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Genetic Analysis of Certain Quantitative Traits in The F_2 Generation of a 8 x 8 Diallel Durum Wheat Population

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Özet

8 x 8 Diallel Makarnalık Melez Buğday Populasyonu F_2 Generasyonunda Bazı Kantitatif Özelliklerin Genetik Analizi

Üçü tescilli (Edirne-1, Kunduru ve Rodur), ikisi ıslah hattı (97mbvd-11 ve 97mbvd-5) ve üçü de yerel (Akbaş, Sorgül ve Karakılçık) olan makarnalık buğday genotipleri 1997-98 yetiştirme sezonunda resiproksuz 8x8 diallel melez programı elde etmek amacıyla melezlenmişlerdir. Sekiz ebeveyn ile 28 F_1 dölü 1998-99 yetiştirme sezonunda yetiştirilmiş ve 1999-2000 yetiştirme sezonunda elde edilen F_2 verileri Hayman tipi diallel analiz ile analiz edilmiştir. Yapılan genetik analiz sonuçları uzun başaklanma tarihi ve yüksek tane veriminin additive gen etkisi altında bulunduğunu ve buna karşın yüksek protein içeriğinin ise dominant genler ile ilişkili olduğunu ortaya koymuştur.

Key words: F_2 Makarnalık buğday melezleri ve genetik analiz**.**

Introduction

Wheat breeder faces the problem of choosing parental combinations, which will ensure the greatest advancement in the trait studied. Improving quantitative traits such as grain yield and protein content in a durum wheat breeding program requires a specific breeding approach due to the physiological and genetic complexity of these traits. Therefore, the recognition of these traits and their parameters, which are mainly under polygenic control, involves the use of principles of quantitative inheritance which plays an important role in formulating approaches in breeding. Determining inheritance of these traits also allows the breeder to study and estimate yield and quality performances among a set of crosses.

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Exploitation of quantitative traits such as grain yield and protein content in durum wheat breeding has a limitation in terms of means of analysing quantitative inheritance to be meaningful to the wheat breeder. To achieve this goal, the diallel analyses developed by Hayman (4) and Jinks (5 and 6) have been widely used. Diallel analysis enables the wheat breeder to assess the merits of a set of crosses for a character under polygenic control. This analysis has been applied to evaluate the performances of parents and their crosses in barley and wheat breeding in terms of grain yield (1 and 2).

The objective of this study was to use the half diallel analysis to investigate the genetic basis of the certain quantitative traits including grain yield and protein content in a number of durum wheat cultivar x landrace crosses and to relate the findings to the actual breeding practice.

Materials and Methods

Eight parents including the three modern durum wheat cultivars (Edirne-1, Kunduru and Rodur), two breeding lines (97mbvd-11 and 97mbvd-5) and three landraces (Akbaş, Sorgül and Karakılçık) originated from Gürünlü, Süleymana and Lice villages in the south eastern part of Turkey were crossed by hand to have an 8x8 diallel crossing program without reciprocals in the 1997-98 growing season. The eight parents and their 28 F_1 progenies were grown at Bornova in the 1998-99 growing season. The seed of each entry was sown in single meter rows spaced 30 cm apart in order to have higher amount of F_2 seed. In the 1999-2000 growing season, the F_2 seed obtained were sown in a plot which consisted of two single one meter rows with one meter length row spaced 30 cm apart. Seed of 20 g was sown in each row. Days to heading (days) and grain yield (g/plot) were measured and protein contents were determined by using the “Near Infrared Reflectance Spectroscopy (NIR-S)” technique (8).

Data obtained from the 28 F_1 progenies and eight parents were analysed by the Jinks-Hayman type diallel analysis (4). Diallel analysis were performed by TarPopGen program developed by Özcan and Açıkgöz (7). The validity of assumptions for a diallel analysis was tested by the regression coefficient of Wr (Covariance) on Vr (Variance). The assumptions were valid for the traits measured.

Results and Discussion

Preliminary analysis of variance indicated that the block effects were not significant whereas there were statistically significant differences among the F_2 progenies for three traits measured (Table 1). These results pointed out that F_2 crosses differed in their mean performance for all the traits and enabled the diallel analysis to be carried out.

Table 1. Mean squares of the certain quantitative traits measured in the F_2 generation of 8x8 durum wheat crosses.

		Mean Squares		
S. V.	d.f.	Days to heading	Grain yield	Protein content
Block	1	231	3857	2.68
F_2 progenies	35	46**	32449**	7.22**
Error	35	2.9	2060	0.226

In the F_2 generation, the graphical analysis of the traits were shown in Figures. The Wr and Vr regression lines for all the traits were found to be significantly different from zero. For the days to heading, the regression line cut the Vr axis to the below of the origin indicating that there was moderately strong average overdominance in the crosses originated from these eight parents (Figure 1). Parents in that order 5 (Kunduru, 127 days) and 8 (Rodur, 127 days) having the highest days to heading can be considered to have recessive genes for this trait. Parents 1 (Akbaş, 121days), 3 (Karakılçık, 122 days) and 2 (Sorgül, 118 days) having similar heading dates in an increasing order had an excess of dominant genes for heading date. The parents such as 4 (Edirne-1, 125 days) and 6 (97mbvd-11, 124 days) having higher heading dates were most likely inherited as a recessive character. In similar way, parent 7 (97mbvd-5, 117 days) had high or moderately high days to heading. The Wr Vr regressions together with the Yr (Wr+Vr) correlations enable a generalized picture of the inheritance of quantitative traits to be obtained (3). Such information could be of use to the wheat breeder in the formulation of a breeding and selection program for the improvement of traits.

The standardized deviations of the Yr and (Wr +Vr) values for days to heading were plotted in Figure 2. The formula $(x_i\text{-}x)$ / s in which x is the parental mean and s is the standard deviation was used to derive the deviations. Yr, the parental measurement, is closely associated with the number of dominant homozygotes while the value of (Wr+Vr) is correlated with the number of recessive homozygotes

(3). A positive value of (Wr+Vr) indicates recessiveness and a negative value dominance. A positive value of Yr denotes a high value for the character and a negative value low expression. The correlation of Yr and (Wr+Vr) values for days to heading was not significant (r=0.26). This relationship indicated that there was a tendency of recessiveness to be associated low and dominance with high days to heading.

The Wr Vr regression line for grain yield closely passed through the origin indicating that this trait exhibited complete dominance averaged over the crosses of the 8x8 diallel (Figure 3). Parents 7 (97mbvd-5, 650 g), 1 (Akbaş, 345 g) and 4 (Edirne-1, 665 g) in decreasing order possessed an excess of dominant over recessive genes for grain yield. Parents 3 (Karakılçık) and 6 (97mbvd-11) had recessive and dominant genes in about equal proportions while 5 (Kunduru), 2 (Sorgül) and 8 (Rodur) in decreasing order had an excess of dominant over recessive genes for this trait.

The point on the graph corresponding to the parent 4 (Edirne-1) with the highest grain yield was on the upper extremity suggesting that high grain yield was genetically recessive to low expression (Figure 4). However, some dominant factors might also determine low expression since there was a lack of close correspondence of points on the graph with the order of parents for grain yield. The position of the Edirne-1, the parent with the highest grain yield lied at some distance from the point of intersection of the regression line with the limiting parabola. Hence, it seemed that there was a reasonable chance of improving grain yield within the range of crosses of the dialled.

The standartized deviations of Yr and (Wr+Vr) were graphically shown in Figure 4. The correlation coefficient between these two variables of (r = +0.44) was significant. This relationship suggested that high grain yield was associated with recessive genes and low grain yield with dominants.

The Wr Vr regression line for protein content for all the parents was shown in Figure 5. Parents, 7 (97mbvd-5), 2 (Sorgül), 4 (Edirne-1), 8 (Rodur) and 6 (97mbvd-11) in increasing order, possessed an excess of recessiveness over dominant genes. These parents had higher protein contents than parents 1 (Akbaş, 14 %) and 3 (Karakılçık, 14 %) which possessed, in increasing order, dominant genes (Figure 6). Therefore, there was an association of dominance with high protein content and conversely recessiveness with low protein content. This result was could not be confirmed since the correlation of Yr with (Wr+Vr) of r=-0.34 was not significant.

Based on the results of the study, it could be concluded that the exact limits of grain yield and protein content considered as highly important traits, obtainable from the 8x8 diallel set studied might not be determined. However, the results could help the breeder to proceed his breeding program more objectively towards end. If the results were interpreted generally, long days to heading and high grain yield would closely follow the laws of additive inheritance. This knowledge would help the breeder to breed these traits in terms of initial parent selection and subsequent crossbred selection and breeding procedure. Therefore, maximum genetic improvement for these characters in breeding would be expected from diverse parents of high expression of these traits.

Summary

Eight parents including three commercial durum wheat cultivars (Edirne-1, Kunduru and Rodur), two breeding lines (97mbvd-11 and 97mbvd-5) and three landraces (Akbaş, Sorgül and Karakılçık) were crossed by hand to have a 8x8 diallel crossing program without reciprocals in the 1997-98 growing season. The eight parents and 28 F_1 progenies were grown at Bornova in the 1998-99 growing season. In the 1999-2000 growing season, F_2 data were analyzed according to Hayman diallel analysis. The results of genetic analysis indicated that long heading date and high grain yield would be under the control of additive genes whereas high protein content could be correlated with dominant genes in the cross population studied.

Key words: F_2 Durum wheat crosses and genetic analysis.

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