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GENETIC ANALYSIS OF SOME LEAF CHARACTERISTICS IN PIGEONPEA [CAJANUS CAJAN (L.) Millsp.]

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ABSTRACT

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A diallel cross involving nine parent types, representing three diverse agronomically promising cultivars each divided into early, medium and late maturity groups, was used to study the inheritance of leaf area, leaf weight, specific leaf weight, petiole length and petiole weight in pigeonpea (Cajanus cajan (L.) Millsp.). Estimates of genetic parameters suggested a primary effect of additive gene action for all the characteristics studied. However, dominance was also significant for specific leaf weight and petiole weight. Ratios computed using these genetic parameters indicated the presence of partial dominance and unequal distribution of positive and negative alleles in the parents. The correlation between Wr + Vr and Yr was positive and significant only for petiole weight. This together with the position of the parents along the regression line clearly showed that high petiole weight was under the control of recessive genes. In the case of specific leaf weight and petiole length the correlations were non-significant but the position of parents along the regression line gave some indication that large and heavy petioles were controlled by recessive genes.

INTRODUCTION

Considerable genetic variation exists for leaf characteristics in pigeonpea (Cajanus cajan (L.) Millsp.). Recently, Rawson and Constable (1981) suggested that selection for large leaves along branches should result in high yield. Leaf area per plant (Singh et al., 1977) and specific leaf weight and leaf fresh weight (Saxena and Sharma, 1981) were found to have positive but moderate association with seed yield (r = 0.47 * *, 0.49 * * and 0.42*, respectively). Specific leaf weight in alfalfa (Pearce et al., 1969) and leaf blade size, petiole length and petiole weight in soybean (Auckland and Lambert, 1974) were recommended as selection criteria for fodder and seed yield respectively. For effectiveness of selection for various leaf characteristics it is im-

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pe: Trive to have information on the genetic control of the traits. In pigeonpeas information on this aspect is completely lacking; therefore, a study was undertaken to determine the genetic nature of some important leaf components.

MATERIALS AND METHODS

Nine cultivars, representing three agronomically promising cultivars each from early, medium and late maturity groups, and their hybrids in all possible combinations, excluding reciprocals, were grown in two replications in a randomized complete block design. The experiment was conducted in vertisol at ICRISAT Center, Patancheru during the 1975 rainy season. Four rows, each 5 m long, constituted a plot. Spacing between and within rows was 150 and 30 cm, respectively. Ten plants in each plot were selected at random for sampling. Our earlier observations (unpublished) indicated that measurements of leaf characteristics from mature leaf samples, obtained from different parts of the pigeonpea plant at flowering, did not differ significantly. Therefore, a sample of five fully developed leaves was taken at random from each plant at the time of flowering. The samples were placed in moist polythene bags to avoid desiccation and immediately processed to determine leaf fresh weight (mg), petiole length (cm) and petiole fresh weight (mg). Leaf area (cm^2) was estimated using an automatic leaf area meter (Model AAM-7). Thereafter, the samples were transferred to glassine bags and dried at 80°C for 40 h before recording dry weight of leaf and petiole. Specific leaf weight (mg/cm^2) was calculated, dividing the sample leaf dry weight by sample leaf area. Genetic analyses of the diallel data were performed according to Jinks (1954) and Hayman (1954a, b). Heritability in the narrow sense was estimated from the mean variance of arrays (Crumpacker and Allard, 1962).

RESULTS AND DISCUSSION

Mean performance of the parents and analysis of variance involving parents and F_1 's exhibited considerable variability for all the leaf characteristics (Table I). Variance of Wr-Vr was also analysed for line and block differences. Non-significant line effects for all the leaf characteristics (Table I) indicated validity of the assumptions involved in a diallel cross analysis.

For all the leaf characteristics studied, significant values of additive effects (D) (Table II) indicated a preponderance of additive gene action, which was supported by relatively high estimates of their narrow sense heritability (60-88%). Dominance components of genetic variation (H_1, H_2) were found to be important only for specific leaf weight and petiole weight. Significant F values (covariance of additive and dominance effects) for specific leaf weight, petiole length and petiole weight uggested non-symmetrical distribution of dominant and recessive alleles in the parents. The

TABLE I

Mean performance of parent plant types a	and analysis of variance fo	r various leaf charac-
tenstics in pigeonpea		

Parent	Leaf area (cm²)	Leaf fresh weight (mg)	Specific leaf weight (mg/cm ²)	Petiole length (cm)	Petiole fresh weight (mg)
Pant A-2	23.04	257	4.75	4.05	38.0
Baigani	25.32	354	4.55	4.45	50.0
Pusa Ageti	25.53	372	6.00	4.95	51.0
ST-1	32.55	491	6.20	4.83	52.0
ICP6997	28.00	454	6.05	5.00	49.5
ICP-7035	50.50	862	6.80	5.90	101.5
ICP—4726	43.48	847	8.10	6.60	105.5
ICP-4711	42.29	832	8.40	5.50	88.5
ICP-4741	39.06	701	6.90	5.05	71.0
LSD 5%	7.76	106.5	0.86	0.73	17.29
CV%	16.28	13.47	9.77	10.20	19.42
Mean square (44 d.f.) (F ₁ 's + parents)	102.74**	51502**	1.51**	0.52*	603.4**
Mean square (8 d.f.) [WrVr]	35.92	1280.93	0.012	0.014	0.18

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

quantity $(H_1/D)^{\frac{1}{2}}$ which measures mean degree of dominance over all loci, was less than unity for all the characteristics, indicating partial dominance for gene action. The estimate of $H_2/4H_1$ (av. value of positive and negative alleles) could be calculated only in the case of petiole weight where H_1 and H_2 were significant. The estimated value of 0.21 approached the expected ratio of 0.25, suggesting an equal distribution of positive (u) and negative (v) alleles of genes in the parent plants that exhibited dominance. For specific leaf weight, petiole length and petiole weight, the ratio KD/KR(proportion of dominance and recessive alleles) exceeded unity, which indicated a preponderance of dominant genes in the parents. The value of h^2 which indicates the extent of dominance effects of the genes was significant only for petiole weight. An h^2/H_2 value of 0.3 for this characteristic indicated a slight excess of recessive genes, which could be an underestimate, either because dominance effects of all genes concerned may not have been equal in size and direction, or because the distribution of genes was correlated (Jinks, 1954). Complementary interactions also depress this ratio (Mather and Jinks, 1971). Values of environmental effect (E) were significant for all the leaf characteristics studied, indicating high environmental influence on the expression of leaf characteristics.

The correlation between order of dominance (Wr + Vr) and parental measurement (Y_r) was significant and positive only for petiole weight

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otation*/ tio	Leaf area	Leaf weight	Specific leaf weight	Petiole length	Petiole weight
	93.86 ± 3.92	513.61 ± 14.67	1.67 ± 0.04	0.58 ± 0.06	6.34 ± 0.16
	1.99 ± 9.15	17.37 ± 34.21	0.61 ± 0.10	0.41 ± 0.14	1.67 ± 0.38
-	12.68 ± 8.66	57.98± 32.37	0.27 ± 0.09	0.27 ± 0.18	1.80 ± 0.36
	10.66 ± 7.44	49.38 ± 27.83	0.14 ± 0.08	0.18 ± 0.12	1.50 ± 0.31
	1.39 ± 4.99	8.23 ± 18.64	0.05 ± 0.06	0.05 ± 0.08	0.45 ± 0.21
	6.67 ± 1.24	58.98 ± 4.64	0.19 ± 0.01	0.13 ± 0.02	0.18 ± 0.05
r,/D) ⁴⁴	0.37	0.41	0.40	0.69	0.53
$_{1}/4H_{1}$	0.21	0.20	0.13	0.17	0.21
/H ₂	0.13	0.12	0.36	0.27	0.30
D/KR	1.06	1.09	2.66	3.19	1.66
eritability (%)	72.00	80.00	79.00	60.00	88.00
Wr+Vr)/Yr	0.35	0.18	- 0.29	-0.45	0.86**
Wr+Vr)/Yr	0.35	0.18	- 0.29	i	-0.45

pigeonpea i. various leaf characteristics variation and their ratios for components of Genetic

extent of average value of u and v alleles; II effects; h² dominance f dominance; $H_1/4H_1 = a^{1/2}$ lleles. covariance dominance; E = environmental effect; $(H_1/D)^{H_1}$ degree of dom h^2/H_2 , KD/KR = proportion of dominance and recessive alleles. H Ŀ. = dominance effects; Ŧ, *D = additive effects; H_1 ,

(Table II). This suggests that high petiole weight was under the control of recessive genes. The correlations for the other traits were non-significant, indicating that dominance was operating in both directions for these characteristics.

In the Wr-Vr graph, the slope of the regression line for all the traits did not deviate significantly from unity, indicating absence of significant epistasis. However, the *b* values for leaf area and specific leaf weight did not differ from zero either. This suggests that the error values for these characters are high; it is difficult to draw definite conclusions about their genetic nature from a Wr-Vr graph based on a small sample size as used in this study. Partial dominance for all the characteristics except petiole length was indicated by positive interception of the Wr axis with the regression line (Fig. 1). In the case of petiole length, dominance seems to be important,



Fig. 1. Regression of Wr-Vr for various leaf characteristics (1, Pant A-2; 2, Baigani; 3, Pusa Ageti; 4, ST-1 ICP-6997; 6, ICP-7035; 7, ICP-4726; 8, ICP-4711; 9, ICP-4741).



Natural Occurrence and Salient Characters of Nonnodulating Chickpea Plants

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ABSTRACT

Nonnodulating (Nod-) lines are a valuable reference for assessing the amount of biologically fixed N_2 in a legume. Chance observation of a Nod- plant in chickpea (Cicer arietinum L.) accession ICC 435 encouraged us to study the frequency of natural occurrence of this trait. Six hundred forty to 36260 plants of each of 11 chickpea accessions, field-grown under conditions favoring good nodulation, were uprooted for nodulation observations at 22 and 112 days after sowing (DAS). Plants identified as Nod[~] at 22 DAS were potted to produce seeds and those at 112 DAS had physiologically mature seeds. Progenies of apparent Nod⁻ plants were inoculated with chickpea Rhizobium strain IC 59 and grown in pots for 28 d for confirmation. The frequency of Nod⁻ plants in four accessions (ICC 435, -4918, -5003 and -4993) ranged from 120 to 490 per million. One Nod- plant from each of the four accessions was used for reconfirmation studies in the postrainy season 1987–1988 and for agronomic evaluation in subsequent studies under field conditions. The Nod- selections were indistinguishable from their respective parent accessions for plant growth except for nodulation, and most yielded similarly to their Nod * accessions when supplied with 50 to 100 kg N ha⁻¹. On a low-N field without fertilizer N, the Nod- plants were light green, grew poorly, had a short internodal distance with small leaves and leaflets, and had reddish-brown pigment on margins of leaflets, rachis, and sometimes branches.

CEREALS or other nonlegume crops are generally used as references in studies assessing amounts of biological N_2 fixation in legumes. These, however, may not be satisfactory reference crops in most such studies because of differences in plant growth rates and rooting patterns between the reference and the test crops (14). Also, cereals may fix some N_2 . Therefore, nonnodulating lines of legumes are preferred as references. The possibility of their use in developing host

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plants with restricted *Rhizobium* specificity, which would circumvent the problem of competition from native rhizobia, has also been indicated (4). The search for Nod⁻ chickpea plants began at ICRISAT Center (18° N lat) in 1975 with initiation of research work on biological N₃ fixation. Nonnodulating plants were occasionally observed during 1976 to 1980 in segregating F_2 and F_3 populations, but could not be saved due to lack of sufficient knowledge and expertise in salvaging the uprooted chickpea plants. Methods developed in the early 1980s (2,9) were used to recover a Nod⁻ plant from a germplasm accession ICC 435, a landrace from Bihar, India. Progenies of this plant were confirmed to be Nod- and were otherwise similar to the parent type (10). Unlike the Nod⁻ groundnut (Arachis hypogaea L.) mutant (5), this Nod-line (named ICC 435M) did not show apparent N-deficiency symptoms when grown on traditional chickpea fields, suggesting good soil-N scavenging ability of its root system. This prompted us to see if Nod - plants could be recovered from other genotypes. Procedures to identify Nod- plants under field conditions at an early plant growth stage and at physiological maturity were proposed based on earlier nodulation studies and are described here. Frequency of occurrence of Nodplants and their characteristics are also discussed.

MATERIALS AND METHODS

Large populations of 11 chickpea accessions (Table 1) were grown on a Vertisol (Kasireddipalli soil series, Typic Pellustert) field with available-N concentration of ≈ 19 mg kg⁻¹ soil in the top 15 cm of the profile, and chickpea *Rhizobium* count of 4700 g⁻¹ dry soil as measured by the most probable number plant infection technique (13). Screening for Nod⁻ plants was conducted on four germplasm accessions at early plant growth stage, 22 DAS, and on 10 accessions (including three studied at 22 DAS) at physiological maturity at 112 DAS (Table 1). Four of the total 11 accessions were Desi type, characterized by lightto dark-brown angular seeds; the other seven were Medi-

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Abbreviations: DAS, days after sowing; Nod⁺, nodulating; Nod⁻, nonnodulating.