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Inheritance of pod and seed traits in chickpea

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Abstract: *A 4 x 4 full-diallel cross was studied to estimate the gene effects and genetic parameters of pod and seed traits. According to Hayman's method, additive genetic variance was significant for pod length and seed length and width, also, both additive and dominance genetic variance were significant for pod thickness and width. As additive gene effects were significant for pod and seed traits, it is suggesting the selection of this traits early generations. Partial dominance was important for traits. The high narrow sense heritability of pod and seed traits was between 86 and 97%.*

Key words: *Cicer arietinum L., Chickpea, Diallel, Heritability, Gene effects*
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Introduction

Chickpea (*Cicer arietinum* L.) is an annual, selfpollinated, diploid (2n=16) grain legume crop grown in a wide range of environments including the Mediterranean, South and West Asia, North America, and North and East Africa (Singh and Saxena, 1999). Vavilov (1926) recognised the Mediterranean, Central Asian, Near Eastern, Indian and Ethiopia as the probable centres of origin (diversity) of the chickpea. Turkey and India are two major centers of diversity. The plant is known to have eight annual and 34 perennial species (Van der Maesen, 1987).

Two main types of chickpea are grown in the world: 'Kabuli' and 'Desi' (Van der Maesen, 1972). The 'Kabuli' types are grown in the Mediterranean region and the 'Desi' types mainly in the Indian subcontinent. The chickpea seed is characteristicly beaked, often angular and strongly wrinkled. The length and width of chickpea seeds vary from 4-12 mm and 3-8 mm, respectively. Generally, three seed size–large, medium and small-are recognised in chickpea.

Many genes control the inheritance of the seed size, a trait that seems to be governed more by additive than by non-additive genes (Singh and Saxena, 1999). Upadhyaya *et al.* (2006) indicated that seed size as determined by seed weight, the normal seed size was dominant over small seed size. The chickpea plant has inflated pods. Pod length, width and thickness are really only one character, that is pod size (Cubero, 1987). Pod size is apperantly an important yield contributing character, but its measurement is difficult. Hence, it is simply classified as small, medium or large. Khattak *et al*. (2002) reported that the additive and dominance gene effects on pod length were highly significant. However, Umaharan *et al*. (1997) reported an additive x dominance and additive x additive interaction effects for pod length in one cross, and pod width showed ambidirectional dominance. This study was carried out determine the genetic control of pod and seed traits in chickpea in 4 x 4 full-diallel cross sets including different chickpea parents.

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Materials and Methods

The experiment was conducted at the experimental farm of the Faculty of Agriculture at Dicle University in Diyarbakir, Southeastern Anatolia of Turkey (37°53´N, 40°16´E, 680 m above sea level), during the spring of 2006.

Four genotypes of chickpea (ILC 3279, Konya, Balikesir and Aknohut) were chosen due to the fact that they were different for seed size. The experimental materials comprised of F_1 hybrids with reciprocals obtained from a 4 x 4 diallel crosses and four parents.

The experimental material was sown by hand during spring of 2006 in a randomized complete block design with three replications. Each replication comprised of 4 parents and 12 F_1 including reciprocals. The plot size was one row of 1.5 m length and 45 cm apart with plants spaced at 10 cm within a row. Number of seeds per row was 15 seed/row. Weeds were controlled by hand several times. Pod length, width and thickness, seed length, width and roughness were measured in 25 pods/seeds for each genotype.

Analysis of variance (ANOVA) in the full diallel set was performed following method described by Hayman (1954) using the microcomputer program "DIALL win 89" developed by Ukai (1989).

Results and Discussion

Genetic variance: ANOVA showed that only additive genetic variance was significant for pod length and seed length and width. In addition additive genetic variance, dominance genetic variance was also significant for pod thickness and width (Table 1).

The "b1" component was highly significant for all the traits, except seed width and indicates that the dominance was

Table - 1: Analysis of variance of diallel tables for pod and seed traits in chickpea according to Haymen (1954)

Source of variation[a]	Pod length	Pod thickness	Pod width	Seed length	Seed roughness	Seed width
Rep	2.69	1.75	1.54	1.23	1.71	0.03
a	38.53**	107.26**	72.39**	141.48**	75.54	149.31**
b	2.04	5.02**	2.51*	1.72	2.07	1.02
b1	5.68*	12.90**	12.80**	5.40*	8.99**	2.36
b2	0.98	5.27**	0.41	1.33	0.48	1.1
b3	1.8	0.72	0.53	0.46	0.99	0.21
c	3.74*	5.91**	0.560*	5.86**	3.68*	5.72**
d	0.33	1.34	0.85	1.68	1.04	1.07

*, ** Significant at the 0.05, and 0.01 probability levels, respectively, [a]a: additive effect, b: dominance effect, b1: mean dominance deviation, b2: dominance deviation due to each parent, b3: dominance deviation due to each crossing combination, c: maternal effect, d: reciprocal differences not ascribable to "c"

Table - 2: Genetic parameters for pod and seed traits in chickpea

Genetic parameters	Pod length	Pod thickness	Pod width	Seed length	Seed roughness	Seed width
D	4.19**	2.02**	1.09**	0.88**	0.31**	2.02**
H_1	0.45	0.28*	0.01	0.02	0.01	0.00
H_2	0.48	0.22*	0.01	0.02	0.02	0.00
F	0.06	0.61	-0.04	0.11	-0.00	0.26
$_h^2$	0.79	0.25	0.28	0.04	0.05	0.03
E	0.22**	0.03**	0.03**	0.01**	0.01**	0.02**
$(H_1/D)^{1/2}$	0.33	0.37	0.28	0.14	0.23	0.03
K_D/K_R	0.51	0.70	0.47	0.73	0.48	1.51
h^2/H_2	2.18	1.47	3.79	2.90	3.58	9.49
h	0.97	0.51	0.55	0.21*	0.24	0.20
$H_2/4H_1$ (uv)	0.27	0.20	0.29	0.24	0.30	0.47
h^2 (bs)	0.91	0.97	0.95	0.97	0.95	0.97
h^2 (ns)	0.86	0.89	0.91	0.96	0.92	0.97

*,** = Significant at 0.05 and 0.01, respectively, D: additive genetic variance, H_1 and H_2: dominance genetic variance and: corrected dominance genetic variance, F: product of additive by dominance, h^2: square of difference P vs All, E: environmental variance, whole, $(H_1/D)^{1/2}$: average of degree dominance, K_D/K_R: proportion of dominance genes, h^2/H_2: number of effective factors, h: average direction of dominance, uv: balance of positive and negative alleles, h^2(bs): heritability for diallel in a broad sense, h^2(ns): heritability for diallel in a narrow sense

predominantly in one direction. The "b2" component was significant for pod thickness. Thus, there was evidence that some parents had a greater ratio of dominant alleles than others. Maternal effects were significant for all the traits studied. However, Niknejad *et al.* (1971) and Upadhyaya *et al.* (2006) reported that no maternal effects were observed for seed size.

Estimation of genetic parameters: The estimates of the genetic parameters are presented in Table 2. The only additive gene effect (D) was significant for pod and seed traits. Both additive (D) and dominance gene effects (H_1 and H_2) were significant for pod thickness. Heterosis (hh) was not significant for all traits, suggesting no dominant effects.

Distribution of alleles: From Table 2 $H_2/4H_1$ was apperant that the positive and negative alleles at these loci were not in equal proportions in the parental genotypes for all traits, except seed length.

The positive F values for pod length and thickness, seed length and width indicate an excess of dominant genes for these characters in the parents.

Degree of dominance: The average degree of the dominance was estimated by $(H_1/D)^{1/2}$, which incomplete dominance for all the traits studied (Table 2). Malhotra *et al.* (1997) noted that partial dominance of normal seed size over large seed size. Martinez *et al.* (1987) reported that full dominance in a negative sense (small values dominant) is shown by pod length.

The ratio of the total number of dominant and recessive genes in all the parents was estimated by K_D/K_R. This ratio indicated the four parental genotypes included in study carried more dominant than recessive genes for pod and seed traits, except seed width. In spite of the excess of dominant alleles, heterosis was not obtained for any of characters.

The ratio of h^2/H_2 estimates the number of groups which control the character and also exhibit dominance to some degree. This ratio was at least two groups genes for pod thickness, at least four groups genes for pod width and seed roughness, and at least nine groups genes for seed width. Niknejad *et al*. (1971) reported that large seeds were partially dominant to small seeds with at least

eight pairs of genes controlling seed size. Upadhyaya *et al.* (2006) indicated that dominance of normal seed size over small seed size with two major genes. However, Malhotra *et al.* (1997) noted partial dominance of normal seed size over large seed size under the control of polygenes with additive effect.

Heritability: The high broad and narrow sense heritability were obtained for all the traits studied. The high broad sense heritability ranged from 91% for pod length to 97% for pod roughness, seed length and width indicated the greater proportion of additive genetic variation compared with dominance in the total inherited genetic variation. Niknejad *et al.* (1971) reported that the 81% heritability estimate for seed size, and indicated that seed size is a predictable trait that relatively uninfluenced by environment. Cobos *et al.* (2007) reported that seed size was the most heritable trait (90%).

Full-diallel cross was studied to estimate the gene effects of the pod and seed traits in chickpea. The additive genetic variance (a) was significant for pod length, seed length and width. Both additive (a) and dominance genetic variance (b) were significant for pod thickness and width. The additive gene effects (D) were significant for pod and seed traits. The average degree of the dominance $(H_1/D)^{1/2}$ was showed partial dominance for all traits. The parental genotypes were carried more dominant than recessive genes for all traits. The high broad and narrow sense heritability were obtained for all the traits. Additive gene effects and high broad sense heritability showed that possible in early generations selection for this traits.

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