

Full Length Research Paper

Genetic analysis of some agronomic characters in chickpea (*Cicer arietinum* L.)

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A 5×5 half-diallel cross set of chickpea (Arman, Hashem, ILC588, ICCV2 and ILC3279) was studied to estimate the gene effects and genetic parameters of twenty traits including days to 50% flowering, days to podding, days to maturity, plant height, basal pod height, plant ordinate, root length, number of primary branches, number of secondary branches, biomass, pods weight per plant, straw yield per plant, 100- Seed weight, number of pods per plant, number of empty pods per plant, number of double seed pods per plant, number of single seed pods per plant, number of seeds per plant, seed yield per plant, seed size, harvest index. This study was carried out at the experimental farm of the Sara-rood dry land research sub institutes, in Kerman Shah Province (west of Iran) during the spring of 2007. According to analysis of variance for diallel, only additive genes effects were found significant for plant height (cm), pod height (cm) and number of primary branches, empty pods and straw yield (gr) per plant. In addition to the significant additive gene effects, dominant gene effects were significant for days to 50% flowering, days to podding, days to maturity, biological yield (gr), 100-seed weight (gr), seed size, harvest index, pod weight (gr), number of pods, single seed pods, seeds number and seed yield per plant (gr), but about plant ordinate and number of double seed pods per plant only dominant gene effects were significant. Additive and dominant gene effects were not found significant for root length and number of secondary branches. Estimates of genetic parameters also revealed that additive and dominance variance were significant for most studied traits in this research. However, both the additive and dominance gene affects together importance to control of most quantitative traits in the chickpea (*Cicer arietinum* L.). The degree of dominance average $(H1/D)1/2$ ($H1$ = dominance variance, D = additive variance) was higher than one, indicating over dominance for all traits except for PHT, BPHT and HI. The narrow-sense heritability was high for HI (67%), 100-seed weight (56%), SS (55%), basal pod height (47%), PHT (42%) and SY/p (37%) indicating that great genetic gain could be achieved for them.

Key words: Additive, chickpea (*Cicer arietinum* L.), half-diallel, dominance, heritability.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a major food legume and an important source of protein in many countries of Asia and its productivity continues to be low (0.78 tha^{-1}) (Upadhyaya et al., 2001). SY/p of Kabuli chickpea genotypes in the Mediterranean countries is low and limited by biotic and abiotic stress factors (Saxena, 1993), challenging plant breeders. Since the seed yield of chickpea is a complex quantitative measure, being affected by many genetic factors as well as environmental ones (Muehlbauer and Singh, 1987), direct selection on the basis of achieved seed yield could be

misleading. Knowledge of genetic components of any multigenic traits and environmental effects are important for the choice of breeding methods, size of populations and intensity of selection (Biçer and Şakar, 2008).

The studies showed that variation for DF, PHT and SS were significant additive gene effects (Singh et al., 1999; Hovav et al., 2003; Şakar and Biçer, 2004; Anbessa et al., 2006), while dominance gene effects were found significant for SY/p, No. PB, No. SB, HSW and DM (Malhotra and Singh, 1989). Also, No. PB and No. P/p (Muehlbauer and Singh, 1987), PHT (Salimath et al., 1996)

revealed significant both additive and dominance gene effects. Most of these reports on gene action have been made using diallel and line \times tester analyses (Muhelbauer and Singh, 1987; Salimath et al., 1996). One of the several biometrical techniques available to plant breeders for evaluating and characterizing genetic variability existing in a crop species is diallel analysis (Singh and Paroda, 1984). Diallel analysis is a useful technique in partitioning phenotypic variance in order to understand the size and proportion of the variation.

The present study was undertaken to elucidate the genetic control of agronomic characters in a 5 \times 5 half-diallel cross set involving in different chickpea parents.

MATERIAL AND METHODS

The experiment was conducted at the experimental farm of the Sara-rood dry land research sub institutes, in Kerman Shah Province (west of Iran) during the spring of 2007. Five Kabuli chickpea (*C. arietinum* L.) genotypes (Arman, Hashem, ILC 588, ICCV2 and ILC 3979) were used in the study. The experimental materials comprised of F1 hybrids obtained from a 5 \times 5 half-diallel crosses and five parents. The experimental materials were sown by hand during early spring of 2008 in a randomized complete block design with three replications. Each replication comprised of 5 parents and 10 F1s. The numbers of seeds per row was 20. Weeds were removed by hand.

Observations were recorded on 10 plants located in middle of the rows, except plants on border of the rows to eliminate border effects. Mature plants were individually harvested. DF and DM observations were taken on row basis when 50% plants were flowered or matured. Plant height, basal pod height, plant ordinate (it is plant diametric), root length, biological yield, seed size, harvest index, pod weight per plant, straw yield, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of single seed pods per plant, number of double seed pods per plant, number of empty pods per plant and number of seeds per plant were recorded for each plant for the laboratory statistical analysis.

Analysis of variance (ANOVA) in the half-diallel set was performed based on the method described by Walters and Morton (1978) using the statistical software of "DIALL for Win 98.

RESULTS AND DISCUSSION

Gene effects

Analysis of variance (ANOVA) in the half-diallel according to Walters and Morton (1978) is showed in (Table 1). In Table 1, (a) and (b) effects: showed genetic variations that were made due to additive and dominance gene effects, respectively. Totally (a), (b) statistics are estimation of from general and specific combining ability (GCA and SCA). The (b) statistics divided into three parts of b1, b2 and b3. Parts of b1 is comparison between parents group and hybrid groups, on the other hand (b1) effect is indicative average of heterosis that only was found significant for DF, DP, HSW, SS, HI, No. PB, No.

DSP/p and SY/p; (b2) effect is specific heterosis in the relative to each of parents that indicated different

dominance and recessive genes frequency in parents, this statistics for all traits except of plant ordinate, root length, secondary branches and HSW was significant. effects of (b3) is most of dominance part and equaled to SCA in Griffing (1954) method that was significant for the DF, the DP and DM, the BPHT, POR, the HSW, the SS and HI, PW/p, STY/p, No. E P/p, the No. DSP/p and SY/p (Table 1). ANOVA showed that only additive gene effects were found significant for the PHT, the BPHT and No. PB, the No. E P/p and STY/p.

In addition additive gene effects, dominance gene effects were also significant for the DF, the DM, the DP, Biomass, the HSW, the SS, the PW/p, the HI and the No. S/p, the No. P/p, the No. SSP/p and the SY/p, whereas only dominance gene effects were found significant for the POR and DSP/p Additive and dominance gene effects were not significant for the RL and secondary branches. The magnitude of the additive gene effects was much higher than dominant ones. These findings showed the possibility of early generation selection for some characters studied (Table 1).

Malhotra and Singh (1989), Singh et al. (1999, 1993), Şakar and Biçer (2004), Biçer and Şakar (2008) reported similar findings for the traits such as PHT, the DM, the HSW but weren't correspond for the other traits of DF, the BPHT the No. P/p and No. S/p. On the other hand the DF, the DP and DM characteristics are very important traits to escape drought in terminal drought environments (Toker et al., 2007). But, they couldn't be used in early generation of the selection because they were regulated by additive and dominance gene actions (Kidambi, 1988). Biçer and Şakar (2008) reported similar findings for DM, but for days to flowering were not corresponded.

As known, the PHT and BPHT are very important traits for the development of chickpea cultivation in the world, because improvement of them is possibility machines harvest of the chickpea, the PHT and the BPHT were mainly governed by additive gene effects, therefore early generation selection for the PHT and the BPHT seemed effective (Table 1). Malhotra and Singh (1989), Singh et al. (1992, 1993), Şakar and Biçer (2004) and Biçer and Şakar (2008), for the plant height, reported similar findings but for basal pod height were not similar. BIM was controlled by additive and dominance gene effects where additive component appeared high in magnitude. Additive gene effects contributed to the variation for the No. PB, No. E P/p and STY/p (Table 1), that indicated genetic gain in selection for these traits could be possible.

Additive and dominance gene effects were not significant for the RL and No. SB, whereas both additive and dominance gene effects were significant for the HSW, SS, HI, PW/p, No. SSP/p, No. S/p and SY/p. However, additive gene effects were higher than dominance gene effects. Singh et al. (1982); Upadhyaya et al. (2006); Dhaliwal and Gill (1973); Şakar and Biçer (2004); Biçer and Şakar (2008) obtained the same results with the exception of pods and seeds number per plant

Table 1. Analysis of variance of a 5×5 half-diallel cross set for most characters in chickpea (according to Walters and Morton 1978).

Source	PW/p (gr)	STY/p	100SW (gr)	No. P/p	No. E P/p	No. DSP/p	No. SSP/p	No. S/p	SY/p(gr)	SS(gr)	I
Rep	164.98**	28.2 ^{ns}	4.7 ^{ns}	812.5*	11.4 ^{ns}	22.2 ^{ns}	864.3**	980.9*	94.3**	0.001**	30.5 ^{ns}
a	440.35**	53.8**	19.8**	2490.3**	35.4**	18.2 ^{ns}	2116.4**	2876.5**	206.2**	0.002**	408.7**
b	123.5**	13.8 ^{ns}	17.6**	593.9**	8.7 ^{ns}	54.6**	459.2**	846.11**	74.7**	0.002**	168.6**
b1	105.8 ^{ns}	1.01 ^{ns}	58.4**	100.02 ^{ns}	5.7 ^{ns}	131.3**	73.2 ^{ns}	658.9 ^{ns}	98.4**	0.006**	531.9**
b2	160.08**	44.6**	5.4 ^{ns}	1351.1**	24.4*	38.5**	983.2**	1365.01**	68.3*	0.006*	36.04**
b3	97.8*	-8.4**	19.2**	86.9 ^{ns}	-3.3**	52.2**	117.12 ^{ns}	468.5 ^{ns}	74.9**	0.0033**	201.9*
Error	27.73	9.5	2.03	168.5	6	7.8	125.2	188.9	14.7	0.0002	12.4

Source	df	DF	DP	DM	PHT(cm)	BPHT (cm)	POR(cm)	RL(cm)	No. PB	No. SB	BIOMAS
Rep	2	4.01 ^{ns}	1.09 ^{ns}	0.67 ^{ns}	82.7**	6.6 ^{ns}	45.6 ^{ns}	2.05 ^{ns}	0.19*	15.9 ^{ns}	331.6*
a	4	124.9**	130.9**	128.9**	152.23**	194.7**	33.10 ^{ns}	1.81 ^{ns}	0.44**	9.8 ^{ns}	565.9**
b	10	120.6**	113.5**	120.8**	25.14 ^{ns}	17.25 ^{ns}	43.9*	1.97 ^{ns}	0.09 ^{ns}	11.12 ^{ns}	183.13*
b1	1	39.34**	17.8*	8.4 ^{ns}	8.5 ^{ns}	32.51 ^{ns}	47.9 ^{ns}	2.5 ^{ns}	0.23*	13.3 ^{ns}	82.4 ^{ns}
b2	4	139.8**	130.34**	156.7**	37.4*	40.07**	23.03 ^{ns}	1.11 ^{ns}	0.17*	12.7 ^{ns}	364.6**
b3	5	121.5**	119.2**	114.5**	18.7 ^{ns}	-4.06**	59.8**	2.6 ^{ns}	-0.01 ^{ns}	9.4 ^{ns}	58.10 ^{ns}
Error	24	4.54	3.07	3.02	11.7	8.15	15.08	1.99	0.04	5.4	64.3

*, ** Significant at the 0.05, and 0.01 probability levels, respectively. 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. DF, days to 50% flowering; DP, days to podding; DM, days to maturity; PHT, plant height; BPHT, basal pod height; POR, plant ordinate; RL, root length; No. PB, number of primary branches; No. SB, number of secondary branches; PW/p, pods weight per plant; STY/p, straw yield per plant; 100-SW (gr), 100- Seed weight; No. P/p, number of pods per plant; No. E P/p, number of empty pods per plant; No. DSP/p, number of double seed pods per plant; No. SSP/p, number of single seed pods per plant; No. S/p, number of seeds per plant; SY/p, seed yield per plant; SS, seed size; HI, harvest index.

that reported only additive gene effects.

Genetic parameters estimated

The estimates of the genetic components for each trait using D2 program were shown in Tables 2 and 3. One of the methods for Hayman (1954) hypothesis test is deviation of regression coefficient (slop) than one; it was not significant for most traits except of DF, DP, DM, BIM, No. P/p, No. DSP/p and STY/p (Tables 2 and 3). Other method for Hayman (1954) hypothesis test is analysis of variance for (Wr–Vr) value that

shown in Table 4. The (Wr–Vr) value only was found significant for three characters including the DF, the DP and the DM (Table 4). That demonstrated for the DF, the DP and the DM definitively Haymans hypothesis don't acceptance and the additive - dominance model was not satisfactory. Hence, in addition to additive and dominance gene effects, epistasis gene effects were effective for controlling DF, DP and the maturity.

These epistatic effects can cause bias in the estimates of the additive and dominance components to which they are confounded. The magnitude of the bias depends on the relative

values of the epistasis effects, comparatively to deviations d and h, type of prevailing epistasis and direction of dominance. For the other characters in this study, Additive-Dominance model appears to be seemed satisfactory. This result is enjoyable for plant breeding researcher because it indicated for most of the important characters in chickpea there were no epistasis effects. Kidambi (1988), Malhotra and Singh (1989) Singh et al. (1992) and Anbessa et al. (2006) reported similar finding. Analysis of variance for (Wr+Vr) value showed in Table 5. The (Wr+Vr) value were significant for DF, DP, DM, BPHT and HI (Table 5). That indicated the

Table 2. Genetic parameters for most traits in chickpea.

Parameter	DF	DP	DM	PHT (cm)	BPHT (cm)	POR (cm)	No. PB	Biomass	PW/p (g)	STY (p)
β	0.005 ± 0.14*	0.017±0.16*	0.29 ± 0.13*	1.12± 0.19 ^{ns}	1.1± 0.15 ^{ns}	0.46 ±0.23*	0.76 ± 0.27 ^{ns}	0.21±0.23*	0.46±0.29 ^{ns}	0.12 ±0.21*
a	23.2 ±6.13	7.6± 25.5	17.8 ±19.04	-4.7±10.3	1.8 ± 37.06	-9.7 ±14.6	-0.003±0.044	6.3 ± 88.5	8.4±53.6	0.92 ±7.8
D±S.E.(D)	37.9 ±15*	41.6±15.1*	42.05±16.9*	46 ±4.3*	61.3±4.09*	2.6±6.2 ^{ns}	0.16 ±0.021*	148.5±44*	125.2 ±20.7*	14.8 ±4.83*
H1±S.E.(H1)	188.2 ±40.5*	172.2±41*	201.2 ± 45.7*	35.9±11.7*	33.7±11.02*	74.3±16.6*	0.16 ± 0.06 ^{ns}	440±118.5*	203.7 ±56*	45.6±13.05*
H2±S.E.(H2)	150.1 ± 36.7	136.8±37*	1604±1.5*	25.3±10.6*	24.8±10*	67 ±15.08*	0.11±0.052*	325.2±108*	154.1±51*	32.06±11.84*
F±S.E.(F)	54 ±37.4 ^{ns}	52.5±37.8 ^{ns}	67.5±42.3 ^{ns}	30.8±10.8*	44.7±10.2*	7.4 ±15.4 ^{ns}	0.16 ±0.054*	213.5±110 ^{ns}	106.2 ± 51.8*	26.6 ±12.08
h2 ± S.E.(h2)	12.8±24.8 ^{ns}	10.1±225 ^{ns}	2.3 ±28 ^{ns}	5.7 ±7.2 ^{ns}	10.5 ±6.8 ^{ns}	5.4±10.2 ^{ns}	0.06 ± 0.04 ^{ns}	12.1 ±72.6 ^{ns}	22.3±34.2 ^{ns}	-1.64 ±7.9 ^{ns}
E±S.E.(E)	4.5±6.2 ^{ns}	3.06±6.2*	3.02 ±7 ^{ns}	11.7±1.8*	8.2 ±1.7*	15.08 ±2.5*	0.044±0.009*	64.5 ±18*	27.5 ±8.5*	9.5 ±1.97*
(H1/D)1/2	2.23	2.035	2.19	0.883	0.742	5.4	1.011	1.7	1.3	1.8
H2/4H1	0.199	0.199	0.194	0.176	0.184	0.23	0.174	0.19	0.19	0.18
KD/KR	1.93	1.89	2.16	2.22	2.93	1.72	2.9	2.43	1.99	3.09
K	0.1	0.1	0.015	0.2	0.4	0.1	0.5	0.037	0.1	-0.1
R(Yr, Wr+Vr)	-0.727	-0.763	-0.41	0.766	0.89	-0.714	-0.25	-0.34	-0.58	0.61
h2NS	0.21	0.25	0.19	0.42	0.47	0.04	0.26	0.15	0.34	0.05
h2BS	0.91	0.94	0.94	0.62	0.70	0.54	0.55	0.62	0.73	0.48
The value of the completely dominant parents	67.11	75.9	95.09	33.5	15.61	27.7	1.84	39.5	33.7	-5.6
The value of the completely recessive parents	49.9	57.95	80.3	68.01	52.97	17.8	1.14	8.5	-12.04	56.7

KD/KR= [(4DH1)1/2 + F]/ [(4DH1)1/2 - F], K = [h2/ H2]. *, ** Significant at the 0.05, and 0.01 probability levels, respectively.

presence of dominant effects for them. Anbessa et al. (2006) and Singh et al. (1992) got the same results. Additive variance was significant for all characters except of POR and No. DSP/p; too, dominance variance was significant for all characters.

Studies suggested that additive (Zafar and Abdullah, 1971; Singh et al., 1992; Biçer and Şakar, 2008) and dominance (Singh et al., 1992; Biçer and Şakar, 2008) variance were important for most of agronomic characters such as days to

flowering, maturity, plant height, basal pod height, number of branches, pods and seeds per plant, seed yield, 100-seed weight and seed size. Environmental variance was found to be significant for all traits except of days to flowering and maturity indicating high level environmental pressure. The degree of dominance average (H1/D)1/2 for all characters except of plant height, basal pod height and harvest index was higher than one, indicating over dominance for most studied traits in this research. But about plant

height, basal pod height and harvest index (H1/D)1/2 was lower than one indicating partial dominance. However, Biçer and Şakar (2008) reported that most characters showed partial dominance, but Muhelbauer and Singh (1987) reported that the No. PB, the No. P/p and the No. S/p showed over dominance. Also, Dhaiwal and Gill (1973) reported that No. P/p and SY/p exhibited positive over dominance but HSW had no dominance.

The proportion of positive and negative genes

Table 3. Genetic parameters for most traits in chickpea.

Parameter	100-SW (g)	No. P/p	No. EP/p	No.DSP/p	No. SSP/p	No. S/p	SY/p(g)	SS(g)	HI (%)
β -1	0.69 \pm 0.18 ^{ns}	0.30 \pm 29 [*]	0.580 \pm .15 ^{ns}	0.22 \pm 0.11 [*]	0.56 \pm 0.37 ^{ns}	0.47 \pm 0.29 ^{ns}	0.47 \pm 0.25 ^{ns}	0.396 \pm 0.156 [*]	0.79 \pm 0.101 ^{ns}
a value	0.076 \pm 2	26.6 \pm 349	-1.7 \pm 5.6	-0.9 \pm 35.4	7.5 \pm 257.6	-10.4 \pm 367.4	3.8 \pm 26.7	0.0001 \pm 0.0002	20.13 \pm 18
D \pm S.E.(D)	6.08 \pm 0.89 [*]	727.02 \pm 145.2 [*]	10.2 \pm 3.9 [*]	1.7 \pm 4.6 ^{ns}	642.04 \pm 91.7 [*]	849.6 \pm 145 [*]	58.03 \pm 10.5 [*]	0.0005 \pm 0.0001 [*]	131.7 \pm 6.3 [*]
H1 \pm S.E.(H1)	9.2 \pm 2.4 [*]	1575 \pm 392.2 [*]	21.3 \pm 10.7 [*]	52.3 \pm 12.3 [*]	944.2 \pm 247.6 [*]	1663.8 \pm 391.2 [*]	101 \pm 28.3 [*]	0.001 \pm 0.0003 [*]	77.8 \pm 17 [*]
H2 \pm S.E. (H2)	7.4 [*] \pm 2.2	1147.6 \pm 255.7 [*]	14.6 \pm 9.7 ^{ns}	39.3 \pm 11.2 [*]	768.3 \pm 224.6 [*]	1218.9 \pm 354.7 [*]	78.5 \pm 25.6 [*]	0.001 \pm 0.0002 [*]	69.12 \pm 15.4 [*]
F \pm S.E. (F)	-1.3 \pm 2.25 ^{ns}	959.6 \pm 362.7 [*]	13.3 \pm 9.9 ^{ns}	-2.9 \pm 11.4 ^{ns}	668 \pm 229.05 [*]	929.03 \pm 261.8 [*]	40.7 \pm 26.12 ^{ns}	-0.0003 \pm 0.0003 ^{ns}	19.6 \pm 15.7 ^{ns}
h2 \pm S.E.(h2)	14.3 \pm 1.5 [*]	5.6 \pm 240.2 ^{ns}	0.5 \pm 6.52 ^{ns}	32.5 \pm 7.5 [*]	21.5 \pm 151.6 ^{ns}	156.2 \pm 239.5 ^{ns}	23.6 \pm 17.3 ^{ns}	0.0014 \pm 0.0002 [*]	130.4 \pm 10.4 [*]
E \pm S.E.(E)	1.85 \pm 0.37 [*]	168.5 \pm 59.3 [*]	5.9 \pm 1.6 [*]	7.8 \pm 1.9 [*]	96.7 \pm 37.4 [*]	188.9 \pm 59.13 [*]	14.7 \pm 4.2 [*]	0.0002 \pm 0.00 [*]	12.4 \pm 2.6 [*]
(H1/D)1/2	1.24	1.47	1.44	5.5	1.25	1.39	1.32	1.56	0.77
H2/4H1	0.198	0.182	0.172	0.19	0.193	0.183	0.195	0.207	0.22
KD/KR	0.85	2.62	2.62	0.73	2.43	2.3	1.72	0.67	1.22
K	1.9	0.0048	0.032	0.80	0.028	0.1	0.3	1.5	1.9
R (Yr, Wr+Vr)	-0.754	0.00	0.46	-0.98	0.032	-0.32	-0.75	-0.57	-0.97
h2NS	0.56	0.18	0.16	0.33	0.26	0.27	0.37	0.55	0.67
h2BS	0.78	0.70	0.48	0.70	0.75	0.72	0.73	0.81	0.86
The value of the completely dominant parents	29.4	52.5	4.9	10.9	38.5	73.04	25.9	0.28	55.2
The value of the completely recessive parents	20.2	53	11.7	-0.01	42.5	3.98	-9.83	0.22	23.11

KD/KR= [(4DH1)1/2 + F]/ [(4DH1)1/2 - F], K = [h2/ H2]. *, ** Significant at the 0.05, and 0.01 probability levels, respectively. β -1(regression coefficient), a (intercept), D \pm S.E.(D) (additive variance), H1 \pm S.E.(H1) (dominance variance), H2 \pm S.E. (H2) (dominance variance), F \pm S.E. (F) (product of add. by dom. effects), h2 \pm S.E.(h2) (square of difference Pvs All), E \pm S.E.(E) (environmental variance whole), (H1/D)1/2 (average of degree dominance), H2/4H1(balance of positive and negative alleles), KD/KR (proportion of dominance genes) , K (number of effective factors), R(Yr, Wr+Vr) (direction of dominance), h2NS (narrow sense heritability), h2BS (broad sense heritability).

(H2/4H1) was unequal showing different distribution of genes among parents. The (H2/4H1) component ranged from (0.17) for the No. PB and the No. EP/p to (0.23) for the POR and the HI. That indicated negative genes had more frequent for these studied traits. Proportion of dominant and recessive genes in the parents (KD/KR) indicated that parents had more dominant than recessive genes for most characters but for HSW, SS and No. DSP/p(KD/KR) value was lower than one showed that parents had more recessive than dominant genes for these traits (Tables 2 and 3). Greater

ratio of dominant to recessive genes (KD/KR) with positive value (F) indicated that dominant genes were more frequent for most studied traits excepts of HSW, No. DSP/p and SS that had (KD/KR<1) and negative value (F) (Tables 2 and 3). Biçer and Şakar (2008) reported that dominant genes were more frequent for PHT, No. PB, SY/p and HSW. The normal (Upadhyaya et al., 2006) or large (Niknejad et al. 1971) SS was dominant over the small SS; however, Kumar and Singh (1995) and Malhotra et al. (1997) found opposite results.

Days to flowering and maturity were controlled by at least one group of genes due to (k=0.1).

Kumar and Van Rheenen (2000), Or et al. (1999) and Cho et al. (2002) reported that days to flowering was determined governed by one major gene, but Biçer and Şakar (2008) and Anbessa et al. (2006) reported DF, governed by three and two major genes, respectively. HSW, SS and HI were controlled by at least two genes due to (K=1.9, 1.5, 1.9), respectively (Table 3). Biçer and Şakar (2008) reported that 100-seed weight in the chickpea was governed by two genes; Upadhyaya et al. (2006) reported that SS in chickpea was controlled by two major genes and Cho et al. (2002) by single major genes. Other characters

Table 4. Analysis of variance for (Wr+Vr).

Source	df	DF	DP	DM	PHT(cm)	BPHT(cm)	POR(cm)	No. PB	BIOMAS	PW/p(gr)	STY/p
Block	2	146.6 ^{ns}	324.2 ^{ns}	96.7 ^{ns}	171.2 ^{ns}	62.14 ^{ns}	1065.1 ^{**}	0.0028 ^{ns}	25684.4 ^{ns}	8160.6 ^{ns}	80.95 ^{ns}
(Wr+Vr)	4	7846.6 ^{**}	347673 ^{**}	10032 ^{**}	91.7 ^{ns}	36.5 ^{ns}	454.8 ^{ns}	0.0021 ^{ns}	21565 ^{ns}	4398.7 ^{ns}	189 ^{ns}
Error	8	82.9	163.62	116.33	110.3	47.9	176.3	0.0017	14369.5	2746.9	158.6

Source	df	100-SW(gr)	No. P/p	No. E P/p	No. DSP/p	No. SSP/p	No. S/p	SY/p(gr)	SS	HI
Block	2	19.4 ^{ns}	329784.5 ^{ns}	27.8 ^{ns}	444.5 ^{ns}	100988 ^{ns}	427118.5 ^{ns}	2152.06 ^{ns}	0.00 ^{ns}	133.3 ^{ns}
Wr-Vr	4	3.13 ^{ns}	272415.5 ^{ns}	25.5 ^{ns}	120.8 ^{ns}	122153.8 ^{ns}	199478.9 ^{ns}	934.6 ^{ns}	0.00 ^{ns}	562.3 ^{ns}
Error	8	4.45	137972.3	64.8	170.6	44877.2	133298.3	805.6	0.00 ^{ns}	269.7

*, ** Significant at the 0.05, and 0.01 probability levels, respectively. 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. DF, days to 50% flowering; DP, days to podding; DM, days to maturity; PHT, plant height; BPHT, basal pod height; POR, plant ordinate; RL, root length; No. PB, number of primary branches; No. SB, number of secondary branches; PW/p, pods weight per plant; STY/p, straw yield per plant; 100 -SW (gr), 100- Seed weight; No. P/p, number of pods per plant; No. E P/p, number of empty pods per plant; No. DSP/p, number of double seed pods per plant; No. SSP/p, number of single seed pods per plant; No. S/p, number of seeds per plant; SY/p, seed yield per plant; SS, seed size; HI, harvest index.

Table 5. Analysis of variance for (Wr+Vr).

Source	df	DF	DP	DM	PHT(cm)	BPHT(cm)	POR(cm)	No. PB	BIOMAS	PW/p(gr)	STY/p
Block	2	186.12 ^{ns}	258.9 ^{ns}	174.8 ^{**}	967.3 ^{ns}	334.8 ^{ns}	1664.9 ^{ns}	0.0072 ^{ns}	6396.2 ^{ns}	568.9 ^{ns}	24.04 ^{ns}
(Wr+Vr)	4	7526.2 ^{**}	7610.2 ^{**}	3714.17 ^{**}	1148.3 ^{ns}	1673.9 [*]	1395.9 ^{ns}	0.012 ^{ns}	34440 ^{ns}	11874.11 ^{ns}	35.12 ^{ns}
Error	8	311.08	428.02	23.8	1208.3	419.7	664.9	0.007	23679	7194.6	322.6

Source	df	100-SW(gr)	No. P/p	No. E P/p	No. DSP/p	No. SSP/p	No. S/p	SY/p(gr)	SS	HI
Block	2	20.61 ^{ns}	76240.5 ^{ns}	500.17 ^{ns}	76.16 ^{ns}	61593.8 ^{ns}	53135 ^{ns}	204.8 ^{ns}	0.00 ^{ns}	3274.4 ^{ns}
(Wr+Vr)	4	59.9 ^{ns}	483247 ^{ns}	384.24 ^{ns}	401 ^{ns}	284170 ^{ns}	545539.5 ^{ns}	369.6 ^{ns}	0.00 [*]	23478.6 ^{**}
Error	8	18.8	248437.9	292.3	293	96565	346246.8	2043.3	0.00 ^{ns}	1296.2

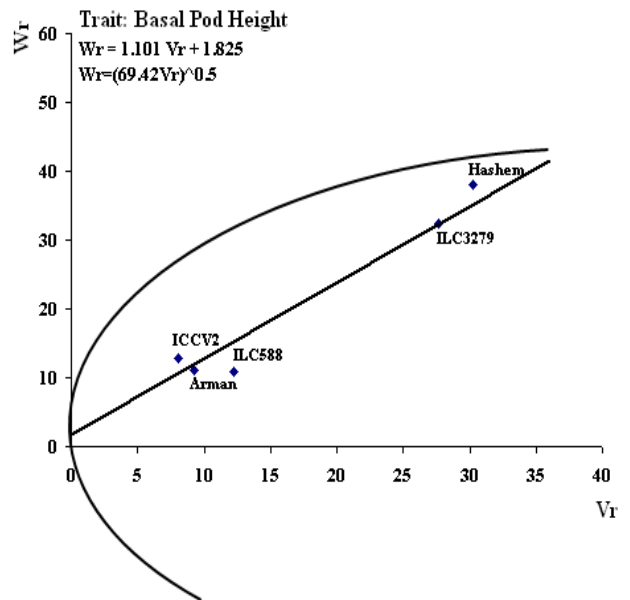
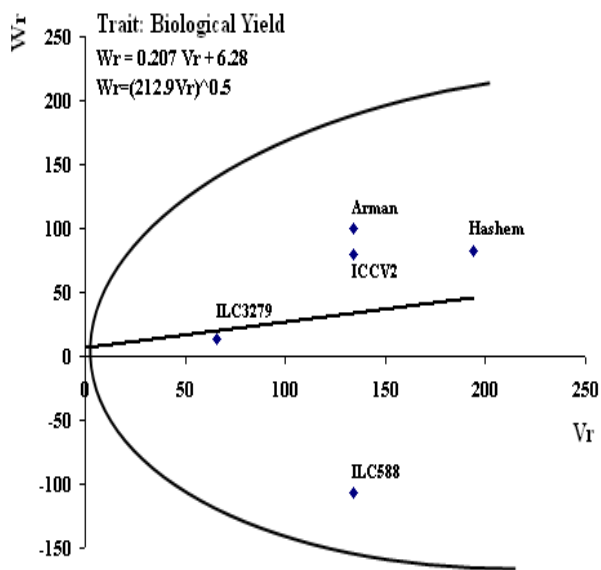
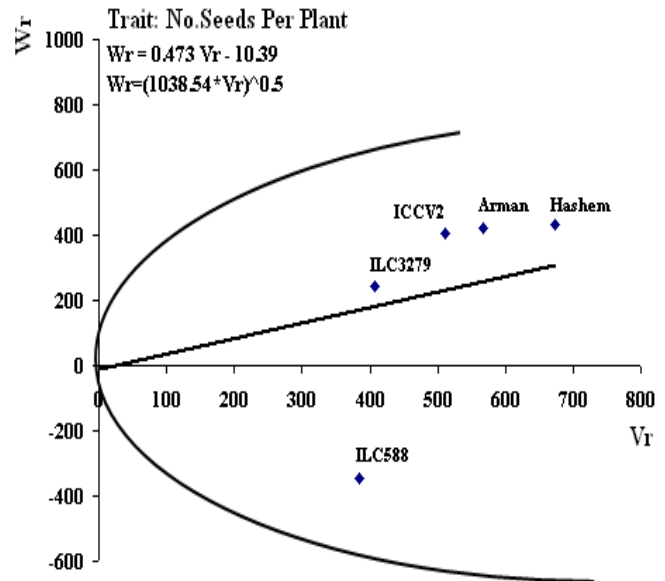
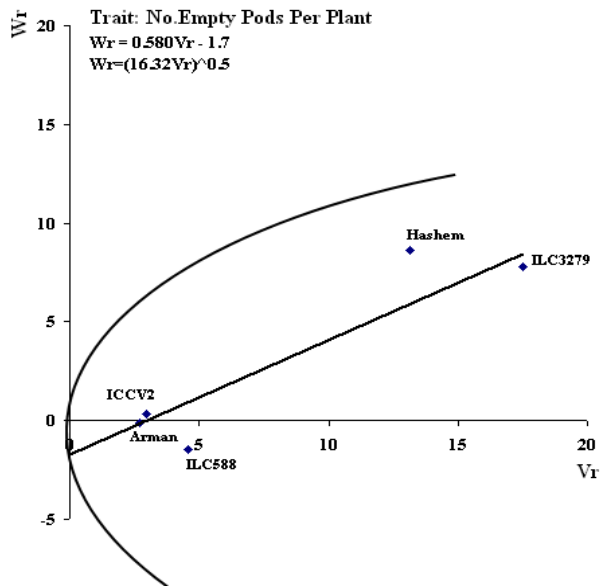
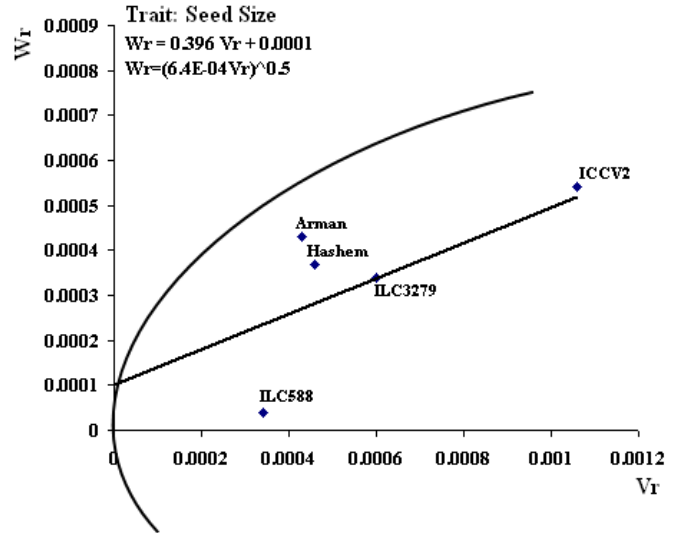
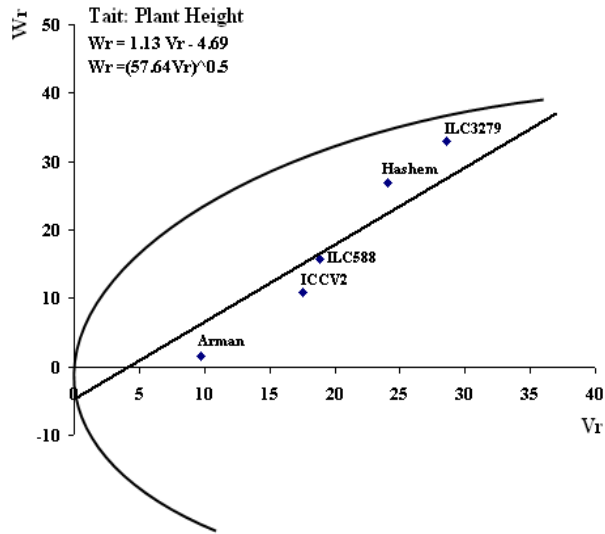
*, ** Significant at the 0.05, and 0.01 probability levels, respectively. a, additive effect; b, dominance effect; b1, mean dominance deviation; b2, dominance deviation due to each parent; b3, dominance deviation due to each crossing combination. DF, days to 50% flowering; DP, days to podding; DM, days to maturity; PHT, plant height; BPHT, basal pod height; POR, plant ordinate; RL, root length; No. PB, number of primary branches; No. SB, number of secondary branches; PW/p, pods weight per plant; STY/p, straw yield per plant; 100 -SW (gr), 100- Seed weight; No. P/p, number of pods per plant; No. E P/p, number of empty pods per plant; No. DSP/p, number of double seed pods per plant; No. SSP/p, number of single seed pods per plant; No. S/p, number of seeds per plant; SY/p, seed yield per plant; SS, seed size; HI, harvest index.

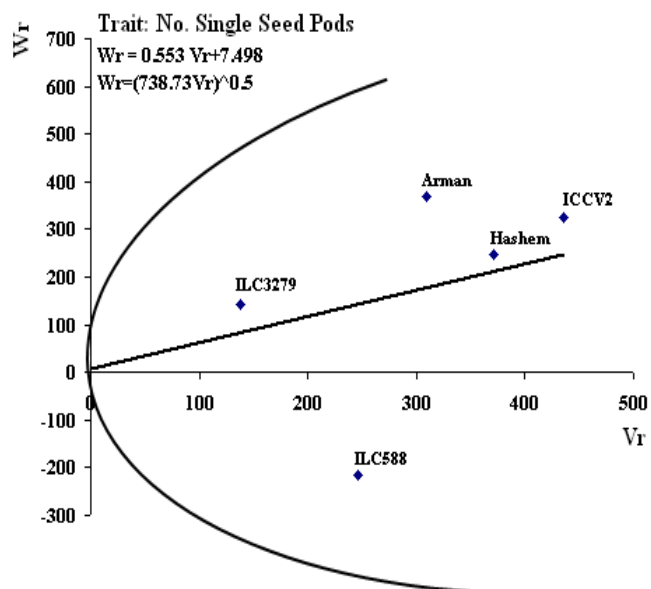
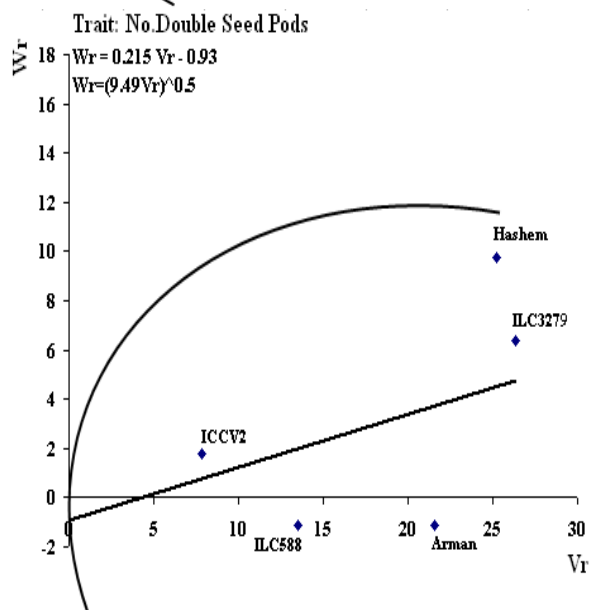
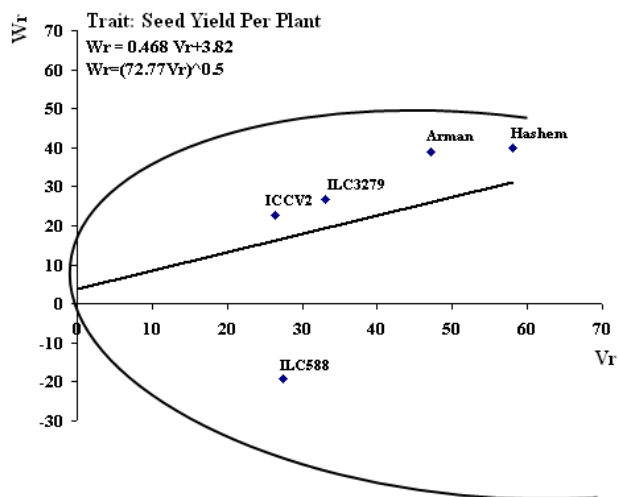
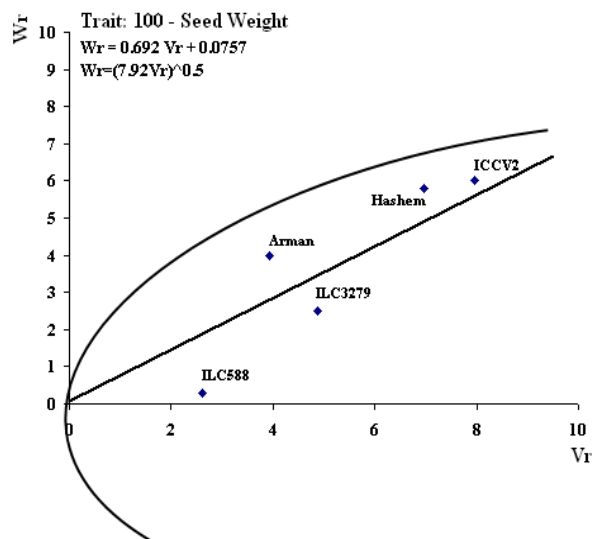
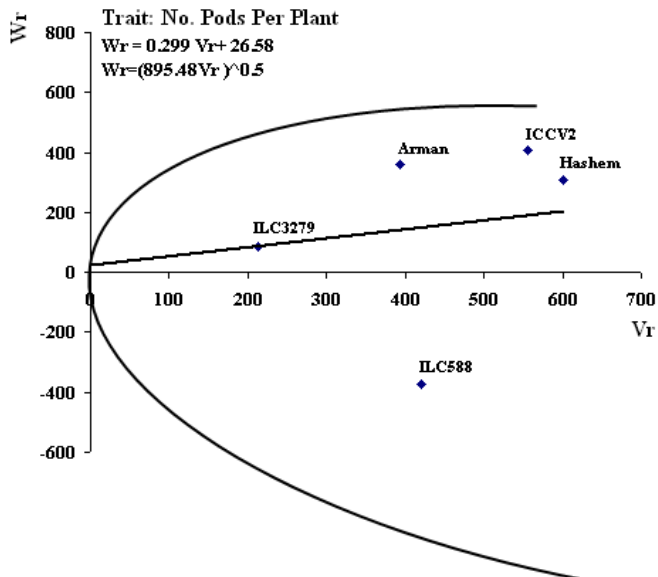
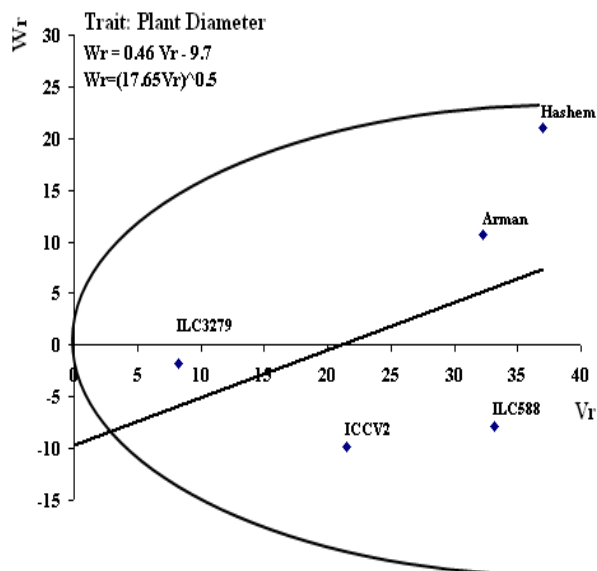
studied in this research were controlled by at least one groups of genes due to (K<1) (Tables 2 and 3).

The sign of (R) (correlation coefficient between averages of joint parent for each row (Yr) and (Wr+Vr) value) indicated dominance direction. The

coefficient of correlation between (Yr) and (Wr+Vr) was negative and high, for DF, DP, DM, PORT, Biomass, HSW, SS, HI, PW/p, No. PB, No. DSP/p, No. S/p and SY/p. Hence for these traits amplifier alleles were dominance but as for PHT, BPHT, STY/p and No. P/p, No. E P/p and No. SSP/p,

with positive and high (R) (Yr, Wr+Vr) (Tables 2 and 3) reducer alleles were dominance. These results are completely corresponding with previous findings in the present research. The highest and lowest of narrow-sense heritability was obtained for HI (0.67) and POR (0.04), respectively.





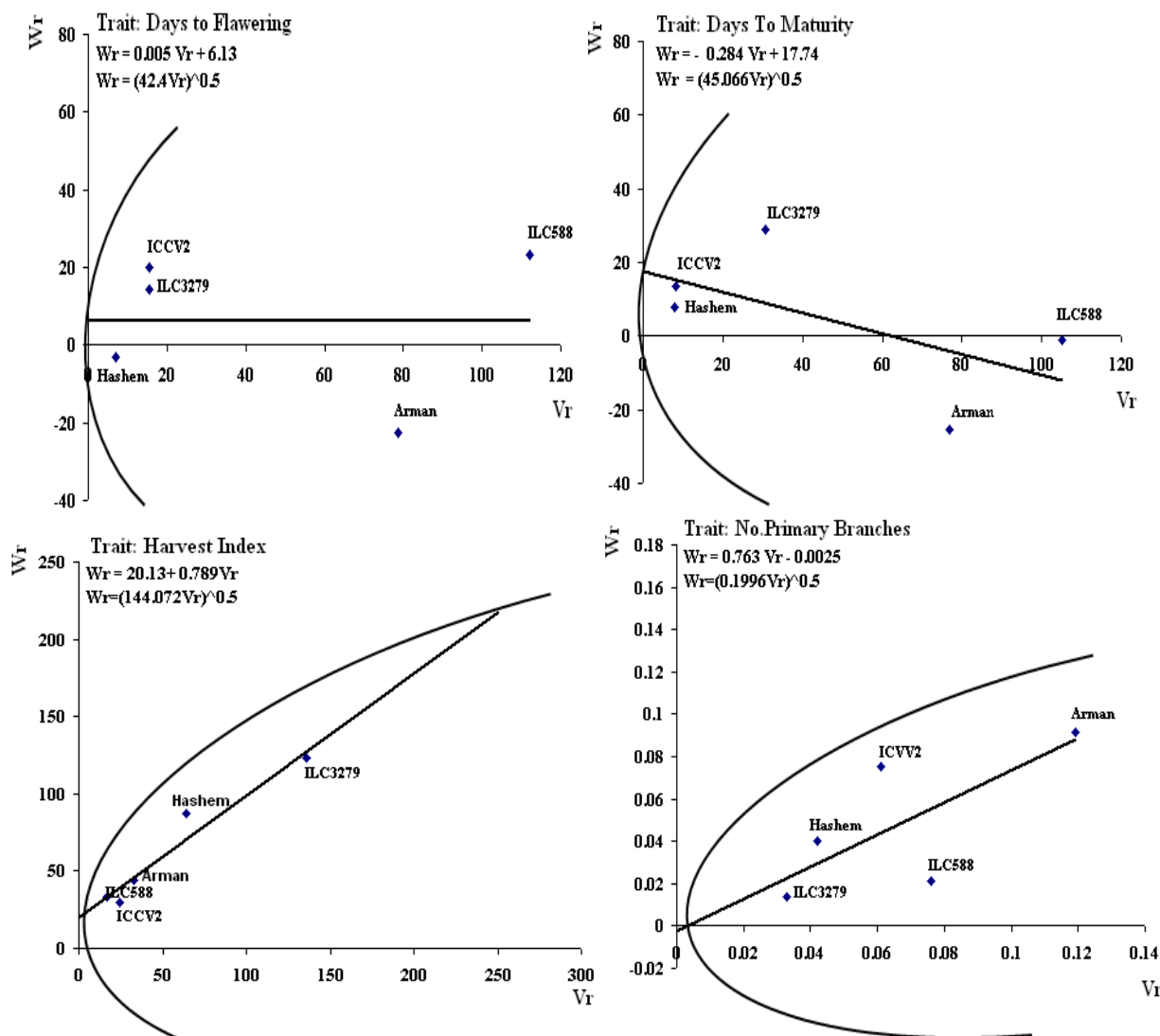


Figure 1. Graphical analysis of different traits for chickpea diallel crosses.

The narrow-sense heritability was relatively the highest for PHT (42%), BPHT (47%), PW/p (34%), HSW (56%), No. DSP/p (33%), SY/p (37%), SS (55%) and HI (67%) indicating that great genetic gain could be achieved for them in the chickpea breeding. Biçer and Şakar (2008) reported more values of narrow-sense heritability for the HSW (96%), DF (84%), No. S/p (78%) and No. P/p (74%). The narrow-sense heritability was the low for DF (20%) and DM (19%), these results were not enjoyable report for breeders that trying to create drought tolerance by early maturity in chickpea. Anbessa et al. (2006) found same results. The broad-sense heritability was found more than narrow-sense heritability for all traits, ranged from 48 to 94% (Tables 2 and 3). This indicated that both additive and non additive components of genetic variances were involved in governing the inheritance of almost all the quantitative traits in the chickpea, whereas dominance component appeared high in magnitude.

Tambal et al. (2000) reported that broad-sense heritability ranged from 11 to 87%, SY/p and PHT had the lowest heritability. Hence early generation selection could not efficacious for most characters in the chickpea. However, Joshi et al. (2004) reported that both additive (fixable) and non - additive (non - fixable) components of genetic variances were involved in governing the inheritance of almost all the quantitative and quality traits in wheat although additive genetic variance was predominant.

Graphical analysis

Graphical analysis of different traits for the chickpea diallel crosses were shown in Figure 1. Rows covariance regression on rows variance was made slope of equal one, on the other hand difference of between covariance and

variance for each row was changeless. The non significant deviation of slope (regression line) from one, when obtained that hadn't epistasis effects. On the base of graphical analysis, (W_r) regression line on (V_r) was crossed parabola in positive regions of (W_r) axis for the DF, DP and DM, BPHT, SS, HSW, Biomass, HI, No. P/p, No. SSP/p, PW/p, SY/p and STY/p, that indicated partial dominance for these characters. Biçer and Şakar (2008) reported similar findings. For the other traits such as PHT, PORT, No. PB, No. DSP/p, No. E P/p and No. S/p (W_r) regression line on (V_r) was crossed parabola in the negative regions of (W_r) axis that indicated over dominance for these traits (Figure 1).

The results of graphical analysis correspond with intercept of regression line (W_r , V_r) in Tables 2 and 3. Muhelbauer and Singh (1987) reported that the number of branches, the pods and seeds per plant showed over dominance. Also, Dhaiwal and Gill (1973) reported that the No. P/p and the seed yield exhibited positive over dominance, DF showed negative over dominance, but the HSW had no dominance. Parents dispersion in the ground of regression line (W_r , V_r) illustrated the proportion of dominance to recessive genes frequency, namely that the nearest parents to crossing of regression line with (W_r) axis had more dominant genes and most far parents had more percentage of recessive genes, therefore for the PORT, No. PB, No. P/p and the No. SSP/p, ILC 3279 cultivar; for the PHT, BPHT, HI, No. DSP/p and No. E P/p, ILC 588, ICCV2 and Arman cultivars; too, for the HSW, SS, PW/p, SY/p and No. S/p, ILC 5588 cultivar and about the DF, DP and DM, Hashem cultivar had least distance through origin (Figure 1).

According to mean differences of genotypes for evaluated traits, cultivars position in side of regression line (W_r , V_r) Figure 1, the value of the completely dominant or recessive parent and sign of correlation coefficient between parents average and (W_r+V_r) value, $R(YR, W_r+V_r)$ (Tables 2 and 3) could be inferring that amplifier genes were dominance for the DF, DP and DM, HSW, SS, HI, No. DSP/p, No. E P/p, No. S/p, PW/p and SY/p, but about PHT, BPHT, PORT, No. PB, No. P/p and No. SSP/p, reducer genes were dominance. That illustrated cross between these genotypes could be caused the product of better hybrids.

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