

A STUDY OF THE HERITABILITY OF AND ENVIRONMENTAL
INFLUENCE ON MAJOR AGRONOMIC AND YIELD CHARACTERS
IN PIGEON PEAS.

By

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DECLARATION

I Masituular Sophy Mwagale Mukwanah-Musaana,
hereby declare that the work described in this thesis,
has not been submitted for a degree in this or any
other University.

Date

Signature.

This thesis is dedicated to my parents:

Asumani Mukwanah and

Fatuma Mugoya

plus my husband:

Zubair Lujja Musaana

in appreciation for the sacrifices they made.

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SUMMARY

Studies reviewed and reported herein showed that single plant selection can be used to improve simple characters such as plant height pods per plant and pod clusters/plant. For the complex characters such as seed yield and protein content phenotypic recurrent selection was more effective. Tall, indeterminate plant types performed best under non-stress water conditions where secondary growth was not affected. The short cultivars, however performed well during both seasons since they escaped the pest population build up at the end of the seasons. Under water stress conditions high population levels (upto 110,000 plants/ha.) with more square arrangements were suitable for tall and short plant types but under non-stress conditions low populations (40,000 plants/ha.) with wide spacings were more suitable for the tall cultivar due to the extra growth. Both population and spacing had little or no effect on yield components.

Up to 37% natural cross-pollination was recorded in the crop and was mostly carried out by insects. Generally the results observed in F_1 regarding the nature of gene action were in agreement with those of F_2 but various degrees of dominance for various characters were observed in F_1 and F_2 generations. The gene action controlling most of the characters was simple and additive. High heterosis with low inbreeding depression was observed for most of the crosses but no reciprocal differences were noted for any character. General combining ability variances were higher than specific combining ability variances in F_1 and F_2 generations indicating the importance of additive gene action. The combining ability of some lines was high indicating that hybrid and composite varieties can be developed.

Phenotypic correlations indicated that plant width and height, days to maturity, pods and pod clusters/plant, seeds/pod and seed size were the main yield components of this crop. A path-coefficient analysis, however, showed that pods and pod clusters/plant, seeds/

pod and seed size were the main yield components having maximum direct effects on yield. High heritability estimates (h^2) were observed for plant height and width, pods/plant, seeds/pod and seed size and low estimates for protein content and seed yield.

INTRODUCTION

Pigeon pea (Cajanus cajan (L) Millsp.) has been grown in Africa for over 4,000 years, where it is found wild (Purseglove, 1968). It originated in tropical Africa and then spread to Malagasy, Egypt, Syria and India during pre-historic times (Purseglove, 1968). India is the secondary centre of diversity where over one hundred cultivars have been identified (Oza, 1972). Two botanical varieties are known. Variety flavus D.C. has members which are early maturing, shorter plants with yellow flowers and usually green pods; and variety bicolour D.C. which has perennial cultivars with red or purple flowers and red pods. These botanical groups may not maintain such distinct boundaries owing to cross-pollination which freely goes on within this genus. Most of the pigeon peas grown in East Africa are of the bicolour D.C. type. The genotypes in the Makerere collection came from India, Latin America, Tropical Africa, parts of South East Asia and the Caribbeans, which are the major world producing areas (Swaminathan

and Jain, 1973). These genotypes are mainly of the flavus D.C. type (Rachie and Wurster, 1971).

This crop grows under a wide spectrum of climatic and adaphic zones, with best adaptability tending towards drier climates (Purseglove, 1968). This is the situation in Uganda with the leading growing areas being Lango, Acholi, Madi, Teso and West Nile districts, which have dry climates (Jameson, 1970). The grain yield of the crop on peasant farms in Uganda was estimated at 1120 kg/ha (Dunbar, 1969) compared to that of 5,000 kg/ha reported in India (Anon, 1967). The difference in these yields is mainly due to the fact that farmers in Uganda are using low yielding varieties. By using higher yielding varieties, Khan and Rachie (1972) and Onim (1974) reported improved yield estimates ranging from 889 to 1228 kg/ha and 1969 to 4229 kg/ha, respectively, at Kabanyolo University Farm.

Khan (1973) and Onim (1974) each started synthesis of composites at Kabanyolo. These composites

need improvement with respect to height, maturity and protein content before they can be released to farmers. Secondly most of the genotypes, in the composites and the Makerere germplasm, have indeterminate growth, so that several harvestings are necessary at the end of each season, which is inconvenient and expensive. This is so because mechanical harvesting is rendered impossible due to the non-uniform ripening of pods on each plant and the uneven levels at which the pods are borne on each plant.

According to the census of Agriculture of 1963/64, 53,000 hectares of pigeon peas were grown in Uganda, but most of this was just broadcasted (Anon, 1965). This method of planting, though good for peasant production, is unsuitable when commercial production is required; because a lot of seed is used and mechanical weeding, spraying and harvesting can not be carried out. Currently a spacing of $100 \times 50 \text{ cm}^2$ (20,000 plants/ha) is being used at Kabanyolo, but no attempt has been made to work out the most suitable distances or population levels required for the different plant

types grown.

Pigeon pea is normally a self-pollinated crop but Khan (1973) reported outcross percentages of 8, 22 and 21 in three successive seasons in plots sprayed regularly with insecticide at Kabanyolo. Therefore, purity of varieties cannot be expected under Kabanyolo conditions. The implication of these observations in the improvement of the crop can not be over emphasized.

The protein content in the seed varies from 18-28% and is of excellent quality (Oland and Starbursvik, 1970 and Rachie and Wurster, 1971). Pigeon peas, therefore, form an important complement to cassava and sweet potatoes which are protein deficient and that are major constituents of the diet of the people in areas where the peas are grown and consumed in Uganda. Kenya is exporting green pigeon pea seed to the export market estimated at an annual value of Ksh 3,000,000 (Rachie and Wurster, 1971), and it is as well developing a canning industry for green pigeon pea seed (Onin, personal communication). Therefore, any excess production of pigeon pea seed in Uganda can be exported to Kenya. In order to get

enough seed for both internal consumption and the export market, high yielding varieties need to be used. Such varieties can be achieved by improving our current low yielding varieties using proper breeding procedures. These breeding methods can be determined after a study of the ^{effects of} individual components of yield on yield itself and the heritability estimates of these components. So far, the use of these two studies to determine breeding methods has not been attempted.

In view of the importance of this crop and the very low average yields in Uganda, an improvement programme was initiated at Makerere in 1968. As part of this continuing programme, the present study was undertaken with the following objectives:-

- (1) To select superior genotypes in the Kabanyolo composites to suit environmental conditions in the different growing areas.
- (2) To determine the optimal populations and spatial arrangements for the different plant types.
- (3) To evaluate the amount of natural cross-pollination and its value in the production of the crop.

- (4) To determine the suitability of producing hybrid varieties and study the inheritance of some quantitative characters.
- (5) To determine the relationships among some agronomic and yield characters and determine their heritability estimates.

LITERATURE REVIEW

Single Plant Selection

Due to the high amount of cross pollination which goes on in this crop, pigeon pea populations are normally highly variable and single plant selection can be a very effective method of improvement (Mehta and Dave, 1931 and Veeraswami and Rathnaswami, 1973). Akinola and Whiteman (1972) found wide variations in plant height, number of primary branches, days to flowering, grain yield, 100-seed weight, seeds per pod and percent protein within 95 pigeon pea introductions from 11 different countries. Pathnaswamy et al. (1973) also found the same wide character variation in a pigeon pea population grown in India. Likewise Khan (1973) and Onim (1974) reported wide character variations in the Makerere composites and within the varieties of the world collection of a pigeon pea germplasm at Makerere University.

Several workers have made effective single plant selections from different pigeon pea populations for

various characters; Anon (1947) and Derieux (1969) for plant height and early maturity, Singh (1973) and Onim (1974) for plant height, early maturity and high yield and Derieux (1969) and Khan (1973) for a high pod number.

Phenotypic Recurrent Selection

Allard (1960) suggested that if phenotypic recurrent selection was used to improve a character that was governed by a few genes, the genetic variability would be lost after a few cycles of selection. Following this, Eberhart (1967) modified the method and outlined it for maize improvement and Dogget and Eberhart (1968) outlined techniques to apply the method to sorghum. Khan (1973) modified the method and outlined it to apply to pigeon peas..

POPULATION AND SPACING

A number of studies have been carried out on pigeon peas to determine the optimal population densities and Spatial arrangements for optimum yields. While using a dwarf pigeon pea variety, Mukherjee (1960) reported that the closest spacing of 2 x 2 feet

consistently gave the highest yields per acre while the lowest spacing of 4 x 4 feet gave the highest yields per plant. Several workers, including Derieux (1969), Veeraswamy et al. (1972) and Abrams and Julia (1973) have since reported similar results. By using wider spatial arrangements, 90 x 45 cm² being the closest, Riollano et al. (1962) and Saurez and Herrera (1971) reported results contrary to the above that spacing had no effect on yield in pigeon peas. Veeraswamy et al. (1972), however, reported that the very wide spacing of 120 x 30 cm gave lower yields than broadcasting.

The effect of population and spacing on yield components and other agronomic characters have been reported by various workers. Plant height, days to flowering, percent protein, seeds per pod and seed size were reported not to be affected by population or spacing in this crop (Presekar and Subramanian, 1961; Abrams and Julia, 1973 and Manjhi et al., 1973). Pods and branches per plant were, however, decreased with increasing population density. Population and spacing requirements of many legumes have been carried out.

Adams (1967) using field beans and Griton and Eastin (1968) using peas reported that these crops were able to compensate among yield components at given population and spatial arrangements, indicating that when one component decreased then there was another that increased with changes in population or spatial arrangements. Leakey and Rubaihayo (1972) reported similar results for soyabeans but showed that pods per plant decreased consistently with increasing population densities.

Genotype x Environmental Interaction

The different behaviour of genotypes when grown in different environmental conditions indicates the reaction of particular genotypes to change in the different environments. A number of studies have been carried out to study the genotype by environmental interaction in pigeon peas. Significant differences have been reported among the yields of different varieties when grown during different years but not when grown at different locations (Abrams et al., 1968 and Laxman Singh et al., 1974). This indicated

that these varieties were not affected by the different soil fertility levels but by changes in the climates of the different years. In fact delays in sowing this crop at the beginning of the season resulted in a loss not only of grain yield but also total biological yield. (Ganguli and Srivastava, 1969; Dahiya et al., 1974; and Onim, 1974). Similar results have been reported for peas (Kurnik et al., 1970) and beans (Singh and Molhotha, 1970).

HYBRIDIZATION

Natural cross-pollination in pigeon peas

Pigeon peas is one of the few grain legumes which are capable of an appreciable amount of potential out-crossing. Reports from India indicate percent natural crossing ranging between 0.0 - 48.0% (Howard et al. 1919; Mehta and Dave, 1931; Deshmukh and Rekhi, 1961; and Veeraswamy et al., 1973). It was observed that most of the cross-pollination was carried out by bees and other large insects (Bateman, 1947; and Khan, 1973). Therefore the amount of these insects in a sprayed or unsprayed crop affects the level of natural

crossing in any one given crop, hence the range that was observed in India. Similar ranges have been reported in Hawaii (Krauss, 1927; and Abrams, 1967), West Indies (Ariyanayagam, 1976) and at the University Farm, Kabanyolo (Khan, 1973). The percent natural crossing of a crop is not only affected by bees and other large insects but also by flower thrips and the basis on which it was calculated, F_1 seed or F_1 plants and the distance between plants (Miranda Colin, 1971 and Ariyanagayam, 1976). In pigeon peas, *seth* pollination is encouraged because pollen is shed a day before a flower opens (Krauss, 1927; and Purseglove, 1968) but by then the stigma is receptive (Prasad et al., 1977). This suggests that for cross-pollination to take place then there must be differential growth rates of pollen from different sources or that some inhibiting physiological or morphological factor prevents selfing before a flower opens.

DIALLEL CROSS

Nature of gene action

Smoothness, apparent normality or unimodality of the F_2 distribution should not be used as an evidence of quantitative inheritance because a character controlled by one gene pair would give a smooth continuous F_2 distribution if 50% of the F_2 variance was non genetic (Burton, 1951). In pigeon peas seed size has been reported to have no dominance deviation in F_1 and F_2 generations (Sharma et al., 1972) but variable degrees of dominance for plant height, branches and pods per plant, days to 50% flowering and grain yield, were reported for F_1 and F_2 generations (Sharma et al., 1973). The deviation of these characters being partial or complete dominance and overdominance for percent protein (Veeraswamy et al., 1973; Sharma et al., 1973).

For certain characters, the nature of gene action cannot be ascertained especially if the segregation is quite small. (Burton, 1951). In pigeon peas, grain yield and percent protein have been reported to be

under the control of non additive gene action (Sharma et al., 1973 and Veeraswamy et al., 1973), the non-additive component being mainly due to epistasis (Mather and Jinks, 1971). On the other hand the nature of gene action controlling plant height, branches and pods per plant, seeds per pod and seed size was reported to be mainly additive (Sharma et al., 1972, and Veeraswamy et al., 1973). Similar results were reported for cowpeas (Rowlands, 1964; Krarup and Davis, 1970 and Kalaidzhieva and Kalinov, 1975) and Phaseolus species (Dickson, 1967 and Albuquerque et al., 1974).

Combining Ability

Sharma et al., (1973) have reported significant ($P < 0.01$) general combining ability (G.C.A) variances for plant height and spread, days to flowering, maturity and seed size. Significant specific combining ability (S.C.A) variances were reported for all the characters recorded above save plant spread and seed yield per plant. G.C.A variances were however higher than S.C.A. variances indicating that the genetic control of these characters was predominantly additive. They

further reported that in some specific crosses which exhibited considerable heterosis there was an indication of the presence of some non-additive gene action. The non-additive effect comprising of dominance, linkage or epistasis (Jinks and Hayman, 1953). Therefore, in pigeon peas characters with high S.C.A. variances, need complex methods of selection to improve them, so as to enter for the non-additive gene action that govern the characters in question. Sharma et al. (1973) further observed that the estimates of G.C.A. effects of the individual parental lines indicated a good agreement between the ranking of the lines for such effects and the ranking based on parental performance. Significant general and specific combining ability effects for plant height, seeds per pod, pods per plant and seed yield per plant have been reported in cowpeas (Singh et al., 1972 and Nandipuri et al., 1973) indicating the importance of both additive and non-additive gene action in this crop. The best specific combining lines have been observed to be the results of crosses between parent with a high x low general combining ability (Khanna and Chaudhary, 1974).

Heterosis and Inbreeding depression

Heterosis and Inbreeding depression are expressions of the same phenomenon. Heterosis has been studied in many self and cross-pollinated crops. The presence of heterosis for a character indicates some degree of genetic diversity between parents for that character (Sprague, 1966), therefore, higher levels of heterosis are expected with increased genetic diversity between parents. Moll et al. (1965), however, cautioned that extreme genetic diversity could result in reduced heterosis. In pigeon peas F_1 hybrids have been reported to yield up to 24.5% more than their corresponding mid-parents (Solomon et al., 1957), but the best yielding hybrid gave lower yields than that of the higher parent, suggesting that the parents used were not highly genetically diversified (Sprague, 1966). High heterotic effects have also been reported in pigeon peas for plant height and grain yield (Sharma et al., 1973 and Veeraswamy et al., 1973a), suggesting that composite varieties could be developed (Khan, 1973). Increases

of 13 to 20% of hybrid seed yield over parents have been reported in soyabeans (Veatch, 1930; Brim and Cockerham, 1961 and Weber et al., 1970). Hybrid vigour for yield and its components has also been reported in phaseolus species (Adams and Duarte, 1961 and Ranamujam et al., 1974); cowpeas (Kheradnam et al., 1975) and tomatoes (Khanna and Chaudhary, 1974). Negative, though non-significant heterosis has, however, been reported for protein content, pod weight and seeds per pod in cowpeas (Kalaidzhieva and Kalinov, 1975).

After a generation of selfing the mean values of F_2 may approach the values of the mid-parent indicating the presence of inbreeding depression. Paroda and Joshi (1970) considered it advantageous to exploit high specific combining ability effects if inbreeding depression effects from F_1 and F_2 were such that F_2 was either superior or equal to the best parental variety. From the available literature inbreeding depression has not been reported in pigeon peas, but Krarup and Davis (1970) and Kherdnam et al. (1975) reported the

presence of inbreeding depression for all the characters that exhibited heterosis in cowpeas.

Reciprocal Effects

Reciprocal effects in pigeon peas have been studied by Dahiya et al. (1976) who reported that the protein content in F_1 hybrids showed maternal effects. Kalaidzhieva and Kalinov (1975) reported that the number and weight of pods in peas were similar to those of the female parent when the latter had a higher value for these characters. Kheradnam et al. (1975), however, reported no reciprocal differences in protein content, pods per plant and other agronomic characters in cowpeas.

RELATIONSHIPS AMONG SOME CHARACTERS

Correlations of some characters:

Several workers have reported on the interrelationships of the major agronomic and yield characters of pigeon peas. Characters that have been reported to be positively and significantly correlated with grain yield are early maturity, high seed number per pod, pods per plant and number of primary branches (Munoz

and Abrams, 1971 and Rubaihayo and Onim, 1975); seed size and plant height (Sharma et al., 1971). Negative and significantly correlated characters with grain are days to flowering (Veeraswamy et al., 1973b) and days to maturity (Rubaihayo and Onim, 1975) while plant height was reported to be negative but non-significantly correlated with grain yield (Khan and Rachie, 1972, Rubaihayo and Onim, 1975). (See Table 1).

Munoz and Abrams (1971) and Veeraswamy et al. (1973b) reported higher genotypic correlations for various characters than their corresponding phenotypic or environmental correlations in pigeon peas. Singh and Molhotha (1970), Srivastava et al. (1975) and Gowda and Pandya (1975) reported similar results for mungbeans, tablepeas and gram, respectively. Seed size has been reported to be negatively and significantly correlated with seeds per pod and pods per plant (Sharma et al., 1971 and Rubainayo and Onim, 1975). Such negative correlations arise primarily from developmentally induced relationships. These developing

Table 1. Correlation coefficients, of some pigeon pea characters with yield, reported by various workers.

Character	Rubaihayo and Onim (1975)	Khan and Rachle (1972)	Sharma <u>et al.</u> (1971)
Plant height	-0.06	0.13	0.56*
Plant width	-0.30*	0.57**	0.71**
Days to flowering	-2.10	-0.44*	-
Days to maturity	-0.30*	-0.25*	-
No of primary branches	0.30*	-2.08	0.21
Branching height	-	-	0.17
Pods per plant	0.86**	2.72**	0.87**
Effective pod bearing length	-	-	0.61**
100 seed weight	-	-	.

*Significant at 5% and **Significant at 1% levels of probability.

structures of the plant body compete for a common nutrient supply and if one structure is more favoured than the other for any reason, a negative correlation may arise between them (Adams, 1967 and Adams and Graffius, 1971). Similar negative correlations were reported by Anand (1962) in soyabeans, Singh and Singh (1969) in peas and Athwal and Sandhu and Gowda and Pandya (1973) in gram.

Path coefficients of some characters

Singh and Molhotha (1973) carried out a path coefficient analysis and regressions studies and concluded that pod clusters per plant was the main yield component in pigeon peas. Veeraswamy et al. (1973) basing his conclusions on phenotypic and genotypic correlations had, however, reported that in addition to pod clusters per plant, branch number, and pods per plant appeared to contribute most to grain yield in pigeon peas.

Abrams (1967); Singh and Molhotha (1970) and Duarte and Adams (1972) reported that seed size, seeds per pod and pods per plant were the most important yield components in phaseolus sp. and that seed size showed

high negative indirect ~~effects~~ via seeds per pod and pods per plant. Singh and Singh (1972) reported that the main yield components in peas were branch number, seeds per pod and seed size. They concluded that in order to improve the yield of the crop it was best to select for a combination of all these characters rather than selecting for yield itself. Bhatt (1973) also made a similar conclusion after carrying out a path-coefficient analysis for yield and its components in wheat. Srivastava et al. (1975) reported that in ~~table~~ pea pods per plant, seeds per pod and pod length which had significant genotypic correlations with yield showed maximum direct effects on yield. They further reported that seeds per pod and pod length ~~have~~ indirect effects on yield as well. They also concluded that these three characters can be used to select higher yielding genotypes. Phadnis et al. (1970) and Gowda and Pandya (1975), however, reported that only two characters, 100 seed weight and pods per plant showed high direct effects on grain yield in ~~grass~~ and that they influence yield negatively via each

other, therefore an optimal combination between them had to be attained in selection programmes.

Heritability of some characters

A number of workers have reported on the heritability of some characters in pigeon peas. High heritability estimates have been reported for plant height $h^2 = 0.36$ to 0.74 , (Munoz and Abrams, 1971) and days to flowering, $h^2 = 0.70$ to 0.90 (Khan and Rachie, 1972 and Rubaihayo and Onim, 1975), suggesting that these characters could be improved by simple methods of selection (Sprague et al., 1959). High heritability estimates have also been reported for seed size and branch number (Govinda Raju et al., 1972), seeds per pod and pods per plant (Heremath and Talawar, 1973) and percent protein (Laxman Singh et al., 1974) in pigeon peas. Low heritability estimates have, however, been reported for grain yield in pigeon peas (Rubaihayo and Onim, 1975).

Krurup and Davis (1970) reported high heritability estimates for seed size, branch number and pods per

plant and low estimates for days to flowering, seeds per pod and grain yield in peas. Similar results were reported for beans (Sarafi et al., 1973).

MATERIALS AND METHODS

Unless otherwise stated all the experimental work in this study was carried out at the University Farm, Kabanyolo. The plant material used came from the pigeon pea world collection of more than 5,000 entries (Rachie and Wurster, 1971). In all the experiments the seed was dressed with Fernasan-D and D.D.T. dust, during storage. The experimental fields received a pre-plant dressing with single super phosphate at a rate of 50 kg/ha. The experiments were kept weed free and sprayed weekly from anthesis to late pod filling with Rogor-E (40% W/V dimethoate and D.D.T. (25% M.D.) at concentrations of 1:600 and 1:100, respectively, of active ingredient to water.

Experiment I(a)

SELECTION

Single Plant Selection

During the first rains season of 1974 (March to September), eight Makerere composites were planted in separate plots. In addition 4-meter single rows of

1400 entries from the world collection of pigeon peas were planted. The entries planted had maturity periods of up to 152 days. A spacing of 75 cm between rows and 25 cm within rows was used. The guard rows comprised of the local selection CIVEI (Khan and Rachie, 1972). After 50% flower bud production, single determinate plants were selected from both the composite populations and the world collection. Selection was based on early maturity, high flower number, good plant vigour, resistance to leaf spots, especially that caused by Mycovellosiella cajani and the amount of flower infestation by Frankniella dampfi. All the selected single plants were selfed by covering the plants with gauze bags fine enough to prevent entry of bees and other large insects, after removing any open flowers and young pods. Cross-pollination by small insects was prevented by spraying with Rogor-E and D.D.T. twice a week. At maturity the following characters were recorded: plant height and width, branching height, primary branch number, effective pod bearing length, pod clusters per plant, pod number per plant, seeds per

pod, seed size; the number of pods and flowers that aborted per plant and dry grain yield per plant. The number of days to maturity were determined when 50% of the pods were ripe. The data were used to determine means and standard deviations of the characters recorded. Phenotypic correlations coefficients among the characters and their heritability estimates were determined by the variance/covariance method and the formula $h^2 = 2b$, respectively (Falconer, 1960).

Experiment I(b)

During the second rains season of 1974 seed from the selected plants of the first rains season was planted out in progeny rows 4 meters long. The parents were also grown as a control. A spacing of 100 cm between rows and 50 cm between plants, was used. At flowering stage selection between the parental lines and within the progenies was made resulting in only 154 out of 770 lines being retained (700 from the world collection and 70 from the composites). From the 154 lines five plants were selected per line and

selfed as in Experiment I(a). The selected plants had the same recordings of plant height, flower colour, leaf shape, plant habit and plant vigour as the parental lines of Experiment I(a). At maturity the same characters measured on the plants in Experiment I(a) were measured on the 5 selected plants per row. Likewise the data recorded was used to determine means and their standard deviations, phenotypic correlations among the characters and heritability estimates for the characters using methods similar to those in I(a).

Experiment II.

Phenotypic Recurrent Selection

A phenotypic recurrent selection experiment was started in the first rains of 1974 in each of the 8 composites and the second cycle population was grown during the second rains season of 1976. The method was suggested by Khan (1973) but modified by omission of the stage for carrying out yield tests in replicated trials in the second cycle of selection. In this case, therefore, 20% of the 100 lines selected from each composite were directly grown in a polycross nursery.

Five replications were used for the yield tests and 6 for the recombination phase. In order to encourage maximum outcrossing during the recombination phase, no insecticidal sprayings were made on these populations. From each population 10 plants were randomly selected and the following characters recorded: Plant height, days to 50% flowering, pods per plant, seeds per pod, seed size, percent protein and dry grain yield per plant. Means were determined for the different characters and for all the eight composites and the percentage change for each character after each cycle of selection for all the composites was determined. In the case of Composite I the percent protein and grain yield per plant in the selected sample of 100 plants and the 20 plants selected as parents were recorded. Percent protein in the seed was determined by an auto-analyser. Phenotypic correlations among the characters were also determined using the method suggested by Falconer (1960). Heritability estimates were determined using the formula $h^2 = br_{xy}$ where r_{xy} = the coefficient of parentage (Smith and Kinman, 1965).

Experiment III

POPULATION AND SPACING

A population and spacing experiment was conducted during the 1975 and 1976 first and second rains seasons. A split plot design was used with varieties in the main plots and planting the row spacings arranged at ratios of 1:1 (30 x 30, 40 x 40 and 50 x 50 cm²); 1:2 (60 x 30, 80 x 40 and 100 x 50 cm²) and 1:4 (60 x 15, 80 x 20 and 100 x 25 cm²), in the sub plots. The experiment had four replications with a plot size of 4m x 4m. At harvesting the outer rows were discarded. Ten plants were randomly selected from parts with good stands, of each plot, and scored for plant height, number of days to 50% flowering and pod yield. Crude protein content of the seed was determined by an auto-analyser. The data were analysed and Duncans Multiple range test used to separate the means.

HYBRIDIZATION

Experiment IV.

Natural Cross-pollination

Two experiments were set up to determine the level of natural outcrossing in pigeon peas. Twenty one determinate plants with pure yellow flowers were selected from the randomly mating population of Composite I grown during the 1974 first rains season. During the second rains season the plants were grown in progeny rows of 50 plants per row. A spacing of $100 \times 50 \text{ cm}^2$ was used. The percentage of natural crossing in each progeny row was determined from the number of off-type plants in each row with respect to plant habit and flower colour. The percent natural crossing for the 21 progeny rows was determined using the method suggested by Kadam et al. (1945). The second experiment was conducted during the first rains of 1975, using the crossing design suggested by Kadam et al. (1945). A randomised complete block design with 4 replicates and a plot size of $10 \times 10 \text{ m}^2$ was used. Three different spacings of $100 \times 50 \text{ cm}^2$,

50 x 50 cm² and 50 x 25 cm² were used. Maximum out-crossing between the pure yellow-flowered plants and those with red veined flowers was encouraged by carrying out insecticidal sprayings on only those plants that were covered with gauze bags. At harvest the pure yellow-flowered plants were harvested from each plot and threshed individually. During the 1975 second rains season these plants were grown in progeny rows and at flowering the number of off-type plants, with respect to flower colour, per progeny row was recorded. Percent natural crossing between strains at each spacing level was then calculated.

Experiment V

Diallel cross

During the 1975 first rains season a complete diallel cross was made using eight lines that were inbred for 2 generations. The lines were selected for wide differences in yield, yield components and other agronomic characters (Table 2). Half of the F_1 seed was grown in greenhouse to get F_2 seed. All possible F_1 's (including reciprocals), F_2 's and parents were

Table 2. Some of the characters of the 8 lines used in the diallel cross

Line	Plant weight	Days to flower	Pods/plant	100-seed weight	% protein	Grain yield/plant
1 (Uc 2568/2)	101	70	272	10.5	21.7	58.8
2 (Uc 2221/6)	110	67	260	9.4	20.0	67.5
3 (Uc 4099/1)	95	67	199	10.0	23.6	54.0
4 (Sel/4)	89	69	260	9.7	20.0	53.3
5 (Uc 1266/2)	99	61	209	10.4	19.7	60.5
6 (Sel/8)	117	73	255	8.9	21.2	60.0
7 (Sel/1)	70	63	135	9.0	19.0	52.7
8 (Uc 5418/2)	108	69	168	13.9	23.0	63.7

Uc = Uganda collection, Sel = Selection from Composite I

/2 = Second plant in the row

grown in the field during the 1976 first rains season, in a randomized complete block design with 4 replicates and a plot size of $4 \times 4\text{m}^2$ in a spacing of 100 cm between rows and 50 cm within rows. At maturity plant height and width, primary branch number, pod clusters and pod number per plant, seeds per pod and seed size were recorded on five randomly selected plants per plot. Days to flowering were recorded when 50% of the plot had bloomed. Percent protein of the seed was determined by an auto-analyser.

Each of the above characters was subjected to the following steps in a series of analysis:

- (1) Analysis of variance
- (2) Half diallel analysis of variance
- (3) Regression of W_r (covariance) on V_r (variance and
- (4) Correlation of Y_r (mean parental value) against $W_r + V_r$ (as a measure of dominance).

The analyses were based on the techniques of Jinks (1954), Hayman (1954a and b) and Mather and Jinks (1971). Heterosis of the characters was calculated as:

$$F_1 - MP$$

———— x 100 and inbreeding depression as:

$$MP$$

$$F_1 - F_2$$

———— x 100 where F_1 and F_2 refer to the

$$F_1$$

first and second filial generations of the diallel and MP = mid parent. The heterosis values were tested on basis of L.S.D. calculated from the analysis of variance of F_1 and parents, and inbreeding depression values were tested using L.S.D. calculated from the analysis of variance including all entries (Parents, F_1 and F_2). The combining ability (general and specific) of the parental and hybrid lines was determined using Method 4 Model 1 of Griffing (1956). The combining ability effects were tested by the F-test as follows:

General combining ability effects = $F_{(P-1)}$, $M = Mg/Me$

Specific combining ability effects = $F_{P(P-3)/2}$, M
 $= Ms/Me$

Where F = 'F' value

P = number of parental lines

RESULTS AND DISCUSSIONS

SELECTION

Experiment I.

Single Plant Selection

The results of the analysis of variance for different characters after two cycles of single plant selection are presented in Table 3. Significant differences ($P < 0.01$) were found for yield, pods per plant and seeds per pod, indicating that these lines had different potentials for yield and some of its components. Significant differences ($P < 0.05$) were found for all the characters measured on the crop, indicating that the parent population was different from the progeny population when grown during the same season. This was so because of the selection pressure imposed on the parent population during the first cycle to yield the progenies of the second cycle of selection. The interaction between the lines and cycles was significant ($P < 0.01$) mainly due to differences in the growing conditions of the two crops, hence making the

varieties to behave differently during each cycle of selection. There were very high rains up to the end of the first rains season while the second rains season had very little rain and none at the pod maturing stage of the crop. Similar views were forwarded by Dahiya et al. (1974).

The results of single plant selections made during the first and second rains seasons of 1974 are presented in Table 4. Each value presented was the combined average of 154 plants for the parent population and 770 plants for the progeny population. The data revealed some variation in the relative performance for various characters and between parental and progeny populations. Variations were mainly observed in grain yield and plant height. The variation in the progeny population for most of the characters was not comparable in extent to that of their corresponding parents, indicating that the parents were not inbred. Significant reduction in yield ($P < 0.01$) between the two parental populations was mainly due to differences in

Table 4. The mean and standard deviation of the mean of some characters for the parents and their progenies after two cycles of single plant selection (grown in Experiment 1(a) and 1(b)).

	Plant height	Plant width	Branch number	Days to flowering	Pods per plant	Seeds per pod	Seed size	Pod clusters per plant	Seed yield per plant
Experiment 1(a) (parents)	76.8 ± 5.9	27.2 ± 0.5	15.8 ± 3.9	61.0 ± 1.6	96.9 ± 1.6	2.0 ± 1.6	9.7 ± 0.6	14.2 ± 0.5	16.20 ± 5.6
Experiment 1(b)									
A (parents)	65.3 ± 3.1	24.5 ± 0.9	12.0 ± 1.7	59.0 ± 1.7	105.9 ± 1.3	2.8 ± 1.5	10.9 ± 0.3	16.2 ± 0.1	24.6 ± 3.8
B (progenies)	62.8 ± 5.8	24.3 ± 2.7	9.8 ± 3.0	58.0 ± 0.6	126.3 ± 0.4	3.9 ± 0.2	12.6 ± 0.1	17.9 ± 0.9	32.3 ± 2.1
L.S.D.									
5%	2.15	1.84	0.57	0.86	3.51	0.70	0.71	0.59	0.33
1%	2.84	2.43	0.75	1.16	4.62	0.93	0.93	0.77	0.44

n = 154 for parents and 770 for progenies.

the amount of rains received during the two seasons when the crops were grown. During the first rains season (Experiment 1) there was a lot of rains throughout the season. The rains that came late in the season were used more for vegetative build up of the plants (Dahiya et al. 1974). With the second offshot of growth, more flowering occurred. This resulted in flowers, flower buds and young pods aborting. Similar results were obtained by Adams (1967) who attributed the abortions to these components competing for the limited supply of available carbohydrates.

Plant height was significantly ($P < 0.05$) decreased from 65.3 to 62.8 cm and days to 50% flowering from 59.0 to 58 days. Onim (1974) and Singh et al. (1976) were also able to significantly change these characters using single plant selection. Significant ($P < 0.01$) increases in mean number of pods per plant, seeds per pod and seed yield per plant were obtained indicating response of these characters to single plant selection. Khan (1973) had obtained similar results in the same environment. The response of these characters to single

plant selection suggests that part of the variation that existed in the parent population was genetic. The results indicate that in unselected populations or land races simple methods of selection can be used to improve most characters in pigeon peas.

Observations were made on the amount of flower and pod abortion that took place during the first and second rains seasons of 1974 and the results are presented in Table 5.

Eight weeks after 50% flowering the percent abortion was at the maximum 30% for the first and 3.5% for the second rains season; but the percent increase in the number of pods and flowers aborted had began to fall, indicating that maximum abortion occurs 7 weeks after 50% flowering. On examination of the aborted flowers, flower buds and young pods, two pests Frankniella dampfi and Heliothis armigera were found in all the flowers and flower buds and the young pods, respectively. Maximum build up of the populations of the two pests occurs 6 to 7 weeks after 50% flowering (Walcott, 1948). Since this corresponded with the

Table 5. Percentages of pod and flower abortion in pigeon peas in the first and second rains of 1974.

	1st rains season			2nd rains season		
Weeks after 50% flowering	No. of pods and flowers	% in- crease	% abortion	No of pods and flowers	% in- crease	% abortion
3	100	-	6.1	41	-	1.1
4	112	12.0	12.3	43	4.9	1.8
5	138	14.3	18.5	46	7.0	2.4
6	175	26.4	22.3	50	8.7	3.1
7	227	29.7	25.4	55	10.0	3.2
8	251	10.6	30.0	60	8.3	3.5

maximum percent increase in abortion then it was suspected that the two pests contributed a lot to the abortion of these reproductive parts of the crop. Similar views were forwarded by Cruz (1975). The attack by II. armigera was higher on determinate plants where pods were borne on a few clusters than where the pods were scattered on the plant.

Correlations among some characters

Results of the phenotypic correlations among major agronomic and yield characters measured on the parent populations of 1974 first and second rains seasons are presented in Table 6. Plant height and width, days to 50% flowering, and number of primary branches were not significantly correlated with grain yield in both populations. Similar results were reported by other workers (Sharma et al. 1971; Singh et al., 1972; and Joshi, 1973). The relationship between grain yield with plant height and width, were negative though non-significant for the population grown during the second rains season, and positive for the population grown

Table 6. Phenotypic correlation coefficients among some characters for the parents, first rains season above the diagonal and second rains season below the diagonal.

Character	1	2	3	4	5	6	7	8	9	10
1) Grain yield		.14	.38	-.29	-.18	.20	.67**	.59**	.74**	.54**
2) Plant height	-.24		.43*	.46*	.04	.13	.37	.72**	.29	.09
3) Plant width	-.37	.14		.37	.11	.28	.52**	.22	.07	.03
4) Days to flower	-.34	.55**	.45*		.19	.42*	-.11	.24	-.08	-.18
5) Days to maturity	-.25	.24	.10	.59**		.12	.17	.14	.11	-.20
6) No of branches	.27	.40*	.02	.54**	.13		.24	.25	.07	.01
7) Pods per plant	.59**	.40*	.69**	.36	.35	.20		.50*	-.39	-.04
8) Pod clusters/plant	.61**	.80**	.19	.37	.16	.50*	.65**		.39	.02
9) Seeds per pod	.63**	-.40*	.36	-.49*	-.48*	-.11	-.33	-.29		.19
10) 100-seed weight	.52**	-.28	.08	-.23	-.42*	.09	-.03	.07	-.22	

* ** Significant at 5 and 1% probability levels, respectively.

during the first rains season. There was a water stress during the second rains season so the tall and wide cultivars planted during this season suffered from the water stress thus giving lower yields than their shorter counterparts (Dahiya et al., 1974).

Negative though non-significant correlations were found for days to flowering and maturity with grain yield. Similar results were reported by Singh et al. (1972) and Rubaihayo and Onim (1975). The relationship indicates that late flowering and maturing cultivars yield less than the early ones. This is so because such genotypes flower at peak pest population build up, especially flower thrips and H. arvensis (Cruz, 1975) while the early genotypes flower before the peak pest populations and at the same time, they miss the drought effects at the end of the season. Similar views were forwarded by Khan and Rachie (1972).

Positive and significant ($P < 0.01$) correlations were found for grain yield with pods per plant, pod clusters per plant seeds per pod and seed size. Since these are some of the components of yield in this crop (Singh and Molhotha, 1973) such a relationship was

expected. The results indicate that increasing any of the above components will increase yield. Since the interrelationships among the components were found to be negative then the compensatory nature of these components for each other (Adams, 1967) should be taken in consideration in selection programmes. Similar results were reported by Sharma et al. (1971) who reported the relationship between grain yield with seed size to be positive, $r = 0.29$, but non-significant.

Plant height was positive and significantly ($P < 0.05$) correlated with plant width and days to 50% flowering in the parent population grown during the 1974 first rains season. This indicated that the tall plants were wider and flowered later than the short plants. The relationship between plant height and pod clusters/plant was positive and significant ($P < 0.01$); indicating that the tall cultivars had more pod clusters. But since the tall cultivars mature when unfavourable weather conditions have set in (Khan and Rachie, 1972 and Dahiya et al., 1974) then the flower buds that are formed on the clusters late in the

season aborted due to lack of available carbohydrates to fill the pods (Adams, 1967). For the population grown during the second rains season, plant height was negative and significantly ($P < 0.05$) correlated with seeds per pod. This indicated that tall plants ~~had~~ ^{had} less seeds per pod due to stress conditions at the end of the season. Similar views were reported by Sharma et al. (1971) who reported that tall plants had less and smaller seeds per pod.

Days to flowering showed a positive and significant ($P < 0.05$) relationship with branch number in the first population. In the second population the relationship was also positive and significant ($P < 0.01$), indicating that the higher the number of primary branches a genotype had the later it tended to flower (Munoz and Abrams, 1971).

Heritability of some characters

Heritability estimates were determined in the narrow sense, for the two seasons of single plant selection, and are presented in Table 7.

Table 7. Heritability estimates of some characters
for the single plant selection experiment

Character	" h^2 " for parent Vs off- spring generations
1 Grain yield	0.27
2 Plant height	0.76**
3 Plant width	0.43*
4 Days to flowering	0.69**
5 No. of branches	0.26
6 Pods per plant	0.67**
7 Seeds per pod	0.66**
8 100 seed weight	0.70**
9 Pod clusters per plant	0.71**
10 Percent protein	0.24

*,**Significant at 5% and 1% probability
levels, respectively.

Low heritability estimates (h^2) were observed for grain yield, primary branch number and percent protein, indicating that these characters can only be improved after several cycles of selection, as was pointed out by Eberhart et al. (1967) and Eberhart (1970). Significant ($P \leq 0.01$) heritability estimates were observed for plant height, days to 50% flowering, pods per plant, seeds per pod, seed size and pod clusters per plant. Similar results have been reported by other workers (Khan and Rachie, 1972; and Rubaihayo and Onim, 1975), indicating that these characters can be improved after a few cycles of selection.

Results contrarily to the ones reported here have been reported by Munoz and Abrams (1971) who reported very high heritability estimates for grain yield in pigeon peas. These workers used heritability in the broad sense (H) their results are, therefore, expected to be higher than those reported in this study. Munoz and Abrams (1971) and Hiremath and

Talawar (1973) also reported high heritability estimates for grain yield and percent protein in pigeon peas. Heritability estimates of the same character may not only be influenced by the experimental procedure used, but also by the seasonal and genetic differences of the material used (Falconer, 1960; and Smith and Kinman, 1965). This accounts for the differences in results between those reported by the above workers and those reported in this study.

Since the aim of this experiment was to select high yielding lines with favourable agronomic characters only a few lines were found interesting. This was attributed to the high pod and flower abortion that took place in most lines. Eight of the selected lines were used in a diallel cross (Table 2) and the high yielding lines will be tested in yield trials before final release to farmers.

Experiment II

Phenotypic Recurrent Selection:

The analysis of variance (Table 8) of the composites after two cycles of phenotypic recurrent selection revealed that there were significant ($P < 0.01$) differences between composites for most of the characters. All the characters were significantly different ($P < 0.01$) for the two cycles indicating that phenotypic recurrent selection was able to change the expression of these characters after each cycle of selection.

Results of the mean yield, pods per plant, seeds per pod, seed size and percent protein plus the percent increase of each character after each cycle of selection are presented in Tables 9 and 10. The mean yield data (Table 9) revealed some variation in the relative performance for various characters and among composites. Variation was mainly observed in grain yield and pods per plant indicating that these two characters were probably governed by many genes.

Table 8. Analysis of variance for the different characters recorded on the composites after two cycles of phenotypic recurrent selection.

Source of variation	d.f.	Mean Squares for:					
		Plant height	Days to flowering	Pods/plant	Seeds/pod	Seed size	Percent protein
Composites	7	291.8*	195.6**	459.9**	94.3**	10.7	68.3**
Cycles	1	1126.1**	989.6**	2750.0**	678.6**	112.4**	964.3**
Composites X cycles	7	167.4	115.0	116.4	11.9	6.5	40.4
Error	48	128.4	87.3	98.9	9.8	6.6	21.6
							0.2

*, and ** = Significant at 5% and 1% levels, respectively.

Table 9. Means and standard deviations of yield and yield components of the selected original population and after one and two cycles of phenotypic recurrent selection.

Composite	Selection cycle	Pods/ plant	Seeds/ pod	Seed size	Percent protein	Grain yield
I	P ₁	245 ± 16.6	3.5 ± 0.5	12.6 ± 0.7	20.6 ± 0.1	51.9 ± 10.1
	1	248 ± 6.9	3.9 ± 0.1	12.7 ± 0.3	21.6 ± 0.2	54.7 ± 6.4
	2	251 ± 6.1	4.7 ± 0.2	12.8 ± 0.1	23.7 ± 0.1	57.7 ± 1.5
II	P ₁	230 ± 11.8	3.4 ± 0.8	11.8 ± 0.5	21.2 ± 0.4	51.1 ± 10.3
	1	239 ± 10.9	3.8 ± 0.5	11.9 ± 0.6	22.0 ± 0.4	53.4 ± 9.6
	2	251 ± 8.7	4.6 ± 0.4	12.1 ± 0.6	24.1 ± 0.1	55.8 ± 6.2
III	P ₁	178 ± 15.1	3.9 ± 0.8	6.7 ± 0.5	20.0 ± 0.9	25.3 ± 10.1
	1	192 ± 15.4	4.1 ± 0.4	6.8 ± 0.4	21.1 ± 1.4	30.3 ± 11.1
	2	200 ± 14.9	4.4 ± 0.3	6.9 ± 0.1	22.9 ± 1.2	35.4 ± 10.7
IV	P ₁	190 ± 10.3	2.6 ± 0.9	7.6 ± 0.4	19.1 ± 2.3	30.8 ± 10.9
	1	200 ± 9.0	2.8 ± 0.8	7.7 ± 0.4	20.3 ± 1.6	36.4 ± 10.9
	2	212 ± 9.1	3.1 ± 0.8	7.9 ± 0.6	22.6 ± 1.1	40.9 ± 11.0
V	P ₁	168 ± 14.6	3.0 ± 0.1	6.1 ± 0.9	20.2 ± 1.9	24.3 ± 11.4
	1	180 ± 14.6	3.4 ± 0.2	6.4 ± 0.7	21.3 ± 2.3	30.6 ± 11.2
	2	190 ± 12.1	4.2 ± 0.2	6.7 ± 0.6	23.3 ± 1.6	37.7 ± 10.5
VI	P ₁	199 ± 10.4	3.1 ± 0.6	8.8 ± 0.9	20.4 ± 2.5	31.6 ± 12.1
	1	211 ± 9.1	3.7 ± 0.4	9.4 ± 0.4	21.9 ± 2.1	37.9 ± 12.0
	2	223 ± 8.2	4.5 ± 0.5	9.8 ± 0.8	23.1 ± 2.2	45.1 ± 10.9
VII	P ₁	171 ± 11.0	2.9 ± 0.3	7.1 ± 0.9	19.6 ± 1.6	28.0 ± 12.9
	1	190 ± 11.6	3.5 ± 0.3	7.3 ± 0.5	20.8 ± 2.1	33.9 ± 12.7
	2	204 ± 10.4	4.3 ± 0.2	7.5 ± 0.3	22.8 ± 1.4	38.4 ± 11.6
VIII	P ₁	232 ± 8.5	3.3 ± 0.7	12.5 ± 0.9	19.5 ± 1.7	50.8 ± 12.6
	1	246 ± 6.6	3.7 ± 0.3	12.6 ± 0.8	20.6 ± 1.2	52.8 ± 11.8
	2	268 ± 6.9	4.3 ± 0.6	12.8 ± 0.8	22.7 ± 0.9	56.2 ± 11.0

P₁, 1 and 2 = Original population, after one and two cycles of phenotypic recurrent selection.

Table 10. Percent increase in mean yield, pods per plant, seeds/pod, seed size and percent protein in composites I to VIII after one and two cycles of phenotypic recurrent selection.

Composite	Selection cycle	Percent increase in				
		Pods/ plant	Seeds/ pod	100-seed weight	% protein	Grain yield
I	1	1.2	11.4	0.8	0.5	5.4
	2	1.2	20.5	0.8	9.7	6.2
II	1	3.9	11.8	0.8	7.5	4.5
	2	5.0	21.0	1.7	5.7	4.5
III	1	7.9	5.1	1.5	5.5	19.8
	2	4.2	7.3	1.5	8.5	16.8
IV	1	10.5	7.7	1.3	5.7	18.2
	2	6.0	10.7	2.6	11.3	12.4
V	1	7.1	13.3	4.9	5.4	25.9
	2	5.5	17.6	4.7	9.4	23.2
VI	1	6.0	19.3	6.8	7.3	19.9
	2	5.7	21.6	4.2	5.5	19.0
VII	1	11.1	20.7	2.8	6.1	20.4
	2	7.4	22.8	2.7	9.6	13.3
VIII	1	6.0	12.1	0.8	5.6	4.0
	2	8.9	16.2	1.6	10.2	6.4

1 and 2 = 1st and 2nd cycle of phenotypic recurrent selection.

Since the aim of the experiment was to compare the relative efficiency of this type of selection in improving yield and other agronomic characters of pigeon peas compared to single plant selection all the composites were found to be interesting. Secondly selection was aimed at improving the yield and agronomic characters of the Makerere composites.

After the first cycle of selection composite I gave the highest yield of 54.7g/plant but the highest percent increase in yield was observed in composite V of 25.9 percent. Composite V was the second lowest yielder after the first cycle of selection. The results indicate that phenotypic recurrent selection was more effective in improving the yield of the low yielding than the high yielding composites. Generally this type of selection was able to increase the yields of the composites by 4 to 25.9 percent. The increases in yield of the composites were mainly attributed to increases in pods/plant and seeds per pod of each composite, indicating that these two are very important

components of yield. Several workers have reported results similar to these while using phenotypic recurrent selection to improve yield, (Sprague et al., 1952; Jinks et al., 1954 and Moll and Robinson, 1966).

Mean yield per plant increased after each cycle of selection but the percent increase in yield of all the composites, except I, II and VIII, was lower after the second cycle of selection. This indicates some loss in genetic variability of most of the composites after one cycle of phenotypic recurrent selection. The random mating phase after intercrossing was omitted during the second cycle of phenotypic recurrent selection resulting in six instead of the seven recommended seasons being used to complete two cycles of phenotypic recurrent selection (Khan, 1973). Omission of this phase probably resulted in fixation of some genes thus resulting in the lower percent increases in yield of the composites after the first cycle of selection as was pointed out by Allard (1960).

After two cycles of selection the protein content of the seed was increased by 5.5 to 10.2%, indicating that phenotypic recurrent selection can be used to improve the nutritive value of pigeon pea seeds. The range of protein content of the seed of the three populations was, 19.1 to 21.2%, 30.3 to 22.0% and 22.6 to 24.1% for the original population, the first cycle and the second cycle, respectively. The range in protein content of the seed that has been reported in pigeon peas varies from 17.0 to 40.0 percent (Rachie and Wurster, 1971, Laxman Singh et al., 1973 and Luse, 1975). These ranges in protein content also indicate some loss in genetic variability after the first cycle of selection. Therefore, by using phenotypic recurrent selection, a random mating population is necessary to conserve genetic variability in pigeon peas. Similar views were forwarded by Sprague et al. (1952) for corn and Khan (1973) for pigeon peas.

Plant height and days to flowering of the composites were significantly ($P < 0.01$) changed (Table 8) after the two cycles of phenotypic recurrent

selection indicating that phenotypic recurrent selection was able to produce early and even maturing composites.

Correlations among some characters

Phenotypic correlation coefficients of yield with its components and other agronomic characters for the phenotypic recurrent selection cycles of Composite I (only) were calculated and are presented in Table 11.

Plant height was positive though non-significantly correlated with grain yield in the original population. In the C_1 and C_2 populations, however, the relationship was negative though non-significant. The negative relationships were found for populations grown during the second rains seasons indicating that during these seasons the plants experienced water stress conditions which made tall genotypes to yield less than their maximum capacities. This was due to a lack of available carbohydrates to fill the late formed pods of the tall plants (Adam, 1967). Similar results were reported by several workers for the tall versus the short genotypes (Joshi, 1973, Veeraswamy et al., 1973b and Rubaihayo and Onim, 1975).

Table 11. Phenotypic correlations of yield with some pigeon pea characters for three different populations of Composite I.

Character	(C ₀) Original population 1974 FR	C ₁ After one cycle 1975 SR	C ₂ After two cycles 1976 SR
Plant height	0.16	-.09	-.21
Plant width	.30*	-.33*	-.30*
Days to 50% flower	-.21	-.18	-.11
Days to maturity	-.24	-.31*	-.30*
No. of branches	.20	.27	.26
Pods per plant	.66**	.56**	.64**
Pod clusters/plant	.38*	.24	.25
Seeds per pod	.70**	.81**	.76**
100-seed weight	.31*	.61**	.78**

*,** Significant at 5% and 1% levels, respectively.

n = 40 plants for all the populations.

The relationship between grain yield with number of branches, pods and pod clusters per plant, seeds per pod and seed size for all the populations were similar to those that were found in the single plant selection experiments. Similar explanations are therefore expected. In the two populations, C_1 and C_2 , however, the relationship between grain yield with days to maturity was negative and significant ($P < 0.05$). This indicated that during the second rains season where a water stress is experienced at the end of the season (as was the case in 1975 and 1976) then late maturing plants are at a disadvantage. Khan and Rachie (1972) got similar results to the ones reported in this study while using the Makerere germplasm at Kabanyolo; University Farm.

The heritability of some characters

Heritability estimates were determined in the narrow sense for the three populations of Composite I and are presented in Table 12.

The heritability estimates that were observed for grain yield, branch number, pods and pod clusters/plant, percent protein, seeds per pod and seed size

Table 12. Heritability estimates of some characters after two cycles of phenotypic recurrent selection in Composite I.

Character	C_1 Vs C_0 (74FR - 75SR)	C_2 Vs C_1 (75SR - 76 SR)
	h^2	h^2
Grain yield	.28	.21
Plant height	.48*	.40*
Plant width	.40*	.40*
Days to flowering	.31	.33
Branch number	.20	.21
Pods per plant	.49*	.47*
Pod clusters/plant	.56**	.61**
Seeds per pod	.56**	.60**
100-seed weight	.55**	.60**
Percent protein	.20	.12

*, ** Significant at 5% and 1% levels, respectively.

were similar to those reported in the single plant selection experiment and similar explanations were offered.

Non-significant heritability estimates were, however, found for days to flowering in these population while in the single plant selection experiment the h^2 estimate was highly significant ($P < 0.01$). The same differences were observed for plant height; in that the level of significance for the single plant selection experiment ($P < 0.01$) was higher than that of the phenotypic recurrent selection experiments ($P < 0.05$). The differences in the results of the two selection experiments was due to differences in the methods of calculating the heritability values. In the single plant selection experiment Falconer's parent-offspring regression equation of $h^2 = 2b$ was used. Smith and Kinman (1965) pointed out that Falconer's parent-offspring regression equation may only be correctly used for estimating heritabilities in an almost completely outbreeding bisexual, diploid population (where outbreeding is greater than 95%). The highest level of

outbreeding reported on pigeon peas was 48% (Mehta and Dave, 1931). It, therefore, seems that Falconer's parent-offspring regression equation may not give correct heritability estimates for pigeon peas which do not fully outbreed. As Smith and Kinman (1965) pointed out, in a case where parents also inbreed, the use of twice the regression coefficient (b) will result in an over-estimation of heritability. This seems to be the explanation for the differences in the results of the single plant selection and the phenotypic recurrent selection experiment where Smith and Kinman's method of estimating heritability was used.

Experiment III.

POPULATION AND SPARTIAL ARRANGEMENTS

The data of air dry seed yield per plot in two successive seasons of 1975 were subjected to analysis of variance and the results are presented in Table 13. The results for 1975 and 1976 were similar so to avoid repetition only those of 1975 will be discussed.

Table 13. Analysis of variance for the seed yields of the different population and spacing arrangements (First and second rains seasons of 1975).

Source	d.f.	First rains		Second rains	
		M.S	F	M.S	F
Main plots	7	791.36	-	460.35	-
Blocks	3	24.22	0.27	32.88	0.65
Varieties	1	1693.35	18.88*	992.36	19.04*
Error (a)	3	89.69	-	52.12	-
Subplots	95	160.21	-	107.58	-
Populations	5	299.05	3.24*	227.74	3.72**
Varieties X population	5	247.36	2.68*	245.49	4.01**
Error (b)	85	92.30	-	61.22	-
Sub-subplots	863	78.20	-	104.10	-
Spacings	8	191.42	1.60	298.80	2.49*
Varieties X spacings	8	245.26	2.05*	238.80	1.99*
Population X spacings	40	169.89	1.42*	189.60	1.58*
Varieties X population X spacings	40	170.56	1.51*	171.60	1.45
Error (c)	767	119.64	-	120.00	-

*,** Significant at 5% and 1% levels, respectively.

There were significant ($P = 0.05$) differences between the yields of the two varieties. Since these varieties came from the selected lines of Experiment I then the results indicate that selection was effective. There were significant, ($P = 0.05$) for the first rains and ($P = 0.01$) for the second rains season, differences between the yields of the different populations. The population by variety interaction was also significant at the same levels as the population factor for both seasons; indicating the presence of variety by population interaction. This suggests that the varieties behaved differently at different population levels. There were plenty of rains throughout the growth of the crop during the first rains season. The rains caused compensatory growth in height and width of the plants at low population levels (Adams, 1967). The compensatory growth increased yield/plant due to increased number of branches/plant. Thus, the variety by population interaction was less noticeable during this season compared to the second rains season which experienced a water stress towards the end. Several workers have re-

ported similar results under similar environments (Sen et al., 1970; Singh et al., 1971 and Veeraswamy et al., 1972). The different spartial arrangements were also non-significantly different during the first rains season for the same reason. There were significant ($P = 0.05$) differences for the interactions between population and spartial arrangements and variety x spacings suggesting that the populations and varieties behaved differently at different spartial arrangements. The second order interaction was significant ($P = 0.05$) suggesting that the two varieties behaved differently at given population levels and spartial arrangements.

The mean yields for each population at the different spartial arrangements are presented in Table 13. The differences among the means were separated out using Duncan's Multiple range test. Low rectangularity (1:1) significantly ($P = 0.05$) out-yielded medium (1:2) and high (1:4) rectangularity for the same population in all the three populations used in each variety. Similar views were forwarded by

Rubaihayo (1969) and Manjhi et al. (1973) while using soyabean and pigeon peas, respectively. There were, however, no significant differences between the yields at the 1:2 and 1:4 spartial arrangements. Contrary views were forwarded by Leakey and Rubaihayo (1972) in soyabean populations that the more rectangular arrangement yielded higher than the square arrangements. In this study the more rectangular arrangements had very wide spaces between plants, which reduced the yield per plot especially during the second rains season where extra growth in width did not take place. But Soyabeans being prostrate, the rectangular arrangement provided room for extra widening of plants thus increasing the yields/plot.

The results of Table 14 showed that the two varieties behaved differently at each spartial arrangement for the two seasons. UC 1266 (tall) gave maximum yields at $40 \times 40 \text{ cm}^2$ during the first rains season and at $50 \times 50 \text{ cm}^2$ during the second rains season. But the yields at both the spacings were not significantly different from the $30 \times 30 \text{ cm}^2$ arrangement. Maximum

Table 14. Summary yield data for the two spartial arrangements of the same populations during the 1975 first and second rains seasons.

Population plants/ha	Spartial arrangement	Seed yield kg/ha			
		UC 1266 (tall)		UC 4099 (Dwarf)	
		1st rains	2nd rains	1st rains	2nd rains
110,000	1:1 (30 x 30 cm ²)	2568ab	2426ab	2306a	3342a
	1:4 (60 x 15 cm ²)	1804bc	1748c	1205bc	2238bc
62,000	1:1 (40 x 40 cm ²)	2937a	2696ab	2254a	2974a
	1:4 (80 x 20 cm ²)	1389c	2073c	1100bc	2231bc
40,000	1:1 (50 x 50 cm ²)	2456ab	2955a	2231a	2778ab
	1:4 (100 x 25 cm ²)	1365c	2201bc	1007bc	2052c
55,000	1:2 (60 x 30 cm ²)	1206c	1571cd	932c	1211d
31,000	1:2 (80 x 40 cm ²)	1196c	1337d	884c	997d
20,000	1:2 (100 x 50 cm ²)	1100c	965d	581c	684d

Conversion gm/plot x 1.794 kg/ha

Tested by Duncans Multiple Range Test

Means followed by a similar letter are not significantly different (P 0.05).

yields for UC 4099 (dwarf) were, however, realised at $30 \times 30 \text{ cm}^2$ for both seasons suggesting that for a tall variety a wider spacing was required especially during the second rains season where water stress conditions were experienced. The second rains yields of UC 4099 were significantly ($P = 0.05$) higher than those of the first rains mainly because the crop matured before the drought effect set in (Onim, 1974) and because there was a less pest population build up during this season (Walcott, 1948 and Cruz, 1975). The very high rains of the first season also hampered pod setting by providing favourable conditions for pest multiplication especial F. dampfi and H. armigera which caused high levels of pod abortion. Similar results were reported by Datta and Arati Deb (1970) for the negative effect of high rains on pod setting in pigeon peas. The spartial arrangement that may be used to plant any given variety should take into consideration the height of the variety and the growing season. Similar views have been forwarded by Abrams and Julia (1973).

The results (Table 13) also indicated that doubling the populations from 20,000 to 40,000; 31,000 to 62,000 and 55,000 to 110,000 plants per hectare more than doubled the mean yields at the 1:1 arrangement and increased the yields by more than a half at the 1:4 arrangement. This gain in yield was due to increased yield per unit area at the higher population levels, though the yield per plant had decreased. Maximum yields for UC 1266 were realised at 62,000 plants/ha with a 1:1 arrangement and at 40,000 plants/ha with the same arrangement during the first and second rains seasons, respectively. The short variety, UC 4099 realised maximum yields at 110,000 plants/ha and 1:1 arrangement for both seasons. The short variety, UC 4099 yielded less/plant than UC 1266, but plant competition for the tall variety set in at a lower population level than that of the short variety. This was more magnified during the second season where the water stress brought the favourable population level for UC 1266 down to 40,000 plants/ha compared with 110,000 plants/ha for UC 4099.

While using a short pigeon pea variety and starting with very low population levels, Manjhi et al.

(1973) also reported increases in yield per unit area with corresponding increases in plant density. An analysis of variance for the different yield components and some agronomic characters was carried out for the two seasons of 1975 and the results are presented in Table 15. Significant ($P < 0.01$) differences were observed for plant height, days to 50% flowering, pods/plant and number of branches between the two seasons, indicating that these characters were affected by changes in the environment. Significant ($P < 0.05$) differences were also observed for percent protein and seeds per pod. Seed size was, however, not affected by changes in the environment provided by the two seasons. Significant ($P < 0.05$) differences were found for pods per plant and branch number with changes in the plant populations, spatial arrangements and the interaction between populations and spacings. This indicated that these characters are affected by changes in both population and row spacing. The interaction between seasons

Table 15. Analysis of variance for some agronomic and yield component characters combined for two seasons data of UC 1266 (First and Second rains seasons of 1975).

Source	d.f	Mean Squares for						
		PH	DF	% PROT	NOPO	NOSE	SWT	NOBR
Main plots	7	518.9	536.3	350.7	295.9	611.2	176.3	139.6
Blocks	3	88.5	71.3	68.3	39.6	40.8	30.1	41.4
Seasons	1	127.5**	146.4*	112.1*	133.1**	49.6*	18.1	129.6**
Error (a)	3	36.1	40.8	9.3	35.1	4.8	5.3	31.2
Sub plots	95	111.3	90.1	52.4	86.6	33.4	13.8	98.3
Populations	5	90.3	71.5	29.1	75.1*	16.9	10.4	78.6*
Seasons x								
Population	5	86.9	63.4	28.4	60.3	10.4	9.1	70.8
Error (b)	85	46.4	36.3	15.6	30.1	9.6	6.2	33.9
Sub-sub plots	863	612.3	520.1	480.1	233.4	112.1	158.7	144.6
Spacings	8	42.1	48.3	18.7	48.5*	19.8	7.3	46.4*
Seasons x								
Spacings	8	52.8*	67.9*	16.1	53.0	15.4	6.2	36.1
Population x								
Spacings	40	20.8	26.0	11.2	39.9*	12.0	3.8	30.2*
Population x								
Seasons x								
Spacings	40	28.1*	34.5*	9.3	37.1*	9.8	3.1	28.9*
Error (c)	767	23.7	26.3	10.1	21.5	11.3	4.5	20.4

PH, DF, % PROT, NOPO, NOSE, SWT and NOBR = plant height, days to flowering, percent protein, pods per plant, Seeds/pod, seed size and branches/plant; respectively.

*, ** Significant at 5% and 1% levels, respectively.

and spacings was significant ($P \leq 0.05$) for plant height and days to flowering, indicating that these characters behaved differently at different spacings and for the two seasons. The second order interaction was significant ($P \leq 0.05$) for all the characters save, percent protein seeds/pod and seed size, indicating changes in the expression of these characters at different population and spatial arrangements and for each season. For different environments, different populations and row widths are to be used to get optimal character expressions.

Means were computed for branches/plant, pod clusters/plant, pods/plant and percent protein for two seasons at different population levels and spatial arrangements and are presented in Table 16. Branch number, pod clusters/plant and pods/plant of different row spacings of the same population showed significant ($P \leq 0.05$) differences indicating that in order to get optimal expression of these characters, there must be careful synchrony between the population level used and the row spacing combination. At high population levels

Table 16. Mean performance of some characters at different population and spacing arrangements for UC 1266.

Population code	Spacing	First rains 1975				Second rains 1975			
		NOBR	CLNO	NOPO	% PROT	NOBR	CLNO	NOPO	% PRCT
P ₁	30 x 30 cm ²	9.8	17.5	241	21.9	8.0	14.6	183	20.6
	60 x 15 cm ²	8.6	16.1	252	21.8	7.2	13.3	187	20.3
P ₂	40 x 40 cm ²	9.6	17.8	280	21.3	8.1	14.0	200	20.7
	80 x 20 cm ²	8.5	16.9	290	21.6	8.0	13.8	216	20.3
P ₃	50 x 50 cm ²	11.3	18.0	314	21.1	9.8	16.1	241	20.5
	100 x 25 cm ²	10.1	16.9	298	21.8	8.3	15.0	263	20.7
P ₄	60 x 30 cm ²	10.4	18.2	306	21.9	9.4	15.9	284	20.5
P ₅	80 x 40 cm ²	11.8	18.5	339	22.0	8.6	16.3	289	21.6
P ₆	100 x 50 cm ²	12.3	18.7	411	22.2	10.9	16.3	290	21.8
	NOBR	CLNO	NOPO	% PROT					
LSD 5%	1.1	1.0	165	1.3					
LSD 1%	1.9	2.8	287	1.9					

NOBR, CLNO, NOPO and % PROT = Branch number, pod clusters/plant, pods/plant and percent protein.

a more square arrangement gave higher pod yields than the rectangular arrangement. Several workers have reported similar results (Presekar and Subramanian, 1961 and Hammerton, 1971). This type of arrangement gave higher seed yields/plant than the rectangular arrangement, thus making it more favourable for use in pigeon peas. Nangju (1975) reported similar results while working on pigeon peas in Nigeria.

The protein content of the seed decreased significantly ($P = 0.05$) during the second rains season. There was, however, no significant effect imposed on this character by changes in population or row spacing. The results indicated that protein content was influenced by seasonal changes but not by changes in population or row spacing. Manji et al. (1973) forwarded similar views for the effect of population and row spacing on the protein content of pigeon pea seeds. These changes came about due to changes in seed yield imposed by the three factors. High seed yields had a diluting effect on seed protein content so that factors

which increased seed yield, reduced seed protein percentages in the seed (Johnson and Raymond, 1964).

Genotype Environmental Interaction

Due to lack of reliable data genotype by location interaction was not calculated, but the genotype by season interaction was observed during the course of growth of the experiments in this study. Significant ($P = 0.01$) differences were found between the seed yields of the two seasons of the single plant selection experiment (Table 4). These differences were attributed to genotype by environmental interaction. Genotype by season interaction was also noted by the differences between the yields of the same population densities and same row spacings, grown during different seasons. Genotype by environmental interaction was also observed by the differences in seed yield, pods per plant, plant height, days to flowering and percent protein at different population levels and spatial arrangements of the same season (Table 15). These results indicated that this crop is greatly affected by changes in the

environment both at population and plant level (Ganguli and Srivastava, 1969). Several workers have reported on the effect of changes in the environment on the yield, yield components and other agronomic characters of pigeon peas (Abrams et al., 1968; and Laxman Singh et al., 1974).

HYBRIDISATION

Experiment IV.

Natural Cross-pollination

Percent natural crossing was determined in 21 progeny rows spaced at 100 x 50 cm and the data are presented in Table 17. When percent natural crossing was determined in respect to plant habit one of the rows showed no segregation. In 21 progeny rows natural crossing varied from 0.0 to 37.3 percent. When percent natural crossing was determined in respect to flower colour, the progeny rows showed natural out-crossing varying between 2.1 to 30.4 percent. The results indicated that percent natural crossing varied with the

Table 17. Percent natural crossing in 21 progeny rows in respect to plant habit and flower colour.

Progeny row	% natural crossing		Progeny row	% natural crossing	
	Plant habit	Flower colour		Plant habit	Flower colour
1	6.6	9.3	12	12.5	10.1
2	6.1	7.8	13	16.6	15.2
3	25.0	14.7	14	14.3	19.0
4	14.3	17.3	15	13.8	25.3
5	15.1	18.1	16	16.6	22.8
6	0.0	2.9	17	21.1	28.3
7	3.7	2.1	18	33.5	30.4
8	28.5	28.9	19	12.5	23.4
9	11.7	16.6	20	37.3	28.0
10	22.4	14.3	21	9.4	10.1
11	16.7	21.6			

basis by which it was determined, plant habit or flower colour. Similar views were forwarded by Miranda Colin (1971) who observed that percent natural crossing in French beans varied with the basis on which it was calculated, F_1 seeds or plants. Several workers have reported on the percent natural crossing in pigeon peas and have found ranges similar to the ones reported in this study (Mehta and Dave, 1931; Kadam et al., 1945 and Khan, 1973).

The results of the percent natural crossing among plant types grown in adjacent rows at each spacing arrangement are presented in Table 18. The percent natural crossing from 5.9 to 8.9 with a mean of 7.5 percent, 15.7 to 19.5 with a mean of 18.1 percent and 31.6 to 38.7 with a mean of 35.2 percent for the $50 \times 100 \text{ cm}^2$, $50 \times 50 \text{ cm}^2$ and $50 \times 25 \text{ cm}^2$ spartial arrangements, respectively. The results showed that highest amounts of natural crossing took place in the closely spaced plants and low amounts in the widely spaced progenies. This suggested that percent natural crossing is inversely proportional to

Table 18. Percent natural crossing in progenies of open pollinated plants.

Spacing between rows (cm)	Replicate No	Plants with yellow flowers	Red-veined flowered plants (segregants)	Total	% natural crossing
50 x 100	1	529	33	562	5.9
	2	788	75	863	8.9
	3	617	50	667	7.5
	4	425	36	461	7.8
Total		2359	194	2553	7.5
40 x 50	1	273	62	335	18.5
	2	566	105	671	15.7
	3	405	92	497	18.6
	4	278	68	346	19.5
Total		1520	327	1849	18.1
50 x 25	1	299	157	456	34.5
	2	394	182	576	31.6
	3	232	130	362	36.0
	4	255	161	416	38.7
Total		1180	630	1810	35.2

the distance between rows. Similar views have been forwarded by Miranda Colin (1971) for French beans, Drozd (1971) and Putntsev (1971) for peas and Ariyanayagam (1976) for pigeon peas.

No natural hybrids were found in the progenies of plants covered with gauze bags and consintantly sprayed with insecticides. This indicated that coverage of plants with gauze bags combined with insecticidal sprays, was an efficient way of maintaining the purity of varieties or stocks. The results also supported the hypothesis that the most important pollen vectors, in pigeon peas, are insects (Abrams, 1967 and Khan, 1973). But in C. cajan the stigma becomes receptive 68 hours before anthers dehisce and remains receptive 20 hours after a flower opens (Prasd et al., 1977). Anthers dehisce 24 hours before a flower opens (Purseglove, 1968). So in order for cross-pollination to take place differential growth rate of pollen from different sources must take place or some inhibiting physiological or morphological factor prevents selfing before a flower opens (Krauss, 1927 and Purseglove, 1968). Minute

insects such as F. dampfi also enter a flower before it opens thus affecting cross-pollination at an early stage (Abrams, 1967). In cases where fertilisation doesn't take place by the time a flower opens, then bees and other large insects effect cross-pollination (Bateman, 1947 and Khan, 1973).

Experiment V: DIALLEL CROSS ANALYSIS

The Nature of Gene Action

The mean performance of the parents their F_1 and F_2 hybrids for ten different characters was worked out and is presented in Table 19. The parents exhibited large variations for plant height, pods/plant seeds/pod, seed size, percent protein and seed yield/plant. The crosses 1 x 2, 2 x 3, 2 x 4, 2 x 7, 2 x 8 and 7 x 8 were among the best in seed yield for both F_1 and F_2 generations. The same crosses had generally high pod numbers/plant and seed size and intermediate number of seeds/pod and pod clusters/plant. Analysis of variance (not shown) carried out on the data in Table 19 showed significant ($P < 0.01$) differences among parents, F_1 's and F_2 's for each character, thus fulfilling the

Table 19. Mean values for parents and the F_1 and F_2 generations of a diallel cross.

Variety	PH	PM	NOBR	DF	MOPO	MOSE	100-SWT	% PROT	CLNO	GY
1	100.6	46.5	13.6	70.0	171.7	3.3	10.5	21.7	16.9	58.8
2	110.5	48.9	10.3	67.9	260.5	5.9	9.4	20.0	16.3	67.5
3	95.4	33.4	10.3	67.5	199.8	4.4	9.8	23.6	16.0	54.0
4	89.9	51.4	12.3	69.6	258.8	3.9	9.7	20.0	15.8	53.3
5	98.6	37.4	12.9	61.2	209.0	3.5	10.4	19.7	16.0	60.5
6	117.6	47.6	17.2	73.0	255.4	5.9	8.9	21.2	16.7	60.1
7	70.0	32.1	14.9	63.6	134.8	4.7	9.0	19.1	15.0	52.7
8	108.4	79.8	16.1	69.2	168.5	7.6	13.8	23.0	18.3	63.7
1 x 2 F_1	106.1	47.8	14.9	67.9	268.8	5.7	12.6	21.9	16.5	72.7
F_2	110.6	47.5	12.6	61.4	262.7	5.0	12.3	19.4	16.2	61.8
1 x 3 F_1	112.4	41.6	12.4	67.4	240.2	4.3	10.1	22.7	16.6	58.7
F_2	105.2	40.9	11.0	63.5	214.7	3.6	9.0	20.5	16.4	51.3
1 x 4 F_1	104.1	49.8	13.0	68.9	261.0	3.4	11.6	21.7	16.0	58.9
F_2	100.1	48.0	11.0	61.9	234.3	2.7	10.9	19.0	15.8	51.0
1 x 5 F_1	112.4	39.9	13.3	61.5	256.7	3.5	11.2	21.0	16.7	61.2
F_2	100.6	39.5	12.7	65.9	230.6	2.8	9.4	19.6	16.4	53.8
1 x 6 F_1	120.9	47.5	18.9	70.1	263.0	4.2	9.8	22.1	16.8	60.0
F_2	110.9	46.6	16.5	64.0	237.9	3.4	8.5	21.6	16.8	52.4
1 x 7 F_1	114.2	43.5	14.9	63.1	194.3	4.6	10.0	20.0	16.1	57.9
F_2	104.0	43.0	12.9	66.2	168.4	3.7	8.7	18.0	15.9	49.9
1 x 8 F_1	115.7	66.9	15.7	69.2	202.8	5.7	12.7	23.3	18.0	64.2
F_2	104.2	66.0	14.0	68.5	176.3	4.9	11.9	22.1	17.8	54.9
2 x 3 F_1	114.6	46.5	11.0	67.4	269.2	6.0	10.7	21.2	18.2	67.1
F_2	112.0	45.9	8.6	67.4	263.9	5.3	10.0	20.1	17.9	56.1
2 x 4 F_1	96.2	50.9	12.9	67.9	259.7	5.4	11.7	18.3	16.0	68.2
F_2	85.7	50.3	11.4	68.7	233.0	5.9	10.8	20.0	15.7	57.0
2 x 5 F_1	116.9	48.0	13.0	62.0	230.8	4.5	9.9	18.7	16.2	66.5
F_2	100.9	47.0	11.7	65.9	204.3	3.3	9.0	21.5	16.0	46.0
2 x 6 F_1	126.0	48.6	17.3	68.1	255.9	6.0	9.0	21.0	14.4	65.0
F_2	115.1	47.9	15.4	62.4	248.1	5.5	8.5	19.7	14.0	54.4
2 x 7 F_1	114.6	40.8	14.9	62.1	278.4	6.8	12.2	19.8	16.5	79.1
F_2	101.3	39.7	13.0	66.0	272.1	6.0	12.3	17.8	16.0	68.0
2 x 8 F_1	112.7	69.7	16.5	68.0	260.8	6.7	12.5	20.9	17.7	68.0
F_2	100.5	69.0	14.1	61.5	253.7	6.1	10.5	18.6	17.5	59.7
3 x 4 F_1	92.3	43.8	11.5	68.9	224.2	4.2	10.5	23.9	15.9	54.0
F_2	89.2	42.9	10.0	62.3	199.4	3.3	8.9	21.1	15.6	46.5
3 x 5 F_1	98.0	37.0	12.0	62.1	203.1	3.7	10.2	23.0	16.0	60.4
F_2	85.2	36.4	10.3	66.1	177.3	3.0	8.6	20.0	15.7	46.5
3 x 6 F_1	118.0	46.6	18.2	68.2	223.7	5.1	9.3	24.2	16.3	56.2
F_2	107.0	45.7	16.1	61.9	197.3	4.5	8.0	23.5	16.1	49.7
3 x 7 F_1	106.1	35.0	13.0	64.6	150.9	4.9	9.8	22.0	15.6	53.4
F_2	94.6	34.5	10.6	67.5	124.0	4.0	7.2	20.1	15.2	45.1
3 x 8 F_1	119.5	56.6	14.0	68.5	181.5	5.6	12.0	23.4	17.6	64.3
F_2	106.0	55.9	12.5	61.8	165.9	4.9	11.0	21.3	17.3	53.4
4 x 5 F_1	106.0	45.4	12.8	63.0	229.8	3.5	10.9	20.3	15.8	55.0
F_2	90.9	44.8	10.8	67.0	203.2	2.7	9.0	18.4	15.5	48.6
4 x 6 F_1	126.6	49.0	18.2	63.1	256.3	4.4	10.1	20.8	15.4	57.4
F_2	116.0	48.5	16.7	64.5	230.0	3.6	8.9	18.6	15.0	50.8
4 x 7 F_1	90.3	42.9	13.2	67.2	194.8	3.6	10.4	19.8	16.6	61.7
F_2	78.0	42.0	11.2	69.3	169.4	2.7	8.7	18.5	16.3	53.9
4 x 8 F_1	119.7	61.9	15.0	67.9	200.2	5.8	12.4	21.7	16.2	60.5
F_2	106.7	60.3	12.7	63.8	174.5	5.3	10.6	20.2	16.0	50.2
5 x 6 F_1	114.7	43.1	17.5	60.4	235.4	4.0	9.2	21.0	15.8	61.0
F_2	100.9	42.4	15.8	61.9	209.8	3.2	7.4	19.5	15.1	53.0
5 x 7 F_1	100.9	37.0	13.1	64.4	161.9	4.1	9.7	19.7	17.0	62.9
F_2	95.7	36.0	11.9	65.6	146.8	3.3	8.5	17.5	16.2	52.7
5 x 8 F_1	110.0	66.1	14.2	60.0	180.5	7.3	12.3	21.4	16.0	59.3
F_2	100.3	64.9	11.8	73.9	154.6	6.8	10.5	21.0	5.7	48.7
6 x 7 F_1	117.9	47.0	17.9	66.5	179.4	6.4	9.0	22.3	16.3	62.2
F_2	110.6	45.9	15.9	70.2	153.1	5.9	7.7	20.6	16.0	50.6
6 x 8 F_1	120.4	59.1	18.9	66.0	201.8	7.7	10.5	23.1	17.7	66.1
F_2	104.9	57.9	16.5	65.0	175.3	7.2	9.0	20.9	17.5	55.0
7 x 8 F_1	108.9	46.2	15.5	65.3	269.0	8.3	14.6	23.0	17.0	67.3
F_2	100.7	44.8	13.0	58.1	259.5	7.7	10.3	21.7	16.6	56.1

requirements for carrying out a diallel cross analysis. The block or block x variety interaction were not significant so the W_r (covariance) and V_r (variance) values were calculated for the blocks combined (Jinks and Hayman, 1953 and Steel and Torrie, 1960).

Plant height

Correlations of the standardised deviations of the two values Y_r against $(W_r + V_r)$, for the F_1 generation, was worked out and are presented in Figure 1a. The positive values of Y_r suggested high expression and negative values low expression of any one given character. The $Y_r, (W_r + V_r)$ relationship for plant height was not significant, $r = - 0.46$, suggesting that there was only a little tendence for tallness to be associated with dorminant genes and shortness with recessiveness (Jinks, 1954 and Hayman, 1954b). The W_r/V_r regression for plant height in F_1 was worked out from the data in Table 17 and is shown Figure 1b. The slope of the regression line, $b = 0.31 \pm 0.07$ was significantly ($P < 0.05$) different from 0 and significantly ($P < 0.05$) different from a

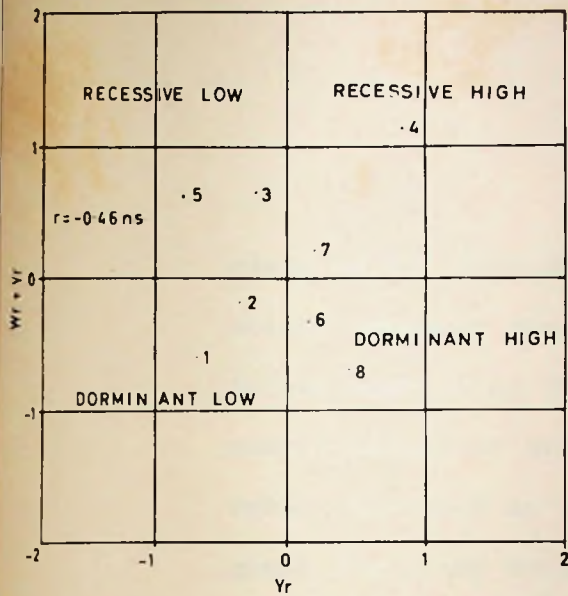


Fig 1a

Correlation of the standardised deviations,
 V_r and $(W_r + V_r)$ for plant height in F_1

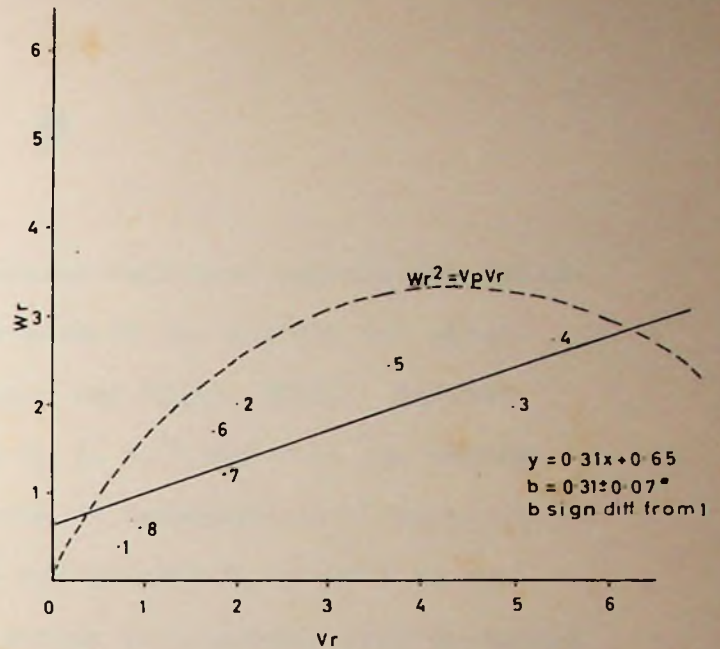


Fig 1b

$W_r | V_r$ regression for plant height in F_1

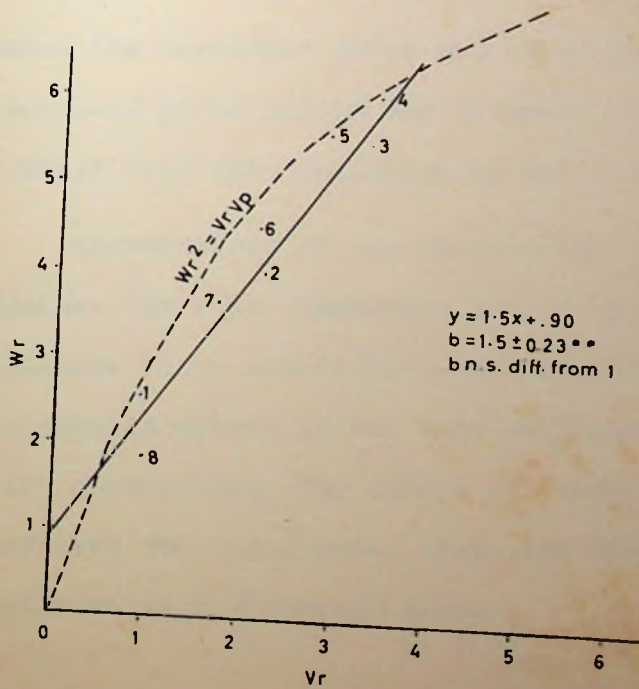


Fig 1c

$W_r | V_r$ regression for plant height in F_2

slope of 1. This behaviour indicated non-allelic interaction amongst the crosses of the diallel for plant height expression (Mather and Jinks, 1971). Parents corresponding to array 2, 6, 7, 8 and 1 in increasing order possessed an excess of dominant over recessive genes for plant height and parents 5, 3 and 4 in increasing order had an excess of recessive over dominant genes. Parents of the recessive arrays were generally short as compared to parents of the dominant arrays. The presence of parent 7, however, which was short among the dominant group indicated that in some instances plant height may be under a different genetic control from that indicated by the results.

Correlations of the standardised deviations of Y_r against $(W_r + V_r)$ indicated only a little tendency for tallness to be associated with dominance while, the regression method showed that tallness was associated with dominance. The method of study, therefore, affected the conclusions drawn for the association of tallness with dominant genes.

The W_r/V_r regression for the F_2 generation (Figure 1c) of slope $b = 1.5 \pm 0.23$ was significantly ($P < 0.01$) different from zero and not significantly different from 1, indicating that plant height was under the control of an additive gene action. The distribution of the parental arrays along the regression line indicated only a slight tendency for tallness to be associated with dominance and shortness with recessiveness (Hayman, 1954 (b) and Sharma et al. 1973).

Plant width

Correlations of the standardised deviations, Y_r with $(W_r + V_r)$ for F_1 (Figure 2a) of $r = -0.48$ ($P < 0.05$) indicated that plants with the highest number of dominant genes were wider than those with an excess of recessive over dominant genes. The W_r/V_r regression for F_1 and F_2 (Figure 2b and 2c, respectively) of slopes, $b = 1.10 \pm 0.21$ for F_1 and $b = 0.98 \pm 0.42$ for F_2 were significantly ($P < 0.01$) different from zero but not significantly different from 1. This relationship indicated that plant width

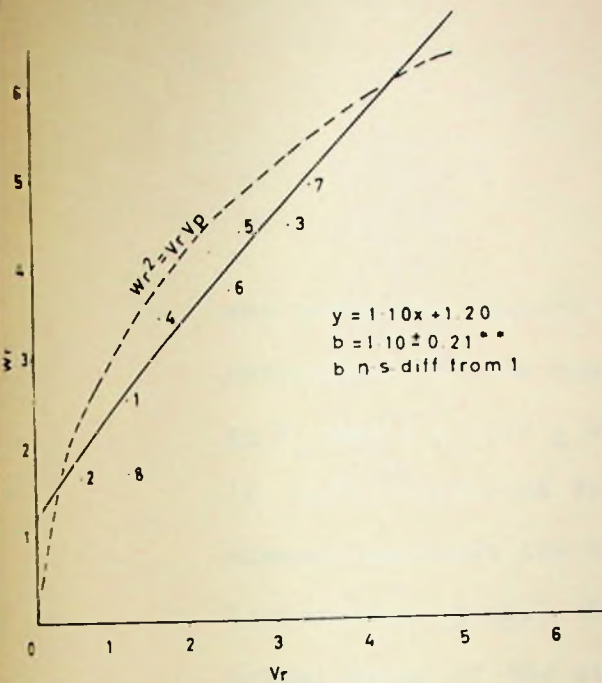


Fig 2b

** significant at 1% level
 $Wr|Vr$ regression for plant width in F_1

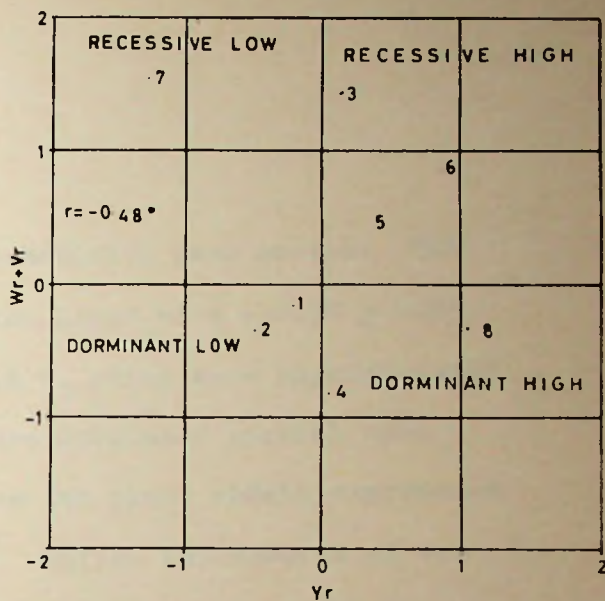


Fig 2a

Correlation of the standardised deviations,
 Vr with $(Wr+Vr)$ for plant width in F_1

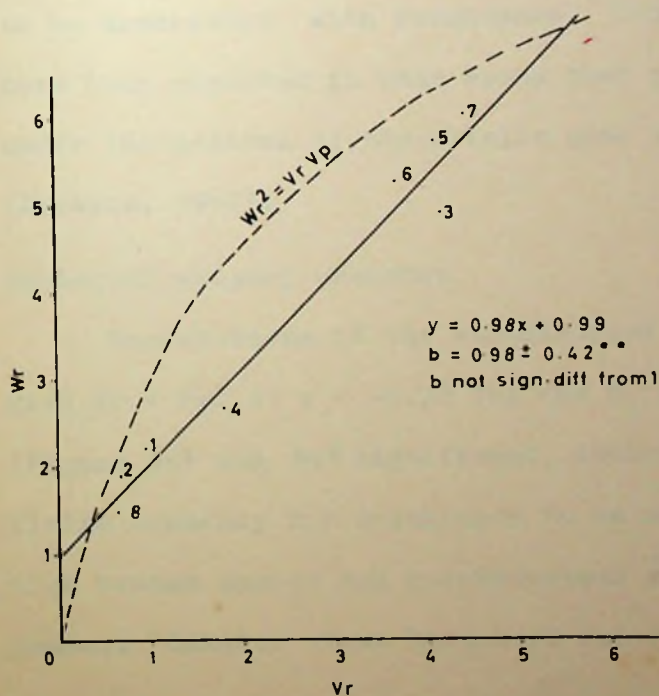


Fig 2c

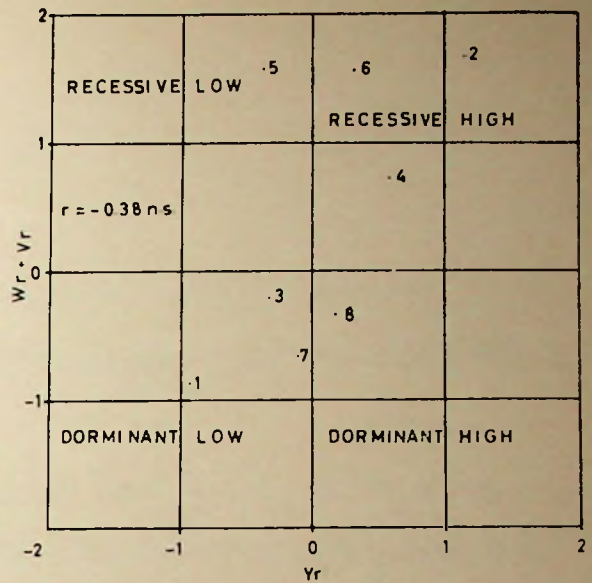
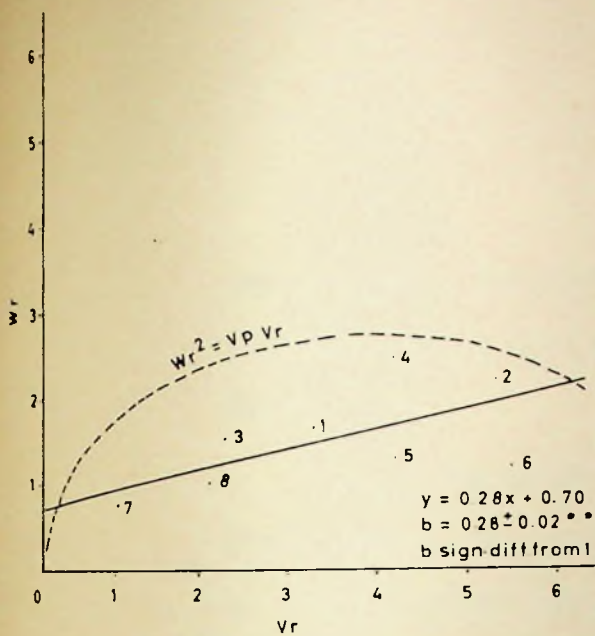
** significant at 1% level

$Wr|Vr$ regression for plant width in F_2

was under the control of an additive gene action. The intercepts, of the regression lines of $a = 0.99 \pm 0.23$ in F_2 and $a = 1.20 \pm 0.10$ in F_1 which were significantly ($P = 0.01$) different from zero indicated partial dominance amongst the crosses for plant width expression (Veeraswamy et al., 1973). Unlike the results of the correlations of the standardised deviations, the distribution of the parental arrays along the regression lines indicated only a slight tendency for wide plants to be associated with dominance. Contrarily results have been reported in snap beans that plant width was under the control of non-allelic gene interactions (Dickson, 1967).

Number of primary branches

Correlations of the standardised deviations of Y_r with $(W_r + V_r)$ of $r = -0.38$ for the F_1 generation (Figure 3a) was not significant, indicating only a little tendency for dorminancy to be associated with a high branch number and recessiveness with a low branch number. Similar views have been reported by other



Correlation of the standardised deviations, Vr with $(Wr + Vr)$ for branch number in F_1

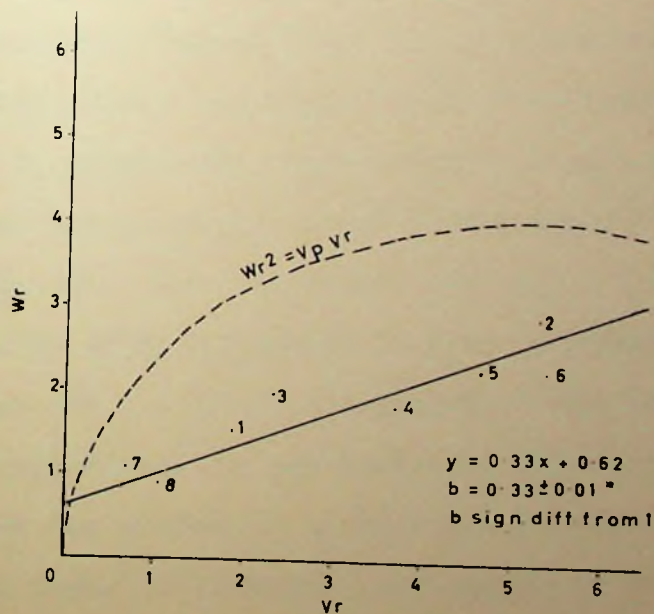


Fig 3c
 Wr/Vr regression of branch number in F_2

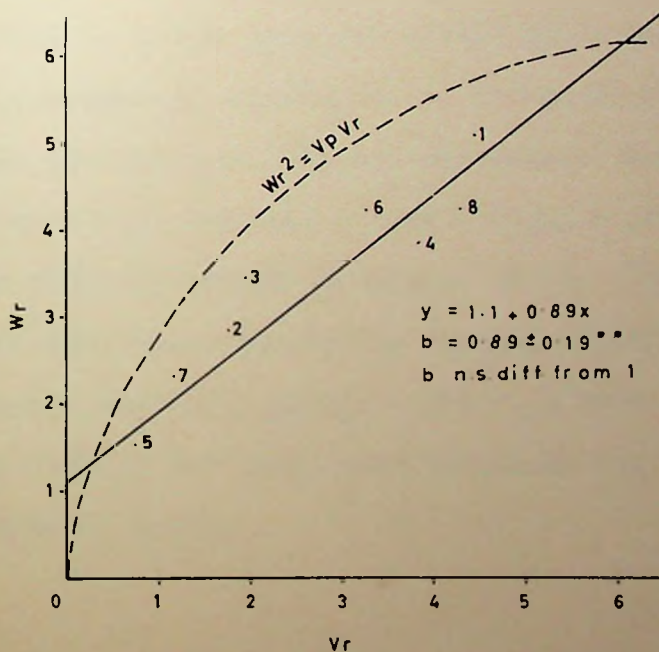
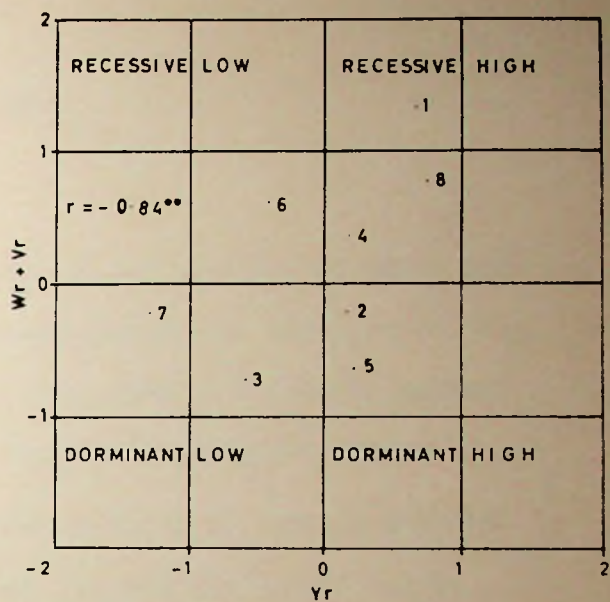
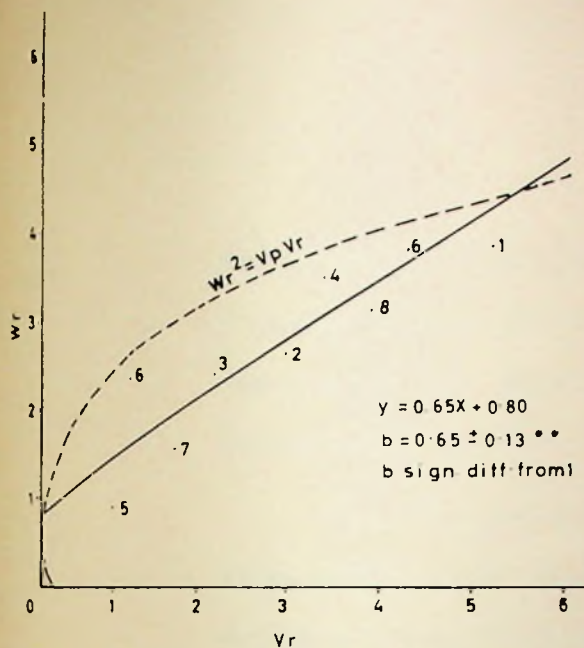
workers while using different legumes (Zafar and Abdallah, 1971; Veeraswamy et al., 1973 and Singh and Singh, 1974).

The W_r/V_r regression lines for F_1 and F_2 generations (Figure 3b and 3c) of slopes $b = 0.28 \pm 0.02$ and $b = 0.33 \pm 0.01$, respectively, were significantly ($P = 0.01$) and ($P = 0.05$) different from zero and significantly ($P = 0.01$) and ($P = 0.05$) different from 1, respectively. This behaviour indicated non-allelic interaction amongst the crosses of the diallel for branch number expression (Mather and Jinks, 1971). In the F_1 generation parents with an excess of dominant genes had generally a high branch number (Figure 3b and Table 17). But the presence of parent 6 in the recessive group and parent 3 in the dominant group which had a high and low branch number, respectively, suggested that in some instances branch number was under the control of a different genetic system, so that high branch number was controlled by recessive genes and low branch number by dominant genes.

(Hallman, 1975). The intercepts of the regression lines on the Y-axis indicated partial dorminance for high branch number over low branch number.

Days to 50% flowering

Correlation of Yr with (Wr + Vr) in F_1 of $r = -0.84$ ($P < 0.01$), Figure 4a, indicated that early flowering was due to an accumulation of dorminant genes and late flowering was associated with recessive genes. Similar views have been forwarded by other workers for the control of flowering time in pigeon peas (Sharma et al., 1973 and Veeraswamy et al., 1973). The regression of Wr on Vr in F_1 gave a line of slope $b = 0.65 \pm 0.13$ which was significantly ($P < 0.01$) different from zero and significantly ($P < 0.05$) different from 1 (Figure 4b). This indicated non-allelic interaction among the parents for days to flowering expression (Mather and Jinks, 1971). The scatter of the parental arrays along the regression line also indicated interaction among the arrays for days to flowering expression (Halloran, 1975).



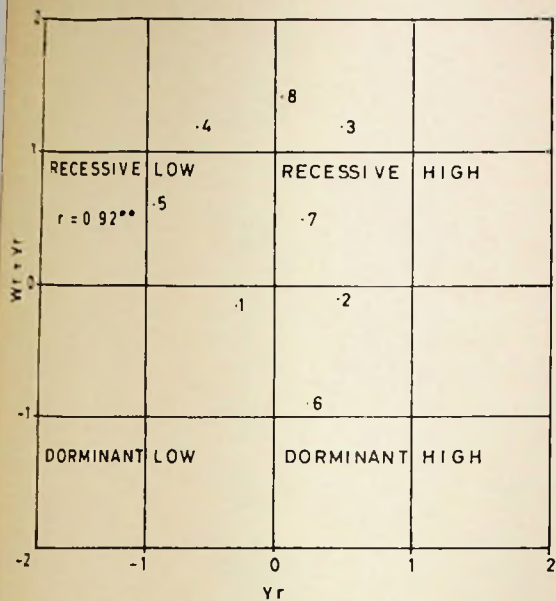
The hybrid resulting from a cross between arrays 5 and 6 showed transgressive segregation for earliness in F_1 , indicating that there is more than one genetic system controlling the days to flowering in pigeon peas.

The regression of W_r on V_r in F_2 gave a line of slope 0.89 ± 0.19 which was significantly ($P = 0.01$) different from zero but not significantly different from 1 (Figure 4c). This indicated additive gene action for the control of days to 50% flowering. The distribution of the parental arrays along the regression line indicated an association of earliness with dominance and lateness with recessiveness. Similar results have been reported on other legumes (Snoad and Arthur 1973b and Singh and Singh, 1974). Contrarily results have been reported by Dickson (1967) for snap beans and Watts et al. (1970) and Snoad and Arthur (1973a) for peas, that earliness was controlled by recessive genes.

Number of pods/plant

The correlation of Y_r with $(W_r + V_r)$ in F_1 of $r = 0.92$ ($P = 0.01$), Figure 5a indicated that high pod number/plant was governed by an accumulation of recessive alleles and low pod number by an accumulation of dominant genes. Similar results have been reported for P. aureus (Singh and Singh, 1972).

The W_r/V_r regression lines for F_1 and F_2 generations of slopes $b = 0.28 \pm 0.17$ and $b = 1.16 \pm 0.02$, respectively, were significantly ($P = 0.01$) different from zero and not significantly different from unity (Figure 5b and 5c). This indicated additive gene action for pod number control in pigeon peas. Dickson (1967) and Veeraswamy et al. (1973) reported similar results for the control of pod number in snap beans and pigeon peas, respectively. Albuquerque et al. (1973), however, reported that the character was controlled by a non-additive gene action in P. vulgaris. The distribution of the parental arrays along the regression lines, like the correlation, method, indicated an association of high pod number with recessiveness and low pod number



** sign. at 1% level

Fig 5a
Correlation of Y_r with $(W_r + V_r)$ for
pods per plant in F_1

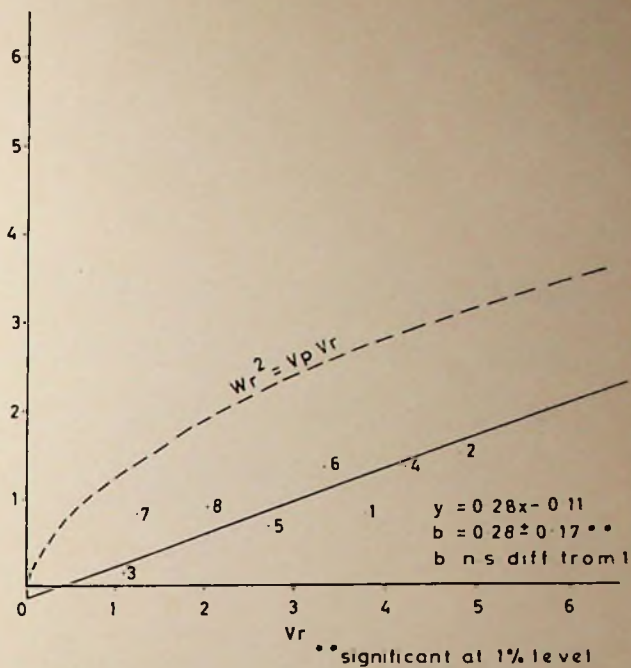
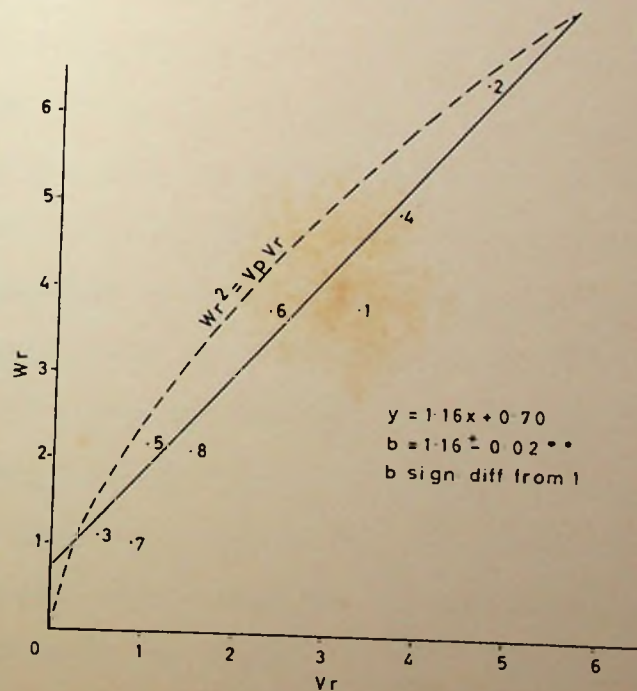


Fig 5b

Regression of W_r on V_r for pods per plant in F_1



** significant at 1% level

Fig 5c

Regression of W_r on V_r for pods per plant in F_2

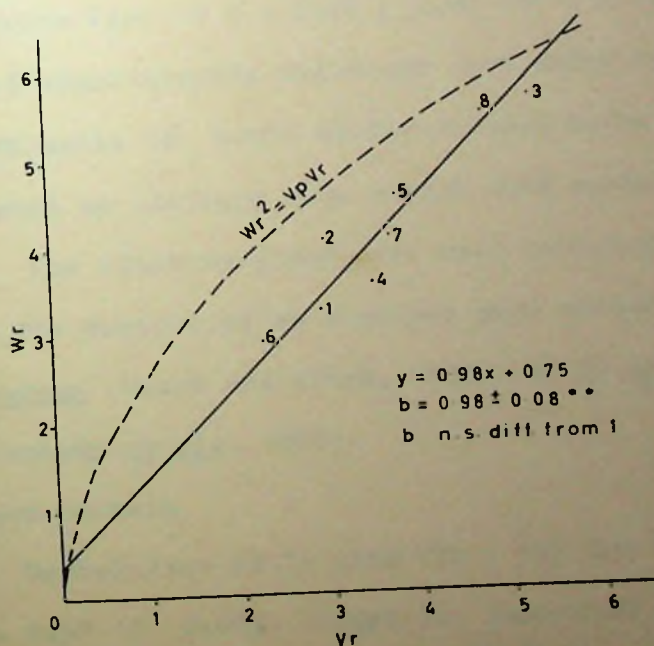
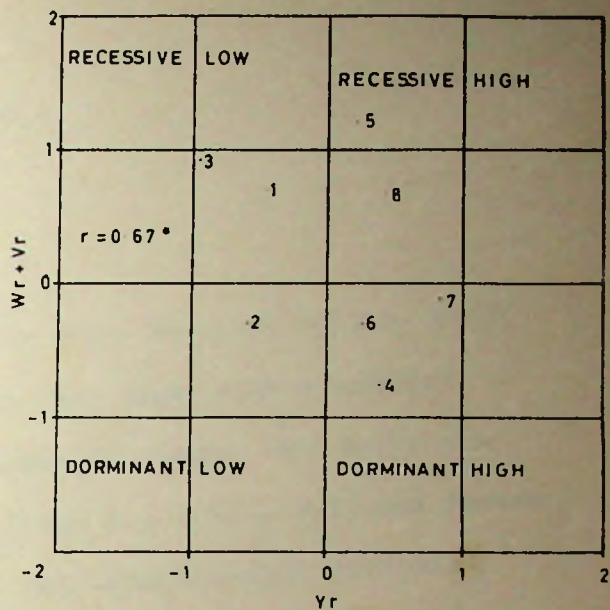
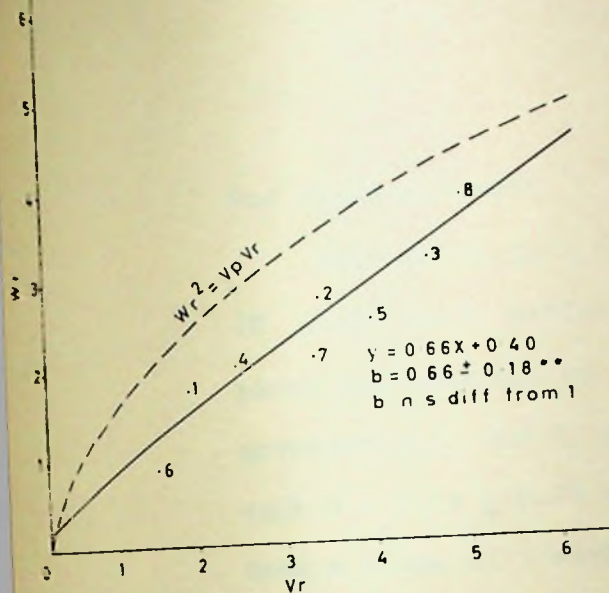
with dorminance. The intercepts of the regression lines on the W_r axes of $a = -0.11 \pm 0.19$ and $a = 0.70 \pm 0.31$ which were significantly ($P = 0.01$) different from zero indicated overdorminance and partial dorminance for F_1 and F_2 , respectively.

Number of seeds/pod

Correlation of Y_r with $(W_r + V_r)$ of $r = 0.31$ was not significant, indicating only a slight tendency for recessiveness to be associated with a high seed number/pod. The regression of W_r on V_r gave lines of slopes $b = 0.89 \pm 0.39$ and $b = 1.15 \pm 0.19$ for F_1 and F_2 , respectively; which were significantly ($P = 0.01$) different from zero but not significantly different from unity. This indicated an additive gene action with partial dorminance since the intercepts were significantly ($P = 0.01$) different from zero at $a = 0.34 \pm 0.21$ and $a = 0.60 \pm 0.34$ for F_1 and F_2 , respectively. Similar results have been reported for the nature of gene action controlling seeds/pod in peas (Krarup and Davis, 1970 and Snoad and Arthur, 1973a). Hybrid 6 x 8 showed transgressive segregation.

Weight of 100-seeds

Correlation of $\bar{Y}_r$ with $(W_r + V_r)$ of $r = 0.67$ ($P = 0.05$), Figure 6a indicated that the genes controlling small seed size were dominant over the genes controlling large seed size. The W_r/V_r regression lines for F_1 and F_2 (Figure 6b and 6c) of slopes $b = 0.66 \pm 0.18$ and $b = 0.98 \pm 0.08$, respectively, were significantly ($P = 0.01$) different from zero but not significantly different from 1. This indicated additive gene action with partial dominance for seed size control. Seed size has also been reported to be simply inherited in lima beans (Allard, 1956) P. aureus (Singh and Singh, 1972) and pigeon peas (Sharma et al., 1972). The distribution of the arrays along the regression lines also indicated that small seed size was dominant over large seed size.



Pod clusters/plant

The correlation of Yr with (Wr + Vr) of $r = -0.73$ (P 0.05) in F_1 indicated that high cluster number/plant was governed by dominant genes. The Wr/Vr regression line for F_1 of slope $b = 1.02 \pm 0.49$ and intercept $a = 0.13 \pm 0.24$ was not significantly different from a slope of 1 with zero intercept. This indicated additive gene action with dominance for the control of pod clusters/plant. For the F_2 generation the Wr/Vr regression line of $b = 0.87 \pm 0.66$ and $a = 0.76 \pm 0.06$ was ~~not~~ significantly different from unity but significantly (P 0.01) different from zero. This indicated an additive gene action with partial dominance. Pod clusters/plant have been reported to be under the control of an additive gene action in Ph. aureus (Singh and Singh, 1972) and C. cajan (Veeraswamy et al., 1973).

Percent protein

Correlation of Yr with (Wr + Vr) for F_1 , of $r = -0.91$ (P 0.01), Figure 7a, indicated that high

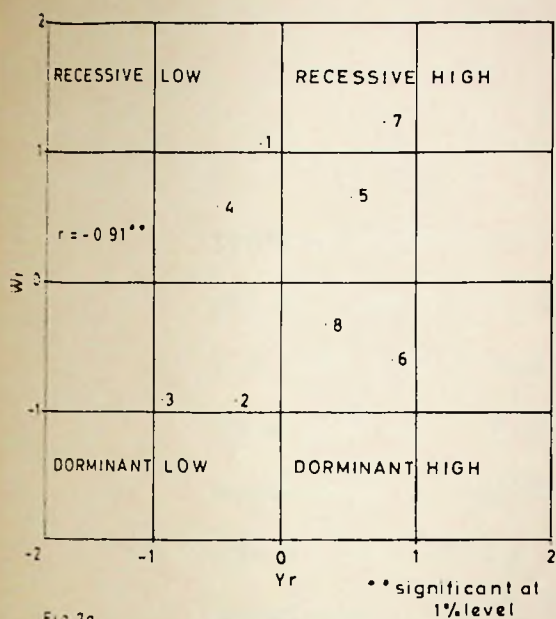


Fig 7a
Correlation of Y_r on $(W_r + V_r)$ for percent
protein in F_1

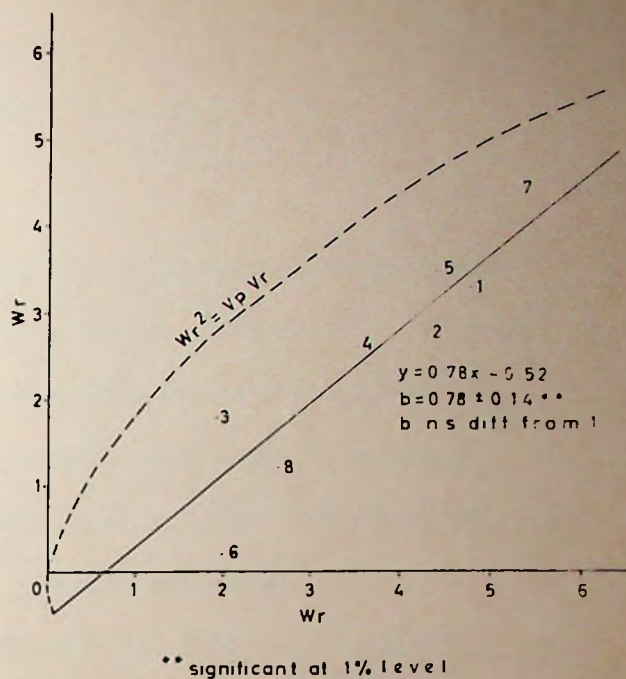


Fig 7b
 W_r/V_r regression for percent protein in F_1

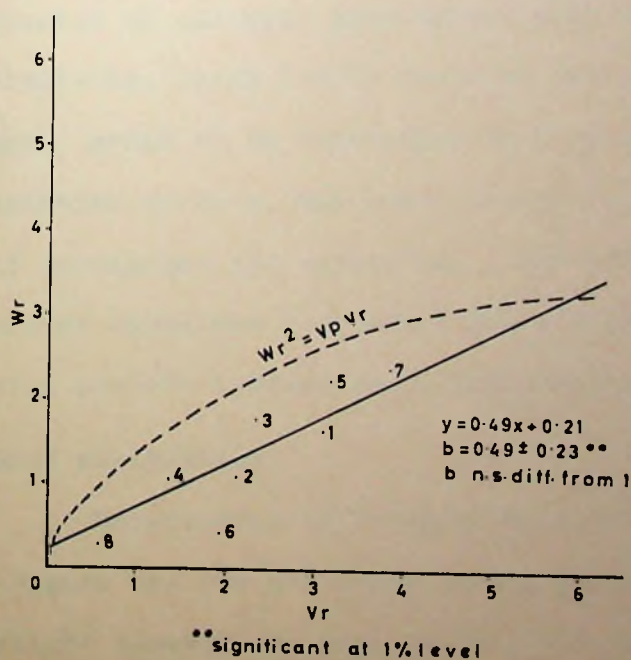
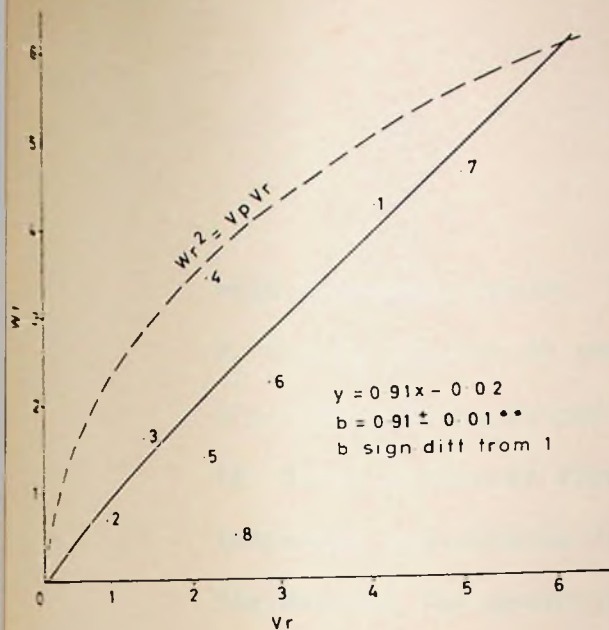


Fig 7c
 W_r/V_r regression for percent protein in F_2

protein content in the seed was controlled by dominant genes. The W_r/V_r regression for F_1 (Figure 7b) of slope $b = 0.98 \pm 0.14$ was significantly ($P = 0.01$) different from zero but not significantly different from unity, indicating an additive gene action. The intercept on the W_r axis of $a = -0.52 \pm 0.17$ indicated over-dominance. In F_2 (Figure 7c) the W_r/V_r regression line of slope $b = 0.49 \pm 0.23$ was not significantly different from unity with zero intercept. This indicated an additive gene action with dominance. Similarly, Singh (1973) reported the protein content of gram grain to be controlled by both additive and non-additive factors, the non-additive component consisting of dominance and epistasis. The distribution of the arrays along the regression lines also indicated that high protein content was controlled by dominant genes.

Seed yield/plant

Correlation of Y_r with $(W_r + V_r)$ of $r = -0.31$ (Figure 8a) was not significant, indicating only a slight tendency for high grain yield to be associated



**significant at 1% level

Fig 8b

$Wr|Vr$ regression for grain yield in F_1

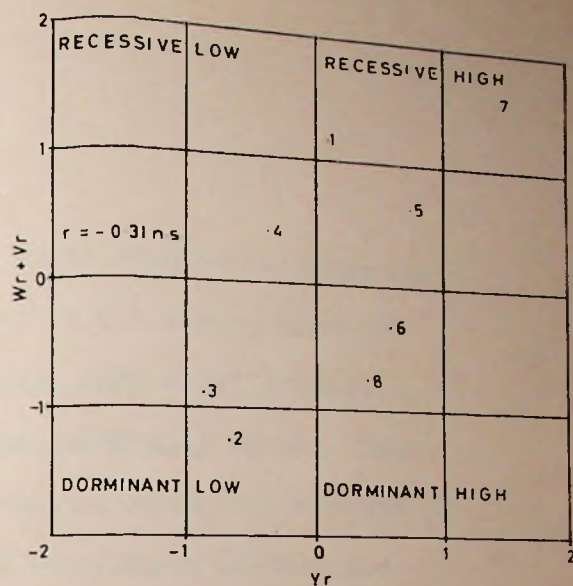
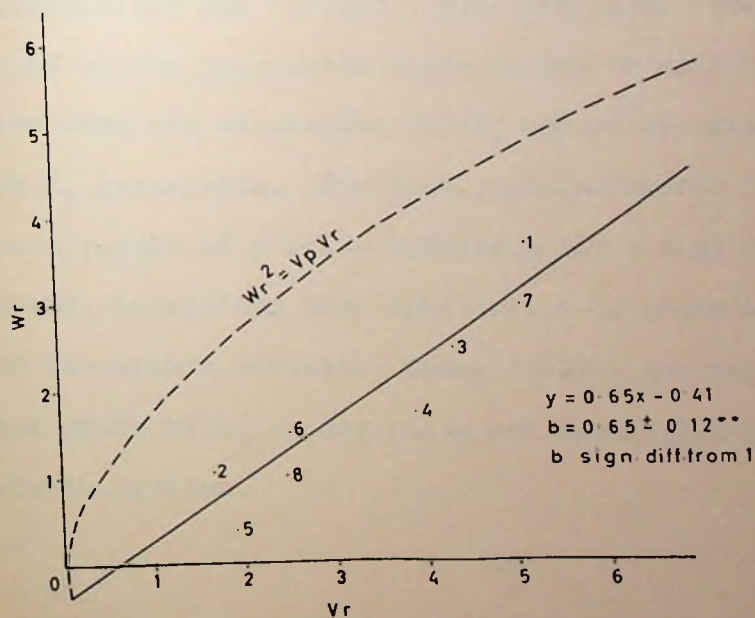


Fig 8a

Correlation of Yr' with $(Wr+Vr)$ for grain yield in F_1



**significant at 1% level

Fig 8c

$Wr|Vr$ regression for grain yield in F_2

with dominant genes. The W_r/V_r regression lines for F_1 and F_2 (Figure 8b and 8c) of $b = 0.91 \pm 0.01$ and $b = 0.65 \pm 0.12$, respectively, were significantly ($P < 0.01$) different from zero with unit slope. This indicated non-allelic interaction among the crosses of the diallel for grain yield expression (Mather and Jinks, 1971). Views similar to these have been forwarded by Abuquer et al. (1974) for Ph. vulgaris and Kalaidzhieva and Kalinov (1975) for peas. The intercepts of the regression lines on the W_r axes indicated near complete dominance for F_1 and overdominance for F_2 generation. The best yielding hybrid (2 x 7) was a result of a cross between a low x high yielding parent, indicating that interaction of genes had strong and favourable effects. Chung (1973), however, reported that grain yield in dry beans was controlled by additive genetic systems.

Heterosis, Inbreeding depression and Reciprical effects

Analysis of variance (Table 20) showed non-significant reciprical effects for all the characters studied. This indicated that for any given character, special care may not be taken as to whether the pollen or mother parent was superior in character expression to their counterparts. Similar results have been reported in cow peas for protein content, pods/plant and other agronomic characters (Furedi, 1970 and Kherdnam et al., 1975). Kalaidzhieva and Kalinov (1975) and Dahiya et al. (1976), however reported the presence of maternal effects for number and weight of pods in peas and protein content in pigeon peas, respectively.

Heterosis was significant ($P = 0.01$) for all the characters studied (Table 20). This indicated expression of joint action of favourable combinations of genes at different loci, for all the characters (Hayman, 1957). Heterosis for grain yield in F_1 ranged from 0.1% to 24.0% more than the mid-parent (Table 20). The crosses 1 x 2, 2 x 3, 2 x 4, 2 x 7, 2 x 8, 4 x 7 and 7 x 8

Table 20. Analysis of Variance for heterosis, Inbreeding and Reciprocal effects for various characters

Character	Plant height	Plant width	Branch number	Days to 50% flowering	Pods/plant	Seeds/pod	100 seed weight	Clusters/plant	Percent protein	Grain yield
Heterosis	22.8**	23.5**	61.7**	198.6**	26076/7**	26.4**	85.7**	523.0**	861.3**	17564.1**
Inbr. depression	6.46*	12.6*	46.0**	186.3**	2530.7**	18.1**	56.2**	124.4**	713.7**	9025.3*
Reci. effects	0.8	6.7	23.0	61.0	11.9	14.0	33.1	68.6	60.7	2256.7
Error	0.6	2.3	10.1	32.4	10.6	6.4	10.5	15.5	19.6	25.9

*Significant at 5% level

.. " " 1%

yielded significantly higher than their respective mid-parents. The crosses 2 x 3, 2 x 4 and 2 x 7 exhibiting significant ($P = 0.05$) heterosis in F_1 , yielded 8.2%, 9.8% and 11.6, respectively, in the F_2 generation, more than their respective mid-parents. This demonstrated partial dorminance which was still evident in the F_2 generation (Nasr and Khayrallah, 1976). Graphical analysis of this character had, however, indicated that seed yield was controlled by dorminance to overdorminance. These results indicate that there was more than one genetic system controlling the degree of dorminance for seed yield in this crop.

The F_1 heterosis for plant height ranged from 0.6% to 25.3% more than the mid-parent. Heterosis for days to 50% flowering ranged from 0.9% more to 14.0 less than the mid-parent value. That for pods/plant ranged from 1.8% to 35% more than the mid-parental value. Heterosis for seed size and percent protein ranged from 0.2% to 6.9% and 0.4% to 13.3%. The significant ($P = 0.05$) heterotic effects observed in

some crosses for these characters indicated non-additive gene action for the control of these characters.

Graphical analysis had however indicated that pods/plant, seed size and percent protein were controlled by additive gene action. The results, thus, suggest that pods/plant, seed size and percent protein are controlled by both additive and non-additive gene actions. Epistatic effects revealed by graphical analysis to control plant height, branch number, days to flowering and grain yield, was responsible for the high heterosis observed for these characters (Comstock and Robinson, 1952). High heterosis for seed yield, days to flowering, plant height and percent protein in pigeon peas has been reported by other workers (Solomon et al., 1957 and Sharma et al., 1973).

Inbreeding depression was found significant at the 5% level for plant height, plant width and cluster number and at the 1% level for the other characters (Table 20), indicating that for all the characters there was some loss in the joint action of favourable

gene combinations at different loci in moving from one generation to another (Hayman, 1957). For pods/plant, seed size and percent protein the crosses with the highest heterosis showed highest inbreeding depression, indicating that the heterosis gained in F_1 was lost in F_2 (Table 21). This indicated these characters were controlled by additive gene effects (Kherdnam et al., 1975). Graphical analysis of these characters had shown similar results. In the rest of the characters the heterosis gained in F_1 was not lost in F_2 ; indicating (like the graphical analysis) non-additive gene action for the control of these characters.

Combining Ability

Combining ability analysis of variance (Table 22) showed significant ($P = 0.01$) general combining ability variencies for all the characters in both generations, indicating the importance of additive gene action for the control of these characters. Specific combining ability variencies were significant ($P = 0.01$) for number of branches, pods/plant, percent protein and grain yield in both generations, indicating the presence

Table 21. Percent heterosis and increasing depression for six characters

Hybrid	Plant height	Days to 50% flowering		Pods per plant		Seed size		% protein		Seed yield/plant		
		a	b	a	b	a	b	a	b	a	b	
1 x 2	14.1	5.9	-1.5	-0.7	19.6*	6.0*	6.4*	1.3*	4.8	2.3	13.2*	5.4*
1 x 3	17.5*	6.3*	-2.0	-0.3	1.8	2.6	7.0*	1.6*	1.0	0.6	3.8	1.5
1 x 4	8.5	3.7	-1.2	-0.2	1.6	1.2	5.0*	0.6	4.0	1.7	4.8	1.6
1 x 5	11.8	4.6	-6.7*	-1.3	16.3	6.3*	6.6*	1.5*	1.6	0.7	2.6	0.9
1 x 6	9.8	4.2	-2.0	-0.0	11.7	3.8	1.6	0.4	2.7	1.3	1.0	0.4
1 x 7	25.3**	9.0*	-5.8*	-1.0	19.4*	6.3*	2.5	0.9	2.9	1.2	3.8	1.0
1 x 8	9.7	4.7	-0.6	-0.0	2.0	0.0	6.9*	1.4*	3.9	1.5	3.1	1.0
2 x 3	17.4*	6.1*	-0.3	-0.0	29.8**	15.6**	0.4	0.0	7.5*	3.0*	19.4*	3.5
2 x 4	8.2	3.2	-1.2	-0.3	26.9**	10.4	1.7	0.4	0.7	0.3	11.4*	3.1
2 x 5	10.6	5.1	-4.1	-0.4	4.4	1.0	0.3	0.1	0.6	0.2	0.1	0.0
2 x 6	1.7	0.8	-3.4	-0.4	15.1*	5.3	2.9	0.9	3.9	1.3	1.9	0.6
2 x 7	21.2**	8.1*	-5.1	-1.0	28.9**	8.7*	0.2	0.0	1.6	0.7	24.0**	5.4*
2 x 8	2.9	1.9	-0.8	-0.0	22.4*	5.4*	6.2*	1.3*	2.0	0.9	13.6*	5.0*
3 x 4	0.6	0.1	0.5	0.0	4.3	1.0	2.5	0.6	4.7	1.3	7.4	3.1
3 x 5	1.0	0.5	-3.6	-0.5	6.3	2.0	1.3	0.1	9.8*	3.7*	5.2	2.2
3 x 6	9.7	4.3	-3.7	-1.0	10.0	1.0	0.3	0.1	7.5*	2.6	2.0	1.0
3 x 7	12.6	5.2	-1.4	-0.0	8.1	1.2	2.6	0.9	13.3**	6.5*	1.8	0.1
3 x 8	14.7	6.2*	0.2	-0.3	7.2	2.2	1.4	0.3	0.5	0.1	8.5	3.1
4 x 5	11.1	4.8	-3.9	-0.3	7.2	2.3	4.9	1.2	2.4	1.3	1.9	0.6
4 x 6	18.1*	8.4*	-2.0	-0.4	8.7	2.0	6.1*	2.3*	0.7	0.3	1.3	0.5
4 x 7	11.4	4.8	-3.2	-1.0	10.0	1.3	0.5	0.1	1.4	0.5	14.0*	6.0
4 x 8	17.2*	7.0*	-0.2	-0.0	9.0	1.2	2.0	0.9	0.9	0.3	6.6	2.9
5 x 6	5.8	2.4	-14.0**	-3.7	12.3	3.8	1.3	0.2	2.5	0.9	1.2	0.5
5 x 7	16.5*	5.2	0.9	0.2	8.3	1.1	0.5	0.1	1.6	0.7	10.0	4.6
5 x 8	5.9	2.4	-0.9	-0.2	6.9	1.2	1.5	0.6	0.5	0.1	3.3	1.1
6 x 7	20.5*	6.2*	-10.7**	-3.6*	6.2	2.1	0.7	0.2	9.8*	3.0*	9.3	3.9
6 x 8	1.7	0.0	-1.7	-0.4	13.3*	3.4	0.8	0.2	4.8*	1.3	6.4	3.2

Table 27. Analysis of variance for combining ability in F_1 and F_2 of the diallel.

Generation	Source	d.f.	Mean Squares for different characters									
			pH	PW	NOBR	DF	NOPO	NOSE	100 SWT	CLNO	% PROT	GY
F_1	E.C.a	7	80.6**	231.2**	76.5**	88.3**	232.7**	224.7**	139.0**	164.7**	94.6**	123.7**
	S.C.a	20	23.7**	30.7*	63.6**	61.1**	13.5**	23.8**	10.3*	14.6	26.6**	30.4**
	Error	27	4.2	14.5	10.1	13.8	2.4	5.3	5.8	10.3	6.4	4.9
F_2	E.C.a	7	77.1	172.4	78.9**	73.6**	201.6**	193.3**	94.9**	123.6**	68.6**	98.1**
	S.C.a	20	16.1*	9.5	52.7**	22.0	16.8**	10.2	3.5	12.1	24.6**	22.3**
	Error	27	8.3	8.4	26.3	20.5	5.4	9.4	4.9	10.9	9.2	8.3

of both additive and non-additive gene effects for the control of these characters. The g.c.a variencies for these characters, however, were greater than s.c.a. variencies, indicating that additive gene action was pre-dominant over the non-additive effects. Graphical analysis had shown these characters to be controlled by only non-additive gene action. The combining ability results are in agreement with the work reported by Sharma et al. (1973) and Nandipuri et al. (1973) for the control of branches, percent protein and seed yield in pigeon peas and cowpeas, respectively. Non-significant s.c.a. variencies for plant width, days to 50% flowering, seeds/pod, seed size and pod clusters/plant in F_2 indicated absence of non-additive gene action for the control of these characters.

General combining ability effects (Table 23) determined from the analysis of F_1 and F_2 generations showed that none of the parents showed consistently positive g.c.a. for all the ten characters. Parents 2 and 8 were high combiners for yield and pods/plant while the other lines were average to low general combiners

for increased yield. G.c.a. effects for yield were influenced by g.c.a. effects of yield components especially, branches/plant, pods/plant, seeds/pod and seed size, for lines having high g.c.a. effects for yield had average to high g.c.a. effects for these components. Significant ($P = 0.05$) differences were noted for the g.c.a. estimates of each parental line for each character, indicating wide genetic divergence between the parental lines. Parents 1 and 3 were high combiners for seed size but average general combiners for yield, indicating that big seeded plant types have a tendency to yield less than the small seeded types. This was not the case from the data in Table 19 mainly due to compensation of seed size with other components of yield for a limited source of nutrients (Adams, 1967). Generally there was good agreement between the g.c.a. for yield of the parents and their performance based on parental means (Table 19 and 22). Other workers have presented similar views (Sharma et al., 1973) for the agreement between the g.c.a. effects for yield of a

parent and its mean yield performance.

Specific combining ability effects (Table 24) revealed that hybrids 2 x 4, 2 x 7, 4 x 8 and 7 x 8 were superior in grain yield. These hybrids were results of crosses that involved parents with high x low g.c.a. for yield. Generally, for all the components of yield hybrids which showed high s.c.a. involved parents with high x low g.c.a. for that particular character. Hybrids 2 x 6, 2 x 7 and 7 x 8 gave superior combinations for yield and most of its components in both generations. The parents involved in these crosses had wide genetic divergence for these characters. The consistent superior performance of these crosses in F_1 and F_2 indicated that dominant gene action was not pre-dominant though present (Griffing, 1956). This was also evident from the low values of inbreeding depression, though graphical analysis had shown dominance to be present for only pods/plant and seed yield and partial dominance for the other yield components. Hybrid vigour shown by the crosses was largely due to concentration of favourable

Table 23. Estimates of General Combining Ability Effects of parents.

Parent No.	Generation	Plant height	Plant width	Branch number	Days to flowering	Pods/plant	Seeds/pod	Seed size	Clusters/plant	Percent protein	Seed yield/plant
1	F ₁	-11.30**	-5.67**	1.98*	-4.16*	1.35	-0.67	8.88*	-1.35	-7.67**	-1.12
	F ₂	-11.92**	-6.34**	1.35	-4.86**	1.24	-0.82	8.31*	-1.98*	-7.81**	-1.34
2	F ₁	-1.49	-2.72*	-1.63	-2.90*	8.62**	-4.40**	-3.51**	1.89*	-3.22**	12.18**
	F ₂	-2.33*	-3.43**	-1.84*	-2.94*	7.34**	-4.72**	-3.69**	1.17	-3.54**	10.37**
3	F ₁	1.63	-2.61*	0.48	3.50**	-2.67*	-2.99*	10.99**	-0.56	-3.68**	-1.29
	F ₂	2.08*	-3.14**	0.41	3.00**	-2.95*	-3.11**	9.72**	-1.98*	-4.32**	-1.23
4	F ₁	2.86*	2.87*	-1.02	-0.62	-0.88	-0.93	0.67	-3.17**	11.25**	-11.96**
	F ₂	2.62*	2.16*	-1.68	-0.87	-1.37	-1.04	0.81	-3.54**	9.56**	-9.19**
5	F ₁	-3.54**	-5.70**	2.54*	5.43**	-8.92**	-1.62	-0.58	4.94**	-2.49*	5.26*
	F ₂	-3.67*	-5.91**	3.61**	4.16**	-8.96**	-2.22*	-1.64	5.00**	-3.42	3.82*
6	F ₁	-1.88*	-1.73	-0.19	1.39	-5.75**	5.17**	1.12	-2.35*	1.81*	4.51*
	F ₂	-2.04*	-1.92*	-0.73	1.02	-6.12**	4.86**	1.01	-2.61*	2.11*	3.99*
7	F ₁	-4.08**	1.80*	-0.05	4.60**	-5.01**	-3.11**	-2.56*	-3.94**	8.20**	-12.80**
	F ₂	-4.43**	1.44	-0.94	4.19**	-5.85	-3.77**	-2.73**	-4.65**	6.95**	-12.14**
8	F ₁	-1.89*	-3.84**	-2.92*	-2.77*	12.00**	1.20	-4.00**	-7.56**	13.32**	10.77**
	F ₂	-2.11*	-3.89	-3.01**	-3.94**	11.34**	0.83	-4.58**	-7.98**	10.86**	9.65**

*Significant at 5% level

**Significant at 1% level

Table 24. Estimates of specific combining ability effects for yield and some of its components

Cross	Pods/Plant		Seeds/Pod		Seed size		Cluster/Plant		Yield/Plant	
	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂	F ₁	F ₂
2 x 2	-0.94	3.61	0.41*	-0.23	-0.18	0.74**	3.64	-0.67	1.82	1.19
2 x 3	-6.37*	-0.34	-0.64**	-0.04	-0.24	-0.77**	1.33	-0.09	12.34*	5.01
2 x 4	-3.93	-0.61	-0.03	0.00	0.31	0.25	2.47	1.34	0.37	0.09
2 x 5	-2.30	0.27	0.35	0.31	0.04	0.21	0.54	0.22	-0.56	-0.41
2 x 6	4.94	0.87	1.98**	0.45	0.56*	-0.61**	-2.21	-2.42	-2.89	-1.74
2 x 7	1.88	0.56	-0.90**	-0.51*	-0.32	0.72**	-6.67*	-3.74	3.67	2.51
2 x 8	4.47	2.75	0.21	-0.77**	-0.29	0.33	-4.56	0.43	3.84	3.11
3 x 3	-3.05	3.47	0.07	0.11	0.93**	-0.51*	8.41*	5.47	-1.30	-4.83
3 x 4	-5.71*	2.33	0.32	0.14	0.57*	-0.34	1.87	-2.44	31.40**	10.11**
3 x 5	8.08**	4.51	-0.02	0.33	0.28	-0.02	-10.42**	-9.97*	1.67	6.52*
3 x 6	6.57*	8.20**	0.61**	0.74**	0.34	-0.08	21.04**	10.12**	1.02	3.57
3 x 7	10.83**	6.59*	-0.24	0.08	0.35	-0.67**	15.33**	11.34**	24.86**	21.01**
3 x 8	-12.63**	5.57*	0.72**	0.21	0.41*	-0.12	11.41**	11.98**	11.85*	8.17*
3 x 4	-0.90	-3.42	-0.13	-0.04	-0.45*	-0.30	8.61*	-4.56	-10.90*	-6.42*
3 x 5	0.63	-0.39	-0.01	-0.19	-0.21	0.33	-0.54	-2.31	-2.30	-0.58
3 x 6	-0.97	1.05	0.84**	-0.52*	0.67**	0.02	0.59	0.21	-6.59*	-9.57*
3 x 7	6.63*	-1.39	0.67**	0.34	0.81**	0.64**	-1.50	0.09	-9.41*	-4.99
3 x 8	8.08**	2.67	0.00	0.09	0.72**	0.24	-4.55	-4.42	-2.38	-5.11
4 x 5	-1.47	3.80	0.09	0.25	0.44*	0.01	20.00**	14.38**	1.69	0.52
4 x 6	0.35	-0.04	-0.23	-0.61**	0.25	0.33	2.60	1.34	1.44	1.19
4 x 7	-2.42	1.12	0.62**	0.33	-0.61**	0.02	3.41	1.86	11.12*	6.32*
4 x 8	14.61**	1.59	0.57*	0.01	-0.20	0.21	-0.59	0.08	42.33**	30.00**
5 x 6	9.31**	-3.33	-0.33	-0.21	-0.09	0.00	6.72*	2.38	-14.89**	-8.16*
5 x 7	-5.82*	-3.98	-0.05	0.00	0.12	0.13	17.64**	6.42**	-3.04	-2.46
5 x 8	11.21**	2.51	1.04*	0.42*	0.03	0.00	10.94**	11.39**	3.96	3.43
5 x 7	-3.91	1.58	0.55*	-0.34	0.51*	0.22	-3.42	1.34	-8.17*	1.47
5 x 8	8.60**	-2.86	-0.56*	-0.45*	0.67**	0.41*	-1.64	-2.88	3.41	-1.04
7 x 8	12.30**	3.13	-0.34	-0.22	0.52*	0.23	-2.33	-0.59	41.47**	27.76**

*Significant at 5% level

** " " 1% "

genes by the parents (Singh and Singh, 1974).

Path coefficient Analysis

Both phenotypic and genotypic correlations were calculated for the F_2 population of the diallel cross for the supposed components of yield and are presented in Table 25.

The phenotypic correlations were lower than the corresponding genotypic correlations. But both the phenotypic and genotypic correlations were close to each other in each instance. This may have been due to the large number of plants (50) used to take the observations per plot which tended to reduce the error (environmental) variance to minor proportions. Had the environmental variance been reduced to zero, the phenotypic and genotypic correlations would have been identical, as was pointed out by Dewey and Lu (1959). Due to resemblance of the two types of correlations, reference will be made only to genotypic correlations to avoid repetition.

It was only plant height that showed a negative correlation with yield. Plant height and seeds per pod

Table 25. Phenotypic and genotypic correlations between yield with its components in the F_2 generation of the diallel cross.

	1	2	3	4	5	6	7
1. Grain yield		(a) -.12 (b) -.28	.44* .48*	.53** .58**	.64** .70**	.57** .59**	.71** .77**
2. Plant height			(a) .24 (b) .29	.40 .44*	.41* .45*	-.52** -.56**	.59** .62**
3. Branch number				(a) .53** (b) .57**	.36 .39	-.48* -.50*	-.25 -.28
4. Cluster number					(a) .36 (b) .38	-.08 -.11	-.15 -.20
5. Pods per plant						(a) -.23 (b) -.30	-.29 -.33
6. Seeds per pod							(a) -.21 (b) -.25
7. 100-seed weight							

*, ** Significant at 5% and 1% levels, respectively.

a, b = Phenotypic and genotypic correlation coefficients, respectively.

were also negatively and significantly ($P < 0.01$) correlated. Seeds per pod and seed size were negatively correlated with branch number, cluster number, and pods per plant. Seeds per pod was also negatively correlated with seed size. What was of interest in this case was that plant size (height) and seed size (100 seed weight) were positively and significantly correlated $r = 0.62$ ($P < 0.01$). This was due to the fact that large plants had greater leaf surface which photosynthesized great quantities of carbohydrates that were directed to seed formation. This combined with the fact that larger plants produced fewer seeds per pod, gave large plants an advantage over small plants with respect to seed size. Similar results were reported by Rathnaswamy et al. (1973) that the seeds of perennials were larger and heavier than those of annuals.

Many of the characters are negatively or positively correlated due to mutual association with other characters. Results of a path coefficient analysis to

separate out the direct and indirect causes of association are presented in Table 26 and the diagram shown in Figure 9.

Yield Vs Plant height

The correlation between yield and plant height was negative and non-significant $r = -0.28$. The direct effect of plant height on yield is high and negative (-0.44). The indirect effect of plant height on seed/pod was high and negative (-0.55) and the indirect influences of plant height on yield through branch number (0.23) and seed size (0.25) were both high and positive. The net effect in the system of opposing influences was that two large negative effects counterbalanced four positive ones making the overall correlation between plant height and grain yield low and negative. The results indicated that plant height was not an important yield component.

Yield Vs number of primary branches

The total correlation between yield and branch number was high and positive $r = 0.48$ ($P < 0.05$). This

Table 26. Partition of genotypic correlation into direct and indirect effects by path-coefficient analysis.

Total correlation of grain yield with effect	Direct effect	Indirect effect via				
		Plant height	Branch number	Cluster number	Pods/plant	Seed/pod
Plant height ($r = -0.28$)	-0.44	-	0.23	0.20	0.03	-0.55
Branch number ($r = 0.48^*$)	0.22	0.20	-	0.46	0.42	-0.56
Clusters/Plant ($r = 0.58^{**}$)	0.79	0.05	0.12	-	0.30	-0.46
Pods/plant ($r = 0.70^{**}$)	1.02	0.01	0.34	0.38	-	-0.85
Seeds/pod ($r = 0.59^{**}$)	0.94	-0.01	-0.03	-0.05	-0.09	-
Seed size ($r = 0.77^{**}$)	1.41	0.25	-0.16	-0.30	-0.30	-0.48
Residuals	-0.21					-

*, ** Significant at 5% and 1% levels, respectively.

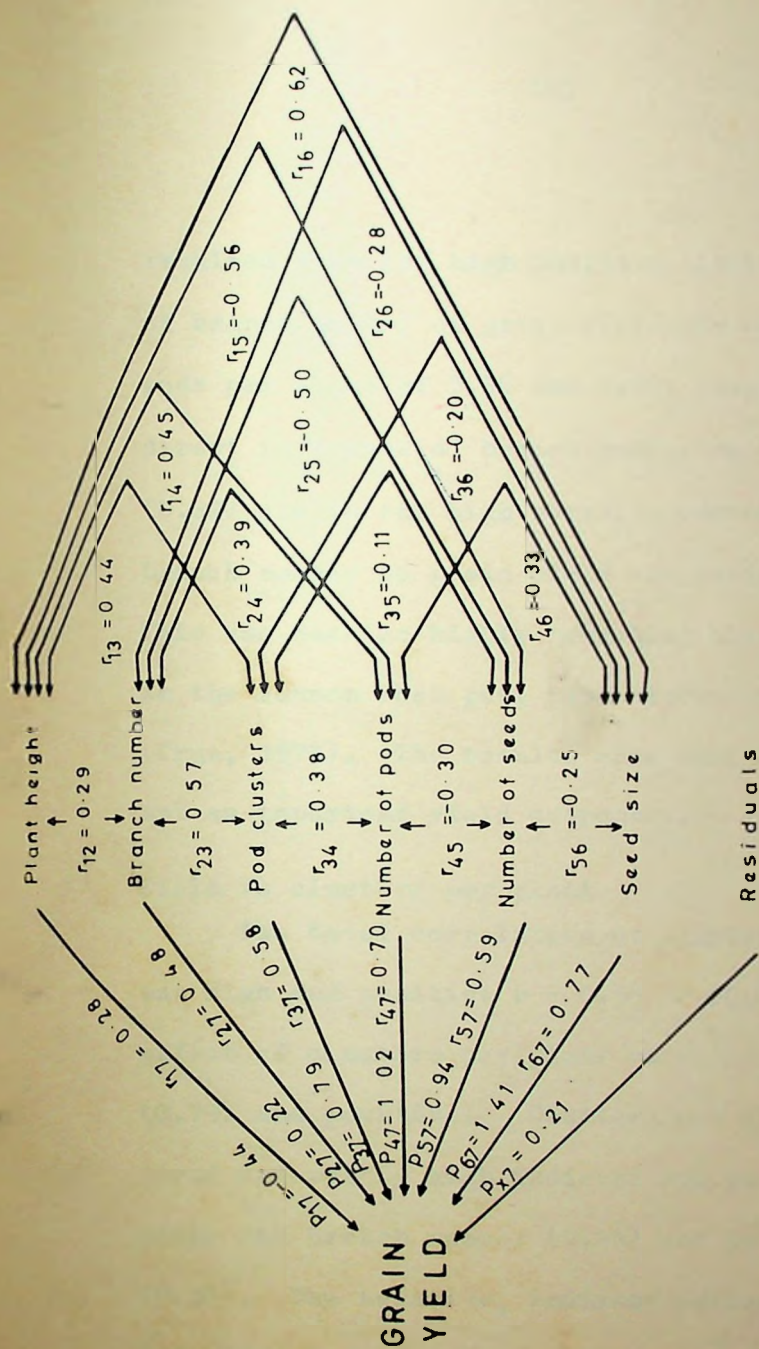


Fig. 9

Path diagram of yield and its components in pigeon peas for the F₂ generation grown during the 1976 rains season. One sided arrows show path coefficients. Two sided arrows show genotypic correlation coefficients.

resulted from the high positive, indirect influences of branch number on grain yield via cluster number and pods per plant of 0.46 and 0.42, respectively. But the direct influence of branch number on grain yield was low (0.22) due to the high negative indirect influence of branch number to grain yield via seed/pod and seed size. This was because highly branching plants matured late in the season when pest populations had built up (Cruz, 1975). The results show that branch number was not an important yield component.

Yield Vs clusters per plant

The total correlation of cluster number with yield was high and positive $r = 0.58$ ($P < 0.01$). The direct effect of clusters per plant on yield was very high (0.79) and positive. Clusters per plant also registered moderately high indirect and positive effects on yield via branch number (0.46) and pods per plant (0.38). The negative, indirect influences of clusters per plant were registered through seed size and seeds/pod. The results indicated that pod clusters/plant were important yield components. Similar views were for-

warded by Singh and Molhotha (1973).

Yield Vs Pods per plant

The correlation between pods per plant and grain yield was high and positive $r = 0.70$ ($P < 0.01$). The direct effect of pods per plant on yield was also high and positive (1.02). A positive, indirect influence of pods per plant on yield was registered via branch number. Negative, indirect influences of pods/plant on yield were registered via seeds per pod and seed size. The high and positive direct influence of pods/plant on yield indicated that this was an important yield component. Veeraswamy et al. (1973b) had also indicated that pods/plant was an important yield component.

Yield Vs Seeds per pod

The correlation between seeds per pod and yield was high and positive $r = 0.59$ ($P < 0.01$). The direct effect of seeds per pod on yield was also high 0.94. The negative indirect effects of seeds per pod on grain yield were low and unimportant. The net effect was

that seeds/pod was an important yield component.

Contrarily views have been forwarded by Singh and Molhotha (1973) and Veeraswamy et al. (1973) who reported that only pod clusters/plant and pods/plant were important yield components.

Yield Vs 100 seed weight (seed size)

The correlation between yield with seed size was high and positive $r = 0.77$ ($P < 0.01$). The direct effect of seed size on grain yield was very high (1.41). The indirect effects of seed size on yield via branch number, clusters per plant, pods per plant and seeds per pod were negative, but unimportant. Seed size was therefore, an important yield component. The residuals were negative and unimportant indicating that there was no need to include more yield components like plant width in the path-coefficient analysis.

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

The results of this study have shown that single plant selection in this crop can be effective if carried out for simple characters like plant height, days to flowering and seed size. In the case of complex characters like yield and percent protein; recurrent selection is more effective (Townly-Smith and Hurd, 1972; Khan, 1973; and Rubaihayo and Onim, 1975). Therefore in polishing up the existing composites recurrent selection was found to be very effective for the improvement of yield and percent protein. High yielding varieties like UC 5418, UC 1266 and UC 2568 have been identified.

The study has shown that the tall indeterminate cultivars perform best under non-stress water conditions at the end of the season where secondary growth is not affected. Short, determinate plant types, however, can be grown suitably during any rainy season. Under conditions of plenty of water, low populations with wide spacings are better for tall plants but under water stress then high populations with narrow, more square

arrangements are best for even the tall plant types. Both population and spartial arrangements were found to have little or no effect on yield components (Singh et al., 1971; Hammerton, 1971; and Abrams and Julia, 1973).

Up to 37% natural crossing has been observed to take place in the crop in this study. Higher percentages (48%) have been reported elsewhere (Mehta and Dave 1931). Therefore, any hybridization programmes should take into account ways of maintaining the purity of parental lines. A high character variation has also been observed in this crop so that hybridization in the crop, for the time being does not necessitate the use of mutagens (Akinola and Whiteman, 1972; Pathnaswamy et al., 1973 and Singh et al., 1973a). The high insect population at flowering makes it difficult to maintain pure line varieties.

Generally the results observed in F_1 regarding the nature of gene action were in agreement with those in F_2 . Various degrees of dorminance for various

characters were, however, observed in F_1 and F_2 generations. But F_1 results should be more reliable since in segregating generations the genic interactions also attribute towards dominance thus causing this factor to be inflated (Singh and Singh, 1972 and Singh, 1974). But regarding the nature of gene action the results of this study indicate that it would be more appropriate to study an additional generation like F_2 to confirm the findings of an F_1 diallel set. The gene action controlling most of the characters was simple and additive (Sharma et al., 1973).

This study has shown that hybrid vigor exists in this crop. It is, therefore, possible to produce hybrid varieties if simpler means of artificial crossing are devised. The high heterosis and low inbreeding depression for yield indicates that composite varieties can be developed (Sharma et al., 1973).

The g.c.a. of parents 2 and 3 were high for yield and pods per plant. Generally g.c.a. variencies were higher than s.c.a. variencies which confirmed that the nature of gene action controlling the characters

studied was principally additive. In fact combining ability analysis served better in detecting the nature of gene action (Singh, 1974) of some characters like pods per plant, than graphical analysis.

Significant ($P < 0.05$) and positive phenotypic correlations were found for grain yield with plant width, pods per plant, seeds per pod, seed size and number of primary branches. The relationship between plant height and grain yield was negative though non-significant. These findings tentatively suggested that these characters were the primary components of yield in this crop. A path coefficient analysis, however, showed that clusters per plant, pods per plant, seeds per pod and seed size were the main yield components having maximum direct effects on yield (Singh and Molhotha, 1973 and Veeraswamy et al., 1973b). Therefore selection for a combination of these characters would be effective in increasing yield in this crop.

High heritability estimates were observed for plant height and width, days to flowering, pods per

plant, seeds per pod, seed size and pod clusters per plant. These characters could, therefore, be improved by simple methods of selection (Ebernart, 1970). But in the case of characters such as plant width, days to flowering and clusters per plant, which are under the control of dominant genes then the breeder should aim at concentration of the favourable dominant genes by following recurrent or biparental progeny selection procedures (Singh, 1974).

From the observations made during the experimental growth of the plant populations used in this study, it appears that there is an urgent need to look into the damage and control of the two pests H. armigera and F. dampfi, on this crop. It was observed that the two pests do most damage during the first than the second rains seasons of the year. H. armigera was observed to incur most damage on plant types where the pods are borne on a few clusters than when the pods are scattered on the plant.

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