DETERMINATION OF INHERITANCE OF SOME YIELD AND QUALITY TRAITS IN WINTER WHEAT (*TRITICUM AESTIVUM* L.)*

E. Aydogan, K. Yagdi
Uludag University, Agriculture Faculty, Department of Field Crops, Bursa, Turkey

ABSTRACT

This study was carried out in Uludag University Agriculture Faculty Research and Application Center between years of 2000-2002 to determine of inheritance of some yield and quality traits in winter wheat.

In this reseach,involving 6 x 6 diallel cross without reciprocals, seed number/spike, seed weight/spike, 1000 kernel weight, protein and gluten content were investigated over F1 plants and parents.

According to the results of diallel analysis,additive and dominance gene variances were found for gluten content, dominance variance was determined for seed number and weight per spike, 1000 kernel weight and protein content. In Wr-Vr graphs about parents,was observed partial domiance in gluten content and over dominance in the other traits.

Narrow and broad heritability sense ranged between in respect of 0.019-0.705 and 0.469 –0.961 in investigated traits. The highest heritability was determined in gluten content (0.705-0.961) and concluded that effective selections can be done in early generations.

Introduction

Wheat, is the most important crop, used in nourishment of human beings, with rice in the world (11). With high adaptation ability, wheat cultivated in the areas where production is difficult. This importance is mostly clarified in countries especially nourishment systems based on grains, like Turkey. In 2002, wheat was grown in 9.400.000 ha area and 20.000.000 ton products were obtained in Turkey. Increasing of seed yield is the first aim of the breeding studies in where the yield is rather low. On the other hand, planning of this studies by involving quality traits, provided to new cultivars sufficiency of this aspect. Crossing method is mostly used in breeding programmes. It is desired that the traits of these genotypes, wanted to improve by superior quality. Determination of inheritance of examining traits are important for breeding.

The methods of diallel analysis, used by Jinks-Hayman (4) is mostly used in the world for this aim. By this method, genetic parameters of agronomic characters can be determined and population analysis can be done between by estimation of these parameters. In this study, 4 cultivars and 2 experimental strains, belongs to genus of Triticum aestivum, were used as plant materials. The genetic structure of parents and F1 hybrids obtained from diallel crosses without resiprocals with these genotypes, were searched by diallel analysis method of Jinks-Hayman.

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At the end it is aimed to determine the genetic parameters and inheritance of some yield and quality traits in winter wheat.

Materials and Methods

This research was conducted at Uludag University Agriculture Faculty in Research and Application Center (Bursa) between the years of 2000-2002. Concerning the region, in production of 1999/2000 563.2 mm, 2000/2001 294.5 mm average precipitation is falled. Long-term average precipitation of the region is approximately 581.3 mm. The soil structure of the trial area was clay, marn and heavy texture. Organic material was insufficient in where usable phosphor and potassium were sufficient (7).

The cultivar of Gönen, Saraybosna ,Köksal-2000 and Atilla-12 (Martonvasari-12), the strains of 15-4 and 22-1 were used as plant genotypes. These genotypes attract attention by their adaptability and high yields in South Marmara province. In parents, especially Gönen is a variety of mostly sowed which is in decrease for quality traits by alternia sp. recently. The variety of Saraybosna and Atilla-12 are resistance to lodging, rust and mildew. Köksal-2000, 15-4 and 22-1 are high quality genotypes.

Hybrid seeds, obtained from 6 x 6 diallel cross,were sown in 1 m rows by 30 cm between rows and 7,5 cm between plants in randomized complete blocks design with three replications. Agronomic observations and measurings were carried out 10 plants per plot. Protein and gluten content were determined by the basis of 14 % moisture to American Association of Cereal Chemists (1). The statistical evalution was done according to Jinks- Hayman (4).

Results and Discussion

Determinated values of seed number/ spike, seed weight/spike, 1000 kernel weight, protein and gluten content are presented in **Table 1**. The result of the analysis of variance the significant differences among genotypes were found for all traits. Controls of hypothesis for application of datas to diallel analysis method, done in two ways. The first one, the value of F in row variance of seed weight/ spike, protein and gluten content were found significant ($P>=0.05$) by the result of variance analysis of Wr-Vr. Differences of regression coefficient, determined from every replications for the investigated traits, from 1 hypothesis was evaluated by t –test. By the result of this evaluation, hypothesis was proved to be valid for all traits. Thus, after the result of controlling of hypothesis, in 6 x 6 diallel cross population, genetic parameters searched for traits. These data were given in **Table 2.**

Seed Number per Spike

As it is presented in Table 2 dominance gene variance (H_1), (H_2) and the value of interaction of additive x dominance effect (F) were found significant statistically. The frequency of dominant and ressesif allels were found 0.23 which indicated equivalence of dominant and ressesif allels. Determination of the ratio of K_D/K_R as 1.00 supported this opinion. In population, narrow and broad heritability sense obtained 0.019 and 0.588, respectively. Being so low of narrow sense, suggested that additive gene effect was not playing an important role for this trait. Different results were reported by the study of determination of inheritance of seed number per spike. Malek and Borojevic (8), Senapati et.al. (15), Singh et.al. (18) and Sameena et.al. (14) were estimated additive gene effects. On the other hand, non-additive gene effects were found by Shahzad et.al. (17), Chowdhry et.al.(2), Rizwan and Khan (13). Karma (6) and Yaðdý and Ekingen (21) were estimated dominance gene effects for this trait. In population, the Wr-Vr graph of parents, regression line cross the Wr axis be-

TABLE 1

Means of the Seed Number/Spike, Seed Weight/Spike, 1000 Kernel Weight, Protein and Gluten Content

GENOTYPES	SEED NUMBER/ SPİKE		SEED WEIGHT/SPİKE (g)		1000 KERNEL WEIGHT (g)		PROTEİN CONTENT (%)		GLUTEN CONTENT (%)	
GONEN	41.3	DCEF	2.09	FGH	41.0	BCDEFG	12.13	J	23.23	L
S.BOSNA	44.0	BCDE	2.11	FGH	36.1	H	12.39	IJ	22.97	L
KOKSAL-2000	42.2	CDEF	2.24	DEFGH	41.7	BCDEF	13.27	EFGH	35.79	D
ATILLA-12	40.6	CDEF	2.19	DEFGH	42.3	BCDE	13.34	EFG	31.16	GH
15-4	32.6	EF	2.28	DEFGH	44.5	ABC	13.64	CDEF	37.93	AB
22-1	32.0	EF	1.44	I	47.6	A	12.68	HIJ	36.72	CD
Gönen x S.Bosna	68.6	A	2.30	DEFGH	36.2	H	13.62	DEF	31.70	FG
Gönen x K.2000	59.6	AB	3.50	A	40.2	CDEFGH	14.64	AB	27.41	K
Gönen x A-12	45.1	BCDE	1.84	HI	44.0	ABCD	14.26	BC	32.08	FG
Gönen x 15-4	36.0	DEF	2.50	BCDEF	37.1	FGH	14.21	BCD	30.58	HI
Gönen x 22-1	46.2	BCDE	2.90	B	36.9	GH	14.98	A	29.54	J
S.Bosna x K.2000	35.7	DEF	2.32	BCDEFG	26.3	J	13.68	CDEF	32.52	F
S.Bosna x A-12	56.0	ABC	2.66	BCDE	31.1	I	13.76	CDEF	36.31	CD
S.Bosna x 15-4	59.9	AB	2.33	CDEFGH	36.4	GH	13.24	FGH	30.10	IJ
S.Bosna x 22-1	52.6	ABC	2.46	BCDEFG	37.0	GH	13.89	CDE	31.70	FG
K.2000 x A-12	34.7	EF	2.04	FGH	37.9	EFGH	14.24	BCD	38.80	A
K.2000 x 15-4	44.7	BCDE	1.96	GHI	45.6	AB	13.69	CDEF	38.32	A
K.2000 x 22-1	27.6	F	2.43	BCDEFG	39.8	DEFGH	14.25	BC	37.18	BC
A-12 x 15-4	51.8	BCD	2.15	EFGH	42.1	BCDE	12.22	J	27.70	K
A-12 x 22-1	45.5	BCDE	2.71	BCD	38.1	EFGH	12.95	GHI	37.10	BC
LSD(%5)	16.2		0.52		4.7		0.62		0.94	

(Symbolizes of cultivars; A-12: Atilla-12, K-2000: Köksal-2000, S.bosna: Saraybosna)

TABLE 2

Genetic Parameters of Investigated Traits

Genetic Parameters	**Seed Number /Spike**	**Seed Weight /Spike**	**1000 Kernel Weight**	**Protein Content**	**Gluten Content**
D	10.46 ± 76.97	0.12 ± 0.30	12.81 ± 13.94	0.46 ± 0.93	46.05 ± 21.59*
H_1	468.19 ± 195.40 *****	1.12 ± 0.76	75.45 ± 35.39 *	3.60 ± 2.36	58.03 ± 54.81
H_2	431.17 ± 174.56 *****	0.94 ± 0.68	86.39 ± 31.61 *	2.96 ± 2.11	59.55 ± 48.96
F	0.16 ± 188.04 *****	0.29 ± 0.37	- 8.98 ± 34.05	0.97 ± 2.27	39.22 ± 52.75
H^2	138.03 ± 117.49	0.44 ± 0.46	47.83 ± 21.23	2.86 ± 1.42	7.84 ± 32.96
E	16.58 ± 29.09	0.03 ± 0.11	2.78 ± 5.27	0.05 ± 0.35	0.11 ± 8.16
D-H1	- 457.73 ± 171.36	- 1.05 ± 0.67	- 62.64 ± 31.03	- 3.14 ± 2.07	- 11.99 ± 48.07
$(H_1/D)^{1/2}$	6.69	3.17	2.43	2.79	1.12
$Uv=H_2/4H_1$	0.23	0.20	0.29	0.21	0.26
K_D/K_R	1.00	2.27	0.75	2.20	2.22
h^2/H_2	0.32	0.45	0.55	0.97	0.13
Narrow Sense	0.588	0.469	0.661	0.579	0.961
Broad Sense	0.019	0.103	0.118	0.141	0.705
Yr,Wr+Vr ,r	-0.33	-.0.73	0.19	-0.60	0.51

*,**: Significant at P:0.05 and P:0.01, respectively

low the point of origin that indicates over dominance (Figure 1a). The genotypes of Köksal-2000 (3) and Atilla-12 (4) were nearer to the origin, inherited dominant genes, 22-1(6), Saraybosna (2),15-4 (5) and Gönen (1) genotypes were found far from the origin and inherited ressesif genes to their hybrids.

Seed Weight per Spike

The parameters found nonsignificant by statistically. Being larger dominance gene effect (H_1) than the additive gene effect, positive F value and determinating the value of the ratio of K_D/K_R by 2.27, larger than 1.00, indicated the more impotant role of dominant genes on the seed weight per spike. In population narrow and broad heritability sense were found in respect of 0.103 and 0.468. So less of heritability, showed that selections in early generation for seed weight per spike which of the more important yield components, so low opportunity of success. The studies about this subject, dominance gene variance by Mou and Kronstad (9), additive gene variance by Singh et.al.(18) were reported significantly. Mou and Kronstad (9) found narrow sense 0.79, in spite of this, Yağdı and Ekingen (21) determinated as 0.27. According to Wr-Vr graph of parents, regression line cross the Wr axis below the the point of the origin (**Fig. 1b**). This result indicated over dominance for the seed weight/spike. Parent of Saraybosna (2) was nearer to the point of origin, inherited dominant genes to their hybrids and Köksal-2000 (3), 22-1 (6) and Gönen (6) inherited ressesif genes.

1000 Kernel Weight

The genetic parameters of dominance gene variance and (H_2) were found significant statistically. It is understood that dominance gene variance was playing important role in the inheritance of 1000 seed weight. In population narrow and broad heritability sense were found 0.118 and 0.661, respectively. This indicated that non–additive effects were important for this trait. Being searched the inheritance of 1000 kernel weight by various workers, different results were found. Malek and Borojevic (8), Taleei and Beigi (19), Shahzad et.al. (16), Rizwan and Khan (13), Sameena et.al. (14) undertaken the existence of additive gene variance. On the other hand, Prodonavic (12) and Wang et.al. (20) obtained dominance variance. As it is seen in Figure 1c, Wr-Vr graph about parents, regression line cross Wr axis below the point of origin indicating the existence of over dominance. Gönen (1) and Saraybosna (2) were nearer to the point of origin inherited dominant genes and Köksal –2000 (3) inherited ressesif genes to the hybrids.

Protein Content

For protein content, dominance gene variance (H_1) was larger than the additive gene variance and positive F parameter suggested that this trait was controlled by dominant genes. The degree of $(H_1/D)^{1/2}$ estimated by 2.79, larger than 1.00, showed the overdominance in population. Similiarly, the ratio of K_D/K_R by 2.20, supported this decision. Narrow and broad heritability sense was found in respect of 0.141 and 0.579 in population. Different results were determinated in the studies for this important quality criteria. Nikitento et.al. (10) reported that additive genes were playing important role for the genetic control of the protein content. The existence of dominant and epistatic gene effecst and importance of the dominance genes were reported by Kanbertay (5) and Huo et. al (3). Wr-Vr graph about parents for this trait was shown in Figure 1d. Regression line cross the Wr axis below the point of origin. This showed the effect of over dominance for the population. Examining of the parents about ranging of regression line, relative dominant genes by Köksal –2000 (3) and

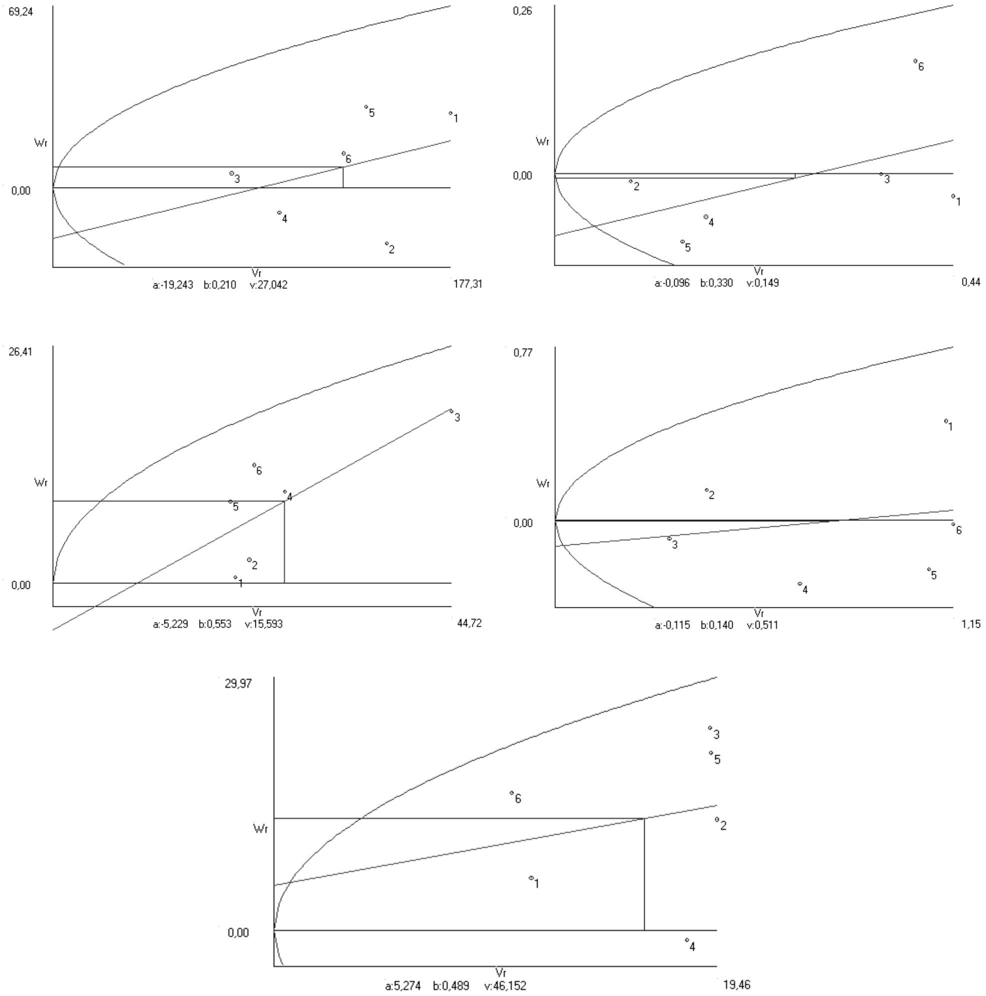

Fig. 1. Wr-Vr Graphs about Parents for Investigated Traits : a. Seed number/ spike; b.Seed weight/ spike; c. 1000 kernel weight; d. Protein Content; e. Gluten Content.

Saraybosna (2), ressesif genes by Gönen (1), 15-4 (5) and 22-1(6) were inherited to their hybrids.

Gluten Content

Being significant of additive genetic variance,suggested that this trait was controlled by additive gene effect, but dominance gene variance was larger than additive gene variance and by positive F parameter, showed the effects of dominant genes in population. With both determination, it is commented that gluten content showed additive and dominant inheritance. Narrow and broad heritability sense for gluten content were found 0.705 and 0.961, in respect. This high heritability indicated that effective selection can be done in early generations. Enough studies about the inheritance of gluten content can not be found. Inheritance of dominant genes and highest heritability was reported by Hou et.al. (3). In Wr-Vr graph, regression line cross Wr axis above the point of origin, indicated partial dominance in population. On the other hand this result was went against over dominance determinated by $(H_1/D)^{1/2}$. Being away from the origin it's seen that nearly all genotypes (especially Parents of 2,3,4,5) inherited ressesif genes to their hybrids.

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