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Inheritance of Some Agronomic Characters in Pea

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ABSTRACT

This study was conducted by using Jinks-Hayman type analyses on four pea genotypes (PS4009, PS3053, PS3073 and Reyna) and their population of the complete diallel reciprocal crosses in order to examine the genetic structure. According to the results of all diallel crosses, environmental variance (E) and additive gene variance (D) was not significant. All the features of the dominant gene variances were higher than the additive gene variances (H_1) and $D-H_1$ value was found to be negative. In the population, dominant genes were found significant for all the characteristics except number of seed per pod. Result of W_r , V_r graphics indicated partial dominance for the number of seed per pod, and over dominance for the rest of the characters studied.

Keywords: Agronomic characters; Diallel; Inheritance; Pea

Bezelyede Bazı Agronomik Özelliklerin Kalıtımı

ESER BİLGİSİ

Araştırma Makalesi

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ÖZET

Bu araştırma, dört bezelye genotipi (PS4009, PS3053, PS3073 ve Reyna) ile bunların tam diallel melezlerinden oluşturulan populasyonun Jinks-Hayman tipi analiz kullanılarak genetik yapısını incelemek amacı ile yapılmıştır. Diallel melez sonuçlarına göre incelenen tüm özelliklerde çevre varyansı (E) ve eklemeli gen varyansı (D) önemsiz bulunmuştur. Tüm özelliklerinde dominant gen varyansları (H_1) eklemeli gen varyanslarından yüksek olup, buna paralel olarak $D-H_1$ değerleri ise negatif bulunmuştur. Populasyonda baklada tane sayısı üzerine resesif genler, bitki boyu, bakla sayısı, yüz tane ağırlığı, bakla verimi ve tane verimi özelliklerine ise dominant genlerin daha etkili olduğu tespit edilmiştir. W_r , V_r grafikleri sonucu baklada tane sayısı için kısmi dominantlık, incelenen diğer özelliklerde ise aşırı dominantlık saptanmıştır.

Anahtar Kelimeler: Agronomik özellikler; Diallel; Kalıtım; Bezelye

1. Introduction

Sources of proteins have undeniable importance in human nutrition. As a leguminous plant, peas are considered a good source of protein and contain 20-30% protein; sufficient carbohydrates; rich in calcium, iron, phosphorus and vitamins (Ceyhan et al 2011). Considering worldwide consumption, human nutrition were made of 22% vegetable proteins, 7% carbohydrates and animal nutrition of 38% proteins and 5% carbohydrates are derived from edible legumes (Sehirali 1988; Adak et al 2010). Thus, peas have a big importance on canned and frozen food industry as a human nutrition.

Success in developing varieties depends on range of variation and right selection from the variations. Pea breeders often make crosses to create new variations. But lack of labor, time, high costs etc. are limiting factors to make numerous crosses. That's why breeders need to choose accurate parental lines to avoid extra expenses and long working hours. Success rate could be higher if the genetic inheritance of parental lines would be identified earlier with different methods. Breeder needs to know effects of the genes on the agronomic characters of interests. Inheritance of genes governing the trait of interest determines the generation for selection in breeding a self-pollinated plant species like peas (Ceyhan & Avci 2004).

Various methods are used in determination of the genetic parameters. With the help of these genetic parameters, information is obtained about the status of the population, the value of a feature to breeding and the effectiveness of the selection. Diallel crossing is one of these methods (Ceyhan & Kahraman 2013). Seed yield and its genetic parameters and heritability were the subject of many researches (Snoad & Arthur 1974; Ceyhan et al 2008; 2014b; Ceyhan & Kahraman 2013).

In this work, a 4x4 complete diallel reciprocal combinations of parents and populations was studied by using Jinks-Hayman type analysis to identify and the genetic structure of agricultural features.

2. Material and Methods

In this study, three pure pea lines (PS4009, PS3053, PS3073) and Reyna a commercial variety were

used. The study was conducted at Selcuk University experimental field in 2012 and 2013. The parental lines were planted on 8 March 2012, followed by five consecutive plantings at 10 days intervals in order to coincide flowering times of the genotypes. For the ease of crossing, parental lines were planted in 3x1 m rows 25 cm apart. The four genotypes were crossed in a 4x4 complete diallel reciprocal according to Eser (1974) and Ceyhan (2003) in 2012.

Soil analysis was made from the soil that was taken from 0-30 cm depth. The results revealed that soil was a clay-loam, light alkaline (pH= 7.8), low in organic matter (1.20%), and has an EC ($\mu\text{S cm}^{-1}$) of 189, available P_2O_5 of 10.74 mg kg^{-1} , Fe of 1.28 mg kg^{-1} , and exchangeable K_2O of 219.96 mg kg^{-1} , Zn of 2.16 mg kg^{-1} , Cu of 0.82 mg kg^{-1} , Mn of 4.95 mg kg^{-1} , and Ca of 5863 mg kg^{-1} .

The study was conducted in Konya where summers are hot and dry and winters are cold. During the vegetation in 2013 for 5 months (March through July) average temperature was 19.5 °C, total rain 63.4 mm, humidity 39.7%.

Parental lines and crosses were planted by hand on March 2013 as three rows 2 m in length with a 50 cm row spacing and 20 cm plant spacing, each plot had 36 seeds which were planted 5 cm deep. Trials were made by "Randomized Block Design" in 3 replicates at Selcuk University Agricultural Department Trial Station. Plots were fertilized with 15 kg DAP (Diammonium phosphate 18-46%) at planting (Ceyhan 2003; Ceyhan et al 2014a). To reinforce the germination after the planting, sprinkle irrigation was used, and by drip irrigation system twice during growing period. Plots were hand-weeded and harvesting was made by hand between 03 and 14 July 2013.

At the parental lines and F_1 plants, plant height, number of pod, number of seed per pod, 100 seed weight, pod yield and seed yield were studied (Ceyhan 2003). Mean values were used to analyze the variation. In the study, the traits under the genetic control were analyzed by Jinks & Hayman (1953) diallel method. After detecting significant statistical differences between parents and among the crosses, validity of hypothesis was checked (Hayman 1954).

The parameters for genetic variation and regression analysis of W_r and V_r values of parents were made according to Jinks & Hayman (1953) and Hayman (1954) diallel analysis method. Statistical analysis was made by using TARPOGEN statistical package programme (Özcan & Açıkgöz 1999).

3. Results and Discussion

Analysis of variance results were shown in Table 1. To apply the Jinks-Hayman type analysis, the validity of the assumption was checked first. All the measurement made from 4x4 peas complete diallel reciprocal were found to be significant at $P=0.01$

Table 1- Mean sum of squares of the measurements

Çizelge 1- İncelenen özelliklere ait kareler ortalaması

Sources	SD	Plant height	Number of pod	Number of seed per pod	100 seed weight	Pod yield	Seed yield
Block	2	178.938	1.021	0.023	3.559	0.764	2.710
Genotype	15	357.950**	144.421**	0.728**	38.138**	78.894**	78.914**
Error	30	94.071	9.888	0.196	2.558	5.708	3.935

** $P<0.01$

Table 2- Sum of squares for W_r , V_r variances

Çizelge 2- İncelenen özelliklere ait W_r , V_r varyans analizi kareler ortalaması

Sources	SD	Plant height	Number of pod	Number of seed per pod	100 seed weight	Pod yield	Seed yield
Replication	2	4307.043	118.231	0.079	61.171	5.788	57.197
Series	3	8162.156	1368.434	0.138	219.802	151.596	174.993
Error	6	14365.334	155.353	0.062	95.980	105.576	71.583

W_r , V_r regression values detected with regression analysis and t values calculated for $b=1$ hypothesis are presented at Table 3. The average regression values and t values obtained from $b=1$ hypothesis showed that $b=1$ hypothesis is suitable.

3.1. Genetic structure of the population

Variance components estimated by Jinks-Hayman method and standard errors are shown in Table 4. In this research environmental variance and additive gene variance were found to be not significant. This result shows that selection would not be successful for the traits studied, similar

level. Results indicated the presence of large enough variation in order to proceed to advanced genetic analysis (Jinks & Hayman 1953; Hayman 1954; Jinks 1954; Ceyhan & Kahraman 2013).

To apply Jinks-Hayman type diallel analysis some of the assumptions have to be valid. Validation of these assumptions (Yıldırım et al 1979) was checked in 2 ways. The W_r , V_r variance analysis results are given in Table 2. The F values deduced from W_r - V_r variance analysis of F_1 populations was found not significant, indicating that W_r , V_r variation differences are uniform. Thus, means of the three replications were used to do genetic analysis.

Table 3- Regression values calculated from means (W_r , V_r) of the blocks and t values calculated for $b=1$ hypothesis

Çizelge 3- Bloklar üzerinden alınmış ortalama (W_r , V_r) değerleri arasındaki regresyon katsayıları ve $b=1$ hipotezi için hesaplanan t değerleri

Features	b	SH	t_i
Plant height	0.503	0.253	1.965
Number of pod	0.704	0.289	1.025
Number of seed per pod	0.449	0.193	2.853
100 seed weight	1.203	0.624	-0.325
Pod yield	0.769	0.351	0.658
Seed yield	0.978	0.666	0.034

Table 4- Variance components of the 4x4 complete diallel pea cross populations

Çizelge 4- 4x4 tam diallel bezelye melez populasyonlarında bazı agronomik özelliklerin genetik varyans komponentleri ve bunlar arasındaki oranlar

Genetic parameters	Plant height	Number of pod	Number of seed per pod	100 seed weight	Pod yield	Seed yield
E	33.13±55.33	3.11±22.65	0.06±0.23	0.87±9.08	1.80±7.54	1.29±8.10
D	19.07±123.71	49.64±50.65	0.33±0.51	42.12±20.30	18.00±16.86	7.97±18.11
F	5.18±317.82	40.58±130.13	-0.15±1.31	46.15±52.15	26.65±43.31	20.42±46.54
H ₁	620.63±359.61	207.69±147.25	1.11±1.48	53.84±59.01	117.07±49.01	122.26±52.65
H ₂	561.47±331.95	202.13±135.92	1.51±1.36	44.13±54.47	97.67±45.24	100.94±48.61
D-H ₁	-601.56±322.89	-158.06±132.21	-0.78±1.33	-11.72±52.99	-99.07±44.01	-114.29±47.28
(H ₁ /D) ^{1/2}	5.71	2.05	1.84	1.13	2.55	3.916
(H ₂ /4H ₁)	0.23	0.24	0.34	0.21	0.21	0.20
KD/KR	1.05	1.50	0.77	2.88	1.82	1.972
h ²	433.83±225.16	282.43±92.19	0.40±0.92	0.02±36.95	161.97±30.69	144.78±32.97
K	1.77	1.40	0.27	1.01	1.66	1.43
GH	0.52	0.70	0.39	0.77	0.75	0.78
DH	0.03	0.22	0.18	0.79	0.16	0.07

results were reported before (Sarawat et al 1994; Ceyhan & Kahraman 2013).

Of all the traits studied, dominant gene variances (H₁) was higher than the additive gene variances, and D-H₁ was negative (Table 4). Similar results were reported elsewhere (Snoad & Arthur 1974; Sarawat et al 1994; Girase & Deshmukh 2000; Ceyhan & Kahraman 2013).

F value that shows direction of recessive and dominant alleles was found to be positive except for the number of pod (Table 4). This indicates dominant and additive gene effects of alleles are together and in increasing direction (Yildirim et al 1979; Ceyhan & Kahraman 2013). Positive F value shows that dominant alleles outnumber the recessive alleles. For the number of seed per pod negative F value opposite effect of above mentioned condition (Yildirim et al 1979; Ceyhan & Kahraman 2013).

The average degree of dominance (H₁/D)^{1/2} indicates the degree of the domination in a population (Table 4). All the data collected in this study, (H₁/D)^{1/2} value was higher than 1 that may mean the population may have over dominance

(Snoad & Arthur 1974; Ceyhan et al 2008; 2014a; 2014b; Ceyhan & Kahraman 2013).

Dominant and recessive alleles (H₂/4H₁) showed similar frequencies for seed yield (0.20) and number of seed per pod (0.34) (Table 4). This may indicate that dominant and recessive alleles frequencies are close to each other (0.5), and multiplication of dominant and recessive alleles frequencies would be around 0.25, a high enough value for successful phenotypic selection (Ceyhan & Kahraman 2013).

Ratio of dominant alleles to recessive alleles (KD/KR) for number of seed per pod was lower than 1 (0.77), indicating number of recessive alleles outnumber dominant alleles (Table 4). For the remaining characters studied, KD/KR value was higher than 1, a strong indication that genes operating on these traits are dominant (Ceyhan & Kahraman 2013). Another factor that was examined in this research which, this means features manages. Therefore in research population, except pea count other features were more dominant than recessive genes.

For the effective number of genes (K), all the traits, except number of seed per pod, had K>1

values (Table 4). This may show that value of K depends largely on dominance. It was reported that K value is associated with dominance and K is underestimated in cases where there is weak dominant effect on traits (Jinks 1954; Yildirim 1974; Ceyhan & Kahraman 2013).

Narrow sense (DH) and broad sense heritabilities (GH) have also been evaluated (Table 4). Low DH values were evident on all traits but 100 seed weight, indicating a low response to selection. The DH for 100 seed weight was 0.79, which would be rather responsive to selection.

3.2. Analysis of W_r , V_r graphics

The W_r and V_r values of parents derived from the means of the 3 blocks are presented in Figure 1 to 6. The regression line for number of seed per pod cut through the W_r on positive side (above 0), indicating presence of a partial dominance for the trait. For all other traits studied, the regression line cut W_r on the negative region, showing over dominance are in effect. Ceyhan & Kahraman (2013) reported that hundred seed weight was under the control of partial dominant genes while seed yield, plant height, and number of pod were under control of over dominant genes.

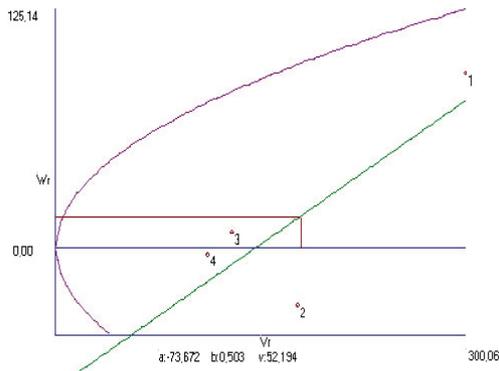


Figure 1- W_r , V_r values for the plant height of parents

Şekil 1- Bitki boyu için ebeveynlere ilişkin W_r , V_r değerleri

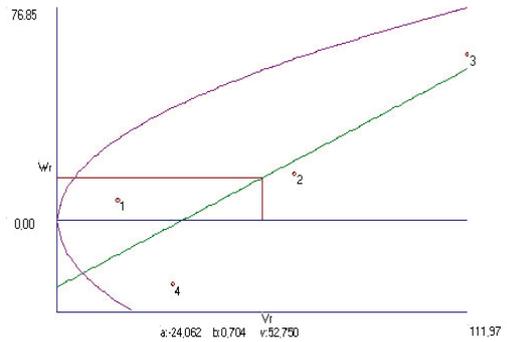


Figure 2- W_r , V_r values for the number of pod per plant of parents

Şekil 2- Bakla sayısı için ebeveynlere ilişkin W_r , V_r değerleri

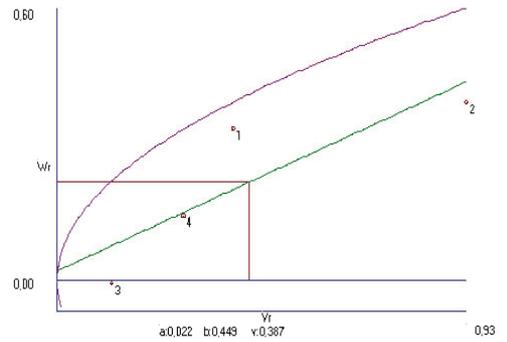


Figure 3- W_r , V_r values for number of seed per pod of parents

Şekil 3- Bakkada tane sayısı için ebeveynlere ilişkin W_r , V_r değerleri

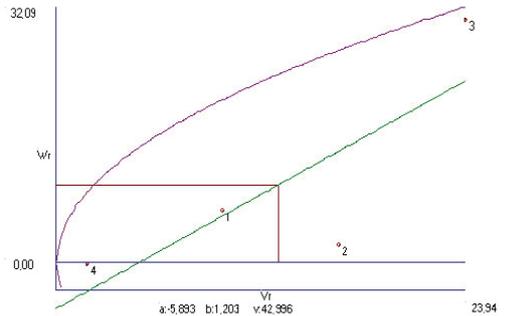


Figure 4- W_r , V_r values for hundred seed weight of parents

Şekil 4- Yüz tane ağırlığı için ebeveynlere ilişkin W_r , V_r değerleri

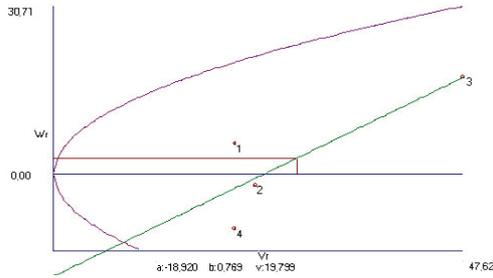


Figure 5- W_r , V_r values for pod yield of parents

Şekil 5- Bakla verimi için ebeveynlere ilişkin W_r , V_r değerleri

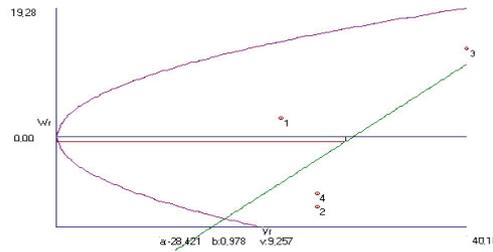


Figure 6- W_r , V_r values for the seed yield of parents

Şekil 6- Tane verimi için ebeveynlere ilişkin W_r , V_r değerleri

At the parental lines shortest plant height were 33.33 cm for PS4009 and PS3073 lines while tallest were Reyna with 46.33 cm. And the shortest hybrid was 42.33 cm (PS3053 x PS3073), and the tallest was 69.00 cm (PS4009 x PS3053) (Table 5).

In terms of plant height, there is no epistatic effect in parental genotypes PS4009, PS3073, and Reyna because they were close to the regression line, while PS3053 was far from regression line, indicative of an epistatic effect in action. Because PS4009 was far from the origin, it transfers recessive gene to crosses. A negative correlation ($r = -0.613$) was found between the hypothetical dominance ($W_r + V_r$) of parents and the average value of the ancestors.

When average number of pod of parents was examined, PS3073 parent had the lowest with 9.00 and Reyna the highest with 26.33. While the PS4009 x PS3053 cross had 21.67 the lowest, and Reyna x PS3053 cross 36.67 the highest (Table 5).

There is an epistatic effect for number of pod in PS4009 and Reyna. The crosses originating from parents with high pot numbers resulted with higher pod numbers. The correlation between hypothetical

Table 5- Agronomic values of the 4x4 full diallel pea cross populations

Çizelge 5- 4x4 tam diallel bezelye melez populasyonlarında bazı agronomik özelliklere ait değerler

Genotypes	Plant height	Number of pod	Number of seed per pod	100 seed weight	Pod yield	Seed yield
PS4009	33.33 ^d	19.33 ^{fg}	4.95 ^{ab}	14.49 ^{de}	14.51 ^c	12.55 ^c
PS3053	42.67 ^{cd}	17.00 ^g	5.45 ^a	16.55 ^{cd}	15.53 ^c	13.90 ^{de}
PS3073	33.33 ^d	9.00 ^h	5.00 ^{ab}	18.45 ^{bc}	13.52 ^c	11.74 ^e
Reyna	46.33 ^{bed}	26.33 ^{edef}	4.14 ^{bc}	28.97 ^a	22.70 ^{cd}	18.28 ^{ed}
Crosses						
PS4009 x PS3053	69.00 ^a	21.67 ^{efg}	4.98 ^{ab}	19.91 ^{bc}	20.91 ^d	19.48 ^c
PS4009 x PS3073	49.33 ^{abcd}	25.00 ^{def}	5.06 ^{ab}	18.66 ^{bc}	23.13 ^{bcd}	21.37 ^{bc}
PS4009 x Reyna	63.67 ^{abc}	27.67 ^{bcde}	4.12 ^{bc}	19.90 ^{bc}	23.14 ^{bcd}	20.65 ^{bc}
PS3053 x PS4009	65.00 ^{ab}	26.67 ^{cde}	4.47 ^{abc}	20.88 ^b	24.83 ^{bcd}	22.31 ^{bc}
PS3053 x PS3073	42.33 ^{cd}	28.67 ^{bcde}	4.19 ^{bc}	19.37 ^{bc}	23.56 ^{bcd}	21.06 ^{bc}
PS3053 x Reyna	43.67 ^{bed}	34.33 ^{ab}	3.51 ^c	12.21 ^c	20.95 ^d	13.14 ^e
PS3073 x PS4009	46.00 ^{bed}	28.33 ^{bcde}	4.58 ^{ab}	17.99 ^{bcd}	23.60 ^{bcd}	21.05 ^{bc}
PS3073 x PS3053	44.67 ^{bed}	30.67 ^{abcd}	4.26 ^{bc}	21.05 ^b	28.17 ^{ab}	24.89 ^b
PS3073 x Reyna	44.33 ^{bed}	29.67 ^{abcd}	4.35 ^{bc}	21.26 ^b	27.29 ^{abc}	24.95 ^b
Reyna x PS4009	51.67 ^{abcd}	27.33 ^{bcde}	4.48 ^{abc}	20.46 ^b	25.19 ^{bcd}	22.64 ^{bc}
Reyna x PS3053	64.00 ^{abc}	36.67 ^a	5.03 ^{ab}	17.90 ^{bcd}	32.65 ^a	29.88 ^a
Reyna x PS3073	54.67 ^{abcd}	33.33 ^{abc}	4.23 ^{bc}	19.33 ^{bc}	27.57 ^{abc}	24.59 ^b

dominance and mean values of parents was negative ($r = -0.947$). This shows that they carry the dominant genes of high pot number.

When number of seed per pod was examined, Reyna had 4.14 peas the lowest, and PS3053 had 5.45 peas the highest counts. The PS3053 x Reyna cross possessed 3.51 peas while PS4009 x PS3073 cross had 5.06 peas per pod (Table 5).

For the number of seed per pod, the parents PS4009 and PS3073 had epistatic effects. Analysis ($W_r + V_r$) indicated that the lower number of peas per pot was dominant in action ($r = 0.582$).

The 100 seed weight ranged from 14.49 g (PS4009) to 28.97 g (Reyna) where PS3053 x Reyna cross had the lowest 100 seed weight with 12.21 g and PS3073 x Reyna cross the highest with 21.26 g (Table 5). The lower hundred seed weight trait (i.e. smaller seed size) was found to be dominant ($r = 0.845$).

When approximate pod yield was examined, PS3073 parent and PS4009 x PS3053 cross had the lowest pod yields with 13.52 g and 22.91 g while Reyna parent and Reyna x PS3053 cross the highest with 22.70 g and 32.65 g, respectively (Table 5). Genetic analysis ($W_r + V_r$) showed that high pod yield was dominant ($r = -0.701$).

The seed yield of parents ranged from 11.74 g (PS3073) to 18.28 g (Reyna) and crosses from 13.14 g (PS3053 x Reyna) to 29.88 g (Reyna x PS3053) (Table 5). All of the parents except the PS4009 showed epistatic effect for seed yield. The parents with PS4009 and Reyna transferred dominant genes to the crosses while the parent with PS3073 transferred recessive gen. The negative correlation ($r = -0.633$) between the theoretical dominance ($W_r + V_r$) and means of the values in the population implied having dominant genes of the parents that are high yielded.

4. Conclusions

A large enough genetic variation exists for the traits studied in the population. It was concluded that recessive genes for number of seed per pod, and

dominant genes for plant height, number of pod, 100 seed weight, pod yield and seed yield are in action. The presence of high DH for hundred seed weight shows that genetic gains are possible at early generation selection for the trait.

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