot diseases than late inbreds but plant height was not affected by the diseases. Rust did not affect inbreds differently (Table 11, top). Plants in high population density were always more affected by all the diseases than plants in low population density (Table 11, bottom). This was probably due to the fact that high population density provided more competitive and more humid conditions favorable to disease development than did low plant density.

A2. Discussion

This study involved four near-isogenic inbreds, that is, inbreds that differ only by a few genes, namely genes affecting early and late maturity and those controlling the plant height (dwarf or tall). Another factor under study was plant population density (high density, 444 000 plants /ha, and low density, 66 000 plants /ha). The results showed that maturity, plant height, and plant spacing, significantly affected the head number per plant, the total head seed weight, 100-seed weight and the yield, even though most of these traits are quantitative and may be affected by environmental conditions especially the water supply that varied during the study (Table 13). But, by using a split

plot design it was possible to detect these environmental effects and remove them from the main effects.

In general, the e_1 gene, controlling early maturity in Tift 23BE and 23DBE, caused plants to flower 25, 18, 26, and 14 days earlier ($p<0.0001$) than plants without the gene (Tift 23B and 23DB) in early and late plantings in 1985 and 1986, respectively. This e_1 gene caused plants to produce 50% more tillers, be 38% shorter, produce 14% less total head seed weight, seed 20% heavier and yield 20% higher than the plants without the gene. The d_2 gene caused Tift 23DB and 23DBE to be 28.7, 61.6, 54.3, and 64.1 cm shorter ($p<0.0001$) than Tift 23B and 23BE in early and late plantings in 1985 and 1986, respectively, and also caused the dwarfs to produce 8% more tillers, 54% more total head seed weight, seeds 20% heavier but yield 70% lower than the tall inbreds.

The high plant population density caused plants to flower 4, 1, 4, and 2 days earlier in early and late plantings in 1985 and 1986, respectively, than the low plant population density . Plants also were 6 cm, 16 cm and 8 cm taller in early planting in 1985 and early and late planting in 1986, respectively. The low plant population density caused plants to produce 136% more tillers, and 19% more total head seed weight than the high population density. Early plantings (57 and 35 days earlier in 1985 and 1986, respectively) caused the plants to flower 7 days later, be 39 cm shorter and produce 42% more tillers on average than late

plantings. Plants also produced 103% more total head seed weight and yielded 99% more in early than in late plantings.

Table 14. Differential effect of intrinsic and induced maturity over both years.

Factor*	Tiller number	Plant height	Head seed weight	Seed size	Yield
Intinsic maturity **					
Early Inb.	50% +	38% shorter	-	20% +	20% +
Late Inb.	-	taller	14% +	-	-
Induced maturity**					
Early Plan.	42% +	40% shorter	103% +	same	99% +
Late Plan.	-	taller	-	same	-

* The late planting was on the average 7 days earlier than the early planting. Early inbreds were about 19 days earlier than late inbreds. Inb. = Inbreds ; Plan. = Planting.
** Each value is the difference between inbreds or planting dates, expressed as the % of the smaller value.

Data in Table 14 above showed that intrinsic late maturity, due to the absence of the e_1 gene, caused 19 days later inbreds to produce 14% more total head seed weight than early inbreds. Therefore, 7 days induced late maturity in early plantings cannot account for the 103% increase in total head seed weight as compared to late plantings. For tiller number, plant height, and yield the effects of early plantings (with their late maturity inducing ability) were opposed to the effects of the intrinsic late maturity in inbreds. Consequently, the causes of the different effects of early and late plantings on plant characteristics must be found elsewhere than in induced differential maturity. The various environmental conditions surrounding plants during each growth season are probably the main causes of the differential responses in early and late plantings. Data in Table 13, for example, showed a net difference in daily rainfall between early and late seasons separated by 56 days in 1985. Among these environmental factors, diseases which manifested themselves by their absence in early plantings, their presence in late plantings, and their severity, may have contributed more to the differences between seasons than other external influences (temperature, moisture etc) which only varied quantitatively from one season to the other. But this seemed not to be the case in this study (see p.68). Data in Table 11 showed that early maturing inbreds averaged 36% higher disease ratings than late inbreds and that plants in

high population density had 31% higher disease ratings than plants in low density conditions. No significant differences were found between dwarf and tall inbreds in their responses to diseases.

To determine the disease impact on plant growth and production, the performances of early and late inbreds were compared in early planting (disease-free condition) and late planting (diseased condition), respectively, (Table 15). Also, high and low density plants were compared in disease-free and diseased conditions, respectively, (Table 16).

Table 15. Disease effect on inbreds over both years of study.

	Tiller number	Plant height	Head seed weight	Seed size	Yield
Disease free Early Plantings**					
Inbreds					
Early	64% +	-	-	21% +	20% +
Late	-	38% +	15% +	-	-
Diseased Late Plantings**					
Inbreds					
Early	38% +	-	-	38% +	11% +
Late	-	34% +	14% +	-	-

*: Early inbreds had 36% higher disease ratings than late late inbreds .

**: Each value is the difference between inbreds expressed as the % of the smaller value.

Data in Table 15 compared early and late inbreds and showed that from disease-free to diseased conditions, the advantage of higher disease rating early inbreds over late inbreds in tiller number per plant and yield, was decreased by 31% and 9%, respectively, while their advantage in seed size was increased by 17%. On the other hand, the advantage of lower disease rating late inbreds over early inbreds in plant height was decreased by 4%. The total head seed weight was not affected by diseases.

Data in Table 16 showed that from disease-free (early planting) to diseased (late planting) conditions, the advantage of lower disease rating plants (low density) over higher disease rating plants (high density) in producing tillers was increased by 142%, while their advantage in seed size was decreased by 9% (from +5% to -4%). The advantage of high density plants was decraesed by 9% (from 12 to 3%) for plant height and also by 9% (from +4% to -5%) for yield. Here again, the total head seed weight was not affected by the diseases.

So, intrinsic susceptibility to disease (early inbreds) and induced susceptibility (high population density) produced similar effects on tillering ability, seed size and yield in diseased conditions but opposite effects on plant height: disease susceptibility reduced yield and tillers number per plant, but increased seed size in both early inbreds and high

density plants. Disease susceptibility tended to increase plant height in inbreds and to decrease plant height in high population density conditions, probably due to the competition effect.

Table 16. Disease effect on plant population density over both years of study.

	Tiller number	Plant height	Head seed weight	Seed size	Yield
Disease free Early Plantings**					
High Density	-	12% +	-	-	4% +
Low Density	100% +	-	21% +	5% +	-
Diseased Late Plantings**					
High Density	-	3% +	-	4% +	-
Low Density	242% +	-	21% +	-	5%

*: Plants in high population density were 31% more susceptible to diseases than in low density conditions.
**: Each value is the difference between levels of density expressed as the % of the smaller value.

Then, the advantage of disease-free early planting over disease prone late planting in producing tillers and yield (Table 14) was due (at least partly) to the disease impact on late planting. The comparison of the percentages from Table 14 to Tables 15 and 16 showed that the early planting had some advantages of its own over late planting that could not be attributed to disease effect on late planting. In particular, the yield increase in early planting was about 10 times more important than the disease effect, and the 103% increase in total head seed weight was totally independent of disease effect. The differences in weather conditions (temperature, relative humidity, precipitation etc.) account more for the differences registered in plant characteristics from early to late plantings than the diseases studied (rust and pyricularia). Nonetheless, early planting did decrease (early planting 1986) or totally escape (early planting 1985) the yield loss due to diseases. The best conditions to study the plants' ability to escape yield lost due to diseases would be the use of resistant and susceptible cultivars and planting early enough (such as in 1985) to have an early growing season free of disease pressure.

B) PLANT BREEDING / GENETIC STUDIES

B1. Results

Data in Tables 17, 18, and 19, on the following pages reported the heterosis values for flowering (maturity), head length, and hundred seed weight (seed size), respectively, in 1987, based on original data.

The mid-parent heterosis for flowering, (Table 17,), ranged from -15% (cross 15) to 9% (cross 7) with an average of -3%, showing that, on the average, the hybrid was a little earlier than the mid-parent. The high-parent heterosis had negative values in all 3 crosses studied with an average of -19% meaning that the hybrid was always earlier than the late parent.

Table 17 : Heterosis for Days to flowering in 1987.

Cross	Mid-parent heterosis	High-parent heterosis	Level of dominance
(3) Late Gero x Early Walor	-3%	-17%	Early > Late
(7) Early T18BE x Late T23B	9%	-12%	Late > Early
(15) Early Togo x Late Gero	-15%	-29%	Early > Late

Jinks' heterosis was not estimated for maturity because in no case was the hybrid earlier than the early parent.

Table 18 : Heterosis for head length in 1987.

Cross	Mid-parent heterosis	High-parent heterosis	Level of dominance
LH Gero x SH T23DBE	-5%	-33%	short head > long head
(3) LH Gero x SH Walor	68%	24% $9^{\hat{d}}$	overdominance over long head
(4) LH Gero x SH Walor	22%	5% $2^{\hat{d}}$	Overdominance over long head
(7) LH T18BE x SH T23B	7%	-25%	long head > short head

(1)

LH = long head ; SH = short head

$\hat{d}$ = Jinks' heterosis value

For head length, the mid-parent heterosis ranged from -5% (Table 18, cross 1) to 68% (cross 4) with an average of 23%. This indicated that the hybrid had a longer head than the mid-parent in general. The high-parent heterosis ranged from -33% to 24% with an average of -7%, and therefore, the hybrid on the average had a shorter head than the high-parent.

Jinks' heterosis for head length (Table 18) was determined for crosses 3 and 4 with 9 and 2 values, respectively.

Seed size or hundred seed weight (Table 19) showed higher mid-parent heterosis mean than did maturity and head length (Tables 17, and 18, respectively).

Cross 9 involving large-seeded Togo and large-seeded Walor as parents showed overdominance.

Table 19 : Heterosis for hundred seed weight in 1987

Cross	Mid-parent heterosis	High-parent hterosis	Level of dominance
(9) LS Togo x LS Walor	22%	6% 0.1[a]	Walor >> Togo
(13) LS Togo x SS T23DBE	30%	-28%	LS > SS

LS = large seed ; MS = mid size seed ; SS = small seed.
[a] = Jinks' heterosis value; >> = overdominance.

The seed size mean mid-parent heterosis for crosses 9 and 13 was 26%. The hybrid had larger seeds than the mid-parent. The mean high-parent heterosis was -11%. This indicated that the hybrid had smaller seeds than the high-parent in both crosses.

Jinks' heterosis for seed size was 0.1 in cross 9 where overdominance was detected.

Broad sense heritability (H^2) values for each of the selected crosses are summarized in Table 20. For maturity, the values ranged from 29% to 98% with an overall mean of 65%. The range was 39% to 81% with a general mean of 58% for headlength, and it was 52% to 93% with a mean of 74% for 100-seed weight or seed size. For each trait, H^2 was also computed using the mean variances of the families across all the crosses studied, and the values (listed as 'Total', in Table 20), were 51%, 60%, and 81% for maturity, headlength, and seed size,respectively.

Table 20 :Broad sense heritability for the traits (%)

Cross	n*	Maturity Range	Maturity Mean	Headlength Range	Headlength Mean	100-seed weight Range	100-seed weight Mean
(1)	6	-	-	64 - 81	73	-	-
(3)	6/4	29 - 64	43	50 - 71	59	-	-
(4)	2	-	-	39 - 51	45	-	-
(7)	5	98 - 98	98	46 - 61	55	-	-
(9)	5	-	-	-	-	52 - 64	61
(13)	6	-	-	-	-	75 - 93	87
(15)	6	47 - 66	55	-	-	-	-
Mean	17/15/11		65		58		74
Total	17/15/11		51**		60**		81**

* : n is the number of F_2s analysed per cross; for cross (3), n = 6 for maturity, and n = 4 for headlength.
** : Computed from the means of variances.

Frequency distributions were plotted to show the variation of the traits (Figures 1, 2, and 3). Cross 7 between the inbred lines late T23B and early T18BE, showed two classes for maturity (Figure 1-B), confirming that the trait is controlled by a single gene with late being dominant over early (Burton, 1981, and Hanna and Burton, 1985a) in these inbreds. However, even in these inbreds maturity seemed to be affected by environmental effects because the observed two classes in Figure 1-B were not distinct.

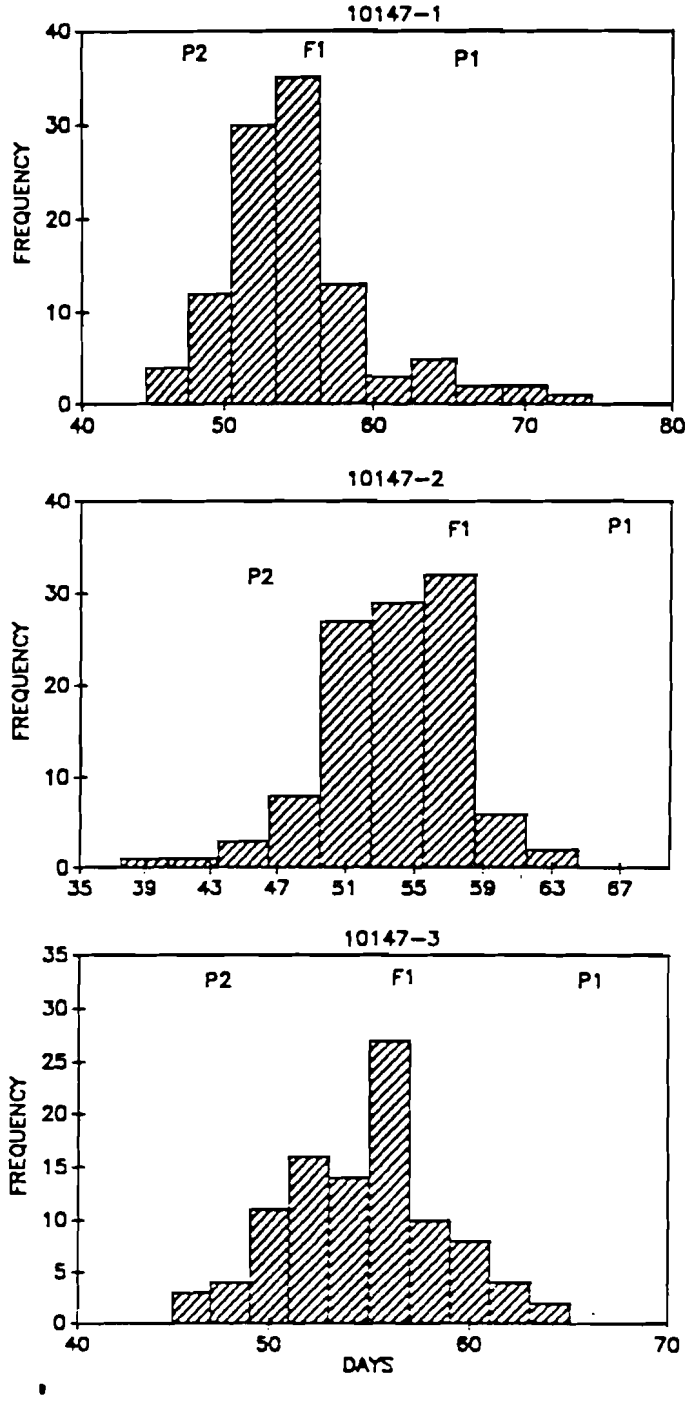

Figure 1A: Cross 3: Maturity (Days)

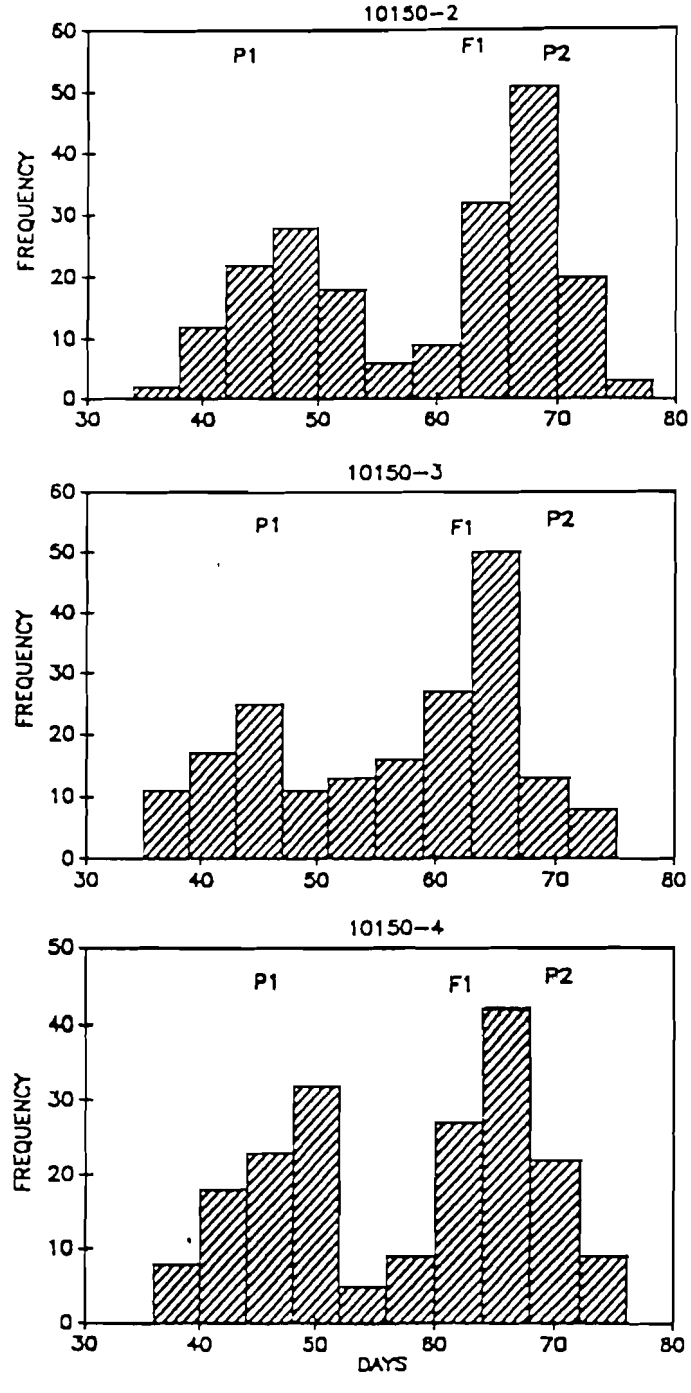

Figure 1B: Cross 7: Maturity (Days)

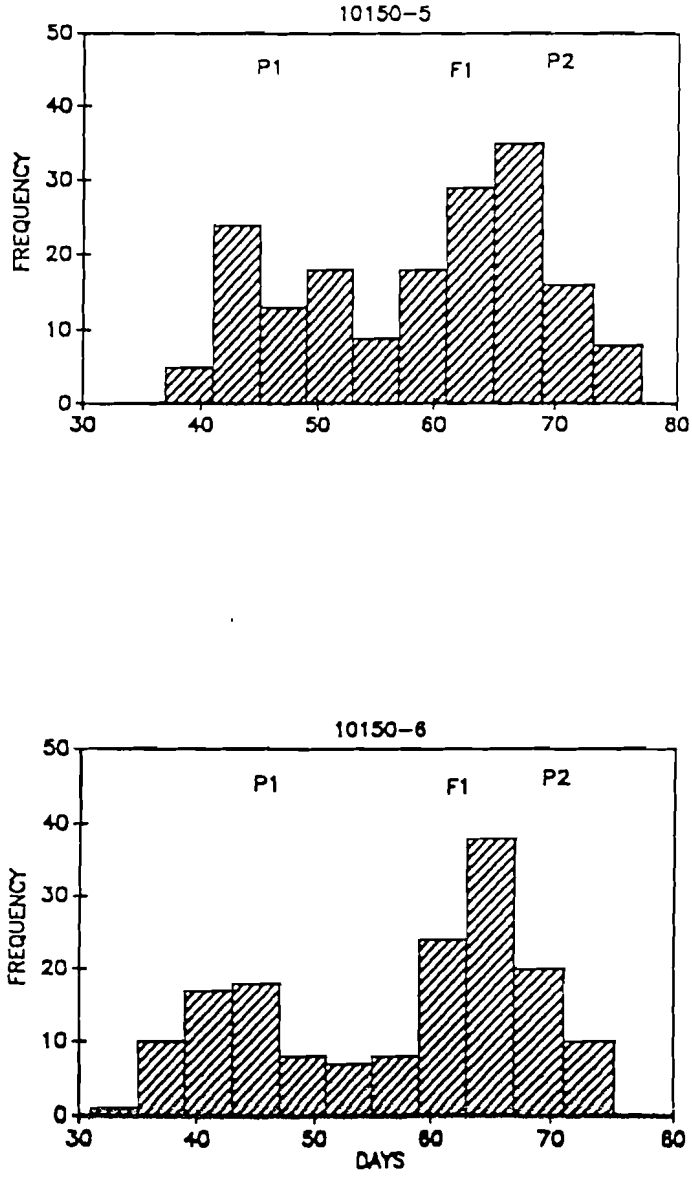

Figure 1B: Cross 7: Maturity (Days)

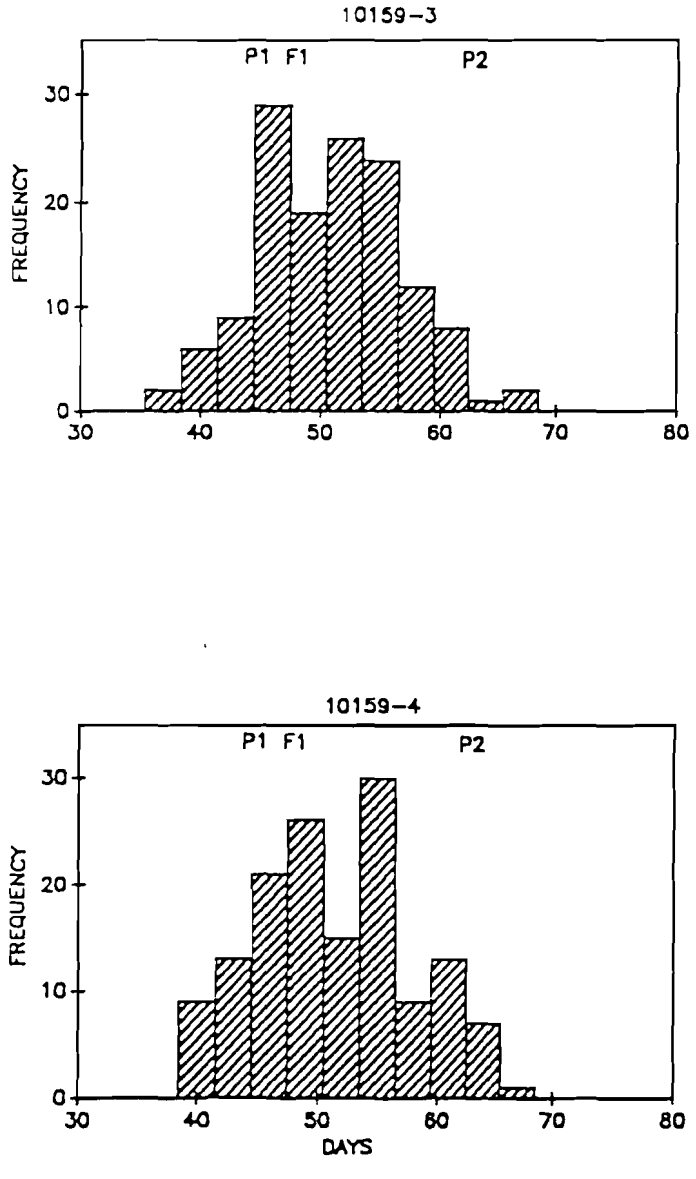

Figure 1C: Cross 15: Maturity (Days)

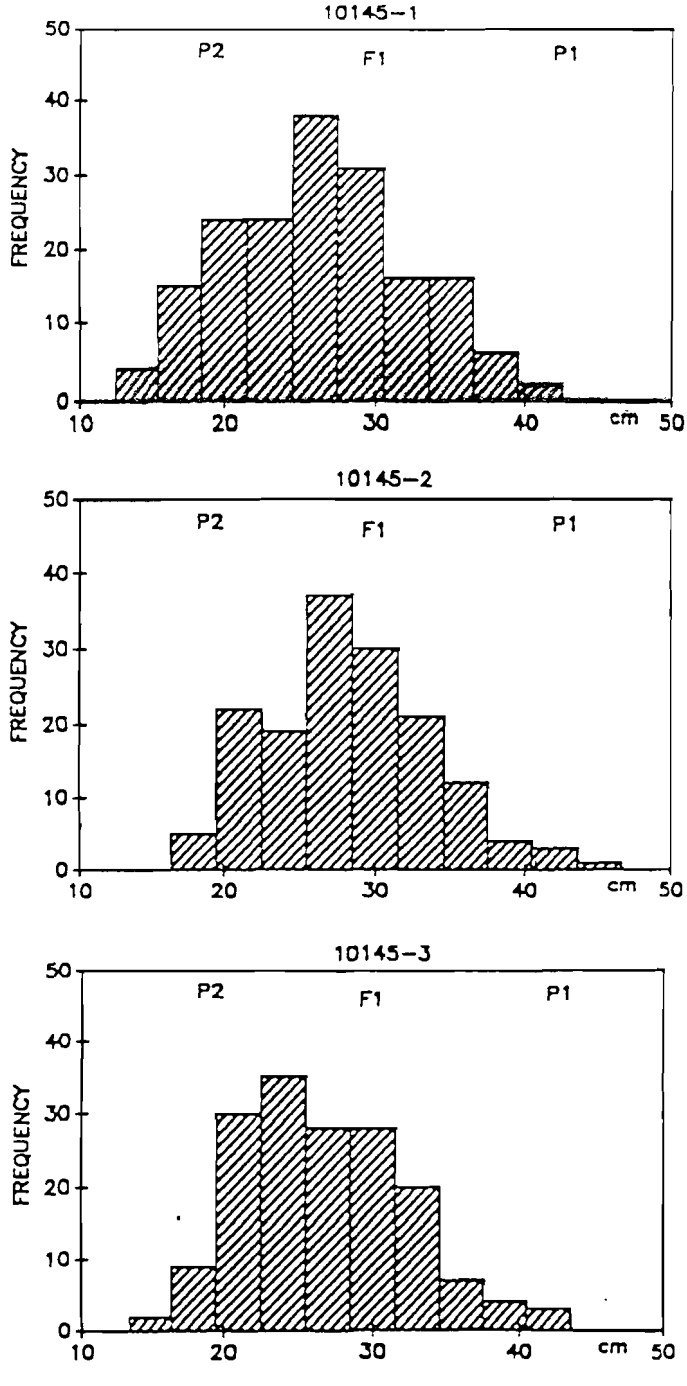

Figure 2A: Cross 1: Head Length (cm)

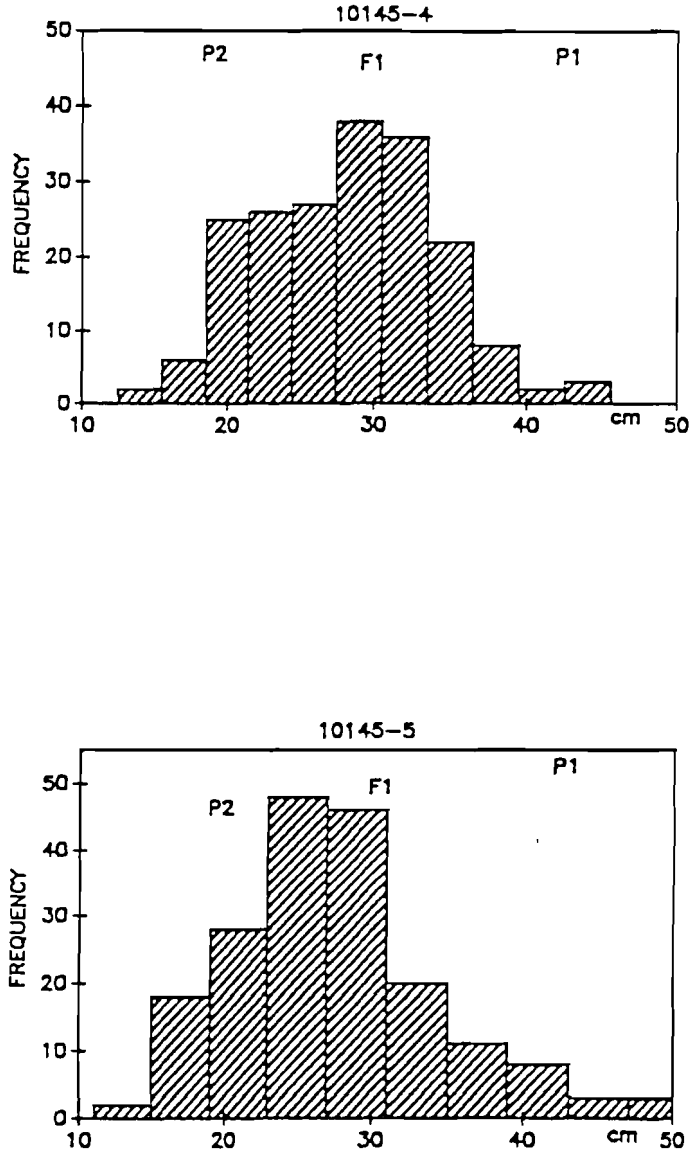

Figure 2A: Cross 1: Head Length (cm)

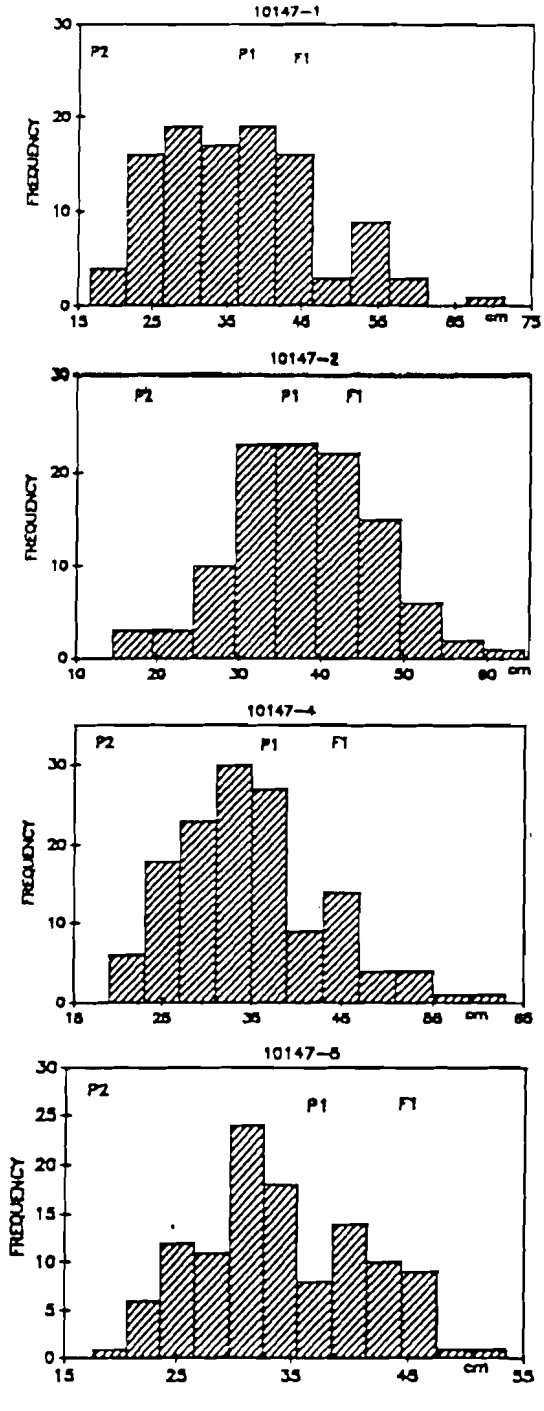

Figure 2B: Cross 3: Head Length (cm)

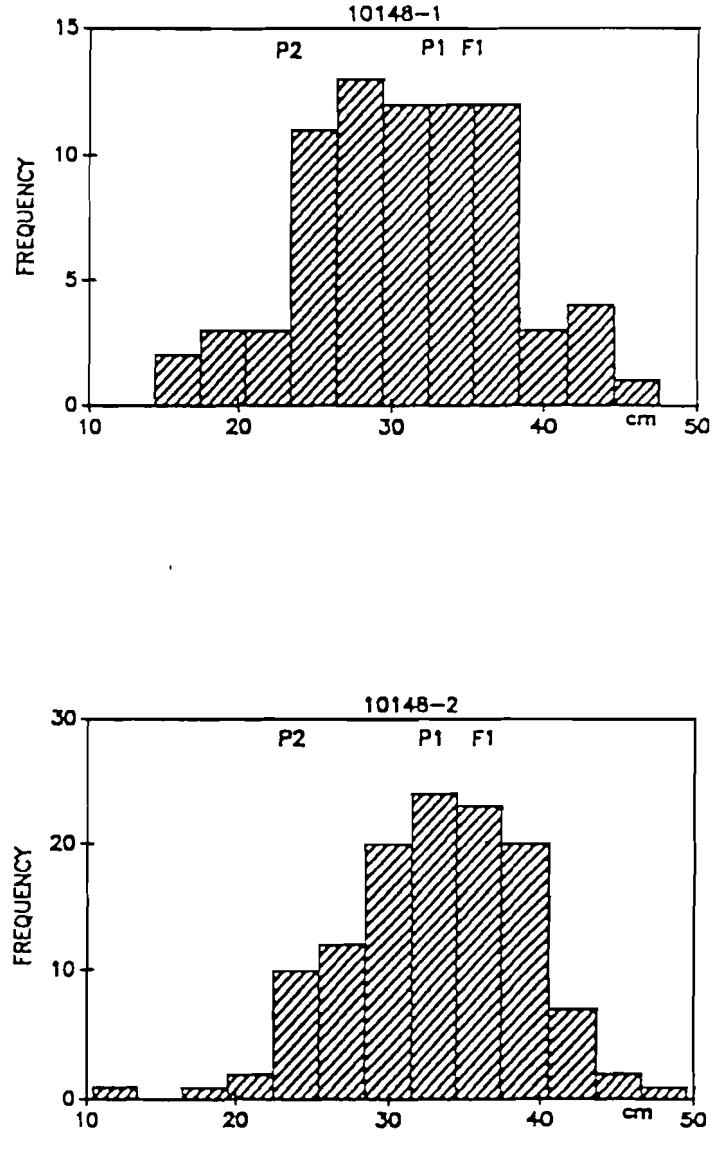

Figure 2C: Cross 4: Head Length (cm)

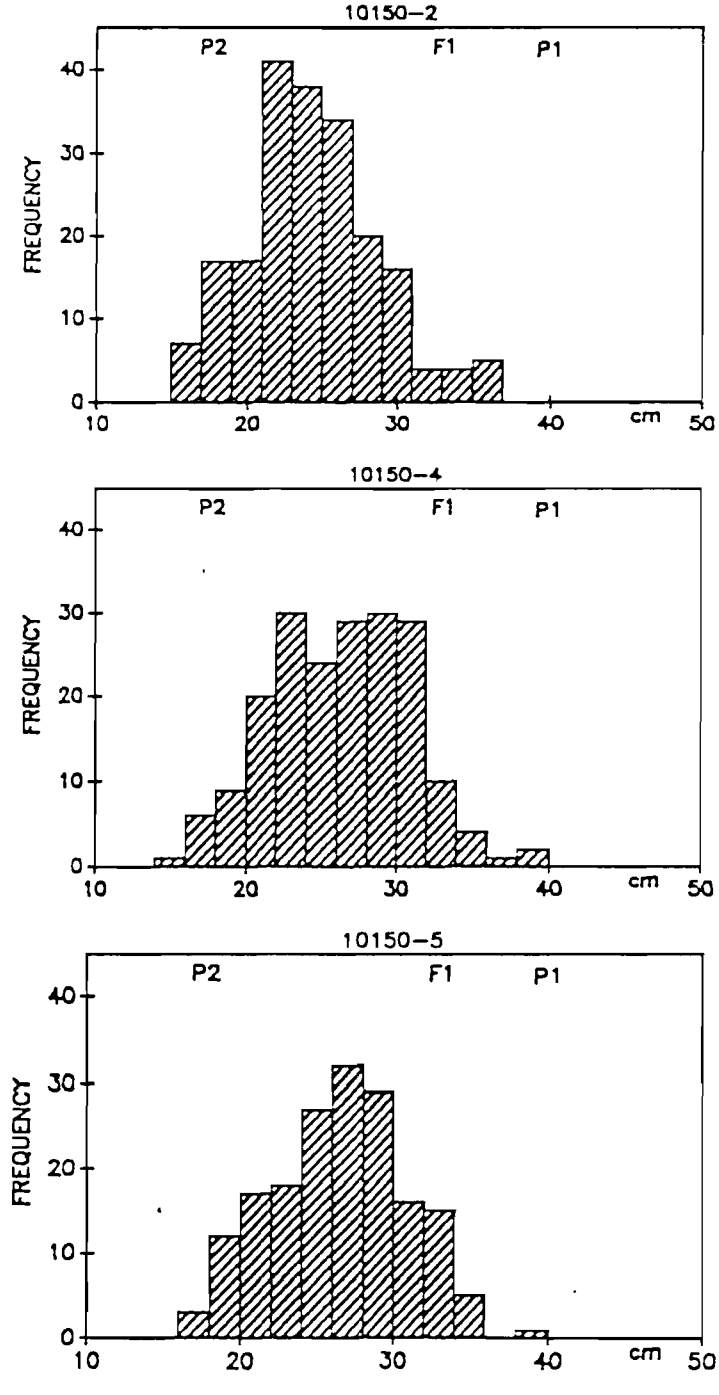

Figure 2D: Cross 7: Head Length (cm)

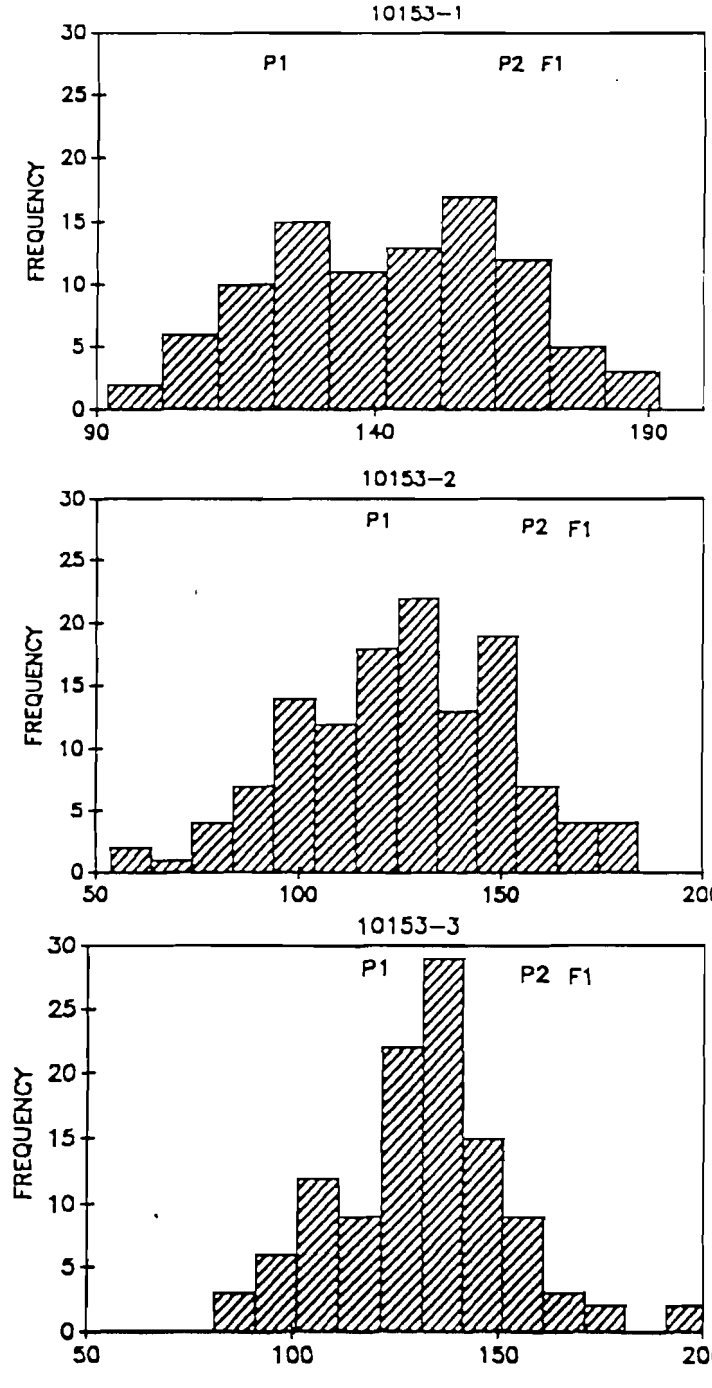

Figure 3A: Cross 9: Seed Size (x 10^{-2} /100 seeds)

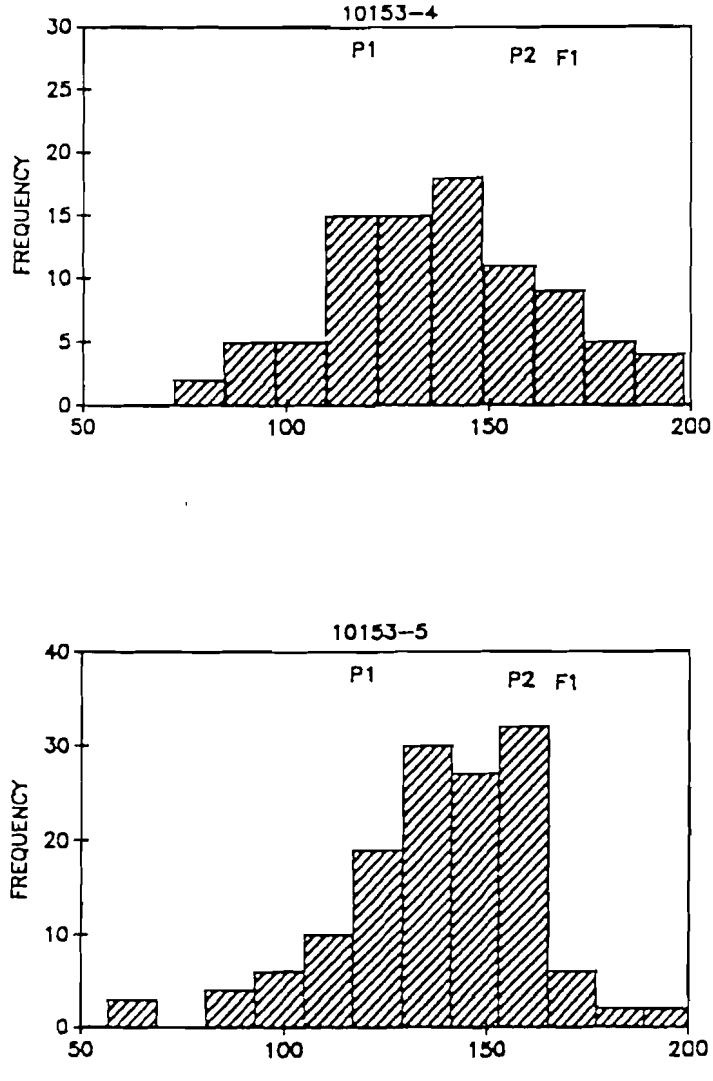

Figure 3A: Cross 9: Seed Size (x 10^{-2} /100 seeds)

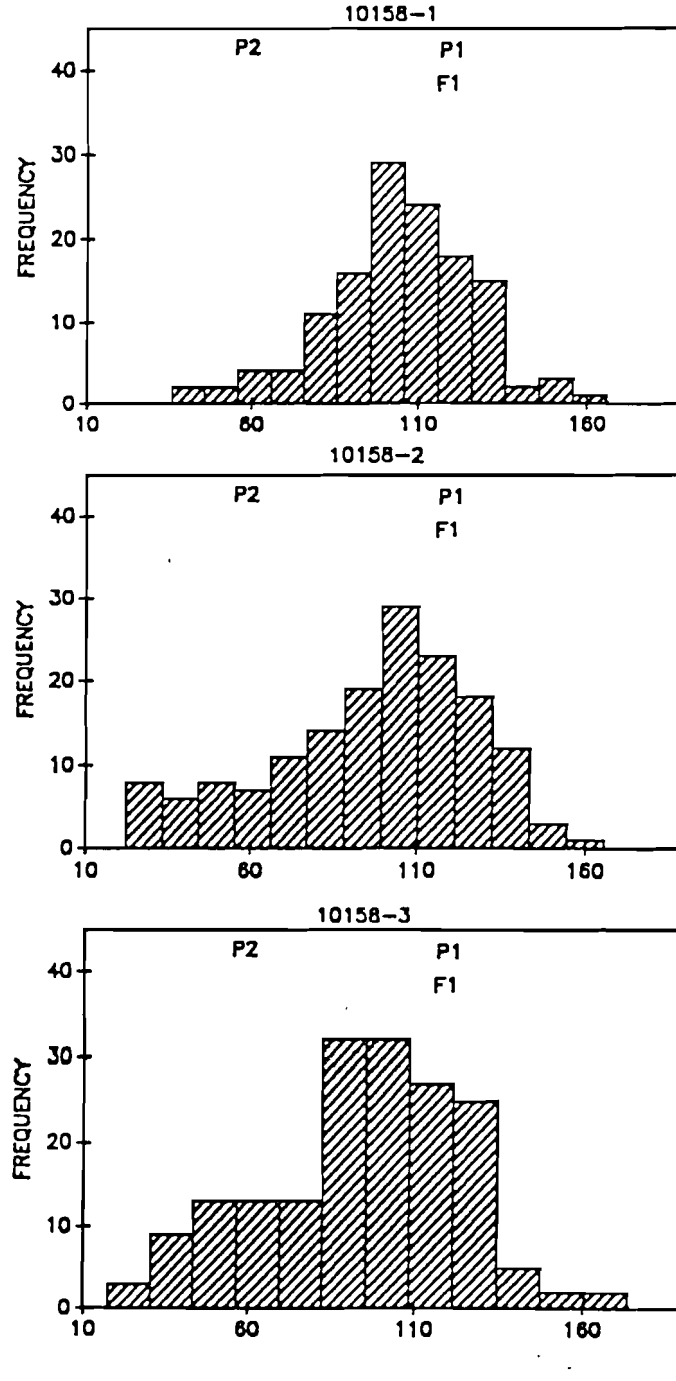

Figure 3B: Cross 13: Seed Size (x 10^{-2} /100 seeds)

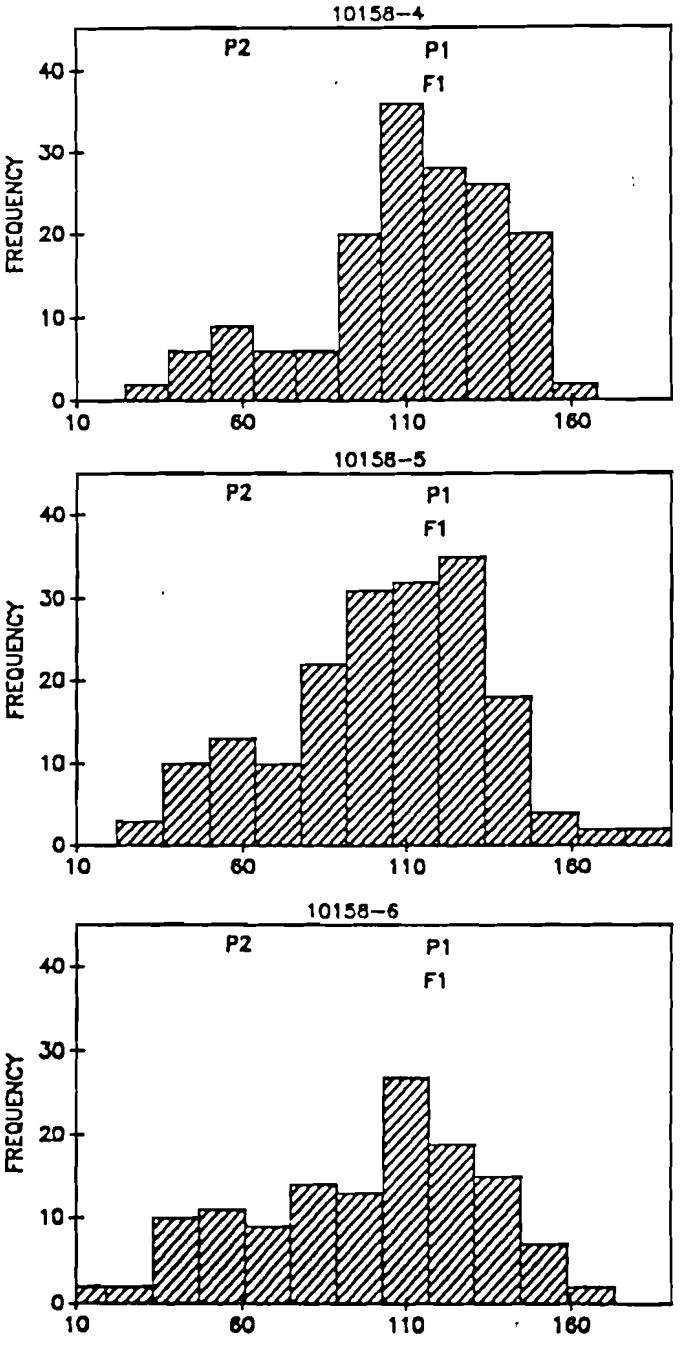

Figure 3B: Cross 13: Seed Size (x 10^{-2} /100 seeds)

The frequency distribution of maturity revealed continuous variation in crosses 3 and 15. Headlength and seed size showed a continuous variation with a tendency for skew to larger seed size (Figures 2, and 3).

Table 21: Gene number per trait in 1987 as estimated through direct calculation.

Days to flowering gene number				Head length gene number				Hundred seed weight gene number			
cross	range	mean		cross	range	mean		cross	range	mean	
3 - 25	12		(1)	3 - 10	6		(9)	1	1		(3)
(7)	1	1		(3)	2 - 11	6		(13)	1 - 2	1	
(15)	4 - 41	14		(4)	1 - 5	2		Total	1 - 2	1	
Total	3 - 41	9		(7)	6 - 11	8					
				Total	1 - 11	6					

The data on the determination of the number of loci controlling each trait were summarized in Table 21. The number of loci was calculated for each single F2 population of a cross. All F2s of a cross were also pooled. The number of F2s in each cross varied from 5 to 6 giving a range of 6 to 7 values including the pooled F2s for the 1987 data.

Single F2 estimations of the number of genes controlling maturity ranged from 3 to 25 and 4 to 41 for crosses between late Gero and early Walor, and between early Togo and late Gero, respectively.

Seed size appeared to be controlled by fewer genes (1 to 2) than maturity and head length, but there were only 2 crosses studied for seed size compared to 3 & 4 for the other traits, respectively.

Determination of the number of genes per trait through the use of the Chi-square test resulted in ratios in Tables 22 (1987) and 23 (1986). These ratios are based on the assumption that epistasis is operating to express each trait. When at least two loci contribute in the expression of one trait, there must necessarily be an interaction between the two or more loci. The interaction can be additive, (each allele in every locus adding a constant specific value to the expression of the trait), or epistatic (one or more alleles from one locus interfering with the expressions of the allele(s) of another locus). There may also be dominance between alleles at any locus.

When the additive interaction is predominant the trait is continuous and no distinctive classes can be observed in the F_2 distribution. When epistatic gene action is operating in a poly-factorial trait with independent loci, then the distinction between classes can be made according to the formulas given by Stansfield, (1983, pp. 53 & 54), and the chi-square test be applied.

When true dominance operates, it will be in association with either additive gene action or epistasis, or both, but never alone to express a quantitative trait.

In reality, a given quantitative trait may depend simultaneously on additive, dominant and epistatic gene actions.

Also, the expression of a quantitative trait may be influenced by environmental effects and this makes it more difficult to determine the genetics of the trait, for when environment effects are in play, the variation is continuous whether the trait is controlled by one or more genes.

Maturity in pearl millet is controlled mainly by dominant and non-additive gene actions (Burton, 1951; Sagar et al., 1985) while both additive and non-additive components control flowering and head length (Upadhyay and Murty, 1971). Grain size was reported to be a quantitative trait mainly under the control of additive and additive by dominant gene actions and greatly influenced by environmental factors (Phul and Atwal, 1969; Hash, 1986).

The chi-square ratios reported here are only an approximation of the extreme case where epistasis only is operating. For two loci controlling a trait, epistatic gene action can yield ratios like 15:1, 13:3, 12:3:1, 9:7, 9:6:1, and 9:3:4, in an F2 in the case of complete dominance at each independent locus. With co-dominance at one or two loci, and assuming that a heterozygote can have an epistatic effect of its own, ratios such as 7:1, 11:5, and 1:1 are also possible in an F2 distribution, (adapted from Stansfield, 1983).

Table 22: Chi-square tests for Maturity in 1987

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values		Number of genes Direct calculation	
Cross(3) F2	Early	Late	Ratio1 63:1	Ratio2 255:1	X^2	N
10147 - 1	97	10	42.1**	220.5**	?	3
10147 - 2	107	1	0.29	0.80	3; 4	8
10147 - 3	94	5	0.24	55.3**	3	6
10147 - 4	137	0	2.18	0.54	3; 4	25
10147 - 5	115	0	1.83	0.45	3; 4	25
10147 - 6	120	1	0.43	0.59	3; 4	12
Pooled	670	17	3.72	77.0**	3	8
5 D.F. Homogeneity X^2 for 63:1			43.4**			
5 D.F. Homogeneity X^2 for 255:1			201.2**			

Cross(7) F2	Late	Early	Ratio1 3:1	Ratio2 13:3	Ratio3 54:10	X^2	N
10150 - 2	180	23	20.2**	7.3**	2.84	3	1
10150 - 3	146	45	0.21	2.90	9.1**	1; 2	1
10150 - 4	158	37	3.78	0.01	1.66	1; 2; 3	1
10150 - 5	146	29	6.6*	0.55	0.12	2; 3	1
10150 - 6	118	43	0.25	6.7**	15.0**	1	1
Pooled	748	177	17.0**	0.09	8.7**	2	1
4 D.F. Homogeneity X^2 for 3:1			14.1**				
4 D.F. Homogeneity X^2 for 13:3			17.4**				
4 D.F. Homogeneity X^2 for 54:10			20.1**				

*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Maturity in 1987 (End)

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values			Number of genes Direct calculation X^2	
Cross(7)	Late	Early	Ratio1	Ratio2	Ratio3	X^2	
BC(1)			3:1	13:3	54:10		
10166 - 1	124	35	0.76	1.11	4.9*	2; 3	
10166 - 2	165	21	18.7**	6.8**	2.65	?	
10166 - 3	69	14	2.93	1.93	0.10	2; 3	
Pooled	358	70	17.0**	1.61	0.17	?	
2 D.F. Homogeneity X^2 for 3:1					5.3ns		
2 D.F. Homogeneity X^2 for 13:3					8.2*		
2 D.F. Homogeneity X^2 for 54:10					7.5*		
Cross(15) F2	Early	Late	Ratio1 7:1	Ratio2 54:10	Ratio3 225:31	X^2	N
10159 - 1	146	19	0.15	2.11	0.06	2; 3; 4	14
10159 - 2	145	23	0.22	0.48	0.40	2; 3; 4	10
10159 - 3	127	11	2.59	6.1*	2.22	2; 4	7
10159 - 4	123	21	0.57	0.12	0.83	2; 3; 4	4
10159 - 5	174	2	20.8**	28.0**	20.0**	?	41
10159 - 6	139	11	3.66	7.8**	3.22	2; 4	?
Pooled	854	87	9.1**	29.1**	7.3**	?	6
5 D.F. Homogeneity X^2 for 7:1					18.9**		
5 D.F. Homogeneity X^2 for 54:10					15.6*		
5 D.F. Homogeneity X^2 for 225:31					19.4**		

*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Headlength in 1987

Cross(1) F2	Number of Plants SH	LH	Ratios with non-significant (p>0.05) Chi-square Values Ratio 1 63:1	Ratio 2 243:13	Number of genes Direct calculation X^2	N
10145 - 1	174	2	0.21	5.7*	3	4
10145 - 2	148	6	5.5*	0.45	4	7
10145 - 3	161	5	2.27	1.47	3; 4	6
10145 - 4	190	5	1.27	2.56	3; 4	5
10145 - 5	173	14	42.7**	2.25	4	3
10145 - 6	143	5	3.17	0.89	3; 4	10
Pooled	989	37	27.9**	4.6*	?	5
5 D.F. Homogeneity X^2 for 63:1				27.2**		
5 D.F. Homogeneity X^2 for 243:13				8.7ns		
Cross(1)	SH	LH	Ratio 1	Ratio 2	X^2	
BC(1)			7:1	13:3		
10162 - 1	88	7	2.29	8.1**	3	
10162 - 2	92	27	11.3**	1.21	?	
Pooled	180	34	2.25	1.15	3	
1 D.F. Homogeneity X^2 for 7:1				11.3**		
1 D.F. Homogeneity X^2 for 13:3				8.1**		

LH = Longhead SH = Shorthead
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values		Number of genes Direct calculation X^2	
Cross(3) F2	LH	SH	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10147 - 1	106	1	0.27	0.81	3; 4	2
10147 - 2	107	1	0.29	0.80	3; 4	4
10147 - 3	99	0	1.57	0.39	3; 4	9
10147 - 4	137	0	2.18	0.54	3; 4	4
10147 - 5	114	1	0.36	0.68	3; 4	5
10147 - 6	121	0	1.92	0.48	3; 4	11
Pooled	684	3	5.7	0.04	4	4
5 D.F. Homogeneity X^2 for 63:1			0.9ns			
5 D.F. Homogeneity X^2 for 255:1			3.7ns			
Cross(3) BC(2)	LH	SH	Ratio 1 63:1		X^2	
10164 - 1	118	2	0.01		?	
10164 - 2	123	2	0.00		?	
10164 - 3	109	2	0.04		?	
10165 - 1	128	0	2.03		?	
10165 - 2	122	1	0.45		?	
10165 - 3	122	1	0.45		?	
Pooled	722	8	2.60		?	
5 D.F. Homogeneity X^2 for 63:1			0.38ns			

LH = Longhead SH = Shorthead
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values		Number of genes X^2 Direct calculation	
Cross(4) F2	LH	SH	Ratio 1 7:1	Ratio 2 55:9	X^2	N
10148 - 1	67	9	0.03	0.31	2; 3	1
10148 - 2	114	9	3.02	4.68	2; 3	1
10148 - 3	114	4	9.0**	11.1**	?	5
10148 - 4	98	12	0.26	0.91	2; 3	2
10148 - 5	103	22	2.97	1.30	2; 3	2
10148 - 6	110	27	6.58*	3.61	3	3
Pooled	606	83	0.13	2.32	2; 3	2
5 D.F. Homogeneity X^2 for 7:1			21.6**			
5 D.F. Homogeneity X^2 for 55:9			19.6**			
Cross(4) BC(2)	LH	SH	Ratio 1 63:1	Ratio 2 243:13	X^2	
10168 - 1	114	2	0.02	2.71	?	

LH = Longhead SH = Shorthead
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Headlength in 1987 (End)

Cross(7) F2	Number of Plants LH	SH	Ratios with non-significant (p>0.05) Chi-square Values Ratio1 15:1	Ratio2 63:1	Ratio3 243:13	Number of genes Direct calculation X^2	N
10150 - 2	179	24	10.8**	139.0**	19.2**	?	6
10150 - 3	194	0	12.9**	3.08	10.4**	3	11
10150 - 4	185	10	0.42	16.1**	0.01	2; 4	6
10150 - 5	166	9	0.37	14.6**	0.02	2; 4	6
10150 - 6	160	1	8.7**	0.93	6.6*	3	9
Pooled	884	44	3.61	61.0**	0.22	2; 4	9
4 D.F. Homogeneity X^2 for 15:1					29.6**		
4 D.F. Homogeneity X^2 for 63:1					112.7**		
4 D.F. Homogeneity X^2 for 243:13					34.0**		
Cross(7) BC(2)	LH	SH	Ratio1 3:1	Ratio2 7:1	Ratio3 55:9	X^2	
10167 - 1	154	40	2.00	11.7**	6.9**	2; 3	
10167 - 2	139	20	13.1**	0.01	0.29	3	
10167 - 3	110	10	17.8**	1.90	3.26	3	
10167 - 4	130	1	41.0**	16.5*8	19.2**	?	
Pooled	533	71	56.5**	0.31	2.66	3	
3 D.F. Homogeneity X^2 for 3:1					17.4**		
3 D.F. Homogeneity X^2 for 7:1					29.8**		
3 D.F. Homogeneity X^2 for 55:9					27.0**		

LH = Longhead SH = Shorthead
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 22: Chi-square tests for Seed Size in 1987

Cross(9) F2	Walor	Togo	Ratios with non-significant (p>0.05) Chi-square Values Ratio1 3:1	Ratio2 13:3	Ratio3 54:10	Number of genes Direct calculation X^2	N
10153 - 1	84	11	8.9**	3.21	1.18	2; 3	1
10153 - 2	87	40	2.86	13.4**	24.3**	1	1
10153 - 3	90	24	0.45	0.40	2.55	1; 2; 3	1
10153 - 4	72	18	1.20	0.09	1.31	1; 2; 3	1
10153 - 5	123	18	11.3**	3.31	0.87	2; 3	1
Pooled	456	111	8.9**	0.25	6.7**	2	1
4 D.F. Homogeneity X^2 for 3:1 15.8**							
4 D.F. Homogeneity X^2 for 13:3 20.3**							
4 D.F. Homogeneity X^2 for 54:10 23.5**							

Cross(13) F2	LS	SS	Ratio 1 7:1	Ratio 2 15:1	X^2	N
10158 - 1	127	4	10.7**	2.28	2	2
10158 - 2	140	19	0.04	9.8**	2	1
10158 - 3	158	18	0.83	4.8*	2	1
10158 - 4	153	8	8.4**	0.45	2	1
10158 - 5	169	13	4.8*	0.25	2	1

Table 22: Chi-square tests for Seed Size in 1987 (End)

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values		Number of genes X^2 Direct calculation	
Cross(13) F2	LS	SS	Ratio 1 7:1	Ratio 2 15:1	X^2	N
10158 - 6	112	20	0.85	17.9**	2	1
Pooled	859	82	12.3**	9.8**	?	1
5 D.F. Homogeneity X^2 for 7:1				13.2*		
5 D.F. Homogeneity X^2 for 15:1				25.6**		
Cross(13) BC(2)	LS	SS	Ratio 1 3:1	Ratio 2 7:1	X^2	
10181 - 1	121	16	13.0**	0.08	3	
10181 - 2	5	4	1.81	8.4**	2; 3	
10181 - 3	128	22	8.6**	0.64	3	
Pooled	254	42	18.5**	0.77	3	
2 D.F. Homogeneity X^2 for 3:1				4.9ns		
2 D.F. Homogeneity X^2 for 7:1				8.4*		

LS = Large Seed ; SS = Small Seed .
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table 23: Chi-square tests for Headlength in 1986

	Number of Plants		Ratios with non-significant (p>0.05) Chi-square Values			Number of genes Direct calculation
						X^2
Cross(1) F2	SH	LH	Ratio 1 63:1		Ratio 2 255:1	X^2
9804	79	0	1.25		0.31	3; 4
Cross(1) BC(2)	SH	LH	Ratio 1 63:1		Ratio 2 255:1	
9801	119	0	1.89		0.47	?
Cross(2) F2	SH	LH	Ratio 1 63:1		Ratio 2 255:1	X^2
9805	78	0	1.24		0.31	3; 4
Cross(2) BC(2)	SH	LH	Ratio 1 63:1		Ratio 2 255:1	
9802	79	0	1.25		0.31	?
Cross(3) F2	SH	LH	Ratio1 15:1	Ratio2 63:1	Ratio3 255:1	X^2
9806	78	1	3.35	0.05	1.56	2; 3; 4
Cross(3) BC(1)	SH	LH	Ratio 1 63:1		Ratio 2 255:1	
9803	116	0	1.84		0.46	?

LH = Longhead ; SH = Shorthead.
*: Chi-square (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Data in Table 24 showed the backcross (BC) ratios expected from different F2 ratios as adapted from Stansfield, 1983.

Data in Table 22 listed chi-square ratios for maturity, head length, and seed size from 1987 data. For each trait

Table 24 : F2 and Backcross ratios.

	a. Two loci controlling a trait							
F2	15:1	13:3	11:5	9:7	7:1	5:3	3:1	1:1
BC	3:1	3:1	1:1	1:3	3:1	1:1	1:1	3:1
	b. Three loci controlling a trait							
F2	63:1	60:4 or 15:1		60:3	57:7	55:9	49:15	45:19
BC	7:1	3:1		6:1	5:3	5:3	3:5	3:5
F2	37:27	27:37	54:10 or 27:5					
BC	5:3	1:7	1:1					
	C. Four loci controlling a trait							
F2	255:1	243:13	225:31 etc,etc.					
BC	15:1	11:5	9:7					

Adapted from Stansfield, 1983.

the ratios varied within crosses and between crosses. When available, the corresponding backcrosses did not confirm the F2 ratios. In 1987, some of the backcrosses were made using stored pollen without testing its viability. A number of the putative BCs may have been F2s because of nonviable inbred pollen. But this hypothesis cannot be entirely true, because backcrosses made in the greenhouse in winter using fresh

pollen and grown in summer 1986 also gave similar BC ratios as in 1987 for head length (Table 23). Also, most BCs in 1987 had an inbred female parent and a male hybrid parent (Table 32). Another explaination would be that the 'mostly' epistatic gene action assumption under which the chi-square test was made may not be true for some crosses, especially because additive gene action was also reported for the three traits of concern here. There may have also been some problems associated with the classification of the F_2 progeny for the test. One of the problems was that sometimes the F_2 did not cover the recessive parent mean, giving a zero value to the recessive class. In other cases the putative recessive class was large (this is when the recessive parent mean was found close to the center, rather than close to one end, of the F_2 distribution), but this may just have been the effect of epistatic gene action (1:1, 9:7 or 27:37 for example).

Comparing tables D8 & D9 to D10, the following analysis of the results can be made:

a.Maturity (days to flowering) study in 1987.

Parents : Togo, T18BE, and Walor are early;
Gero, and T23B are late.

The gene number varied from 3 to 25 with an average of 12, for cross 3 (Table 22), between late Gero and early Walor, meaning not necessarily that the trait is controlled

by 12 loci but that at least three loci are involved, and therefore, the chi-square ratios 63:1 and 255:1 which showed perfect homogeneity may both be possible. Since the backcross over the recessive Gero was not available, neither ratio could be confirmed.

The calculated gene number for maturity in cross 7 between early T18BE and late T23B, (Table 22), was 1. The corresponding 3:1 F2 ratio was found in three replications out of four but was not supported by the backcross ratio.

Cross 15 between early short head Togo and late long head Gero, gave very high calculated gene numbers (4 to 41) with an average of 14 in 1987 (Table 21, cross 15). A wide range of F2 ratios was also recorded : 13:3, and 14:2 or 7:1 for 2 loci, 55:9, 54:10 or 27:5, 60:3, and 63:1 for 3 loci, and 225:31, 243:13, and 255:1 for 4 loci. The most frequent ratios were 7:1, 225:31 and 27:5. No backcross data were available to support the F2 ratios. There seems to be a conflict between the two methods of gene number determination here. The chi-square test suggests a minimum of 2 genes, while the direct calculation supports a minimum of 4.

b. Head length study in 1987 and in 1986.

Parents : Gero, and T18BE are long headed;
Walor has small to mid-size heads;
T23B, and T23DBE are short-headed.

Cross 1 between Gero long head and T23DBE gave a

calculated gene number (n) of 3 to 10 with a mean of 6 in 1987 (Tables 21 and 22). The three pairs of F_2 and BC families of the same cross grown in 1986 (Table 23 crosses 1, 2, & 3) yielded n = 3, 4, and 2; with a mean of 3 genes. It can, therefore, be concluded that head length was controlled by at least 2 loci in that cross. The chi-square ratio 243:13 was more frequent and homogeneous in 1987, but it was not supported by the observation of its expected BC ratio 11:6. The F2 ratio 63:1 and its expected BC ratio 7:1 were observed, but the F2 ratio, even though found in 4 of 6 replicates, showed a high degree of heterogeneity. There may be at least 2 loci for head length in the cross 1, but the exact number of loci could not be specified. In 1986, (Table 23, crosses 1, 2, 3), the F2 and BC progeny segregated into the same 63:1 and 255:1 ratios, respectively. These BCs were made in the greenhouse using fresh pollen and must be genuine. Then why did the BC ratios appear to be F^2 ratios? This is a question without an answer. Since the F2 family with a gene number of 2 (Cross 3), also showed the 15:1 ratio that was expected, the hypothesis of at least 2 genes can be postulated.

Crosses 3 and 4 (Table 22) involved different families of the same cultivars of long head Gero and short to medium head Walor. The gene number varied from 2 to 11 with a mean of 6 in cross 3, and from 1 to 5 with a mean of 2 in cross 4. In both crosses, the BC ratios paralleled F2 ratios, yet the female parent for the BC in the cross 4 was the inbred Walor,

not the F1 (Table 32, 1987). The F2 ratios 63:1 (3 loci) and 255:1 (4 loci) were non-significant and homogeneous across the 6 replicates in cross 3, but the 2 loci ratios were highly significant, so that here at least 3 genes (instead of 2) may be operating. However, this did not agree with the calculated gene number. In cross 4, F2 ratios for 1, 2, 3 and 4 loci hypotheses were found, but were very heterogeneous, i.e. associated with chi-square values non-significant for some replicates and highly significant for others. Only the 2 most frequent ratios, 7:1 and 55:9, were presented in Table 22. For cross 4, a minimum of 2 genes is proposed. No Gero x Walor F2s were grown in 1986.

Cross 7, in Table 22, between T18BE and T23B showed a high calculated number of genes, 6 to 11 with a mean of 8. The more frequent F2 ratio was 15:1 (2 loci), but the associated chi-square value was variable in its significance (highly heterogeneous). The F2 ratios for four loci, 255:1 and 243:13, were also found even though their chi-square values were more heterogeneous. The two methods of gene number determination only agreed on the fact that there was variation among the replicates of the F2s, but while the chi-square test indicated a variation from 2 to 4 loci or more, the gene number calculation showed a range of 6 to 11 loci. Similar F2s were not available in 1986.

c. Seed size (100-seed weight) study in 1987.

Parents: Togo, and Walor, are large-seeded;

T23DBE is small-seeded.

Cross 13 (Table 22) was a cross between the large-seeded cultivar Togo and the small seed size inbred T23DBE. Cross 9 had Togo and Walor as parents.

Cross 13, (Togo x T23DBE), with a calculated gene number of 1 to 2 (average 1) showed F2 ratios of 15:1, and 14:2 or 7:1 more frequently, and associated with heterogeneous chi-square values. No single gene ratio was observed. The cross between the two large-seeded cultivars Togo and Walor showed overdominance over Walor (Table 22). For this cross, the number of genes determined through direct calculation was 1. The most frequent F2 ratios, 13:3 and 54:10 in the cross, showed heterogeneous chi-square values. The 3:1 ratio supporting the one gene hypothesis was observed in 3 of 5 replications.

Data in Table 25 summarize the linkage study between maturity and headlength. The study was based on the most frequent F_2 ratios discussed for each trait in each cross. As the table indicates, there was apparently no linkage between the traits for the limited number of crosses studied.

Table 25: Linkage Study in 1987: Maturity/Headlength

Cross (3) Ratio	Early > Late 63:1		LH > SH 63:1		Linkage 3969: 63: 63: 1	
Family	Early LH	Early SH	Late LH	Late SH	Chisq.	D.F.
10147-1	96	1	10	0	0.839 ns	3
10147-2	106	1	1	0	0.001 ns	3
10147-3	94	0	5	0	0.124 ns	3
10147-4	137	0	0	0	0.035 ns	3
10147-5	114	1	0	0	0.006 ns	3
10147-6	120	0	1	0	0.007 ns	3
Pooled	667	3	17	0	0.129 ns	3
Homogeneity					0.882 ns	15

Cross (7) Ratio	Late > Early 13:3		LH > SH 15:1		Linkage 195: 13: 45: 3	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10150-1	159	21	20	3	0.172 ns	3
10150-2	146	0	45	0	0.193 ns	3
10150-3	151	7	34	3	0.692 ns	3
10150-4	138	8	28	1	0.129 ns	3
10150-5	118	0	42	1	0.000 ns	3
Pooled	712	36	169	8	0.027 ns	3
Homogeneity					1.160 ns	12

ns = non significant at p = 0.05.
SH = short head; LH = long head.

Table 25: Linkage Study in 1987: Maturity/Headlength (End)

Cross (7) Ratio	Late > Early 3:1		LH > SH 15:1		Linkage 45: 3: 15: 1	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10150-1	159	21	20	3	0.718 ns	3
10150-2	146	0	45	0	0.014 ns	3
10150-3	151	7	34	3	0.711 ns	3
10150-4	138	8	28	1	0.056 ns	3
10150-5	118	0	42	1	0.189 ns	3
Pooled	712	36	169	8	0.015 ns	3
		Homogeneity			1.673 ns	12

ns = non significant at p = 0.05.
SH = short head; LH = long head.

B2. Discussion

The study of heterosis in the selected crosses showed no overdominance for maturity but, the hybrid F1s were on the average earlier than the mid-parent and the late-parent. The direction of dominance varied from cross 7 (late > early) to crosses 3 and 15 (early > late). For head length, the mean hybrid head length was between those of the mid-parent and the high-parent, but some overdominance was observed towards the high-parent (crosses 3 and 4 between Gero and Walor, with a mean Jinks' heterosis of 5.5 cm). For seed size, the hybrids had smaller seed than the high-parent but were higher than the mid-parent for the two selected crosses.

Since heterosis is widely accepted as mainly due to dominant gene action (Hallauer and Miranda,1981), low heterosis means low dominant gene effects and high heritability, while high heterosis means high dominant gene effects, low additive gene effects and low heritability. Because heterosis varied from cross to cross, heritability can be expected to also vary from cross to cross.

The environmental effect was higher for head length (42%) than for maturity (35%) and seed size (26%). The mean broad sense heritabilities (H^2) were consequently higher for seed size (74%) than for maturity (65%), and head length (58%). H^2 calculated from the totals of variances across crosses was different from the mean H^2 above for each cross.

The differences (H^2 - 'total' H^2) were 14% for maturity, -2% for head length, and -7% for seed size. The non similarity in the differences showed that they arose from other causes than the method of calculation. The environmental effect, for example, may not be the same from one trait to another. Genotype-environment interaction effects may be higher for head length than for seed size and maturity.

The environmental effect and its interaction with the genotype may be one of the causes for the continuous variation showed by the frequency distribution charts of the traits. The variation in the expression of maturity (continuous for crosses 3 and 15, and single gene effect in cross 7) seems to indicate that the trait is probably under the control of several independent additive loci as in wheat kernel color inheritance reported by Nilsson-Ehle in 1910 (Allard, 1960). When two cultivars only differ in alleles of a single gene, (this is probably the case between the Tift inbreds 18E and 23B), the trait displays discontinuous variation and high heritability, while continuous variation appears in other cases.

The broad sense heritability for seed size reported here for two crosses seems very high compared to the reports from Hash (1986) who found heritability of pearl millet grain size moderately low and from Phul and Athwal (1969) who found pearl millet seed size controlled by additive plus additive by dominance gene actions, and greatly influenced by environment. It may be because of the limited number of

crosses evaluated in this study, or genetic differences in the cultivars used here in the crosses. The hypothesis for independent additive gene actions could apply, continuous variation arising only when entries differ by more than one locus.

The number of genes per trait

Even though the number of crosses was limited, a general conclusion on the genetics was difficult to reach, especially for maturity.

When selfing plants, errors can result from bagging secondary tillers instead of intended main tillers. In this experiment, that kind of error was minimized since the heads were bagged regularly. Cautiously recording data on maturity and head length can easily eliminate errors. But total head seed weight and resulting seed weight per cm of head can be a source of errors, because a head can lose seed before and during threshing, or during seed transfer into envelopes. For this reason the seed weight per cm of head was not studied. There may also be errors in 100-seed count, because the machine does not count exactly 100 seeds each time. At least three repetitions of each count would have been more accurate. However, given the amount of seeds to count in a limited time this could not be done. If there was any human or technical errors associated with the data, it would be in 100-seed weight. Some unusual results were observed for maturity and head length.

One unusual result was the high gene number estimated for maturity in the crosses between early short head Togo and late long head Gero (cross 15,1987) and between late Gero and early Walor (cross 3, 1987). The heritability (H^2) was 56% and 46%, respectively for these crosses with a mean calculated gene number of 14 and 12, respectively. These numbers appear to be high even for quantitative traits but maybe not impossible since Stansfield, (1983), gave a gene number range for such traits that varied from 10 to 100. The gene number for head length was a little lower but also consistent with the moderate H^2 of the trait. The small seed size calculated gene number was also consistent with its high H^2. Further investigation using carefully chosen material would be necessary to verify this information.

In general, data from this study showed that the number of genes controlling maturity was higher than has been reported for pearl millet. Considering all crosses the average gene number was 9 (direct calculation) and 3 (chi-square method) for maturity, 6 (calculation) and 4 (chi-square method) for head length, and 1 (calculation) and 2 (chi-square method) for seed size.

The purpose for analyzing the data with a chi-square test was to use it as a check to decide which calculated

gene number fits the data better, but this did not appear useful in some crosses.

Since heterosis is largely due to dominance and to a

lesser degree due to epistasis, the amount of heterosis can give an idea of the importance of epistasis in the material. The mean heterosis for maturity was 20% at most. Attributing 50% of this heterosis (probably overestimated), there would be at most 10% of epistatic effects. Similarly, for head length and seed size with about 25% heterosis each, epistasis would account for about 13% . If this approximation can be made, then this clearly means that the 'mostly' epistatic gene action hypothesis behind the chi-square test would not hold in general. In fact, the epistatic effect is very small compared to the dominance effect (Halluer and Miranda, 1981) and not similar to it as supposed above. This may be one reason why the gene number and the chi-square ratios did not match very often. Another reason may be that the calculated gene number may not be accurate some times since it was based on the assumption that dominance existed and this could not be verified directly. Despite all these limitations, both methods estimated the gene number with similar results for some crosses.

For maturity, there was at least partial agreement between the calculated gene number and the chisquare ratios in crosses 3 and 7, so that, at least 3 genes in cross 3, and 1 to 3 genes maximum in cross 7 control the trait. Similarly, at least 2 genes were probably controlling maturity in cross 15 where the upper limit could not be set.

Partial agreement was found for head length in crosses 1, 3, and 4, in 1987. At least 2 genes probably control head

length in cross 4, and maybe 3 genes were operating in cross 1 and 3. Crosses 3 and 4 did not seem to be the same even though both involved the same cultivars Gero and Walor.

There was no agreement between the calculated gene numbers (greater than 6) in cross 7, and the chisquare ratios suggesting 2 genes minimum.

There was full agreement between the calculated gene number and the chisquare ratios in cross 9 regarding the minimum gene number that expresses seed size. Both methods suggested a minimum of 1 gene in the cross.

The calculated minimum gene number in cross 13 was 1 while the chi-square test indicated at least 2 genes. One gene probably controlled seed size in this cross.

The maximum gene number controlling seed size was 3 for both crosses 9 and 13.

Data in Table 26 summarized the minimum and the reasonable maximum gene numbers that are proposed for each cross as discussed above. Several reasons may account for the fact that a clearer estimate of the number of genes controlling each character was not determined:

- Quantitative traits in general are not suitable for this kind of analysis because their variation is continuous.
- Such traits are affected by environmental effects which are not easy to remove from their phenotypic variances.

- Small effects of modifier genes also add to the

phenotypic variances of the quantitative traits and this may bias the gene number determination.

The fact that the linkage chisquare test between head length and maturity was not significant does not necessarly mean that there was no linkage between them. If it is true that many genes are involved in maturity and head length, then, chances are that linkage is somewhere between these traits. Since the calculated number of genes seemed to be high and only ratios corresponding to low gene number (1 to 4 genes) were used in the test, the existing linkage could easily be missed.

Table 26: Summary of the minmum number of genes per cross

M A T U R I T Y I N 1 9 8 7

Cross(3) Late Gero * Early Walor

Family	Minimum gene number	Maximum gene number
10147 - 1	3	?
10147 - 2	3	8
10147 - 3	3	6
10147 - 4	3	?
10147 - 5	3	?
10147 - 6	3	?
Pooled	3	8

Cross(7) Early T18BE * Late T23B

Family	Minimum gene number	Maximum gene number
10150 - 2	1	3
10150 - 3	1	2
10150 - 4	1	3
10150 - 5	1	3
10150 - 6	1	1
Pooled	1	2

Table 26: Summary of the minmum number of genes per cross

M A T U R I T Y I N 1 9 8 7 (End)

Cross(15) Early Togo * Late Gero

Family	Minimum gene number	Maximum gene number
10159 - 1	2	?
10159 - 2	2	?
10159 - 3	2	7
10159 - 4	2	4
10159 - 5	?	?
10159 - 6	2	?
Pooled	?	6

Table 26: Summary of the minmum number of genes per cross

H E A D L E N G T H		
Cross(1) IN 1987 Longhead Gero * Short head T23DBE		
Family	Minimum gene number	Maximum gene number
10145 - 1	3	4
10145 - 2	4	7
10145 - 3	3	6
10145 - 4	3	5
10145 - 5	3	4
10145 - 6	3	?
Pooled	5	?
Cross(1) in 1986 Longhead Gero * Short head T23DBE		
Family	Minimum gene number	Maximum gene number
9804	3	4
Cross(2) in 1986 Longhead Gero * Short head T23DBE		
Family	Minimum gene number	Maximum gene number
9805	3	4
Cross(3) in 1986 Longhead Gero * Short head T23DBE		
Family	Minimum gene number	Maximum gene number
9806	2	4
Cross(3) in 1987 Longhead Gero * Short head Walor		
Family	Minimum gene number	Maximum gene number
10147 - 1	2	4
10147 - 2	3	4
10147 - 3	3	9
10147 - 4	3	4
10147 - 5	3	5
10147 - 6	3	?
Pooled	4	4

Table 26: Summary of the minmum number of genes per cross

H E A D L E N G T H (End)

Cross(4) in 1987 Longhead Gero * Short head Walor Family	Minimum gene number	Maximum gene number
10148 - 1	1	3
10148 - 2	1	3
10148 - 3	?	5
10148 - 4	2	3
10148 - 5	2	3
10148 - 6	3	3
Pooled	2	3

Cross(7) in 1987 Longhead T18BE * Short head T23B Family	Minimum gene number	Maximum gene number
10150 - 2	?	6
10150 - 3	3	?
10150 - 4	2	6
10150 - 5	2	6
10150 - 6	3	9
Pooled	2	9

Table 26: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7		
Cross(9) Family	Large seed Togo * Minimum gene number	Large seed Walor Maximum gene number
10153 - 1	1	3
10153 - 2	1	1
10153 - 3	1	3
10153 - 4	1	3
10153 - 5	1	3
Pooled	1	2
Cross(13) Family	Large seed Togo * Minimum gene number	Small seed T23DBE Maximum gene number
10158 - 1	2	3
10158 - 2	1	2
10158 - 3	1	2
10158 - 4	1	2
10158 - 5	1	2
10158 - 6	1	2
Pooled	1	?

(V) SUMMARY AND CONCLUSION

In an attempt to provide more information on the factors influencing grain yield and its components in pearl millet, Pennisetum glaucum (L.) R. Br., a plant management study and a genetic study were conducted for two years.

The plant management study lead to the observations that tillering ability of the plants, total head seed weight, weight of 100 seeds (or seed size), and yield, were significantly affected by maturity, plant height, plant population density and planting date.

Earlier maturing plants produced more but shorter tillers, less but heavier seed, and higher grain yields.

Shorter plants had higher seed weight per head, lighter seeds and lower yield.

It appeared that yield increase depended more on seed size increase than on total head seed weight increase.

Plant populations that were less dense, matured later, produced more tillers, had higher total head seed weight, and were shorter. Yield and seed size were not affected significantly by plant population density.

Plants in early plantings took longer to mature seeds, produced more tillers, produced more total head seed weight, were higher yielding, and were shorter than plants in the late plantings. Seed size was not significantly affected by

the planting date.

Tillering ability of plants was negatively correlated with plant height: shorter plants always produced more tillers than taller plants. Tillering can be manipulated through plant spacing, planting date, or choice of inbreds.

It was also noticed that the total head seed weight, an important yield component, could be increased substantially by planting early.

The disease effects were not agronomically important.

The overall conclusion of the plant management study was that yield and its more important components can be increased by choosing an early maturing semi-dwarf inbred, planting early, and thinning to one plant per hill, with hills spaced 15 to 20 cm on rows about 90 cm apart.

The plant breeding / genetic study showed that headlength, seed size, and even maturity, (days to flowering), appeared to be quantitative traits. Even though the genetics of such traits is not easy to study, the combination of the Chi-square method outlined by Hanna et al., (1978), and the gene number calculation method attributed to Sewell Wright by Burton, (1951), provided some information about the minimum number of genes expressing each trait. Also, the study of heterosis, heritability, and frequency distribution, provided information on the traits.

The material studied seemed very complex. Each cross appeared to be very specific, suggesting the need to use the

pedigree method in crosses. Further investigations are needed to check the inbreeding level in the cultivars (for a better choice of parents in a breeding program) and to clarify the genetics of the traits studied.

In particular, crosses within each cultivar, (Gero, Togo, and Walor at least), may give some information on the level of diversity. If a within-cultivar diversity were found, then selection of parents within each cultivar would become necessary before making intercultivar crosses. Each selection within a cultivar would need also to be crossed to several known inbreds for each trait, with all the reciprocals and backcrosses. Crosses between established inbreds like T23B, T23DBE, and T18BE, would be made at the same time and used as checks. This would allow collection of more accurate information and better hypotheses would be generated.

From the limited number of crosses examined, seed size was about 10% more heritable than maturity which in turn was 7% more heritable than head length.

Epistasis estimated from heterosis was less than 10% for maturity and less than 13% for head length and seed size. The chi-square test based on epistasic gene action for these quantitative characters may not, therefore, have been suitable for the data. Nonetheless, the test was helpful in making a decision about the gene number in some of the crosses.

Only in one cross out of 3 was maturity found to be

controlled by one gene. For the other two crosses, the minimum gene number was 2 or 3, and there was no way to set the upper limit which went up to 9 genes on the average.

The mininmum gene number found in the material for head length was 1, 2, 3, or 6 depending on the cross. The upper limit gene number for this trait was 2 for cross 1, 6 for two crosses, and 8 for the last one.

The minimum gene number mostly found for seed size was 1 in both crosses with a maximum of 3 in one cross and 2 in the second.

The gene number, or more precisely the range of gene numbers, per trait proposed here has to be considered with caution. It just gives an idea of what may be going on in the expression of each trait. The main conclusion here is that:

a) maturity can be more complex in some pearl millet material than it has been previously reported. It may be controlled by a number of additive independent genes like the inheritance of the kernel color in wheat;

b) the head length of pearl millet seems to be a complex trait probably more influenced by environment than maturity and seed size; and

c) seed size seemed to depend on only a few genes (1 to 3), in the material studied.

No linkage was detected between any two of the traits (maturity, head length, and seed size).

The minimum gene number found in the pearl millet material studied can reasonably be summarized as following:

Maturity : 1 to 3 genes minimum, no speculation could be made about the maximum.

Headlength: 2 to 3, most probably 3, genes minimum; no speculation could be made about the maximum.

Seed size: 1 to 3, most probably 1 or 2, genes minimum; the maximum not to exceed 5.

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APPENDIX

Table A1: Generation means for Head length (cm) in 1986

Cross	Family	N	Range	Mean	Variance	CV	Trait
Fem.Par.	9499-G*	6	30-61	46.7	191.0	29.6	Long head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1	9497	12	31-46	35.8	18.1	11.9	Long head
(1) F2	9804	79	14-50	31.1	42.8	21.0	
BC(1)	9784	109	17-51	31.3	40.0	20.2	
BC(2)	9801	119	17-36	26.1	12.4	13.5	
Fem.Par.	9499-G	6	30-61	46.7	191.0	29.6	Long head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1	9497	12	31-46	35.8	18.1	11.9	Long head
(2) F2	9805	78	19-44	28.4	31.3	19.7	
BC(1)	9803	79	16-42	26.5	22.9	20.3	
Fem.Par.	9500-G	7	38-72	54.6	155.0	22.8	Long head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1	9497	12	31-46	35.8	18.1	11.9	Long head
(3) F2	9806	79	13-53	30.5	46.2	22.3	
BC(1)	9803	116	20-50	32.5	43.6	20.3	
Fem.Par.	9615-T	3	18-25	20.7	14.4	18.3	Short head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1	9612*	7	15-27	26.1	0.8	3.4	Short head+
(9) F1	9613*	21	20-26	23.6	3.5	8.0	
F2	9838	78	16-33	22.4	11.2	14.9	
F2	9839	66	15-30	22.2	11.3	15.2	
F2	9840	89	15-40	21.4	12.0	16.2	

Table A1: Generation means for Head length (cm) in 1986 (Cont.)

Cross	Family	N	Range	Mean	Variance	CV	Trait
F2 (9)	9841	39	15-30	21.2	10.4	15.2	
F2	9842	73	17-31	22.4	7.6	12.3	
BC(1)	9845	108	12-31	22.7	11.2	14.7	
BC(1)	9846	59	14-30	22.3	15.0	17.4	
BC(2)	9843	78	15-32	22.7	12.5	15.6	
BC(2)	9844	107	15-30	22.1	7.3	12.3	
Fem.Par.	9650-W	6	19-26	21.7	5.9	11.2	Short head
Mal.Par.	9734-T	7	18-20	18.7	0.6	4.0	Short head
F1 (10)	9660*	11	20-31	25.1	11.7	13.6	Shorthead+
F2	9850	102	15-29	22.1	7.5	12.4	
F2	9851	83	13-28	21.3	10.4	15.2	
F2	9852	29	8-23	18.4	8.2	15.6	
F2	9853	58	15-28	20.3	9.8	15.4	
BC(1)	9792	63	16-30	22.2	7.9	12.6	
BC(1)	9793	100	17-28	22.7	4.7	9.8	
Fem.Par.	9650-W	6	19-26	21.7	5.9	11.2	Short head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1	9655	18	20-29	25.7	4.9	9.4	Shorthead+
F1 (11)	9656	14	38-47	41.8	7.84	6.7	Long head
F2	9895	75	14-31	22.1	9.3	13.8	
F2	9896	70	16-30	21.9	9.3	13.9	
F2	9897	79	14-30	22.4	10.9	14.7	
F2	9898	70	16-28	22.4	8.0	12.7	

Table A1: Generation means for Head length (cm) in 1986 (Cont.)

Cross	Family	N	Range	Mean	Variance	CV	Trait
	F2	9899	79	13-28	20.5	9.7	15.2	
	F2	9900	129	12-28	21.1	11.2	15.9	
	F2	9901	82	16-27	21.4	7.2	12.6	
(11)	BC(1)	9796	63	15-30	23.5	8.4	12.3	
Fem.Par.	9662-W		4	24-28	26.3	2.9	6.5	Short head
Mal.Par.	T23DBE		20	18-23	19.9	2.7	5.0	Short head
	F1	9659	11	21-29	25.1	6.3	10.0	Walor
(12)	F2	9889	80	15-26	21.1	5.9	11.5	
	F2	9890	62	18-33	24.3	11.2	13.8	
	F2	9893	117	13-27	20.7	6.1	11.9	
	F2	9894	96	15-27	20.6	6.1	12.0	
	BC(1)	9794	85	19-36	27.2	14.0	13.8	
	BC(1)	9795	90	16-34	25.6	9.0	11.7	
	BC(2)	9893	117	13-27	20.7	6.1	11.9	
Fem.Par.	9724-T		7	17-21	19.4	3.0	8.8	Short head
Mal.Par.	9499-G		6	30-61	46.7	191.0	29.6	Long head
	F1	9726	17	23-41	34.7	21.1	13.2	Long head
(13)	F2	9854	98	15-39	27.3	16.1	14.7	
	F2	9855	91	18-35	26.8	15.7	14.8	
	F2	9856	83	16-36	25.5	18.8	17.0	
	F2	9857	97	15-38	27.3	21.7	17.0	
	F2	9858	84	17-40	29.0	23.0	16.6	
	F2	9859	81	20-38	26.8	18.5	15.9	
	--	9860	86	16-32	24.9	10.2	12.8	

Table A1: Generation means for Head length (cm) in 1986 (End.)

Cross	Family	N	Range	Mean	Variance	CV	Trait
BC(1) (13)	9797	89	15-35	25.0	15.0	15.5	
BC(1)	9798	103	16-36	24.4	14.6	15.6	
BC(1)	9799	58	17-31	24.2	11.0	13.7	
Fem.Par.	9737-T	9	18-20	19.2	0.4	3.5	Short head
Mal.Par.	T23DBE	20	18-23	19.9	2.7	5.0	Short head
F1 (14)	9742	19	21-27	23.6	1.5	6.4	Short head+
F1	9743	11	21-27	24.5	3.7	7.8	Short head+
F2	9861	100	16-28	21.3	6.7	12.1	
F2	9864	90	16-28	21.3	9.1	14.2	
F2	9866	105	15-34	21.8	11.0	15.2	
F2	9867	99	14-26	20.5	6.9	12.9	
F2	9868	74	16-27	21.1	7.1	12.6	
F2	9869	102	15-27	21.3	7.1	12.5	
BC(1)	9888	54	14-27	21.1	6.7	12.3	
BC(2)	9880	103	14-29	21.8	11.2	15.4	
BC(2)	9881	96	12-26	20.7	7.1	12.9	

* : E = T18BE ; G = Gero ; T = Togo ; W = Walor.
N = number of obser vations per family.
Short head+ = overdominance.

Table A2A: Generation Means for Days to flowering in 1987.

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10080-G	67	4.3	18.6	6.5	Late
Mal.Par.	23DBE	48	1.5	2.2	3.1	Early
F1	10123	53	9.9	97.6	18.7	Early
(1) F2	10145	52	7.8	57.4	14.6	
BC(1)	10162	63	6.3	40.0	10.1	
BC(2)	10175	49	4.9	23.8	9.9	
Fem.Par.	10084-G	68	3.1	9.5	4.6	Late
Mal.Par.	10097-W	48	2.5	6.3	5.2	Early
F1	10126	56	3.2	10.1	5.7	
(3) F2	10147	56	3.9	15.1	7.0	
BC(2)	10164	55	3.8	14.6	7.0	
BC(2)	10165	55	3.3	10.9	16.6	
Fem.Par.	10085-G	65	2.8	8.1	4.4	Late
Mal.Par.	10100-W	45	2.5	6.4	5.6	Early
F1	10127	58	4.7	22.1	8.1	Late
(4) F2	10148	57	4.8	22.6	8.3	
BC(2)	10168	47	2.8	7.9	6.0	
Fem.Par.	10086-G	63	3.6	12.7	5.7	Late
Mal.Par.	T23DBE	48	1.5	2.2	3.1	Early
F1	10128	53	5.4	28.9	10.1	Early
(5) BC(1)	10173	59	8.2	66.7	14.4	

Table A2A: Generation Means for days to flowering in 1987 (End)

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10090-E	44	1.4	1.9	3.1	Early
Mal.Par.	T23B	70	1.3	1.6	1.8	Late
F1	10131	61	3.4	11.2	5.5	Early
(7) F2	10150	59	10.7	115.4	18.2	
BC(1)	10166	60	11.2	124.7	18.6	
BC(2)	10167	65	5.3	28.3	8.2	
Fem.Par.	10115-T	42	2.7	7.1	6.3	Early
Mal.Par.	10086-G	63	3.6	12.7	5.7	Late
F1	10141	45	4.7	21.7	10.5	Early
(15) F2	10159	52	6.1	36.7	11.6	

Table 28B : Generation Means for Head length in 1987.

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10080-G	43	4.8	23.1	11.1	Longhead
Mal.Par.	T23DBE	18	1.3	1.6	7.3	Shorthead
F1	10123	29	3.7	13.7	12.9	Shorthead
(1) F2	10145	29	6.1	36.6	21.1	
BC(1)	10162	34	6.0	35.5	17.5	
BC(2)	10175	27	4.9	23.7	17.8	
Fem.Par.	10081-G	37	7.1	50.0	19.3	Longhead
Mal.Par.	T23B	17	2.3	5.4	13.5	Shorthead
F1	10125	31	3.3	10.8	10.7	Longhead
(2) F2	10146	27	4.3	18.6	15.8	

Table A2B: Generation Means for Head length in 1987. (CONT.)

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
BC(1) (2)	10163	33	3.7	13.5	11.1	
BC(2)	10161	24	3.7	13.9	15.7	
Fem.Par.	10084-G	35	7.5	56.9	21.3	Longhead
Mal.Par.	10097-W	17	1.7	3.0	10.2	Shorthead
F1	10126	44	4.9	24.3	11.1	Longhead
F2	10147	36	8.2	67.4	22.7	
BC(2) (3)	10164	34	7.8	60.7	23.0	
BC(2)	10165	32	6.8	45.8	21.1	
Fem.Par.	10085-G	32	4.8	23.1	15.0	Longhead
Mal.Par.	10100-W	23	4.0	15.8	17.1	Shorthead
F1	10127	34	3.9	15.4	11.6	Longhead
F2	10148	32	5.5	30.0	17.2	
BC(2) (4)	10168	31	3.5	12.1	11.1	
Fem.Par.	10089-E	41	4.1	17.1	10.1	Longhead
Mal.Par.	T23DBE	18	1.3	1.7	7.3	Shorthead
F1	10130	33	2.3	5.3	7.0	Longhead
F2	10149	29	4.9	23.6	16.5	
BC(2) (6)	10176	27	5.4	30.0	20.5	
Fem.Par.	10090-E	40	4.2	17.5	10.5	Longhead
Mal.Par.	T23B	17	2.3	5.4	13.5	Shorthead
F1	10131	33	4.2	17.2	12.4	Longhead
F2 (7)	10150	29	5.8	33.9	20.2	
BC(1)	10166	29	5.5	30.3	19.2	

Table A2B: Generation Means for Head length in 1987. (End)

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
(7) BC(2)	10167	24	3.9	14.9	16.2	
Fem.Par.	10092-E	40	3.8	12.1	8.6	Longhead
Mal.Par.	10100-W	23	4.0	15.8	17.1	Shorthead
F1	10132	37	3.4	11.6	9.3	Longhead
F2	10152	32	5.6	31.6	17.7	
(8) BC(2)	10169	31	4.9	24.1	15.6	
Fem.Par.	10115-T	19	1.7	2.8	9.0	Shorthead
Mal.Par.	10086-G	50	10.4	107.8	20.7	Longhead
F1	10141	27	5.6	31.4	20.6	Shorthead
(15) F2	10159-1	27	4.5	20.0	16.9	

Table 28C :Generation Means for Total head seed weight in 1987

Cross	Family	Mean	Standard Ddeviation	Variance	C.V.
Fem.Par.	10080-G	4.1	6.4	40.9	157.9
Mal.Par.	T23DBE	0.8	0.6	0.4	78.6
F1	10123	20.4	6.8	46.0	33.2
(1) F2	10145	10.7	8.0	63.3	74.4
BC(1)	10162	17.4	11.8	140.2	68.1
BC(2)	10175	9.1	7.3	53.3	80.5

Table A2C: Generation Means for Total head seed weight in 1987 (Cont.)

Cross	Family	Mean	Standard Deviation	Variance	C.V.
Fem.Par.	10081-G	4.9	5.0	25.3	102.6
Mal.Par.	T23B	1.0	0.6	0.4	60.9
F1	10125	13.9	7.5	55.5	53.8
F2	10146	10.4	7.2	52.0	69.6
(2) BC(1)	10163	16.9	8.6	74.2	51.0
BC(2)	10161	12.1	7.6	58.2	63.1
Fem.Par.	10084-G	9.9	11.6	134.4	117.7
Mal.Par.	10097-W	2.9	3.0	8.8	101.4
F1	10126	25.1	10.0	100.8	40.0
F2	10147	10.4	9.2	84.6	88.4
(3) BC(2)	10164	10.4	9.4	88.2	90.5
BC(2)	10165	14.7	10.8	117.2	73.6
Fem.Par.	10085-G	11.0	9.2	85.2	83.8
Mal.Par.	10100-W	10.8	10.8	116.7	100.0
F1	10127	22.6	10.6	112.7	47.0
(4) F2	10147	10.1	7.0	49.6	69.7
BC(2)	10168	27.1	9.7	93.6	35.7
Fem.Par.	10089-E	3.5	1.8	3.2	51.7
Mal.Par.	T23DBE	0.8	0.6	0.4	78.6
F1	10130	13.1	3.2	10.1	24.3
F2	10149	8.3	5.2	26.9	62.8
(6) BC(2)	10176	7.6	6.1	37.5	81.1

Table A2C: Generation Means for Total head seed weight in 1987 (Cont.)

Cross	Family	Mean	Standard Deviation	Variance	C.V.
Fem.Par.	10090-E	2.9	1.5	2.3	52.2
Mal.Par.	T23B	1.0	0.6	0.4	60.9
F1	10131	16.7	6.3	40.2	38.0
(7) F2	10150	7.6	6.0	36.1	78.7
BC(1)	10166	5.9	4.5	20.5	76.7
BC(2)	10167	7.1	5.0	25.4	71.5
Fem.Par.	10092-E	3.2	1.6	2.7	50.6
Mal.Par.	10100-W	10.8	10.8	116.7	100.0
F1	10132	19.3	6.8	45.7	35.0
(8) F2	10152-1	17.2	10.4	107.4	60.3
BC(2)	10169	25.8	9.1	83.0	35.3
Fem.Par.	10095-T	2.8	1.8	3.2	65.1
Mal.Par.	10101-W	12.2	12.2	149.7	100.7
(9) F1	10135	21.8	9.5	89.5	43.3
F2	10153	11.7	8.5	72.5	72.6
Fem.Par.	10105-W	10.3	7.4	54.0	71.5
Mal.Par.	T23DBE	0.8	0.6	0.4	78.6
(10) F1	10136	23.0	7.0	49.2	30.5
F2	10154	10.8	6.7	44.6	61.9
Fem.Par.	10111-T	1.1	1.5	2.4	136.5
Mal.Par.	10108-W	6.7	5.0	24.8	74.8
F1	10137	20.2	9.0	81.9	44.8
(11) F2	10155	9.9	8.7	75.4	87.8

Table A2C: Generation Means for Total head seed weight in 1987 (End)

Cross	Family	Mean	Standard Deviation	Variance	C.V.
Fem.Par.	10113-T	2.6	2.8	7.9	108.7
Mal.Par.	10101-W	12.2	12.2	149.7	100.7
F1 (12)	10138	24.8	10.7	114.9	43.2
F2	10156	11.4	10.0	100.0	88.3
Fem.Par.	10114-T	3.4	2.9	8.4	85.1
Mal.Par.	T23DBE	0.8	0.6	0.4	78.6
F1 (13)	10139	23.1	6.1	37.4	26.5
F2	10158	8.1	6.4	41.4	79.5
BC(2)	10181	8.8	5.9	34.6	66.8
Fem.Par.	10113-T	2.6	2.8	7.9	108.7
Mal.Par.	10109-W	6.8	8.5	72.3	125.4
F1 (14)	10138*	24.8	10.7	7.9	108.7
F2	10157	9.7	7.7	58.5	79.3
BC(2)	10172	3.6	6.1	37.3	170.1
Fem.Par.	10115-T	2.1	2.0	4.0	94.8
Mal.Par.	10087-G	9.5	8.7	76.1	91.6
F1 (15)	10141	29.6	10.3	105.1	34.6
F2	10159	19.2	12.2	148.3	63.4
Fem.Par.	10118-T	2.7	2.9	8.3	107.3
Mal.Par.	T23DBE	0.8	0.6	0.4	78.6
F1 (16)	10142	22.8	4.9	24.4	21.7
F2	10160	12.3	9.9	97.3	80.1
BC(2)	10183	3.0	4.2	18.0	142.9

Table A2D: Generation Means for 100-seed weight (g) 1987

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10084-G	0.69	0.29	0.08	41.4	MS
Mal.Par.	10097-W	1.08	0.19	0.04	17.8	LS
F1	10126	1.52	0.19	0.04	12.6	LS+
F2	10147	1.31	0.28	0.08	21.6	
(3) BC(2)	10164	1.37	0.26	0.07	19.1	
BC(2)	10165	1.45	0.22	0.05	15.0	
Fem.Par.	10085-G	0.78	0.16	0.03	21.1	
Mal.Par.	10100-W	1.48	0.29	0.08	19.2	
F1	10127	1.00	0.26	0.07	25.7	
(4) F2	10147	1.08	0.22	0.05	20.1	
BC(2)	10168	1.48	0.16	0.02	10.4	
Fem.Par.	10092-E	0.74	0.11	0.01	14.7	
Mal.Par.	10100-W	1.48	0.29	0.08	19.2	
F1	10132	1.26	0.19	0.04	14.9	
(8) F2	10152	1.44	0.25	0.6	17.1	
Fem.Par.	10095-T	1.18	0.13	0.02	10.8	
Mal.Par.	10101-W	1.60	0.24	0.06	15.0	
F1	10135	1.70	0.20	0.04	11.6	
(9) F2	10153	1.39	0.25	0.06	18.1	
Fem.Par.	10105-W	1.08	0.28	0.08	25.7	
Mal.Par.	T23DBE	0.51	0.08	0.01	15.8	
F1	10136	1.24	0.14	0.02	11.3	
(10) F2	10154	1.18	0.32	0.10	27.0	
BC(2)	10177	0.57	0.20	0.04	35.5	

Table A2D: Generation Means for 100-seed weight (g) in 1987 (Cont.)

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10111-T	1.06	1.19	0.03	18.0	LS
Mal.Par.	10108-W	1.00	0.30	0.09	30.2	LS
F1	10137	1.80	0.22	0.05	12.0	LS+
(11) F2	10155	1.45	0.30	0.09	21.0	
BC(2)	10171	1.00	0.31	0.10	31.4	
Fem.Par.	10113-T	1.33	1.55	2.39	116.2	LS
Mal.Par.	10101-W	1.60	0.24	0.06	15.0	LS
F1	10138	1.85	0.26	0.07	14.3	W+
(12) F2	10156	1.41	0.33	0.11	23.4	
BC(2)	10170	1.31	0.24	0.06	18.1	
Fem.Par.	10114-T	1.24	0.19	0.04	15.7	LS
Mal.Par.	T23DBE	0.51	0.08	0.01	15.8	SS
F1	10139	1.19	0.14	0.02	12.1	LS
(13) F2	10158	1.07	0.30	0.09	28.4	
BC(2)	10181	0.87	0.26	0.07	29.6	
Fem.Par.	10113-T	1.33	1.55	2.40	116.2	LS
Mal.Par.	10109-W	1.05	0.25	0.06	23.5	LS
F1	10138*	1.85	0.26	0.07	14.3	T+
(14) F2	10157	1.35	0.31	0.10	23.3	
BC(2)	10172	0.99	0.24	0.06	24.3	

Table A2D: Generation Means for 100-seed weight (g) in 1987 (End)

Cross	Family	Mean	Standard Deviation	Variance	C.V.	Trait
Fem.Par.	10115-T	1.09	0.26	0.07	23.8	LS
Mal.Par.	10087-G	0.85	0.18	0.03	20.9	MS
F1	10141	1.40	0.20	0.04	14.5	LS+
(15) F2	10159	1.17	0.26	0.07	22.1	
Fem.Par.	10118-T	1.19	0.24	0.06	20.8	LS
Mal.Par.	T23DBE	0.51	0.08	0.01	15.8	SS
F1	10142	1.15	0.13	0.02	11.1	LS
(16) F2	10160	1.05	0.27	0.07	25.6	
BC(2)	10183	0.54	0.08	0.03	33.8	

E = T18BE; G = Gero; MP = mid-parent ; T = Togo;
W = Walor; N = number of observations per family.
LS = large seed; MS = mid-sized seed; SS = small seed.
LS+ = overdominance.
F2's and BC's are pooled in this table.

Table A3A : Generation Means for $\log_{10}$(Days to flowering) in 1987.

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
Fem.Par.	10080-G	45	1.75-1.88	1.82	0.0008	1.57	Late
Mal.Par.	23DBE	41	1.67-1.67	1.67	0.0000	0.00	Early
F1	10123	60	1.56-1.85	1.72	0.0060	4.53	Early
F2	10145-1	176	1.57-1.85	1.72	0.0046	3.90	
(1) F2	10145-2	154	1.58-1.83	1.71	0.0046	3.90	
F2	10145-3	166	1.56-1.84	1.72	0.0044	3.80	
F2	10145-4	195	1.57-1.81	1.70	0.0032	3.40	
F2	10145-5	187	1.48-1.88	1.72	0.0045	3.90	
F2	10145-6	148	1.54-1.85	1.71	0.0042	3.80	
BC(1)	10162-1	95	1.38-1.88	1.81	0.0031	3.10	
BC(1)	10162-2	119	1.67-1.87	1.78	0.0011	1.90	
BC(1)	10162-3	33	1.67-1.86	1.78	0.0020	2.60	
Fem.Par.	10084-G	49	1.78-1.87	1.82	0.0004	1.10	Late
Mal.Par.	10097-W	59	1.64-1.76	1.68	0.0005	1.31	Early
F1	10126	51	1.70-1.80	1.75	0.0006	1.53	
F2	10147-1	107	1.66-1.83	1.75	0.0014	2.20	
(3) F2	10147-2	108	1.59-1.81	1.74	0.0009	1.70	
F2	10147-3	99	1.66-1.82	1.75	0.0010	1.80	
F2	10147-4	137	1.69-1.80	1.75	0.0007	1.50	
F2	10147-5	115	1.62-1.80	1.74	0.0007	1.50	
F2	10147-6	121	1.66-1.81	1.74	0.0008	1.60	

Table A3A : Generation Means for $\log_{10}$(days to flowering) in 1987 (continued).

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
BC(2) (3)	10164-1	120	1.66-1.83	1.74	0.0007	1.60	
BC(2)	10164-2	125	1.66-1.79	1.73	0.0010	1.90	
BC(2)	10164-3	112	1.67-1.81	1.74	0.0008	1.70	
Fem.Par.	10085-G	72	1.76-1.86	1.81	0.0004	1.06	Late
Mal.Par.	10100-W	28	1.60-1.70	1.66	0.0006	1.47	Early
F1	10127	62	1.70-1.83	1.76	0.0012	1.98	Late
F2 (4)	10148-1	76	1.70-1.85	1.76	0.0008	1.63	
F2	10148-2	123	1.70-1.84	1.77	0.0008	1.56	
F2	10148-3	118	1.66-1.79	1.71	0.0011	1.96	
F2	10148-4	110	1.69-1.82	1.76	0.0006	1.42	
F2	10148-5	125	1.56-1.86	1.77	0.0013	2.04	
F2	10148-6	137	1.57-1.86	1.76	0.0009	1.69	
BC(2)	10168-1	116	1.60-1.75	1.67	0.0007	1.54	
Fem.Par.	10090-E	76	1.61-1.67	1.64	0.0002	0.83	Early
Mal.Par.	T23B	57	1.83-1.86	1.84	0.0000	0.32	Late
F1	10131	43	1.75-1.83	1.79	0.0002	0.76	Late
F2 (7)	10150-1	00					
F2	10150-2	203	1.56-1.88	1.77	0.0066	4.58	
F2	10150-3	191	1.57-1.88	1.75	0.0072	4.86	
F2	10150-4	195	1.58-1.88	1.76	0.0069	4.71	
F2	10150-5	175	1.59-1.88	1.77	0.0061	4.41	
F2	10150-6	161	1.36-1.88	1.76	0.0085	5.26	

Table A3A : Generation Means for $\log_{10}$(days to flowering) in 1987 (End).

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
BC(1) (7)	10166-1	159	1.40-1.88	1.76	0.0090	5.40	
BC(1)	10166-2	186	1.32-1.88	1.78	0.0071	4.80	
BC(1)	10166-3	83	1.57-1.87	1.76	0.0076	5.00	
Fem.Par.	10118-T	54	1.59-1.72	1.63	0.0007	1.62	Early
Mal.Par.	10087-G	52	1.73-1.83	1.79	0.0005	1.28	Late
F1	10141	11	1.56-1.74	1.65	0.0020	2.74	Early
F2	10159-1	166	1.59-1.86	1.72	0.0023	2.76	
F2	10159-2	168	1.57-1.85	1.73	0.0024	2.84	
F2	10159-3	138	1.57-1.84	1.72	0.0026	2.98	
F2	10159-4	144	1.60-1.84	1.72	0.0031	3.24	
F2	10159-5	177	1.60-1.81	1.72	0.0020	2.58	
F2	10159-6	150	1.60-1.81	1.72	0.0020	2.61	

N = the number of observations in the family.
E = T18BE ; G = Gero ; T = Togo ; W = Walor.

Table A3B : Generation Means for $\log_{10}$(Head length) in 1987.

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
Fem.Par.	10080-G	45	1.52-1.73	1.63	0.0024	3.00	Long Head
Mal.Par.	T23DBE	41	1.18-1.32	1.25	0.0009	2.40	Short Head
F1	10123	60	1.34-1.60	1.46	0.0032	3.87	Long Head
(1) F2	10145-1	176	1.15-1.62	1.42	0.0098	6.90	
F2	10145-2	154	1.26-1.66	1.46	0.0071	5.80	
F2	10145-3	166	1.27-1.64	1.43	0.0077	6.20	
F2	10145-4	195	1.15-1.66	1.45	0.0086	6.40	
F2	10145-5	187	1.11-1.72	1.45	0.0112	7.30	
F2	10145-6	148	1.26-1.68	1.47	0.0059	5.20	
BC(2)	10175-1	11	1.30-1.53	1.44	0.0064	5.60	
BC(2)	10175-2	87	1.26-1.58	1.44	0.0059	5.40	
BC(2)	10175-3	8	1.30-1.51	1.38	0.0040	4.60	
BC(2)	10175-4	22	1.28-1.54	1.40	0.0066	5.80	
Fem.Par.	10081-G	63	1.28-1.71	1.55	0.0078	5.70	Long Head
Mal.Par.	T23B	57	1.15-1.34	1.24	0.0020	3.59	Short Head
F1	10125	62	1.40-1.61	1.49	0.0021	3.07	Long Head
(2) F2	10146-1	127	1.26-1.59	1.43	0.0052	5.00	
F2	10146-3	127	1.32-1.59	1.46	0.0029	3.70	
F2	10146-4	150	1.20-1.58	1.40	0.0056	5.40	
F2	10146-5	105	1.30-1.56	1.43	0.0030	3.90	
BC(2)	10161-1	193	1.15-1.51	1.35	0.0036	4.45	
BC(2)	10161-2	164	1.26-1.56	1.39	0.0042	4.68	

Table A3B : Generation Means for $\log_{10}$(Head length) in 1987. (Cont.)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
BC(2) (2)	10161-3	155	1.20-1.54	1.36	0.0037	4.46	
BC(2)	10161-4	149	1.18-1.54	1.37	0.0045	4.88	
BC(2)	10161-5	144	1.23-1.61	1.39	0.0050	5.09	
Fem.Par.	10084-G	49	1.32-1.71	1.55	0.0077	5.69	Long Head
Mal.Par.	10097-W	59	1.11-1.30	1.23	0.0021	3.69	Short Head
F1	10126	51	1.56-1.74	1.64	0.0023	2.90	Long Head
F2 (3)	10147-1	107	1.28-1.85	1.57	0.0139	7.50	
F2	10147-2	108	1.23-1.79	1.59	0.0102	6.40	
F2	10147-3	99	1.36-1.70	1.56	0.0055	4.80	
F2	10147-4	137	1.32-1.79	1.55	0.0090	6.10	
F2	10147-5	115	1.28-1.72	1.53	0.0081	5.90	
F2	10147-6	121	1.30-1.63	1.49	0.0048	4.70	
BC(2)	10164-1	120	1.28-1.69	1.52	0.0090	6.20	
BC(2)	10164-2	125	1.28-1.75	1.51	0.0108	6.90	
BC(2)	10164-3	112	1.28-1.72	1.51	0.0106	6.80	
Fem.Par.	10085-G	72	1.34-1.62	1.50	0.0045	4.46	Long Head
Mal.Par.	10100-W	28	1.18-1.49	1.36	0.0058	5.58	Short Head
F1	10127	62	1.41-1.64	1.53	0.0026	3.31	Long Head
F2 (4)	10148-1	76	1.20-1.67	1.50	0.0088	6.28	
F2	10148-2	123	1.08-1.68	1.52	0.0071	5.52	
F2	10148-3	118	1.38-1.67	1.52	0.0037	4.01	
F2	10148-4	110	1.26-1.61	1.49	0.0055	4.98	

Table A3B : Generation means for $\log_{10}$(Head length) (Cont.).

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
F2	10148-5	125	1.15-1.64	1.48	0.0059	5.22	
(4) F2	10148-6	137	1.26-1.60	1.46	0.0046	4.66	
BC(2)	10168-1	116	1.38-1.60	1.49	0.0022	3.18	
Fem.Par.	10090-E	74	1.51-1.70	1.61	0.0019	2.74	Long Head
Mal.Par.	T23DBE	41	1.18-1.32	1.25	0.0009	2.40	Short Head
F1	10130	58	1.43-1.57	1.52	0.0009	2.03	Long Head
F2	10149-1	166	1.20-1.78	1.41	0.0048	5.28	
(6) F2	10149-2	168	1.26-1.58	1.42	0.0037	6.49	
F2	10149-3	138	1.28-1.57	1.44	0.0034	4.65	
F2	10149-4	144	1.11-1.61	1.40	0.0059	4.94	
F2	10149-5	177	1.23-1.95	1.40	0.0044	4.70	
F2	10149-6	150	1.23-1.54	1.43	0.0037	5.00	
BC(2)	10176-1	49	1.20-1.60	1.44	0.0074	5.97	
BC(2)	10176-2	112	1.15-1.58	1.40	0.0090	6.80	
BC(2)	10176-3	36	1.26-1.60	1.42	0.0085	6.50	
Fem.Par.	10090-E	76	1.46-1.67	1.59	0.0023	2.98	Long Head
Mal.Par.	T23B	57	1.15-1.34	1.24	0.0020	3.59	Short Head
F1	10131	43	1.40-1.66	1.52	0.0025	3.25	Long Head
F2	10150-1	00					
(7) F2	10150-2	203	1.20-1.57	1.39	0.0058	5.46	
F2	10150-3	191	1.36-1.67	1.51	0.0042	4.29	
F2	10150-4	195	1.18-1.61	1.42	0.0058	5.37	
F2	10150-5	175	1.23-1.60	1.42	0.0053	5.16	

Table A3B : Generation Means for $\log_{10}$(Head length). (End.)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
F2 (7)	10150-6	161	1.26-1.66	1.51	0.0046	4.46	
BC(2) (7)	10167-2	194	1.17-1.54	1.34	0.0044	4.80	
Fem.Par.	10092-E	79	1.45-1.68	1.60	0.0016	2.46	Long Head
Mal.Par.	10100-W	28	1.18-1.49	1.36	0.0058	5.58	Short Head
F1	10132	31	1.48-1.64	1.56	0.0016	2.59	Long Head
F2 (8)	10152-1	164	1.32-1.65	1.49	0.0052	4.85	
F2	10152-2	107	1.26-1.68	1.50	0.0071	5.58	
F2	10152-3	122	1.26-1.67	1.49	0.0069	5.53	
F2 (8)	10152-4	96	1.28-1.64	1.51	0.0045	4.42	
F2	10152-5	115	1.28-1.68	1.50	0.0067	5.46	
F2	10152-6	123	1.28-1.66	1.48	0.0066	5.50	
BC(2)	10169-1	63	1.32-1.60	1.48	0.0037	4.12	
BC(2)	10169-2	61	1.28-1.65	1.50	0.0058	5.03	
Fem.Par.	10118-T	54	1.15-1.34	1.27	0.0016	3.20	Short Head
Mal.Par.	10087-G	52	1.40-1.86	1.71	0.0128	6.62	Long Head
F1	10141	11	1.34-1.61	1.43	0.0064	5.59	Short Head
F2 (15)	10159-1	166	1.20-1.78	1.41	0.0048	4.86	
F2	10159-2	168	1.26-1.58	1.42	0.0037	4.27	
F2	10159-3	138	1.28-1.57	1.44	0.0034	4.04	
F2	10159-4	144	1.11-1.61	1.40	0.0055	5.52	
F2	10159-5	177	1.23-1.95	1.40	0.0045	4.74	
F2	10159-6	150	1.23-1.54	1.43	0.0037	4.30	

E = T18BE; G = Gero; T = Togo; W = Walor;
N = number of observations

Table A3C : Generation Means for $\log_{10}$(100*100-seed weight) in 1987.

Cross		Family	N	Range	Mean	Variance	C.V.	Trait
Fem.Par.		10084-G	48	1.30-2.11	1.80	0.0351	10.39	MS
Mal.Par.		10097-W	54	1.87-2.19	2.02	0.0061	3.85	LS
	F1	10126	51	2.02-2.29	2.18	0.0027	2.37	LS
	F2	10147-1	97	1.52-2.30	2.10	0.0144	5.70	
(3)	F2	10147-2	87	1.67-2.28	2.10	0.0128	5.40	
	F2	10147-3	95	1.74-2.28	2.15	0.0100	4.60	
	F2	10147-4	112	1.78-2.24	2.08	0.0092	4.70	
	F2	10147-5	95	1.86-2.37	2.12	0.0083	4.30	
	F2	10147-6	98	1.65-2.27	2.11	0.0088	4.50	
Fem.Par.		10085-G	71	1.62-2.08	1.80	0.0090	5.03	MS
Mal.Par.		10100-W	28	1.92-2.30	2.16	0.0087	4.32	LS
	F1	10127	62	1.54-2.17	1.98	0.0183	6.83	MP
	F2	10147-1	66	1.93-2.24	2.07	0.0037	2.93	
	F2	10147-2	121	1.82-2.22	2.08	0.0042	3.12	
(4)	F2	10147-3	111	1.08-2.20	2.03	0.0130	5.63	
	F2	10147-4	110	1.76-2.17	1.97	0.0079	4.53	
	F2	10147-5	124	1.62-2.14	1.97	0.0081	4.60	
	F2	10147-6	136	1.73-2.20	2.03	0.0079	4.36	
BC(2)		10168-1	116	2.02-2.26	2.17	0.0022	2.17	
Fem.Par.		10092-E	76	1.69-2.06	1.87	0.0034	3.12	MS
Mal.Par.		10100-W	28	1.92-2.30	2.16	0.0087	4.32	LS
	F1	10132	30	1.99-2.21	2.10	0.0027	2.47	LS
(8)	F2	10152-1	163	1.78-2.27	2.12	0.0071	3.94	

Table A3C : Generation Means for $\log_{10}$(100*100-seed weight) in 1987.(Cont.)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
	F2 10152-2	104	1.95-2.33	2.16	0.0066	3.77	
	F2 10152-3	122	1.81-2.29	2.16	0.0074	3.98	
	F2 10152-4	96	1.74-2.26	2.16	0.0052	3.35	
(8)	F2 10152-5	113	1.88-2.32	2.16	0.0058	3.50	
	F2 10152-6	122	1.92-2.30	2.15	0.0056	3.50	
Fem.Par.	10095-T	15	1.96-2.15	2.07	0.0024	2.35	LS
Mal.Par.	10101-W	35	2.04-2.32	2.20	0.0045	3.06	LS
	F1 10135	49	2.05-2.32	2.23	0.0027	2.34	W
	F2 10153-1	94	1.99-2.32	2.16	0.0088	18.13	
(9)	F2 10153-2	127	1.77-2.28	2.10	0.0088	4.45	
	F2 10153-3	113	1.75-2.30	2.11	0.0083	17.21	
	F2 10153-4	90	1.72-2.31	2.14	0.0088	4.37	
	F2 10153-5	141	1.80-2.31	2.15	0.0067	3.82	
Fem.Par.	10105-W	53	1.79-2.20	2.03	0.0110	5.17	LS
Mal.Par.	T23DBE	1	1.76-1.76	1.76	0.0000	0.00	SS
	F1 10136	45	1.93-2.17	2.09	0.0030	2.52	LS
	F2 10154-1	165	1.72-2.25	2.08	0.0086	4.45	
	F2 10154-2	159	1.62-2.88	2.05	0.0144	5.83	
(10)	F2 10154-3	133	1.75-2.21	2.00	0.0074	4.32	
	F2 10154-4	174	1.34-2.29	2.06	0.0108	5.07	
	F2 10154-5	152	1.78-2.30	2.09	0.0076	4.16	
	F2 10154-6	162	1.86-2.27	2.08	0.0066	3.88	

Table A3C: Generation Means for $\log_{10}$(100*100-seed weight) in 1987. (Cont.)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
Fem.Par.	10111-T	13	1.86-2.15	2.02	0.0062	3.91	LS
Mal.Par.	10108-W	42	1.53-2.22	1.98	0.0218	7.48	LS
F1	10137	31	2.16-2.32	2.26	0.0015	1.73	T
(11) F2	10155-1	82	1.78-2.29	2.14	0.0085	4.29	
F2	10155-2	103	1.52-2.32	2.14	0.0125	5.22	
F2	10155-3	136	1.74-2.30	2.12	0.0125	5.26	
F2	10155-4	108	2.01-2.34	2.19	0.0048	3.17	
F2	10155-5	110	1.65-2.31	2.14	0.0110	4.91	
F2	10155-6	80	1.93-2.36	2.18	0.0094	4.46	
Fem.Par.	10113-T	45	1.78-2.25	2.03	0.1016	2.01	LS
Mal.Par.	10101-W	35	2.04-2.32	2.20	0.0045	3.06	LS
F1	10138	41	2.14-2.35	2.28	0.0019	1.93	W
F2	10156-1	121	1.41-2.35	2.14	0.0193	6.25	
F2	10156-2	85	1.59-2.29	2.09	0.0154	5.94	
(12) F2	10156-3	53	1.63-2.26	2.09	0.0193	6.56	
F2	10156-4	65	1.79-2.29	2.16	0.0072	3.92	
F2	10156-5	97	1.75-2.31	2.05	0.0130	18.50	
F2	10156-6	111	1.72-2.30	2.15	0.0132	5.33	
Fem.Par.	10114-T	45	1.93-2.21	2.09	0.0050	3.39	LS
Mal.Par.	T23DBE	1	1.76-1.76	1.76	0.0000	0.00	SS
F1	10139	48	1.96-2.19	2.07	0.0028	2.53	LS
(13) F2	10158-1	131	1.61-2.21	2.03	0.0104	5.03	
F2	[illegible]	159	1.45-[illegible]21	1.98	0.0272	8.32	

Table A3C: Generation Means for $\log_{10}$(100*100-seed weight) in 1987.(Cont.)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
F2 (13)	10158-3	176	1.38-2.25	1.98	0.0231	7.66	
F2	10158-4	161	1.49-2.24	2.05	0.0182	6.57	
F2	10158-5	182	1.46-2.28	2.02	0.0210	7.17	
F2	10158-6	131	1.08-2.23	1.99	0.0346	9.38	
BC(2)	10181-1	137	1.15-2.18	1.92	0.0237	8.03	
BC(2)	10181-2	9	1.58-2.07	1.82	0.0279	9.14	
BC(2)	10181-3	150	1.60-2.18	1.92	0.0180	6.98	
Fem.Par.	10113-T	45	1.78-2.25	2.03	0.0103	2.01	LS
Mal.Par.	10109-W	57	1.74-2.18	2.02	0.0103	5.03	LS
F1	10138	41	2.14-2.35	2.28	0.0019	1.93	LS+
F2 (14)	10157-1	123	1.75-2.29	2.11	0.0100	4.76	
F2	10157-2	117	1.66-2.30	2.09	0.0147	5.80	
F2	10157-3	131	1.26-2.36	2.14	0.0180	6.25	
F2	10157-4	123	1.73-2.37	2.14	0.0106	4.80	
F2	10157-5	116	1.63-2.31	2.14	0.0108	4.84	
F2	10157-6	131	1.76-2.34	2.08	0.0094	4.66	
Fem.Par.	10118-T	45	1.93-2.21	2.09	0.0050	3.39	LS
Mal.Par.	10087-G	44	1.52-2.10	1.90	0.0167	6.82	MS
F1	10141	48	1.96-2.19	2.07	0.0028	2.53	LS
F2 (15)	10159-1	158	1.34-2.30	2.01	0.0161	6.32	
F2	10159-2	165	1.65-2.30	2.09	0.0104	4.88	
F2	10159-3	130	1.68-2.23	2.07	0.0100	4.84	

Table A3C: Generation Means for $\log_{10}$(100*100-seed weight) in 1987. (End)

Cross	Family	N	Range	Mean	Variance	C.V.	Trait
F2 (15)	10159-4	141	1.68-2.22	2.04	0.0100	4.90	
F2	10159-5	175	1.77-2.21	2.04	0.0072	4.18	
F2	10159-6	150	1.68-2.24	2.09	0.0121	5.28	
Fem.Par.	10118-T	25	1.80-2.24	2.07	0.0100	4.84	LS
Mal.Par.	T23DBE	1	1.76-1.76	1.76	0.0000	0.00	SS
F1	10142	56	1.94-2.18	2.06	0.0023	2.32	LS
F2 (16)	10160-1	164	1.41-2.16	1.98	0.0135	5.84	
F2	10160-2	161	1.43-2.28	2.03	0.0195	6.90	
F2	10160-3	157	1.36-2.24	2.02	0.0224	7.40	
F2	10160-4	142	1.18-2.18	1.97	0.0228	7.64	
F2	10160-5	173	1.38-2.22	2.01	0.0161	6.33	
F2	10160-6	140	1.20-2.26	2.00	0.0180	7.00	
BC(2)	10183-1	25	1.46-2.03	1.71	0.0152	7.22	

E = T18BE; G = Gero; MP = mid-parent ; T = Togo;
W = Walor; N = number of observations per family.
LS = large seed; MS = mid-sized seed; SS = small seed.
LS+ = overdominance.

Table A4: ANOVA over within cultivar data (log_{10}) in 1987

Cultivar	Source of var.	ANOVA	Maturity	Head length	Head SW	Seed size
Late long-head Gero	Family	F test	30.0 **	36.0*	11.2**	13.5**
		Prob.	0.0001	0.0001	0.0001	0.0001
	Reps	F test	3.1 *	2.5 *	3.2*	16.5**
		Prob.	0.0145	0.0443	0.0141	0.0001
	Fam.*Reps	F test	1.1 ns	1.3 ns	1.0ns	3.0**
		Prob.	0.3628	0.1662	0.4590	0.0001
Early long-head T18BE	Family	F test	6.1 **	5.9 **	5.1**	8.3**
		Prob.	0.0001	0.0001	0.0002	0.0001
	Reps	F test	20.8 **	4.5 **	0.9ns	3.6**
		Prob.	0.0001	0.0001	0.4665	0.0070
	Fam.*Reps	F test	3.2 **	4.0 **	2.6**	2.7**
		Prob.	0.0001	0.0001	0.0002	0.0001
Early large seed Togo	Family	F test	17.8 **	4.6 **	3.8**	2.0*
		Prob.	0.0001	0.0001	0.0039	0.0447
	Reps	F test	2.2 ns	0.9 ns	0.5ns	2.3ns
		Prob.	0.0713	0.4774	0.7757	0.0627
	Fam.*Reps	F test	5.9 **	1.9 **	0.9ns	2.3**
		Prob.	0.0001	0.0039	0.6690	0.0006
Early large seed Walor	Family	F test	16.9 **	40.7 **	15.4**	16.9**
		Prob.	0.0001	0.0001	0.0001	0.0001
	Reps	F test	4.4 **	5.4 **	0.2ns	2.8*
		Prob.	0.0016	0.0003	0.9441	0.0252
	Fam.*Reps	F test	2.7 **	1.4 *	1.8**	1.3ns
		Prob.	0.0001	0.0456	0.0011	0.0937

Table A4: ANOVA over within cultivar data (log_{10}) in 1987 (End)

Cultivar	Source of var.	ANOVA	Maturity	Head length	Head SW	Seed size
Early dwarf T23D-BE & Late tall T23B	Family	F test	51482.4**	1.8 ns	1.9ns	3.3ns
		Prob.	0.0001	0.1891	0.1818	0.0796
	Reps	F test	1141.8**	0.5 ns	3.3*	1.9ns
		Prob.	0.0001	0.7228	0.0256	0.1443
	Fam.*Reps	F test	0.00	0.5 ns	-	-
		Prob.	1.00	0.7643	-	-

ns : non significant at p = 0.05; * : significant at p = 0.05; ** :significant at p < 0.01;
SW = seed weight; Seed size = 100 seed weight.

Table A5: Within cultivar means (log_{10}) comparisons in 1987

Cultivar	Family	Days to Flowering (number)	Head Length (cm)	Head seed weight (cm)	Hundred seed weight (g)
Gero	10080	1.83 ab*	1.63 b	2.18 c	1.74 e
-	10081	1.83 ab	1.55 c	2.39 c	1.83 cd
-	10082	1.78 e	1.63 b	2.85 ab	1.89 b
-	10083	1.82 bc	1.57 c	2.30 c	1.87 bc
-	10084	1.83 a	1.55 c	2.71 b	1.81 d
-	10085	1.81 c	1.50 d	2.84 ab	1.88 b
-	10086	1.80 d	1.69 a	2.70 b	1.92 b
-	10087	1.80 d	1.71 a	2.80 ab	1.90 b
Gero	10088	1.79 d	1.56 c	3.0 a	2.0 a
T18BE	10089	1.64 bc	1.61 bc	2.49 ab	1.89 bc
-	10090	1.64 bc	1.60 cd	2.41 bc	1.89 b
-	10091	1.64 c	1.61 ab	2.33 c	1.88 bc
-	10092	1.65 a	1.60 bcd	2.45 b	1.87 c
-	10093	1.643 b	1.62 a	2.41 bc	1.87 bc
T18BE	10094	1.640 bc	1.59 d	2.55 a	1.92 a
Walor	10096	1.678 a-e	1.273 ef	2.38 bc	2.03 cd
-	10097	1.683 abc	1.230 f	2.25 c	2.02 cd
-	10098	1.682 a-d	1.282def	2.00 c	2.09 bc
-	10099	1.670 a-f	1.339a-d	2.92 a	1.97 d
-	10100	1.655 efg	1.360 ab	2.70 ab	2.16 ab
-	10101	1.670 b-f	1.350abc	2.75 ab	2.20 a
-	10102	1.663 c-g	1.360 ab	2.31 c	2.19 a

Table A5: Within cultivar means (log_{10}) comparisons in 1987 (End.)

Cultivar	Family	Days to Flowering (number)	Head Length (cm)	Head seed weight (cm)	Hundred seed weight (g)
Walor	10103	1.671 a-f	1.370 a	2.95 a	2.22 a
-	10104	1.690 ab	1.334 a-d	2.95 a	2.20 a
-	10105	1.694 a	1.308 b-e	2.92 a	2.03 cd
-	10106	1.656 efg	1.240 f	2.82 a	2.03 cd
-	10107	1.641 g	1.240 f	2.80 a	2.08 bc
-	10108	1.657 d-g	1.300 cde	2.72 ab	1.99 cd
-	10109	1.648 fg	1.150 g	2.71 ab	2.02 cd
Walor	10110	1.658 c-g	1.256 ef	2.96 a	2.06 cd
Togo	10095	1.677 a	1.283 ab	2.35 a	2.07 abc
-	10111	1.642 b	1.279 ab	1.84 c	2.02 c
-	10112	1.621 e	1.276 ab	2.34 a	2.07 ab
-	10113	1.637 bc	1.252 c	2.22 a	2.05 abc
-	10114	1.622 e	1.285 ab	2.36 a	2.09 a
-	10115	1.628 cde	1.268 bc	2.12ab	2.05 abc
-	10116	1.633 bcd	1.282 ab	2.01bc	2.03 bc
-	10117	1.628 cde	1.278 ab	2.05bc	2.05 abc
Togo	10118	1.626 de	1.289 a	2.17ab	2.07 abc
T23B	10119	1.845 a	1.238a	1.92 a	1.608 a
T23DBE	10120	1.672 b	1.248 a	1.59 a	1.756 a

* : means with the same letter (s) are not significantly different ;Duncan's multiple range test at p = 0.05. a-f = abcdef and so forth

Table A6: The parents of the backcrosses in 1986 and 1987

(1986)				(1987)			
		Parents				Parents	
Cross	BC	Female	Male	Cross	BC	Female	Male
(1)	9784	Gero	F1	(1)	10175	T23DBE	F1
	9801	F1	T23DBE		10162	Gero	F1
(2)	9789	Gero	F1	(2)	10161	F1	T23B
	9802	F1	T23DBE	(3)	10165	F1	Walor
(3)	9803	F1	Gero	(4)	10168	Walor	F1
(7)	9821	F1	Gero	(5)	10173	Gero	F1
(9)	9843	F1	T23DBE	(6)	10176	T23DBE	F1
	9844	F1	T23DBE	(7)	10166	F1	T18BE
	9845	F1	Togo		10167	F1	T23B
	9846	F1	Togo	(8)	10169	Walor	F1
(10)	9792	Walor	F1	(10)	10177	T23DBE	F1
	9793	Walor	F1		10178		
(11)	9796	Walor	F1		10179		
(12)	9794	Walor	F1		10180		
	9795	Walor	F1	(11)	10171	Walor	F1
	9893	F1	T23DBE	(12)	10170	Walor	F1
(13)	9797	Togo	F1	(13)	10181	T23DBE	F1
	9798	Togo	F1		10182		
	9799	Togo	F1	(14)	10172	Walor	F1
(14)	9870	F1	T23DBE	(16)	10183	T23DBE	F1
	9881	F1	T23DBE		10184		
	9888	F1	Togo		10185		
					10186		

Table A7: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings on 13 May, 1985

Treatment	Plant # per plot	Plant height*	Days to 50% heading	Head no. per plot	Head no. per plant	Head length	Head seed wt (g.)	100 seeds weight (g)	Yield kg/ha
INBRED(I)[1]									
T23B	32a	89a	75.6b	94b	3.3c	21.9a	9.2a	0.5c	2380a
T23BE	30ab	56b	54.1c	144a	5.4b	17.9c	6.5b	0.7a	2570a
T23DB	28b	50c	79.1a	93b	3.6c	18.0c	5.5c	0.4d	1400b
T3DBE	18c	37d	50.9d	141a	8.5a	19.2b	3.7d	0.6b	1460b
DENSITY(D)[1]									
HIGH	37a	61a	62.7b	130a	3.9b	18.9b	5.7b	0.5b	2010a
LOW	17b	55b	67.2a	106b	6.5a	19.5a	6.7a	0.6a	1900a
				A N O V A					
INBRED(I)	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
DENSITY(D)	0.0001	0.0001	0.0001	0.0001	0.0001	0.0004	0.0170	0.0007	0.2700
I x D	0.0001	0.0001	0.0001	0.2953	0.0002	0.0003	0.6817	0.0034	0.0140
CV	13	3	2	8	16	3	20	9	20
Overall Mean	27	58	64.9	118	5.2	19.2	6.2	0.5	1630

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for p > 0.05.
* : Plant height and head length are in cm.

Table A8: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings on 09 July, 1985

Treatment	Plant # per plot	Plant height*	Days to 50% heading	Head no. per plot	Head no. per plant	Head length	Head seed wt (g.)	100 seeds weight (g)	Yield kg/ha
INBRED(I)[1]									
T23B	70a	202a	62.2b	115c	2.6c	20.5a	4.8a	0.6a	1550a
T23BE	68a	130b	47.3c	163a	3.7b	19.0b	3.0b	0.5b	1350b
T23DB	70a	118c	65.4a	105d	2.4d	17.6c	1.1c	0.2c	310d
T23DBE	45b	92d	45.9d	137b	4.0a	19.2b	1.4c	0.5b	510c
DENSITY(D)[1]									
HIGH	101a	135b	54.8b	137a	1.5b	18.8b	2.4b	0.5a	940a
LOW	25b	137a	55.5a	123b	4.9a	19.4a	2.7a	0.4b	930a
				A N O V A					
INBRED(I)	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001	0.0001
DENSITY(D)	0.0001	0.1354	0.0023	0.0009	0.0001	0.0053	0.156	0.0008	0.8900
I x D	0.0001	0.0019	0.0016	0.4885	0.0002	0.5005	0.3888	0.2933	0.9100
CV	8	2	1	7	9	3	21	14	21
Overall Mean	63	136	55.2	130	3.2	19.1	2.6	0.5	780

[1]: Duncan's multiple range test at 5% level ; The F test is non significant for $p > 0.05$.
* : Plant height and head length are in cm .

Table A9: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings on 13 June, 1986

Treatment	Plant # per plot	Plant height*	Maturity (days	Head no. per plot	Head no. per plant	Head length	Head seed wt (g.)	100 seeds weight (g)	Yield kg/ha
INBRED(I)[1]									
T23B	33b	188a	74.1a	98c	3.6b	18.2b	5.9b	0.60c	1630b
T23BE	39a	133b	47.9c	122a	3.9a	18.9ab	7.0a	0.61bc	2350a
T23DB	37ab	115c	72.2b	72d	2.7c	18.1b	6.3ab	0.63b	1270c
T23DBE	37ab	96d	46.8d	106b	3.7ab	19.2a	6.4ab	0.70a	1830b
DENSITY(D)[1]									
HIGH	55a	141a	58.4b	110a	2.0b	18.5a	5.9b	0.6a	1780a
LOW	18b	125b	62.2a	90b	4.9a	18.8a	6.9a	0.6a	1755a
				A N O V A					
INBRED(I)	0.0737	0.0001	0.0001	0.0001	0.0016	0.0179	0.2866	0.0001	0.0001
DENSITY(D)	0.0001	0.0006	0.0017	0.0056	0.0001	0.2080	0.0396	0.5243	0.7500
I x D	0.1029	0.1085	0.1488	0.0021	0.0339	0.0218	0.0027	0.0329	0.0060
CV	14	4	2	6	10	4	14	6	16
Overall Mean	37	133	60.3	100	3.5	18.6	6.4	0.6	1470

[1]: Duncan's multiple range test at 5% level; The F test is non significant for $p > 0.05$; * : Plant height and head length are in cm .

Table A10: Plant and seed characteristics of four near-isogenic pearl millet inbreds planted at two spacings on 18 July, 1986

Treatment	Plant # per plot	Plant height*	Days to 50% heading	Head no. per plot	Head no. per plant	Head length	Head seed wt (g.)	100 seeds weight (g)	Yield kg/ha
INBRED(I)[1]									
T23B	47b	187a	62.7b	92c	2.7c	17.9b	5.2a	0.4c	1320a
T23BE	53a	146b	49.6c	116a	3.2a	18.8a	3.9b	0.6a	1210b
T23DB	46b	110c	64.0a	85d	2.7c	16.4c	2.0c	0.5b	470d
T23DBE	46b	95d	49.1c	103b	3.0b	18.9a	3.4b	0.6a	950c
DENSITY(D)[1]									
HIGH	75a	138a	55.4b	107a	1.4b	17.5b	3.1b	0.5a	900b
LOW	21b	130b	57.4a	91b	4.4a	18.5a	4.2a	0.5a	1070a
				A N O V A					
INBRED(I)	0.0006	0.0001	0.0001	0.0001	0.0053	0.0001	0.0001	0.0001	0.0001
DENSITY(D)	0.0001	0.0130	0.0062	0.0154	0.0001	0.0009	0.0160	0.7990	0.0004
I x D	0.0012	0.0098	0.0666	0.0087	0.0407	0.3002	0.0004	0.0014	0.0005
CV	7	2	2	6	8	3	14	6	12
Overall Mean	48	134	56.4	99	2.9	18.0	3.6	0.9	820

[1]: Duncan's multiple range test at 5% level; The F test is non significant for p > 0.05. * : Plant height and head length are in cm .

Table A11: Chi-square tests for Maturity in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(3) F2	Early	Late	Ratio1 63:1	Ratio2 255:1	X^2	N
10147 - 1	97	10	42.1**	220.5**	?	3
10147 - 2	107	1	0.29	0.80	3; 4	8
10147 - 3	94	5	0.24	55.3**	3	6
10147 - 4	137	0	2.18	0.54	3; 4	25
10147 - 5	115	0	1.83	0.45	3; 4	25
10147 - 6	120	1	0.43	0.59	3; 4	12
Pooled	670	17	3.72	77.0**	3	8
5 D.F. Homogeneity X^2 for 63:1			43.4**			
5 D.F. Homogeneity X^2 for 255:1			201.2**			
Cross(4) F2	Late	Early	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10148 - 1	75	0	1.21	0.30	3; 4	7
10148 - 2	123	0	1.95	0.48	3; 4	7
10148 - 3	117	1	0.39	0.63	3; 4	25
10148 - 4	110	0	1.75	0.43	3; 4	5
10148 - 5	123	2	0.0	4.7*	3	37
10148 - 6	136	1	0.62	0.41	3; 4	9
Pooled	685	4	4.3*	0.64	4	20
5 D.F. Homogeneity X^2 for 63:1			1.61ns			
5 D.F. Homogeneity X^2 for 255:1			6.3ns			
Cross(4) BC(2)	Late	Early	Ratio 1 1:1	Ratio 2 9:7	X^2	
10168 - 1	62	[illegible]	0.55	[illegible]7	2; 3; 4	

Table A11: Chi-square tests for Maturity in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(3) F2	Early	Late	Ratio1 63:1	Ratio2 255:1	X^2	N
10147 - 1	97	10	42.1**	220.5**	?	3
10147 - 2	107	1	0.29	0.80	3; 4	8
10147 - 3	94	5	0.24	55.3**	3	6
10147 - 4	137	0	2.18	0.54	3; 4	25
10147 - 5	115	0	1.83	0.45	3; 4	25
10147 - 6	120	1	0.43	0.59	3; 4	12
Pooled	670	17	3.72	77.0**	3	8
5 D.F. Homogeneity X^2 for 63:1			43.4**			
5 D.F. Homogeneity X^2 for 255:1			201.2**			
Cross(4) F2	Late	Early	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10148 - 1	75	0	1.21	0.30	3; 4	7
10148 - 2	123	0	1.95	0.48	3; 4	7
10148 - 3	117	1	0.39	0.63	3; 4	25
10148 - 4	110	0	1.75	0.43	3; 4	5
10148 - 5	123	2	0.0	4.7*	3	37
10148 - 6	136	1	0.62	0.41	3; 4	9
Pooled	685	4	4.3*	0.64	4	20
5 D.F. Homogeneity X^2 for 63:1			1.61ns			
5 D.F. Homogeneity X^2 for 255:1			6.3ns			
Cross(4) BC(2)	Late	Early	Ratio 1 1:1	Ratio 2 9:7	X^2	
101	62	54	0.55	0.37	2; 3; 4	

Table A11: Chi-square tests for Maturity in 1987 (End)

Cross(15) F2	Number of Plants Early	Late	Ratios with non-significant (p>0.05) Chisquare Values Ratio1 7:1	Ratio2 54:10	Ratio3 225:31	Number of genes Direct calculation X^2	N
10159 - 1	146	19	0.15	2.11	0.06	2; 3; 4	14
10159 - 2	145	23	0.22	0.48	0.40	2; 3; 4	10
10159 - 3	127	11	2.59	6.1*	2.22	2; 4	7
10159 - 4	123	21	0.57	0.12	0.83	2; 3; 4	4
10159 - 5	174	2	20.8**	28.0**	20.0**	?	41
10159 - 6	139	11	3.66	7.8**	3.22	2; 4	?
Pooled	854	87	9.1**	29.1**	7.3**	?	6
5 D.F.	Homogeneity X^2 for 7:1				18.9**		
5 D.F.	Homogeneity X^2 for 54:10				15.6*		
5 D.F.	Homogeneity X^2 for 225:31				19.4**		

*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Maturity in 1987 (End)

Cross(15) F2	Number of Plants Early	Late	Ratios with non-significant (p>0.05) Chisquare Values Ratio1 7:1	Ratio2 54:10	Ratio3 225:31	Number of genes X^2 Direct calculation X^2	N
10159 - 1	146	19	0.15	2.11	0.06	2; 3; 4	14
10159 - 2	145	23	0.22	0.48	0.40	2; 3; 4	10
10159 - 3	127	11	2.59	6.1*	2.22	2; 4	7
10159 - 4	123	21	0.57	0.12	0.83	2; 3; 4	4
10159 - 5	174	2	20.8**	28.0**	20.0**	?	41
10159 - 6	139	11	3.66	7.8**	3.22	2; 4	?
Pooled	854	87	9.1**	29.1**	7.3**	?	6
5 D.F. Homogeneity X^2 for 7:1					18.9**		
5 D.F. Homogeneity X^2 for 54:10					15.6*		
5 D.F. Homogeneity X^2 for 225:31					19.4**		

*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(2) F2	LH	SH	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10146 - 1	125	2	0.00	4.6*	3	5
10146 - 3	127	0	2.02	0.50	3; 4	18
10146 - 4	136	14	58.9**	308.3**	?	4
10146 - 5	105	0	1.67	0.41	3; 4	16
Pooled	493	16	8.3**	99.1**	?	5
3 D.F. Homogeneity X^2 for 63:1			54.3**			
3 D.F. Homogeneity X^2 for 255:1			214.7**			
Cross(2) BC(2)	LH	SH	Ratio 1 7:1	Ratio 2 225:31	X^2	
10161 - 1	165	28	0.71	1.04	3	
10161 - 2	151	13	3.14	2.70	3	
10161 - 3	135	20	0.02	0.09	3	
10161 - 4	134	15	0.81	0.58	3	
10161 - 5	139	5	10.7**	10.1**	?	
Pooled	724	81	4.4*	3.17	?	
4 D.F. Homogeneity X^2 for 7:1			11.0*			
4 D.F. Homogeneity X^2 for 225:31			11.3*			

*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.
LH = Longhead SH = Shorthead

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation X^2	
Cross(3) F2	LH	SH	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10147 - 1	106	1	0.27	0.81	3; 4	2
10147 - 2	107	1	0.29	0.80	3; 4	4
10147 - 3	99	0	1.57	0.39	3; 4	9
10147 - 4	137	0	2.18	0.54	3; 4	4
10147 - 5	114	1	0.36	0.68	3; 4	5
10147 - 6	121	0	1.92	0.48	3; 4	11
Pooled	684	3	5.7	0.04	4	4
5 D.F. Homogeneity X^2 for 63:1			0.9ns			
5 D.F. Homogeneity X^2 for 255:1			3.7ns			
Cross(3) BC(2)	LH	SH	Ratio 1 63:1		X^2	
10164 - 1	118	2	0.01		?	
10164 - 2	123	2	0.00		?	
10164 - 3	109	2	0.04		?	
10165 - 1	128	0	2.03		?	
10165 - 2	122	1	0.45		?	
10165 - 3	122	1	0.45		?	
Pooled	722	8	2.60		?	
5 D.F. Homogeneity X^2 for 63:1			0.38ns			

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
[illegible] at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(4) F2	LH	SH	Ratio 1 7:1	Ratio 2 55:9	X^2	N
10148 - 1	67	9	0.03	0.31	2; 3	1
10148 - 2	114	9	3.02	4.68	2; 3	1
10148 - 3	114	4	9.0**	11.1**	?	5
10148 - 4	98	12	0.26	0.91	2; 3	2
10148 - 5	103	22	2.97	1.30	2; 3	2
10148 - 6	110	27	6.58*	3.61	3	3
Pooled	606	83	0.13	2.32	2; 3	2
5 D.F. Homogeneity X^2 for 7:1				21.6**		
5 D.F. Homogeneity X^2 for 55:9				19.6**		
Cross(4) BC(2)	LH	SH	Ratio 1 63:1	Ratio 2 243:13	X^2	
10168 - 1	114	2	0.02	2.71	?	

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987(Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation X^2	
Cross(6) F2	LH	SH	Ratio 1 63:1	Ratio 2 243:13	X^2	N
10149 - 1	195	6	2.65	1.83	3; 4	4
10149 - 2	204	5	0.94	3.13	3; 4	2
10149 - 3	187	3	0.00	4.8*	3	5
10149 - 4	200	5	1.02	2.96	3; 4	4
10149 - 5	215	1	1.70	0.03	3; 4	5
10149 - 6	190	4	0.31	3.66	3; 4	4
Pooled	1191	24	1.35	24.3**	3	4
5 D.F. Homogeneity			X^2 for 63:1	5.3ns		
5 D.F. Homogeneity			X^2 for 243:13	7.8ns		
Cross(6) BC(2)	LH	SH	Ratio 1 7:1	Ratio 2 55:9	X^2	
10176 - 1	43	5	0.19	0.53	3	
10176 - 2	92	20	2.94	1.33	3	
10176 - 3	32	4	0.06	0.26	3	
Pooled	167	29	0.95	0.09	3	
2 D.F. Homogeneity			X^2 for 7:1	2.24ns		
2 D.F. Homogeneity			X^2 for 55:9	2.03ns		

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation	
Cross(7) F2	LH	SH	Ratio1 15:1	Ratio2 63:1	Ratio3 243:13	X^2	N
10150 - 2	179	24	10.8**	139.0**	19.2**	?	6
10150 - 3	194	0	12.9**	3.08	10.4**	3	11
10150 - 4	185	10	0.42	16.1**	0.01	2; 4	6
10150 - 5	166	9	0.37	14.6**	0.02	2; 4	6
10150 - 6	160	1	8.7**	0.93	6.6*	3	9
Pooled	884	44	3.61	61.0**	0.22	2; 4	9
4 D.F. Homogeneity X^2 for 15:1					29.6**		
4 D.F. Homogeneity X^2 for 63:1					112.7**		
4 D.F. Homogeneity X^2 for 243:13					34.0**		
Cross(7) BC(2)	LH	SH	Ratio1 3:1	Ratio2 7:1	Ratio3 55:9	X^2	
10167 - 1	154	40	2.00	11.7**	6.9**	2; 3	
10167 - 2	139	20	13.1**	0.01	0.29	3	
10167 - 3	110	10	17.8**	1.90	3.26	3	
10167 - 4	130	1	41.0**	16.5*8	19.2**	?	
Pooled	533	71	56.5**	0.31	2.66	3	
3 D.F. Homogeneity X^2 for 3:1					17.4**		
3 D.F. Homogeneity X^2 for 7:1					29.8**		
3 D.F. Homogeneity X^2 for 55:9					27.0**		

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		tios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation	
Cross(8) F2	LH	SH	Ratio1 7:1	Ratio2 55:9	Ratio3 225:31	X^2	N
10152 - 1	146	18	0.35	1.29	0.20	2; 3; 4	2
10152 - 2	83	14	0.33	0.01	0.49	2; 3; 4	2
10152 - 3	105	17	0.23	0.00	0.3	2; 3; 4	2
10152 - 4	90	6	3.43	4.9*	3.10	2; 4	3
10152 - 5	99	16	0.21	0.00	0.35	2; 3; 4	2
10152 - 6	102	21	2.35	0.92	2.85	2; 3; 4	2
Pooled	625	92	0.07	0.90	0.35	2; 3; 4	2
5 D.F. Homogeneity X^2 for 7:1					6.8ns		
5 D.F. Homogeneity X^2 for 55:9					6.2ns		
5 D.F. Homogeneity X^2 for 225:31					7.2ns		
Cross(8) BC(2)	LH	SH	Ratio 1 7:1		Ratio 2 55:9	X^2	
10169 - 1	56	7	0.11		0.45	3	
10169 - 2	54	7	0.06		0.34	3	
Pooled	110	14	0.17		0.79	3	
1 D.F. Homogeneity X^2 for 7:1					0.0ns		
1 D.F. Homogeneity X^2 for 55:9					0.0ns		

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Headlength in 1987 (Cont.)

	Number of Plants		tios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation
Cross(8) F2	LH	SH	Ratio1 7:1	Ratio2 55:9	Ratio3 225:31	X^2 N
10152 - 1	146	18	0.35	1.29	0.20	2; 3; 4 2
10152 - 2	83	14	0.33	0.01	0.49	2; 3; 4 2
10152 - 3	105	17	0.23	0.00	0.3	2; 3; 4 2
10152 - 4	90	6	3.43	4.9*	3.10	2; 4 3
10152 - 5	99	16	0.21	0.00	0.35	2; 3; 4 2
10152 - 6	102	21	2.35	0.92	2.85	2; 3; 4 2
Pooled	625	92	0.07	0.90	0.35	2; 3; 4 2
5 D.F. Homogeneity X^2 for 7:1					6.8ns	
5 D.F. Homogeneity X^2 for 55:9					6.2ns	
5 D.F. Homogeneity X^2 for 225:31					7.2ns	
Cross(8) BC(2)	LH	SH	Ratio 1 7:1	Ratio 2 55:9		X^2
10169 - 1	56	7	0.11	0.45		3
10169 - 2	54	7	0.06	0.34		3
Pooled	110	14	0.17	0.79		3
1 D.F. Homogeneity X^2 for 7:1				0.0ns		
1 D.F. Homogeneity X^2 for 55:9				0.0ns		

LH = Longhead SH = Shorthead
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Seed Size in 1987

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation X^2	
Cross(3) F2	LS	MS	Ratio1 15:1	Ratio2 60:3	Ratio3 243:13	X^2	N
10147 - 1	93	4	0.75	0.09	0.18	2; 3; 4	2
10147 - 2	84	3	1.17	0.33	0.48	2; 3; 4	2
10147 - 3	91	4	0.67	0.06	0.15	2; 3; 4	1
10147 - 4	107	5	0.61	0.02	0.09	2; 3; 4	1
10147 - 5	94	1	4.4*	2.88	3.19	3; 4	4
10147 - 6	96	2	2.96	1.60	1.88	2; 3; 4	4
Pooled	565	19	9.0**	2.93	4.1*	3	3
5 D.F.	Homogeneity X^2 for 15:1				1.6ns		
5 D.F.	Homogeneity X^2 for 60:3				2.1ns		
5 D.F.	Homogeneity X^2 for 243:13				1.9ns		
Cross(4) F2	MS	LS	Ratio1 15:1	Ratio2 60:3	Ratio3 243:13	X^2	N
10148 - 1	61	5	0.20	1.15	0.85	2; 3; 4	1
10148 - 2	105	16	10.0**	19.1**	16.7**	?	1
10148 - 3	108	3	2.38	1.04	1.30	2; 3; 4	2
10148 - 4	109	1	5.4*	3.60	4.0*	3	1
10148 - 5	124	0	8.3**	6.2*	6.6*	?	1

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation	
Cross(4) F2	MS	LS	Ratio1 15:1	Ratio2 60:3	Ratio3 243:13	X^2	N
10148 - 6	129	7	0.28	0.04	0.00	2; 3; 4	1
Pooled	636	32	2.43	0.00	0.12	2; 3; 4	1
5 D.F.	Homogeneity X^2 for 15:1				24.1**		
5 D.F.	Homogeneity X^2 for 60:3				31.1**		
5 D.F.	Homogeneity X^2 for 243:13				12.6*		
Cross(4) BC(2)	LS	MS	Ratio 1 2:1		Ratio 2 11:5	X^2	
10168 - 1	72	44	1.10		2.41	4	
Cross(8) F2	LS	MS	Ratio 1 63:1		Ratio 2 255:1	X^2	N
10152 - 1	161	2	0.12		2.90	3; 4	3
10152 - 2	104	0	1.65		0.41	3; 4	3
10152 - 3	119	3	0.64		13.4**	3	3
10152 - 4	95	1	0.17		1.05	3; 4	5
10152 - 5	112	1	0.34		0.71	3; 4	4
10152 - 6	122	0	1.94		0.48	3; 4	4
Pooled	713	7	1.63		6.3*	3	3
5 D.F.	Homogeneity X^2 for 63:1				3.2ns		
5 D.F.	Homogeneity X^2 for 255:1				12.7*		

*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(10) F2	LS	SS	Ratio 1 63:1	Ratio 2 255:1	X^2	N
10154 - 1	163	2	0.13	2.86	3; 4	3
10154 - 2	155	4	0.94	18.5**	3	2
10154 - 3	132	1	0.57	0.45	3; 4	4
10154 - 4	173	1	1.10	0.15	3; 4	2
10154 - 5	152	0	2.41	0.60	3; 4	4
10154 - 6	164	0	2.60	0.64	3; 4	5
Pooled	939	8	3.17	5.0*	3	3
5 D.F. Homogeneity			X^2 for 63:1	4.6ns		
5 D.F. Homogeneity			X^2 for 255:1	18.1**		
Cross (10) BC(2)	SS	LS	Ratio1 1:1	Ratio2 3:1	Ratio3 5:3	X^2
10177 - 1	5	3	0.50	0.67	0.00	1; 2; 3
Cross(9) F2	Walor	Togo	Ratio1 3:1	Ratio2 13:3	Ratio3 54:10	X^2 N
10153 - 1	84	11	8.9**	3.21	1.18	2; 3 1
10153 - 2	87	40	2.86	13.4**	24.3**	1 1
10153 - 3	90	24	0.45	0.40	2.55	1; 2; 3 1
10153 - 4	72	18	1.20	0.09	1.31	1; 2; 3 1
10153 - 5	123	18	11.3**	3.31	0.87	2; 3 1
Pooled	456	111	8.9**	0.25	6.7**	2 1
4 D.F. Homogeneity			X^2 for 3:1	15.8**		
4 D.F. Homogeneity			X^2 for 13:3	20.3**		
4 D.F. Homogeneity			X^2 for 54:10	23.5**		

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes X^2 Direct calculation	
Cross(11) F2	Togo	Walor	Ratio 1 7:1	Ratio 2 55:9	X^2	N
10155 - 1	73	9	0.17	0.65	2; 3	3
10155 - 2	94	9	1.33	2.42	2; 3	2
10155 - 3	118	18	0.07	0.08	2; 3	2
10155 - 4	107	1	13.2**	15.4**	?	5
10155 - 5	98	12	0.26	0.91	2; 3	2
10155 - 6	74	6	1.83	2.85	2; 3	2
Pooled	564	55	7.4**	13.7**	?	2
5 D.F. Homogeneity X^2 for 7:1				9.5ns		
5 D.F. Homogeneity X^2 for 55:9				8.6ns		
Cross(11) BC(2)	Walor	Togo	Ratio1 3:1	Ratio2 5:3	Ratio3 39:25	X^2
10171 - 1	39	37	22.7**	4.1*	2.96	?
10171 - 2	16	4	0.27	2.61	3.05	2; 3
Pooled	55	41	16.1**	1.11	0.54	3
1 D.F. Homogeneity X^2 for 3:1				7.0**		
1 D.F. Homogeneity X^2 for 5:3				5.6*		
1 D.F. Homogeneity X^2 for 39:25				5.5*		

*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation	
						X^2	
Cross(12) F2	Walor	Togo	Ratio1 3:1	Ratio2 13:3	Ratio3 54:10	X^2	N
10156 - 1	101	20	4.6*	0.40	0.07	2; 3	1
10156 - 2	62	23	0.91	3.9*	8.4**	1	1
10156 - 3	38	15	0.31	3.17	6.5*	1; 2	1
10156 - 4	59	6	8.6**	3.9*	2.02	3	2
10156 - 5	86	11	9.7**	3.50	1.35	2; 3	1
10156 - 6	97	14	9.1**	2.54	0.76	2; 3	1
Pooled	443	89	19.4**	1.43	0.50	2; 3	1
5 D.F. Homogeneity X^2 for 3:1			13.80*				
5 D.F. Homogeneity X^2 for 13:3			15.90**				
5 D.F. Homogeneity X^2 for 54:10			18.60**				
Cross(14) F2	Togo	Walor	Ratio 1 13:3		Ratio 2 54:10	X^2	N
10157 - 1	99	24	0.05		1.41	2; 3	2
10157 - 2	87	30	3.65		8.9**	2	1
10157 - 3	113	18	2.16		0.353	2; 3	1
10157 - 4	111	12	6.5*		3.21	3	2
10157 - 5	103	13	4.3*		1.72	3	2
10157 - 6	96	35	5.5*		12.2**	?	2
Pooled	609	132	0.43		2.69	2; 3	1
5 D.F. Homogeneity X^2 for 13:3			21.8**				
5 D.F. Homogeneity X^2 for 54:10			25.1**				

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation	
Cross (14) BC(2)	Togo	Walor	Ratio1 1:1	Ratio2 3:1	Ratio3 5:3	X^2	
10172 - 1	3	3	0.00	2.00	0.40	1; 2; 3	
Cross(15) F2	LS	MS	Ratio1 15:1	Ratio2 225:31	Ratio3 243:13	X^2	N
10159 - 1	135	23	18.6**	0.89	29.5**	4	1
10159 - 2	157	8	0.55	8.2**	0.02	2; 4	2
10159 - 3	122	8	0.00	4.3*	0.31	4	2
10159 - 4	129	12	1.23	1.72	3.45	2; 4	2
10159 - 5	159	15	1.67	1.99	4.5*	2; 4	3
10159 - 6	138	12	0.78	2.38	2.66	2; 4	1
Pooled	840	78	7.9**	11.3**	22.3**	?	1
5 D.F. Homogeneity X^2 for 15:1					15.0*		
5 D.F. Homogeneity X^2 for 225:31					8.2ns		
5 D.F. Homogeneity X^2 for 243:13					18.2**		
Cross(13) F2	LS	SS	Ratio 1 7:1		Ratio 2 15:1	X^2	N
10158 - 1	127	4	10.7**		2.28	2	2
10158 - 2	140	19	0.04		9.8**	2	1
10158 - 3	158	18	0.83		4.8*	2	1
10158 - 4	153	8	8.4**		0.45	2	1
10158 - 5	169	13	4.8*		0.25	2	1

Table A11: Chi-square tests for Seed Size in 1987 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(13) F2	LS	SS	Ratio 1 7:1	Ratio 2 15:1	X^2	N
10158 - 6	112	20	0.85	17.9**	2	1
Pooled	859	82	12.3**	9.8**	?	1
5 D.F. Homogeneity X^2 for 7:1				13.2*		
5 D.F. Homogeneity X^2 for 15:1				25.6**		
Cross(13) BC(2)	LS	SS	Ratio 1 3:1	Ratio 2 7:1	X^2	
10181 - 1	121	16	13.0**	0.08	3	
10181 - 2	5	4	1.81	8.4**	2; 3	
10181 - 3	128	22	8.6**	0.64	3	
Pooled	254	42	18.5**	0.77	3	
2 D.F. Homogeneity X^2 for 3:1				4.9ns		
2 D.F. Homogeneity X^2 for 7:1				8.4*		

Cross(16) F2	LS	SS	Ratio1 15:1	Ratio2 60:3	Ratio3 243:13	X^2	N
10160 - 1	156	8	0.53	0.00	0.01	2; 3; 4	1
10160 - 2	153	8	0.45	0.02	0.00	2; 3; 4	1
10160 - 3	147	10	0.00	0.90	0.54	2; 3; 4	1
10160 - 4	129	13	2.05	6.0*	4.9*	2	1
10160 - 5	164	9	0.32	0.07	0.01	2; 3; 4	1

Table A11: Chi-square tests for Seed Size in 1987 (End)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation X^2	
Cross(16) F2	LS	SS	Ratio1 15:1	Ratio2 60:3	Ratio3 243:13	X^2	N
10160 - 6	132	8	0.07	0.28	0.12	2; 3; 4	1
Pooled	881	56	0.12	3.05	1.57	2; 3; 4	1
5 D.F.	Homogeneity		X^2 for 15:1		3.3ns		
5 D.F.	Homogeneity		X^2 for 60:3		4.3ns		
5 D.F.	Homogeneity		X^2 for 243:13		4.0ns		

LS = Large Seed ; MS = Medium Seed ; SS = Small Seed .
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A12: Chi-square tests for Headlength in 1986

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes X^2	Direct calculation
Cross(1) F2	SH	LH	Ratio 1 63:1		Ratio 2 255:1	X^2	N
9804	79	0	1.25		0.31	3; 4	3
Cross(1) BC(2)	SH	LH	Ratio 1 63:1		Ratio 2 255:1		
9801	119	0	1.89		0.47	?	
Cross(2) F2	SH	LH	Ratio 1 63:1		Ratio 2 255:1	X^2	N
9805	78	0	1.24		0.31	3; 4	4
Cross(2) BC(2)	SH	LH	Ratio 1 63:1		Ratio 2 255:1		
9802	79	0	1.25		0.31	?	
Cross(3) F2	SH	LH	Ratio1 15:1	Ratio2 63:1	Ratio3 255:1	X^2	N
9806	78	1	3.35	0.05	1.56	2; 3; 4	2
Cross(3) BC(1)	SH	LH	Ratio 1 63:1		Ratio 2 255:1		
9803	116	0	1.84		0.46	?	
Cross(10) F2	Walor	Togo	Ratio1 5:3	Ratio2 11:5	Ratio3 39:25	X^2	N
9850	74	28	4.3*	0.69	5.8*	2	5
9851	50	33	0.18	2.80	0.02	2	3
9852	22	7	2.21	0.68	2.71	2	1
9853	33	25	0.78	3.79	0.40	2	4
pooled	179	93	1.27	1.09	2.71	2	-
3 D.F. Homogeneity X^2 for 5:3					6.2ns		
[illegible] Homogeneity X^2 for 11:5					6.9ns		

Table A12: Chi-square tests for Headlength in 1986 (Cont.)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes X^2 irect calculation	
Cross(9) F2	Togo	T23DBE	Ratio1 3:1	Ratio2 11:5	Ratio3 49:15	X^2	N
9838	56	22	0.43	0.34	0.99	1; 2; 3	?
9839	47	19	0.51	0.19	1.1	1; 2; 3	1
9841	25	14	2.47	0.39	3.37	1; 2; 3	1
9842	55	18	0.01	1.48	0.06	1; 2; 3	2
Pooled	183	73	1.69	0.89	3.68	1; 2; 3	-
3 D.F. Homogeneity			X^2 for 3:1		1.7ns		
3 D.F. Homogeneity			X^2 for 11:5		1.5ns		
3 D.F. Homogeneity			X^2 for 49:15		1.8ns		
Cross(9) F2	Togo	T23DBE	Ratio 4 45:19			X^2	N
838	56	22	0.08			3	?
9839	47	19	0.03			3	1
9841	25	14	0.72			3	1
9842	55	18	0.89			3	2
Pooled	183	73	0.17			3	-
3 D.F. Homogeneity			X^2 for 45:19		1.6ns		

Table A12: Chi-square tests for Headlength in1986 (Cont.)

	of Plants		Ratios with non-significant (p>0.05) Chisquare Values			Number of genes Direct calculation X^2	
Cross(9) BC(2)	Togo	T23DBE	Ratio1 3:1	Ratio2 11:5	Ratio3 45:19	X^2	
9843	54	24	1.39	0.01	0.04	2; 3; 4	
9844	80	27	0.00	1.80	1.02	2; 3; 4	
Pooled	134	51	0.65	1.17	0.40	2; 3; 4	
1 D.F. Homogeneity X^2 for 3:1 0.74ns							
1 D.F. Homogeneity X^2 for 11:5 0.64ns							
1 D.F. Homogeneity X^2 for 45:19 0.7ns							
Cross(13) F2	LH	SH	Ratio1 7:1	Ratio2 55:9	Ratio3 225:31	X^2	N
9854	90	8	1.69	2.82	1.43	2; 3; 4	33
9855	83	8	1.14	2.10	0.94	2; 3; 4	49
9856	66	17	4.8*	2.83	5.5*	3	12
9857	84	13	0.07	0.04	0.15	2; 3; 4	8
9858	78	6	2.20	3.33	1.95	2; 3; 4	12
9859	72	9	0.14	0.58	0.08	2; 3; 4	24
9860	74	12	0.17	0.00	0.28	2; 3; 4	39
Pooled	547	73	0.30	2.69	0.07	2; 3; 4	-
6 D.F. Homogeneity X^2 for 7:1 9.9ns							
6 D.F. Homogeneity X^2 for 55:9 9.0ns							
6 D.F. Homogeneity X^2 for 225:31 10.2ns							

Table A12: Chi-square tests for Headlength in 1986 (End)

	Number of Plants		Ratios with non-significant (p>0.05) Chisquare Values		Number of genes Direct calculation	
Cross(13) BC(1)	LH	SH	Ratio 1 3:1	Ratio 2 13:3	X^2	
9797	72	17	1.65	0.01	2; 3	
9798	80	23	0.39	0.87	2; 3	
9799	45	13	0.21	0.51	2; 3	
Pooled	197	53	1.93	0.99		
2 D.F. Homogeneity X^2 for 3:1				0.32ns		
2 D.F. Homogeneity X^2 for 13:3				0.40ns		
Cross(12) F2	Walor	T23DBE	Ratio 1 9:7	Ratio 2 37:27	X^2	N
9889	49	31	0.80	0.39	2; 3	3
9893	60	57	1.17	2.05	2; 3	3
9894	52	44	0.17	0.52	2; 3	3
Pooled	161	132	0.10	0.99	2; 3	-
2 D.F. Homogeneity X^2 for 9:7				2.04ns		
2 D.F. Homogeneity X^2 for 37:27				2.0ns		

LH = Longhead ; SH = Shorthead.
*: Chisquare (X^2) significant at p = 0.05
**: X^2 significant at p = 0.01; ns = nonsignificant X^2.

Table A13A: Linkage Study in 1987: Maturity/Headlength

Cross (1) Ratio	Early > Late 15:1		SH > LH 63:1		Linkage 945: 15: 63: 1	
Family	Early SH	Early LH	Late SH	Late LH	Chisq.	D.F.
10145-1	164	1	10	1	4.827 ns	3
10145-2	133	6	15	0	1.518 ns	3
10145-3	146	5	15	0	0.990 ns	3
10145-4	189	5	1	0	0.108 ns	3
10145-5	156	12	17	2	6.062 ns	3
10145-6	139	5	4	0	0.398 ns	3
Pooled	927	34	62	3	0.491 ns	3
Homogeneity					13.411 ns	15

Cross (1) Ratio	Early > Late 7:1		SH > LH 63:1		Linkage 441: 7: 63: 1	
Family	Early LH	Early SH	Late LH	Late SH	Chisq.	D.F.
10145-1	164	1	10	1	2.870 ns	3
10145-2	133	6	15	0	1.804 ns	3
10145-3	146	5	15	0	1.026 ns	3
10145-4	189	5	1	0	0.206 ns	3
10145-5	156	12	17	2	0.322 ns	3
10145-6	139	5	4	0	0.638 ns	3
Pooled	927	34	62	3	0.235 ns	3
Homogeneity					6.630 ns	15

ns = non significant at p = 0.05.
SH = short head; LH = long head.

Table A13A: Linkage Study in 1987:Maturity/Headlength (Cont.)

Cross (3) Ratio	Early > Late 63:1		LH > SH 63:1		Linkage 3969: 63: 63: 1	
Family	Early LH	Early SH	Late LH	Late SH	Chisq.	D.F.
10147-1	96	1	10	0	0.839 ns	3
10147-2	106	1	1	0	0.001 ns	3
10147-3	94	0	5	0	0.124 ns	3
10147-4	137	0	0	0	0.035 ns	3
10147-5	114	1	0	0	0.006 ns	3
10147-6	120	0	1	0	0.007 ns	3
Pooled	667	3	17	0	0.129 ns	3
Homogeneity					0.882 ns	15
Cross (4) Ratio	Late > Early 255:1		LH > SH 7:1		Linkage 1785: 255: 7: 1	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10148-1	67	9	0	0	0.000 ns	3
10148-2	114	9	0	0	0.012 ns	3
10148-3	113	4	1	0	0.137 ns	3
10148-4	98	12	0	0	0.001 ns	3
10148-5	101	22	2	0	1.421 ns	3
10148-6	110	26	0	1	11.999 **	3
Pooled	603	82	3	1	0.895 ns	3
Homogeneity					12.675 ns	15

ns = non significant at p = 0.05.
SH = short head; LH = long head.

Table A13A: Linkage Study in 1987: Maturity/Headlength (Cont.)

Cross (4) Ratio	Late > Early 255:1		LH > SH 55:9		Linkage 14025:2295:55:9	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10148-1	67	9	0	0	0.001 ns	3
10148-2	114	9	0	0	0.018 ns	3
10148-3	113	4	1	0	0.151 ns	3
10148-4	98	12	0	0	0.004 ns	3
10148-5	101	22	2	0	1.516 ns	3
10148-6	110	26	0	1	10.672 *	3
Pooled	603	82	3	1	0.746 ns	3
		Homogeneity			11.615 ns	15
Cross (7) Ratio	Late > Early 13:3		LH > SH 15:1		Linkage 195: 13: 45: 3	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10150-1	159	21	20	3	0.172 ns	3
10150-2	146	0	45	0	0.193 ns	3
10150-3	151	7	34	3	0.692 ns	3
10150-4	138	8	28	1	0.129 ns	3
10150-5	118	0	42	1	0.000 ns	3
Pooled	712	36	169	8	0.027 ns	3
		Homogeneity			1.160 ns	12

ns = non significant at p = 0.05.
SH = short head; LH = long head.

Table A13A: Linkage Study in 1987: Maturity/Headlength (Cont.)

Cross (7) Ratio	Late > Early 3:1		LH > SH 15:1		Linkage 45: 3: 15: 1	
Family	Late LH	Late SH	Early LH	Early SH	Chisq.	D.F.
10150-1	159	21	20	3	0.718 ns	3
10150-2	146	0	45	0	0.014 ns	3
10150-3	151	7	34	3	0.711 ns	3
10150-4	138	8	28	1	0.056 ns	3
10150-5	118	0	42	1	0.189 ns	3
Pooled	712	36	169	8	0.015 ns	3
		Homogeneity			1.673 ns	12

Cross (15) Ratio	Early > Late 7:1		SH > LH 63:1		Linkage 441: 7: 63: 1	
Family	Early LH	Early SH	Late LH	Late SH	Chisq.	D.F.
10159-1	146	0	19	0	0.002 ns	3
10159-2	145	0	23	0	0.003 ns	3
10159-3	127	0	11	0	0.041 ns	3
10159-4	123	0	21	0	0.009 ns	3
10159-5	174	0	2	0	0.330 ns	3
10159-6	139	0	11	0	0.058 ns	3
Pooled	854	0	87	0	0.145 ns	3
		Homogeneity			0.299 ns	15

ns = non significant at p = 0.05.
SH = short head; LH = long head.

Table A13A: Linkage Study in 1987: Maturity/Headlength (End.)

Cross (15) Ratio	Early > Late 225:31		SH > LH 63:1		Linkage 14175:225:1953:31	
Family	Early LH	Early SH	Late LH	Late SH	Chisq.	D.F.
10159-1	146	0	19	0	0.001 ns	3
10159-2	145	0	23	0	0.006 ns	3
10159-3	127	0	11	0	0.035 ns	3
10159-4	123	0	21	0	0.013 ns	3
10159-5	174	0	2	0	0.316 ns	3
10159-6	139	0	11	0	0.051 ns	3
Pooled	854	0	87	0	0.115 ns	3
		Homogeneity			0.307 ns	15

Table D11B: Linkage Study in 1987: Maturity/Seed size

Cross (3) Ratio	Early > Late 63:1		LS > MS 60:3		Linkage 3780:189:60:3	
Family	Early LS	Early MS	Late LS	Late MS	Chisq.	D.F.
10147-1	86	1	7	3	94.862 **	3
10147-2	84	3	0	0	0.005 ns	3
10147-3	86	4	5	0	0.798 ns	3
10147-4	107	5	0	0	0.000 ns	3
10147-5	94	1	0	0	0.046 ns	3
10147-6	95	2	1	0	0.001 ns	3
Pooled	552	16	13	3	13.855 **	3
		Homogeneity			81.856 **	15

SH = short head; LH = long head.
ns = non significant at p = 0.05.

Table A13B: Linkage Study in 1987: Maturity/Seed size (Cont.)

Cross (3) Ratio	Early > Late 63:1		LS > MS 243:13		Linkage 15309:819:243:13	
Family	Early LS	Early MS	Late LS	Late MS	Chisq.	D.F.
10147-1	86	1	7	3	87.371 **	3
10147-2	84	3	0	0	0.008 ns	3
10147-3	86	4	5	0	0.825 ns	3
10147-4	107	5	0	0	0.001 ns	3
10147-5	94	1	0	0	0.051 ns	3
10147-6	95	2	1	0	0.000 ns	3
Pooled	552	16	13	3	12.798 **	3
		Homogeneity			75.457 **	15

Cross (3) Ratio	Early > Late 63:1		LH > MS 15:1		Linkage 945: 63: 15: 1	
Family	Early LS	Early MS	Late LS	Late MS	Chisq.	D.F.
10147-1	86	1	7	3	66.287 **	3
10147-2	84	3	0	0	0.019 ns	3
10147-3	86	4	5	0	0.930 ns	3
10147-4	107	5	0	0	0.010 ns	3
10147-5	94	1	0	0	0.070 ns	3
10147-6	95	2	1	0	0.000 ns	3
Pooled	552	16	13	3	9.820 *	3
		Homogeneity			57.495 **	15

LS = large seed ; MS = medium seed .
ns = non significant at p = 0.05.

Table A13B: Linkage Study in 1987: Maturity/Seed size (Cont.)

Cross (4) Ratio	Late > Early 255:1		MS > LS 60:3		Linkage 15300:765:60:3	
Family	Late MS	Late LS	Early MS	Early LS	Chisq.	D.F.
10148-1	61	5	0	0	0.005 ns	3
10148-2	105	16	0	0	0.075 ns	3
10148-3	108	3	1	0	0.075 ns	3
10148-4	109	1	0	0	0.014 ns	3
10148-5	122	0	2	0	0.238 ns	3
10148-6	128	7	1	0	0.103 ns	3
Pooled	633	32	4	0	0.309 ns	3
		Homogeneity			0.200 ns	15

Cross (4) Ratio	Late > Early 255:1		MS > LS 15:1		Linkage 3825:255:15:1	
Family	Late MS	Late LS	Early MS	Early LS	Chisq.	D.F.
10148-1	61	5	0	0	0.001 ns	3
10148-2	105	16	0	0	0.039 ns	3
10148-3	108	3	1	0	0.086 ns	3
10148-4	109	1	0	0	0.021 ns	3
10148-5	122	0	2	0	0.317 ns	3
10148-6	128	7	1	0	0.103 ns	3
Pooled	633	32	4	0	0.294 ns	3
		Homogeneity			0.274 ns	15

LS = large seed ; MS = medium seed.
ns = non significant at p = 0.05.

Table A13B: Linkage Study in 1987: Maturity/Seed size (End)

Cross (4) Ratio	Late > Early 255:1		MS > LS 243:13		Linkage 61965:3315:243:13	
Family	Late MS	Late LS	Early MS	Early LS	Chisq.	D.F.
10148-1	61	5	0	0	0.003 ns	3
10148-2	105	16	0	0	0.065 ns	3
10148-3	108	3	1	0	0.077 ns	3
10148-4	109	1	0	0	0.016 ns	3
10148-5	122	0	2	0	0.255 ns	3
10148-6	128	7	1	0	0.103 ns	3
Pooled	633	32	4	0	0.304 ns	3
		Homogeneity			0.214 ns	15

LS = large seed; MS = medium seed .
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size

Cross (3) Ratio	LH > SH 63:1		LS > MS 15:1		Linkage 945: 63: 15: 1	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10147-1	92	4	1	0	0.010 ns	3
10147-2	83	3	1	0	0.008 ns	3
10147-3	91	4	0	0	0.011 ns	3
10147-4	107	5	0	0	0.010 ns	3
10147-5	93	1	1	0	0.003 ns	3
10147-6	96	2	0	0	0.047 ns	3
Pooled	562	19	3	0	0.014 ns	3
		Homogeneity			0.074 ns	15
Cross (3) Ratio	LH > SH 63:1		LS > MS 60:3		Linkage 3780: 189: 60: 3	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10147-1	92	4	1	0	0.021 ns	3
10147-2	83	3	1	0	0.015 ns	3
10147-3	91	4	0	0	0.001 ns	3
10147-4	107	5	0	0	0.000 ns	3
10147-5	93	1	1	0	0.001 ns	3
10147-6	96	2	0	0	0.025 ns	3
Pooled	562	19	3	0	0.000 ns	3
		Homogeneity			0.063 ns	15

MS = medium seed; LS = large seed;
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (Cont.)

Cross (3) Ratio	LH > SH 63:1		LS > MS 243:13		Linkage 15309:819:243:13	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10147-1	92	4	1	0	0.018 ns	3
10147-2	83	3	1	0	0.013 ns	3
10147-3	91	4	0	0	0.002 ns	3
10147-4	107	5	0	0	0.001 ns	3
10147-5	93	1	1	0	0.001 ns	3
10147-6	96	2	0	0	0.030 ns	3
Pooled	562	19	3	0	0.000 ns	3
		Homogeneity			0.065 ns	15

Cross (4) Ratio	LH > SH 7:1		MS > LS 60:3		Linkage 420: 21: 60: 3	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	1.018 ns	3
10148-2	98	15	7	1	0.727 ns	3
10148-3	101	3	3	0	0.027 ns	3
10148-4	97	1	12	0	0.003 ns	3
10148-5	103	0	21	0	0.112 ns	3
10148-6	104	6	25	1	0.137 ns	3
Pooled	561	29	71	3	0.099 ns	3
		Homogeneity			1.925 ns	15

MS = medium seed; LS = large seed;
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (Cont.)

Cross (4) Ratio	LH > SH 7:1		MS > LS 15:1		Linkage 105: 7: 15: 1	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	0.970 ns	3
10148-2	98	15	7	1	0.397 ns	3
10148-3	101	3	3	0	0.109 ns	3
10148-4	97	1	12	0	0.000 ns	3
10148-5	103	0	21	0	0.149 ns	3
10148-6	104	6	25	1	0.220 ns	3
Pooled	561	29	71	3	0.045 ns	3
	Homogeneity				1.800 ns	15

Cross (4) Ratio	LH > SH 7:1		MS > LS 243:13		Linkage 1701 91: 243: 13	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	1.003 ns	3
10148-2	98	15	7	1	0.638 ns	3
10148-3	101	3	3	0	0.041 ns	3
10148-4	97	1	12	0	0.002 ns	3
10148-5	103	0	21	0	0.119 ns	3
10148-6	104	6	25	1	0.154 ns	3
Pooled	561	29	71	3	0.084 ns	3
	Homogeneity				1.874 ns	15

LS = large seed; MS = medium seed;
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (Cont.)

Cross (4) Ratio	LH > SH 55:9		MS > LS 60:3		Linkage 3300:165:540:27	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	0.831 ns	3
10148-2	98	15	7	1	1.016 ns	3
10148-3	101	3	3	0	0.039 ns	3
10148-4	97	1	12	0	0.001 ns	3
10148-5	103	0	21	0	0.042 ns	3
10148-6	104	6	25	1	0.130 ns	3
Pooled	561	29	71	3	0.092 ns	3
	Homogeneity				1.968 ns	15

Cross (4) Ratio	LH > SH 55:9		MS > LS 15:1		Linkage 825: 55: 135: 9	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	0.841 ns	3
10148-2	98	15	7	1	0.550 ns	3
10148-3	101	3	3	0	0.145 ns	3
10148-4	97	1	12	0	0.007 ns	3
10148-5	103	0	21	0	0.056 ns	3
10148-6	104	6	25	1	0.178 ns	3
Pooled	561	29	71	3	0.018 ns	3
	Homogeneity				1.760 ns	15

LS = large seed;
MS = medium seed; ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (Cont.)

Cross (4) Ratio	LH > SH 55:9		MS > LS 243:13		Linkage 13365:715:2187:117	
Family	LH MS	LH LS	SH MS	SH LS	Chisq.	D.F.
10148-1	58	4	3	1	0.830 ns	3
10148-2	98	15	7	1	1.890 ns	3
10148-3	101	3	3	0	0.058 ns	3
10148-4	97	1	12	0	0.002 ns	3
10148-5	103	0	21	0	0.045 ns	3
10148-6	104	6	25	1	0.140 ns	3
Pooled	561	29	71	3	0.069 ns	3
	Homogeneity				1.897 ns	15

Cross (8) Ratio	LH > SH 7:1		LS > MS 63:1		Linkage 441: 7: 63: 1	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10152-1	143	2	18	0	0.165 ns	3
10152-2	81	0	13	0	0.002 ns	3
10152-3	102	3	17	0	0.789 ns	3
10152-4	89	1	6	0	0.006 ns	3
10152-5	97	1	15	0	0.101 ns	3
10152-6	102	0	20	0	0.027 ns	3
Pooled	614	7	89	0	0.647 ns	3
	Homogeneity				0.444 ns	15

LS = large seed; MS = medium seed ;
ns = non significant at p =0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (Cont.)

Cross (8) Ratio	LH > SH 7:1		LS > MS 255:1		Linkage 1785: 7: 255: 1	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10152-1	143	2	18	0	0.835 ns	3
10152-2	81	0	13	0	0.001 ns	3
10152-3	102	3	17	0	2.808 ns	3
10152-4	89	1	6	0	0.252 ns	3
10152-5	97	1	15	0	0.343 ns	3
10152-6	102	0	20	0	0.007 ns	3
Pooled	614	7	89	0	2.539 ns	3
	Homogeneity				1.707 ns	15
Cross (8) Ratio	LH > SH 55:9		LS > MS 63:1		Linkage 3465: 55: 567: 9	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10152-1	143	2	18	0	0.138 ns	3
10152-2	81	0	13	0	0.000 ns	3
10152-3	102	3	17	0	0.776 ns	3
10152-4	89	1	6	0	0.003 ns	3
10152-5	97	1	15	0	0.076 ns	3
10152-6	102	0	20	0	0.009 ns	3
Pooled	614	7	89	0	0.503 ns	3
	Homogeneity				0.499 ns	15

LS = large seed ; MS = medium seed ;
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A13C: Linkage Study in 1987: Headlength/Seed size (End)

Cross (8) Ratio	LH > SH 55:9		LS > MS 255:1		Linkage 14025:55:2295:9	
Family	LH LS	LH MS	SH LS	SH MS	Chisq.	D.F.
10152-1	143	2	18	0	0.896 ns	3
10152-2	81	0	13	0	0.000 ns	3
10152-3	102	3	17	0	3.093 ns	3
10152-4	89	1	6	0	0.275 ns	3
10152-5	97	1	15	0	0.354 ns	3
10152-6	102	0	20	0	0.002 ns	3
Pooled	614	7	89	0	2.558 ns	3
		Homogeneity			1.962 ns	15

LS = large seed; MS = medium seed ;
ns = non significant at p = 0.05.
LH = long head; SH = short head.

Table A14: Summary of the minmum number of genes per cross

M A T U R I T Y I N 1 9 8 7

Cross (1) Late Gero * Early T23DBE Family	Minimum gene number	Maximum gene number
10145 - 1	2	2
10145 - 2	2	3
10145 - 3	2	3
10145 - 4	1 ?	?
10145 - 5	2	3
10145 - 6	2	2
Pooled	2	2

Cross(3) Late Gero * Early Walor Family	Minimum gene number	Maximum gene number
10147 - 1	3 ?	?
10147 - 2	3 ?	8 ?
10147 - 3	3 ?	6
10147 - 4	3 ?	?
10147 - 5	3 ?	?
10147 - 6	3 ?	?
Pooled	3 ?	8 ?

Table A14: Summary of the minmum number of genes per cross

M A T U R I T Y I N 1 9 8 7 (Cont.)

Cross(4) Late Gero * Early Walor Family	Minimum gene number	Maximum gene number
10148 - 1	3 ?	7 ?
10148 - 2	3 ?	7 ?
10148 - 3	3 ?	?
10148 - 4	3 ?	5 ?
10148 - 5	3 ?	?
10148 - 6	3 ?	9 ?
Pooled	3 ?	?

Cross(7) Early T18BE * Late T23B Family	Minimum gene number	Maximum gene number
10150 - 2	1 ?	3
10150 - 3	1	2
10150 - 4	1	3
10150 - 5	1 ?	3
10150 - 6	1	1
Pooled	1 ?	2

Table A14: Summary of the minmum number of genes per cross

M A T U R I T Y I N 1 9 8 7 (End)		
Cross(15) Early Togo * Late Gero Family	Minimum gene number	Maximum gene number
10159 - 1	2 ?	?
10159 - 2	2 ?	?
10159 - 3	2 ?	7 ?
10159 - 4	2 ?	4
10159 - 5	?	?
10159 - 6	2 ?	?
Pooled	?	6 ?

Table A14: Summary of the minmum number of genes per cross

H E A D L E N G T H

Cross(1) IN 1987 Longhead Gero * Short head T23DBE

Family	Minimum gene number	Maximum gene number
10145 - 1	3 ?	4
10145 - 2	4 ?	7 ?
10145 - 3	3 ?	6 ?
10145 - 4	3 ?	5 ?
10145 - 5	3 ?	4 ?
10145 - 6	3 ?	?
Pooled	5 ?	?

Cross(1) in 1986 Longhead Gero * Short head T23DBE

Family	Minimum gene number	Maximum gene number
9804	3	4

Cross(2) in 1986 Longhead Gero * Short head T23DBE

Family	Minimum gene number	Maximum gene number
9805	3 ?	4

Cross(3) in 1986 Longhead Gero * Short head T23DBE

Family	Minimum gene number	Maximum gene number
9806	2	4

Cross(2) in 1987 Longhead Gero * Short head T23B

Family	Minimum gene number	Maximum gene number
10146 - 1	3 ?	5 ?
10146 - 3	3 ?	?
10146 - 4	4 ?	?
10146 - 5	3 ?	?
Pooled	?	5 ?

Table A14: Summary of the minmum number of genes per cross

H E A D L E N G T H (Cont.)

Cross(3) in 1987 Longhead Gero * Short head Walor Family	Minimum gene number	Maximum gene number
10147 - 1	2 ?	4
10147 - 2	3 ?	4
10147 - 3	3 ?	9 ?
10147 - 4	3 ?	4
10147 - 5	3 ?	5 ?
10147 - 6	3 ?	?
Pooled	4	4

Cross(4) in 1987 Longhead Gero * Short head Walor Family	Minimum gene number	Maximum gene number
10148 - 1	1 ?	3
10148 - 2	1 ?	3
10148 - 3	?	5 ?
10148 - 4	2	3
10148 - 5	2	3
10148 - 6	3	3
Pooled	2	3

Table A14: Summary of the minmum number of genes per cross

H E A D L E N G T H (Cont.)

Cross(6) in 1987 Longhead T18BE * Short head T23DBE Family	Minimum gene number	Maximum gene number
10149 - 1	3 ?	4
10149 - 2	2 ?	4
10149 - 3	3 ?	5 ?
10149 - 4	3 ?	4
10149 - 5	3 ?	5 ?
10149 - 6	3 ?	4
Pooled	3 ?	4 ?

Cross(7) in 1987 Longhead T18BE * Short head T23B Family	Minimum gene number	Maximum gene number
10150 - 2	?	6 ?
10150 - 3	3 ?	?
10150 - 4	2 ?	6 ?
10150 - 5	2 ?	6 ?
10150 - 6	3 ?	9 ?
Pooled	2 ?	9 ?

Cross(8) in 1987 Longhead T18BE * Short head Walor Family	Minimum gene number	Maximum gene number
10152 - 1	2	3
10152 - 2	2	3
10152 - 3	2	3
10152 - 4	2 ?	3
10152 - 5	2	3
10152 - 6	2	3
Pooled	2	3

Table A14: Summary of the minmum number of genes per cross

H E A D L E N G T H (Cont.)

Cross(15) in 1987 Shorthead Togo * Longhead Gero Family	Minimum gene number	Maximum gene number
10159 - 1	3 ?	?
10159 - 2	3 ?	9 ?
10159 - 3	3 ?	8 ?
10159 - 4	3 ?	?
10159 - 5	3 ?	?
10159 - 6	3 ?	?
Pooled	4 ?	?

Cross(13) in 1986 Shorthead Togo * Longhead Gero Family	Minimum gene number	Maximum gene number
9854	2 ?	?
9855	2 ?	?
9856	3 ?	?
9857	2 ?	8 ?
9858	2 ?	?
9859	2 ?	?
9860	2 ?	?
Pooled	2 ?	?

Cross(10) in 1986 Shorthead Walor * Shorthead Togo Family	Minimum gene number	Maximum gene number
9850	2 ?	5
9851	2 ?	3
9852	1 ?	2
9853	2 ?	4
pooled	2 ?	?

Table A14: Summary of the minmum number of genes per cross

H E A D L E N G T H (End)

Cross(9) in 1986 Shorthead Togo * Longhead Gero Family	Minimum gene number	Maximum gene number
9838	1 ?	?
9839	1	3
9841	1	3
9842	1 ?	3
Pooled	1 ?	?

Cross(12) in 1986 Shorthead Togo * Longhead Gero Family	Minimum gene number	Maximum gene number
9889	2 ?	3
9893	2 ?	3
9894	2 ?	3
Pooled	2 ?	3 ?

Table A14: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7		
Cross(3) Family	Medium seed Gero * Minimum gene number	Large seed Walor Maximum gene number
10147 - 1	2	4
10147 - 2	2	4
10147 - 3	1 ?	4
10147 - 4	1 ?	4
10147 - 5	3 ?	4
10147 - 6	2 ?	4
Pooled	3	3
Cross(4) Family	Medium seed Gero * Minimum gene number	Large seed Walor Maximum gene number
10148 - 1	1 ?	4
10148 - 2	1 ?	?
10148 - 3	2	4
10148 - 4	1 ?	3
10148 - 5	1 ?	?
10148 - 6	1 ?	4
Pooled	1 ?	4

Table A14: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7 (Cont.)

Cross(8) Family	Medium seed T18BE * Large seed Walor Minimum gene number	Maximum gene number
10152 - 1	3	4
10152 - 2	3	4
10152 - 3	3	3
10152 - 4	3 ?	5
10152 - 5	3 ?	4
10152 - 6	3 ?	4
Pooled	3	3

Cross(10) Family	Large seed Walor * Small seed T23DBE Minimum gene number	Maximum gene number
10154 - 1	3	4
10154 - 2	2 ?	3
10154 - 3	3 ?	4
10154 - 4	2 ?	4
10154 - 5	3 ?	4
10154 - 6	3 ?	5
Pooled	3	3

Cross(9) Family	Large seed Togo * Large seed Walor Minimum gene number	Maximum gene number
10153 - 1	1 ?	3
10153 - 2	1	1
10153 - 3	1	3
10153 - 4	1	3
10153 - 5	1 ?	3
Pooled	1 ?	2

Table A14: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7 (Cont.)

Cross(11) Family	Large seed Togo * Minimum gene number	Large seed Walor Maximum gene number
10155 - 1	2 ?	3
10155 - 2	2	3
10155 - 3	2	3
10155 - 4	2	5 ?
10155 - 5	2	3
10155 - 6	2	3
Pooled	?	2 ?

Cross(12) Family	Large seed Togo * Minimum gene number	Large seed Walor Maximum gene number
10156 - 1	1 ?	3
10156 - 2	1	1
10156 - 3	1	2
10156 - 4	2 ?	3
10156 - 5	1 ?	3
10156 - 6	1 ?	3
Pooled	1 ?	3

Table A14: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7 (Cont.)		
Cross(14) Family	Large seed Togo * Large seed Walor Minimum gene number	Maximum gene number
10157 - 1	2	3
10157 - 2	1 ?	2
10157 - 3	1 ?	3
10157 - 4	2 ?	3
10157 - 5	2 ?	3
10157 - 6	2 ?	?
Pooled	1 ?	3
Cross(15) Family	Large seed Togo * Medium seed Gero Minimum gene number	Maximum gene number
10159 - 1	1 ?	4
10159 - 2	2	4
10159 - 3	2 ?	4
10159 - 4	2	4
10159 - 5	2 ?	4
10159 - 6	1 ?	4
Pooled	1 ?	?

Table A14: Summary of the minmum number of genes per cross

S E E D S I Z E I N 1 9 8 7 (End)		
Cross(13) Family	Large seed Togo * Minimum gene number	Small seed T23DBE Maximum gene number
10158 - 1	2 ?	3
10158 - 2	1 ?	2
10158 - 3	1 ?	2
10158 - 4	1 ?	2
10158 - 5	1 ?	2
10158 - 6	1 ?	2
Pooled	1 ?	?
Cross(16) Family	Large seed Togo * Minimum gene number	Small seed T23DBE Maximum gene number
10160 - 1	1 ?	4
10160 - 2	1 ?	4
10160 - 3	1 ?	4
10160 - 4	1 ?	2
10160 - 5	1 ?	4
10160 - 6	1 ?	4
Pooled	1 ?	4

RESUME EN FRANCAIS DE LA THESE AYANT POUR TITRE :

FACTORS INFLUENCING GRAIN YIELD IN PEARL MILLET PENNISETUM glaucum (L.) R. Br.

by

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Facteurs influençant le rendement en grains du mil, Pennisetum glaucum (L.) R. Br.

Par Widi TCHALA / Sous la direction de Wayne W. HANNA[1]

RESUME

Pour avoir suffisamment d'aliments de bonne qualité pour la population humaine galopante, il est nécessaire d'augmenter les rendements d'une plante hautement digestiblie et nourrissante comme le mil, Pennesetum glaucum (L.) R. Br.
Entre 1985 et 1987, deux études parallèles ont été memées à la station exprérimentale de Tifton, Georgia aux USA (*Coastal Plain Experiment Station, Tifton, Georgia, USA)*, l'une concernant les méthodes de vulgarisation et l'autre traitant de l'aspect amélioration génétique, en vue d'identifier les facteurs influençant le rendement en grains du mil et ses composants.

LE VOLET AMENAGEMENT/GENETIQUE DES PLANTES

L'objectif scientifique du volet qui a trait à la vulgarisation était de déterminer les effets agronomiques de la date du semis, de la densité, du nanisme, de la précocité et des maladies foliaires (la pyriculariose causée par Pyricularia grisea (Cke) Salc., et la rouille causée par Puccinia substriata var indica) sur les caractéristiques des plantes.
Pour cela, quatre lignées proches-isogéniques (différant seulement au niveau de quelques loci) ont été cultivées pendant deux années consécutives (1985 et 1986), en split plot avec deux facteurs, la densité à deux niveaux et la variété représentée par les quatre lignées. Les deux niveaux de densité (la haute densité avec 444 000 plants à l'hectare, et la faible densité avec 66 000 plants à l'hectare) occupaient chacune une parcelle principale portant chacune des quatre lignées sur des parcelles secondaires. Le dispositif expérimental utilisé était le système de blocs complètement randomisés (Completly Randomised Bloc Design ou CRBD en anglais) avec 8 répétitions en 1985 et 5 répétitions en 1986. Deux semis décalés ont été effectués chaque année pour étudier l'effet de la date de semis. En vue d'étudier les effets des maladies foliaires sur le rendement des lignées, des débris de mil

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infecté en pépinière et hâché à la machine ont été uniformément répandus dans le champ à chaque saison de culture, au moment opportun.

Les résultats ont montré que la précocité des lignées a augmenté leur sensibilité aux maladies foliaires, le tallage, la taille des grains et le rendement, mais a diminué la taille des plants. Le nanisme des lignées a augmenté le tallage mais a diminué la productivité (masse des grains d'une chandelle) et le rendement. La forte densité de population des plantes a plus favorisé la maturité des plants et leur sensibilité aux maladies foliaires, et plus augmenté la taille des plants, mais moins favorisé le tallage et la productivité en comparaison avec la faible densité de population. Le semis tardif a eu tendance à réduire le temps de maturité, le tallage, la productivité et le rendement en grains, mais a augmenté la taille des plants. L'effet des maladies foliaires, bien que statistiquement significatif sur le tallage, la productivité et le rendement, n'était pas agronomiquement important.

LE VOLET AMELIORATION / GENETIQUE DES PLANTES

Ce volet amélioration devrait permettre de déterminer d'une part les bases génétiques de la précocité (ou maturité), de la longueur des chandelles et de la taille (grosseur) des grains, et d'autre part, les possibilités de créer des cultivars nains, précoces, à longues chandelles et à gros grains. Trois lignées de mil Tift (crées à Tifton, Georgia) et trois lignées introduites à Tifton, soit au total six lignées ont été croisées jusqu'aux backcross et à la génération F_2, en passant par la F_1, dans le cadre de cette étude.

L'analyse des résultats a permis de noter que l'hétérosis était faible (-11 à 8 %) pour la précocité (maturité), la longueur des chandelles et la taille des grains, alors que l'héritabilité au sens large mesurée au niveau des parcelles était respectivement de 65 %, 58 % et 74 %, pour ces trois caractères. La fréquence de distribution en F_2 était continue pour la longueur des chandelles et la taille des grains mais à pics pour la précocité. Le phénotype gros grain était dominant sur petit grain. Pour la précocité et la longueur de la chandelle le sens de la dominance était variable selon les croisements. La superdominance a été notée en ce qui

concerne la taille des grains et la longueur des chandelles. Le nombre minimal de loci (gènes) contrôlant chaque caractère révélé par l'étude est de 1 ou 2 pour la taille des grains, au moins 2 pour la longueur de la chandelle et 1 à 3 gènes pour la précocité.

Mots clés : mil à chandelle, *Pennisetum glaucum*, dates de semis, précocité, densité, nanisme, maladies foliaires, longueur de chandelle, taille des grains, Tifton, lignées Tift, nombre de gènes, loci

(I) INTRODUCTION

Le mil à chandelle, Pennisetum glaucum, est par ordre d'importance socio-économique, la sixième céréale du monde et la céréale la plus cultivée dans les zones semi-arides où, selon Burton (1983), il peut croître et produire une récolte sur des sols sableux ou caillouteux, trop acides, trop secs ou trop stériles pour le sorgho (Sorgum bicolor(L.) moench) ou pour le maïs (Zea mays (L.)). Selon le même auteur, le mil a un grand potentiel de production fourragère et peut produire plus de fourrage que le sorgho ou le maïs (Burton,1983), dont les meilleurs hybrides surclassent cependant ceux du mil en rendement en grains en conditions optimales. Frère (1982) a en effet montré que les rendements moyens en grains du maïs, du sorgho et du mil sont respectivement de 4500, 3000 et 1250 kg/ha dans les meilleures conditions de culture et de 1000, 875 et 600 kg/ha, respectivement, dans des conditions moins favorables.

Ce faible rendement en grains du mil mérite d'être corrigé par le développement de cultivars plus productifs surtout à cause du fait qu'il est irremplaçable dans certaines zones semi-arides et que par conséquent une meilleure production permettrait de mieux satisfaire les besoins des populations qui ne peuvent cultiver que cette céréale.

De meilleurs rendements chez le mil permettraient aussi d'encourager l'intérêt croissant pour le sorgho et le mil en Amérique Latine (560%), en Asie (100%) et en Afrique (66%), selon Frère (1982) et aux USA où le mil passe progressivement de culture fourragère en culture céréalière, selon Hanna (1985, communication personnelle) utilisable pour l'alimentation de la vollaille.

D'une façon plus générale, l'amélioration de la production du mil est une nécessité pour l'alimentation en zones tropicales à croissance démographique rapide et aux conditions climatiques défavorables pour la culture d'autres céréales. Cette augmentation des rendements de mil peut se faire par le développement de cultivars de mil précoce à longues chandelles, à gros grains, résistant à la sécheresse et aux maladies. Mais parallèlement on peut aussi augmenter les rendements par l'utilisation de bonnes méthodes de vulgarisation.

Selon les informations disponibles (prospections à travers les zones de culture, Rachie and Majmudar (1980), etc), les potentialités pour accroître les rendements de mil existent déjà mais elles ne sont pas rassemblées dans un même cultivar. On peut citer par exemple les cultivars 'Bajra' à gros grains de l'Inde ; 'Sanio' à gros grains, résistant à la sécheresse mais tardif au Sénégal ; 'Zongo', mil tardif à très longues chandelles (jusqu'à 100 à 150 cm) au Niger ; 'Maiwa', mil tardif du Nigéria, résistant au mildiou ou maladie de l'épi vert, causé par Sclerospora graminicola (Sacc.) Schroet ; et les mils très précoces à gros grains mais à courtes chandelles 'Missi' ou 'Gnari' du Togo.

La combinaison des caractéristiques de bons rendements au niveau d'un seul cultivar nécessite d'être faite surtout aux USA où les conditions économiques peuvent permettre la culture rentable des hybrides et des lignées hautement performantes.

Les objectifs du thème de la présente thèse étaient d'étudier les effets agronomiques des gènes controllant la précocité, la taille des grains, la longueur des chandelles, le nanisme (pouvant permettre la récolte à la machine), et la résistance/tolérance à la rouille causée par Puccinia substriata var indica Zimm et à la pyriculariose causée par Pyricularia grisea (Cke) Salc. Deux projets avaient été conçus pour atteindre ces objectifs, l'un concernant l'aménagement des plantes et la génétique, et l'autre l'amélioration des plantes et la génétique.

1. Aménagement/Génétique des Plantes

(Management/Genetic studies)

L'objectif poursuivi est la détermination des effets de la date de semis, de la densité de population des plants, du nanisme et de la précocité des lignées de mil, et des maladies foliaires sur le rendement en grains du mil et ses composantes.

2. Amélioration/Génétique des Plantes

(Plant breeding/Genetic studies)

Les objectifs poursuivis étaient :

a) La détermination des bases génétiques de la longueur des chandelles et de la taille des grains de mil ;
b) L'étude des possibilités du développement de lignées de mil précoce, à longues chandelles et à gros grains.

(II) REVUE BIBLIOGRAPHIQUE

D'immenses progrès ont été réalisés en agriculture et en amélioration des plantes dans différentes parties du monde et cependant il y a encore un grand besoin d'aliments de bonne qualité pour nourrir la population humaine en croissance rapide et pour éviter de grandes famines telles que celle qu'a connu l'Ethiopie en 1985.

Pour accroître la production mondiale en aliments :

- les domages causés par les ravageurs et les maladies doivent être minimisés ;
- les rendements agricoles augmentés ;
- de nouvelles variétés vulgarisées partout où besoin est ;
- de nouvelles cultures introduites dans des zones où, à cause de barrières géographiques ou culturelles, elles n'étaient pas cultivées.

Tel est le cas du mil à chandelles largement cultivé comme plante fourragère au sud des Etats Unis (Burton, 1951, 1980, 1981 and 1983; Hanna and Burton, 1985a) mais dont les grains ne sont pas en alimentation animale et humaine. but its grain is not used as human food or for animal feed. Cependant, récemment, Smith (1987) a montré que les grains de mil et de sorgho peuvent valablement remplacer le maïs dans la ration alimentaire des poussins. Ceci peut amener les agriculteurs américains à s'intéresser à la culture du mil dans le future, mais la réussite de cette culture dans ce pays nécessite de bons rendements, des variétés adaptées au travail (récolte en particulier) à la machine et des lignes de conduite sur l'aménagement des plantes et la production.

Le développement de lignées et de variétés hybrides de mil nain, précoce, à longues chandelles et gros grains, et un bon programme d'aménagement des plantes permettraient d'encourager et d'augmenter la production en grains du mil aus USA. Et puis pareils cultivars (lignées et hybrides de mil) pourraient être cultivés ailleurs dans le monde pour augmenter la production alimentaire.

Bien que le mil a connu un certain nombre de changements de nom au cours de son histoire, (Chase, 1921; Terrel, 1976; Brunken et al., 1977 and Jauhar, 1981), le nom scientifique utilisé ici sera celui publié tout récemment, Pennisetum glaucum (L.) R. Br., par Terrel et al., (1986).

Le reste de cette revue bibliographique parle de :

- la biologie et morphologie du mil ;
- l'aménagement associé à la génétique du mil ;
- l'amélioration et génétique du mil (taille des grains, longueur des chandelles, précocité).

Elle a permis essentiellement de montrer que, malgré les travaux de recherche importants effectués sur le mil à travers le monde, des informations manquent sur l'aménagement des plantes et l'hérédité des caractères liés au rendment du mil que sont la longueur des chandelles, la taille des graines et la précocité.

(III) MATERIELS ET METHODES

Le thème de cette thèse était décomposée en deux projets de recherche. L'un devrait fournir des informations sur :
a) les effets agronomiques de la taille des plantes, de la maturité (le temps mis pour fleurir) et la densité de population basée sur la distance entre deux plants voisins, sur le rendement en grains et ses composants, et
b) les effets des maladies foliaires (le complexe pyriculariose-rouille) sur le rendement.
Le second projet devait déterminer les bases héréditaires de la longueur de la chandelle et de la taille des graines et étudier la faisabilité de la création de lignées et d'hybrides de mil nain, précoce, à longues chandelles et à gros grains.
Les deux projets ont été conduits à Coastal Plain Experiment Station, à Tifton/Georgia aux USA, au champ et en serre.

A. Aménagement/Génétique des Plantes

(1) Matériels

Quatre lignées proches-isogéniques (différentes seulement au niveau de quelques loci) de mil ont été utilisées.

1. La lignée Tift 23B vulgarisée le 1er Juillet 1963 (Burton, 1965a), était décrit comme il suit : " 1.8 à 2.4 m de hauteur avec des grains de couleur gris bleu sur des chandelles de 12.5 à 20 cm de long.
Semée en début Mai, cette lignée fleurit en 90 jours et arrive à maturité 3 à 4 semaines plus tard, mais semée en mis Août elle fleurit en 70 jours. Elle est entièrement fertile et constitue le mainteneur de stérilité de la lignée mâle stérile Tift 23A ".

2. La lignée Tift 23BE a été développée par sélection d'un mil précoce d'une population de backcross 2 ou BC_2, (Hanna and Burton, 1985a, 1985b). Elle diffère de Tift 23B par sa plus petite taille moyenne (1.4 m contre 1.9 m), ses plus courtes chandelles (17.8 cm contre 20.0 cm), son plus petit diamètre de la tige (15 mm contre 20 mm), ses plus courts pédoncules (21.8 cm contre 24.5 cm), et son nombre réduit d'entre-noeuds (6 contre 9). Plantée en fin Mai-début Juin, "Tift 23BE peut fleurir en 45 à 50 jours et arriver à maturité en 70 à 75 jours alors que la lignée Tift 23B, dans les

mêmes conditions, fleurit en 75 à 80 jours après le semis et arrive à maturité en 100 à 105 jours".

3. La lignée Tift 23DB a été crée par transfert du gène de nanisme d_2 de la lignée Tift 239 à la lignée Tift 23B. Elle ressemble à Tift 23B sauf pour sa plus petite taille. Le gène d_2 réduit la longueur des entre-noeuds sans modifier celles du pédoncule et de la chandelle (Burton, 1967).

4. La lignée Tift 23DBE a été crée par transfert du gène récessif e_1, du mil 'Katherine' d'origine africaine, à la lignée naine tardive Tift 23DB. Tift 23DBE est insensible à la photopériode et peut donc fleurir entre 45 et 55 jours après le semis à n'importe quel moment de l'année (Burton, 1981).

Le tableau suivant montre quelques caractères de ces quatre lignées enregistrés à la suite des deux années d'étude :

Lignée	Précocité (50% floraison femelle)	Taille Plante	Longueur Chandelle
1. Tift 23B	71-81 jours	2.30 m	18-28 cm
2. Tift 23BE	54 jours	1.60 m	16-23 cm
3. Tift 23 DB	76-83 jours	1.30 m	16-20 cm
4. Tift 23DBE	51 jours	0.90-1 m	15-24 cm

(2) Méthodes

Deux semis par an ont été effectués en 1985 et 1986 à Tifton/Georgia à Coastal Plain Experimental Station, en split plot, avec 8 répétitions en 1985 et 5 en 1986. Chaque répétition comportait deux parcelles principales différant par leur densité de population et quatre parcelles secondaires représentant chacune des quatre lignées. Chaque parcelle secondaire comportait 6 lignes de 4.8 m de long distantes l'une de l'autre de 0.9 m. Une bordure de deux lignes entourait tout le champ et les parcelles principales

étaient distantes de 1,20 m tandis que 0,80 m séparait les parcelles secondaires.

Le semis étant fait à la machine et en ligne continue, il était nécessaire de démarier en respectant les distances de 2,5 cm ou de 17 cm entre les plants selon la densité de population de plants voulue sur les parcelles principales.

Pour assurer à la fois l'infection et son uniformité en deuxième saison où les plantes sont naturellement exposées aux maladies foliaires, des débris de plantes infectées en pépinière et hachées à la machine étaient uniformément répandus dans le champ, environ 40 jours après le semis.

Chaque semis était toujours précédé par l'épandage de 280 kg/ha de l'engrais NPK 5-10-50. L'entretien a été fait à la fois à l'aide d'herbicides et de sarclage à la machine. Pour lutter contre les insectes et les oiseaux granivores, des sachets en papier kaki spécial (papier *kraft*) traités par trempage dans une solution d'insecticide ont été utilisés pour protéger les chandelles récoltables, juste au début de la formation des grains issus de la fécondation libre.

Au besoin, les plantes sont traitées à l'Azodrin ou dimethyl, cis-1-methyl-2-methylcarbamoylvinyl phosphate (McEwen et al.,1979), au taux recommandé pour le contrôle des insectes.

Les données recueillies concernaient 10 caractères : le nombre de plants par parcelle (number of plants per plot), la date de floraison (heading date), le nombre de chandelles par parcelle, (Head number per plot), la hauteur des plants (Plant height) en cm, la tolérance/sensibilité aux maladies foliaires (Disease rating) en utilisant une échelle de 0 à 5 (la note 0 étant attribuée aux plantes saines et la note 5 aux plantes sévèrement attaquées), la

longueur des chandelles (Head length) en cm, la masse des grains d'une chandelle (Total head seed weight) en g, la masse de 100 grains (Weight of 100 seeds) en g, le nombre moyen de chandelles par plante (Average head number per plant), et le rendement (Yield) en kg/ha. L'analyse de variance pour le split plot et la comparaison des moyennes par le test de Duncan ont permis d'organiser les données pour une meilleure analyse.

B. AMELIORATION/GENETIQUE DES PLANTES

(1) Matériels

L'objectif de ce projet était de déterminer les bases génétiques de la taille des grains et de la longueur de la chandelle de mil et d'étudier la faisabilité de la création d'un mil précoce, nain, à gros grains et à longues chandelles. Six origines supposées être des lignées ont été utilisées pour ce projet :

1) La lignée Tift 23DBE décrite plus haut : naine, précoce, à petits grains (0.51 g /100 grains) et à courtes chandelles (environ 20 cm en moyenne), (Burton, 1969).

2) La lignée Tift 23B : géante, tardive, à petits grains (0.44 g/100 grains) et à courtes chandelles, proche-isogénique de Tift 23DBE.

3) La lignée Tift 18BE : c'est une mutation précoce de la lignée tardive Tift 18B vulgarisée en Mai 1965 (Burton, 1965b) comme le mainteneur de stérilité de la lignée mâle stérile Tift 18A et décrite, (cette lignée Tift 18B), comme insensible à la photopériode qui fleurit à Tifton en 90 jours pour un semis au printemps et en 70 jours pour un semis en été (mis Août). Tift 18BE fournit des plants de taille moyenne portant des grains blancs sur

de chandelles de 45 à 90 cm et fleurissant en 45 ou 35 jours après le semis, selon la date de semis.

4) Le cultivar 'Gero' à longues chandelles : Il a été introduit à Tifton par Dr. Glenn Burton en 1962. Il est insensible à la photopériode et ses chandelles de taille semblable à celle des chandelles de Tift 18BE mais plus grosses et plus robustes. Bien que décrit au Nigéria comme un mil précoce lorsqu'on le compare au mil photopériodique 'Maïwa' (Rachie and Majmudar, 1980), Gero est tardif à Tifton (floraison de 70 à 90 jours après le semis) comparé à Tift 23DBE, 23BE ou 18E.

Les deux mils à longues chandelles ont des grains de petite à moyenne taille (0.76 g / 100 grains, en moyenne).

5) Le cultivar 'Togo' : Il est d'origine togolaise comme son nom l'indique avec des plants précoces de taille moyenne, de courtes grosses chandelles et à gros grains (1,18 g / 100 grains) qui a transité par le Niger où il fleurit en 36 jours. A Tifton, Togo est aussi précoce que Tift 23DBE et est hautement male-stérile.

6) Le cultivar 'Walor Kassens' : C'est une introduction du Ghana en 1966. C'est un mil précoce qui fleurit 45 jours après le semis et qui porte de courtes chandelles à grosses graines (1.26 g /100 grains).

(2) Méthodes

Pour atteindre les objectifs fixés, tous les croisements possibles successifs ont été effectués, au champ et en serre, en 1985 et 1986, entre les six origines. La possibilité de conserver le pollen au froid pour une utilisation ultérieure même après un an, (Hanna et al., 1983), a permis de résoudre le problème du décalage de floraison entre les précoces et les tardifs. Parfois, les semis décalés à cause de la diversité des expériences sur la même station

mais utilisant les mêmes cultivars ont permis de transporter du pollen d'un champ à un autre pour résoudre le même problème.
Les parents, les hybrides, les backcross et les générations F_2 ont été semés ensemble en parcelles répétées au champ en 1986 et 1987 pour mesurer les différents paramètres à analyser. Pour les parents et les hybrides F_1 qui sont génétiquement homogènes les parcelles avaient 4,45 m de long alors que les populations hétérogènes backcross et F_2 occupaient des parcelles de 28,45 m de long en 1986 et de 62 m en 1987.

Le démariage nécessaire après le semis en ligne continue à la machine laissait 17 à 20 cm entre les plants individuels de la même ligne, deux lignes étant distantes l'une de l'autre de 0,90 m. Les conditions de culture sont identiques à celles du volet aménagement des plantes.

Les autofécondations nécessaires pour maintenir les lignées parentales ou pour obtenir les générations F_2 étaient réalisées à l'aide des sachets en papier *kraft* traités à l'insecticide et mis à temps pour éviter la contamination par du pollen extérieur. Ces sachets sont agrafés contre l'effet du vent et des oiseaux.
Pour les croisements, des sachets en papier plastifié (*glassine*) non traités à l'insecticide étaient utilisés pour éviter la contamination génétique, puis, à la sortie des stigmates qui se voyaient à travers ce papier spécial, un sachet *kraft* traité renfermant le pollen du parent mâle remplaçait soigneusement le papier en *glassine*. Tout comme pour l'autofécondation ce sachet de fécondation portant le nom du parent mal est agrafé pour empêcher le vent de l'emporter.
Pour les longues chandelles de Tift 18E et de Gero les sachets de

35 cm utilisés ne pouvaient théoriquement couvrir que le sommet de la chandelle qui seul a été utilisé pour la suite.

Collection des données

Pour ce second sujet les traits suivants ont été étudiés :

1. La date de floraison des plantes autofécondées (en jours)
2. La longueur des chandelles (en cm)
3. La masse moyenne des grains d'une chandelle par plante (en g)
4. La masse de 100 grains (en g)

Méthodes d'analyses

L'analyse des moyennes brutes enregistrées a montré des coefficients de variation trop élevés pour certains traits et cela a conduit à des transformations de données comme le suggérait Hoyle (1973) en pareil cas. Cependant, les données originelles ont pu être directement utilisées pour des raisons pratiques.

L'analyse des variances a été effectué sur les données recueillies au niveau des parents croisés et de leurs hybrides après leur culture en 1987 avec le dispositif expérimental CRBD à 5 répétitions.

Les résultats (Tables 30 & 31) ont montré pour certains traits des variations intra cultivar qui étaient dues soit aux variations de type environnemental, soit à des différences génétiques entre plants du même cultivar qui était pourtant considéré comme une lignée.

La comparaison des variances intra-cultivar en prenant celles des lignées certifiées Tift comme références, a montré que les cultivars 'Géro', 'Walor' et 'Togo' étaient trop variables

intérieurement pour être des lignées (voir tableaux 1 et 2 de la thèse originale).

Pour chaque croisement entre deux lignées parentales (P_1 et P_2) la hiérarchie des variances jusqu'en F_2, en passant par la F_1 et les backcross (BC) s'établit comme il suit :

$$Var\ (F_2) > Var\ (BC) > Var\ (F_1) = Var\ (P_1) = Var\ (P_2).$$

L'analyse a montré que cette hiérarchie n'a été respectée que pour certains croisements et la littérature disponible montrait que pareille déviation a été déjà enregistrée (Burton, 1951).

Ces déviations et la variabilité sûrement génétique au sein de certains cultivars considérés au départ comme des lignées ont conduit à l'abandon de certaines données et ont donc réduit le nombre de croisements à utiliser pour l'étude génétique envisagée au départ.

Pour les croisements retenus surtout, l'hétérosis a été calculé en utilisant les formules proposées par Fehr (1987, p. 175) et Jinks (Frankel, 1983 p. 4).

L'héritabilité au sens large a été calculée selon la méthode de Allard (1960), mais les données retenues ne permettaient pas d'estimer l'héritabilité au sens strict.

La distribution des fréquences a été faite à l'aide du logiciel SIGMAPLOT.

Pour des raisons techniques le nombre de gènes contrôlant la précocité, la longueur des chandelles et la taille des grains a été estimé à la fois par la méthode attribuée par Burton (1951) à Sewell Wright et par la méthode du chi deux suggérée par Hanna et al., en 1978, qui ont aussi proposé le test de chi deux pour la détermination de la liaison génétique également utilisé dans ce projet.

RESULTATS ET DISCUSSION

A. Aménagement/Génétique des Plantes

Les principaux résultats et la discussion concernant cette partie sont reportés dans l'article en français joint à ce même dossier et intitulé *EFFETS DES GENES d_1 et e_1 SUR LES CARACTERISTIQUES DES GRAINS ET DES PLANTES CHEZ LE MIL Pennisetum glaucum (L.) R. Br.* (Actes des Journées Scientifiques de l'U.B., N°4, Vol. II, pp. 139 à 152.

B. AMELIORATION/GENETIQUE DES PLANTES

Pour cette partie les figures et les tableaux auxquels il sera fait référence ne sont pas traduits en français et le lecteur est prié de se reporter à la thèse en anglais. Merci pour la gymnastique nécessaire. Il est rappelé aussi que ce sont trois caractères qui sont étudiés ici : la maturité (maturity) ou précocité des plantes, la longueur des chandelles (head length) et la taille des grains (seed size) exprimée par la masse de 100 grains (100 seed weight). Les tableaux 17, 18 et 19 (pp. 70 à 72 de la thèse en anglais) donnent les valeurs de l'hétérosis pour les trois traits. Ces résultats montrent que :

1. L'hybride était plus précoce que le parent tardif et en moyenne plus précoce aussi que le parent moyen (la moyenne des deux parents croisés).
2. L'hybride avait des chandelles en moyenne plus longues que celles du parent moyen et mais plus courtes que celles du parent à longues chandelles.
3. L'hybride avait des grains dont la taille est intermédiaire

entre celle des grains du parent moyen et du parent supérieur (parent à gros grains). Certains croisements ont montré une superdominance pour la taille des grains.

Le tableau 20 concerne l'héritabilité au sens large pour les trois traits qui peut être résumée comme il suit :

Caractère	Héritabilité Limites	moyenne
Maturité	29% - 98%	65%
Longueur de chandelle	39% - 81%	58%
Taille des grains	52% - 93%	74%

Les moyennes ci-dessus peuvent être comparées aux moyennes obtenues à partir des moyennes des variances des différentes générations de chaque croisement et qui sont respectivement de 51%, 60%, 81% pour la maturité, la longueur des chandelles et la taille des grains mais on remarque que l'ordre est un peu inversé pour les deux premiers traits.

Les figures (pp. 74 à 86 de la thèse) indiquent les fréquences de distribution des individus F_2 selon leurs phénotypes respectifs, avec indicatif de la place qu'occupe chacun des parents et l'hybride F_1 dans cette distribution. Ceci permet de voir si chaque parent est représenté ou non en F_2 et si le trait envisagé est analysable qualitativement ou non. A cet effet les figures 1B de la page 75 indiquent deux classes avec la domination partielle du parent tardif P_2 et suggèrent l'influence d'un gène à deux allèles pour la maturité comme l'avaient signalé Burton (1981), and Hanna and Burton, (1985a) chez les lignées concernées.

La longueur des chandelles et la taille des grains montrent une distribution continue (figures 2 et 3) suggérant la nature quantitative et une analyse mendélienne (qualitative) difficile pour les deux traits. Malgré tout, la détermination du nombre de gènes contrôlant chaque caractère a été tentée et les résultats sont consignés dans le tableau 21 (p. 87 de la thèse). Avec toutes les réserves émises plus hauts, en particulier sur la nature génétique des cultivars utilisés, on peut dire que la taille des grains semble dépendre d'un plus petit nombre de gènes que la longueur des chandelles. Peut-être aussi que la maturité ne dépend

pas toujours d'un seul locus chez tous les cultivars du mil.
Le test du chi deux suggéré également pour la détermination du nombre de gènes (Hanna et al. 1978) ne s'applique en réalité que pour les caractères dont les effets épistasiques sont prédominants alors même que les effets additifs et semblent être importants chez le mil (Burton, 1951 ; Upadhyay et Murty, 1971). Ainsi les chiffres des tableaux n°26 relatifs à ce test sont plutôt indicatifs.

CONCLUSION

A. Aménagement/Génétique des Plantes

Voir l'article '*EFFETS DES GENES d_1 et e_1 SUR LES CARACTERISTIQUES DES GRAINS ET DES PLANTES CHEZ LE MIL Pennisetum glaucum (L.) R. Br.*' (Actes des Journées Scientifiques de l'U.B., N°4, Vol. II, pp. 139 à 152.

B. AMELIORATION/GENETIQUE DES PLANTES

Cette étude génétique nous a permis d'essayer un certain nombre de méthodes de travail mais le matériel végétal ne nous semblait pas très approprié. Bien que la base génétique de la maturité, de la longueur de la chandelle et de la taille des grains n'a pas pu être clairement élucidé, la méthode originale utilisée pour déterminer la nature (lignée ou pas lignée) des cultivars reste un acquis important qui pourrait rendre service dans les études ultérieures.