

Inheritance of Some Yield Components Through F₃ and F₄ in Durum Wheat (*T. durum* Desf)

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ABSTRACT

This study aimed to assess the inheritance of some of important yield components such as ‘number of grain spike⁻¹ (NOGS⁻¹)’ and ‘grain weight spike⁻¹ (GWS⁻¹)’ through the segregating generations of F₃-F₄ in durum wheat. Field experiments were carried out in 2006/07 cropping season in Şanlıurfa - Turkey. P₁, P₂ and 6 F₃ and F₄ families derived from P₁ × P₂ were tested employing a randomized complete block design with 3 replications and 4 samplings in each plot. h²_n and h²_b were estimated through the methods of ‘components of variance’ and h²_n by ‘parents-offspring regression’. Results, obtained from components of variance revealed that h²_ns (=h²_b) were 11.37% and 35.13% for NOGS⁻¹ and GWS⁻¹ respectively in F₃. In F₄, h²_b estimates were 16.6% and 32.77% for above characteristics respectively. Parents-offspring regressions revealed that average narrow heritability estimates for NOGS⁻¹ were h²_{n (P1)} = 75.74%, h²_{n (P2)} = 64.02% and h²_{n (mid parent)} = 55.34% in F₃ and h²_{n (P1)} = 0%, h²_{n (P2)} = 38.09% and h²_{n (mid parent)} = 33.85% in F₄. Average narrow heritability estimates for GWS⁻¹ were 57.38% for the first parent, 51.41 % for the second parent and 86.64% for mid parental in F₃. They turned out to be 114.76%, 116.94% and 129.44% for mid parental in F₄ respectively. It was found that the reliability of h²_n estimates depend on the fulfillment of all assumptions accepted prior to analysis. It was concluded that narrow heritability estimates for GWS⁻¹ were higher than those of NOGS⁻¹ in both methods and generations. Selection can be practiced for GWS⁻¹ in F₃ and F₄ whereas, selection can also be practiced for NOGS⁻¹ with some reservations in segregating material in durum wheat..

Key words: durum wheat, grain weights, grain numbers, components of variance, covariance, inheritance

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Introduction

One correlation that has been observed widely in describing wheat yield is between number of grain and final yield (Savin and Slafer, 1991; Fischer, 1993; Sayre et al., 1997; Gonzalez et al., 2003a). Indeed, there are suggestions that the route to increasing wheat yields is to “breed for increased grain numbers” (Reynolds et al., 2004). The belief in grain number as a determinant of yield is bolstered by the observation, that grain number is correlated with conditions favoring growth during an interval that precedes flowering (Fischer, 1985; Demotes-Mainard and Jeuffroy, 2004).

An alternative view is that yield is a consequence of resource accumulation and use by a crop. Carbon and nitrogen are two likely candidates determining yield, and these in turn are dependent on other resources such as light and water. From this view, the availability and use of these resources are the fundamental determinants of yield and the number of grain are adjusted in the plant to match the resource-defined yield level (Sinclair and Jamieson, 2006).

All florets are initiated before spike emergence (Kirby, 1988; Sibony and Pinthus, 1988) and the fate of individual florets is fairly well defined at that point. Only florets that develop all floral organs by the time of spike emergence continue to develop any further (Langer and

Hanif, 1973; Sibony and Pinthus, 1988). The critical stage that a floret must reach to be a strong candidate for grain set is to have pollen and ovules fully formed by spike emergence (Langer and Hanif, 1973; Sibony and Pinthus, 1988). Florets that have not reached this stage of development commonly do not produce grains (Whingwiri and Stern, 1982).

Experiments carried out in Turkey (Genç *ve ark.* 1992, Özberk *ve Özberk* 1993, Korkut *ve ark.* 1993, Akkaya *ve ark.* 1996, Özberk *ve ark.* 2002, Özberk *ve Özberk* 2004) showed that the number of grain spike⁻¹ was highly related to final grain yield of wheat. Furthermore the result of experiments carried out in South-east Turkey (Özberk *ve Özberk* 1993, Akkaya *ve ark.* 1996, Özberk *ve ark.* 2002, Özberk *ve Özberk* 2004) revealed that the grain weight per spike was highly correlated with the final grain yield of wheat.

This study aimed to assess heritability estimates of both characteristics through F₃ and F₄ generations and help the durum wheat breeding programs.

Material and Methods

Field experiments were carried out in 2006/07 cropping season in Şanlıurfa - Turkey. P₁, P₂ and 6 F₃ and F₄ families derived from P₁ x P₂ were tested employing a randomized complete block design with 3 replications and 4 samplings in each plot. Narrow (h^2_n) and broad heritability (h^2_b) were estimated through the methods of ‘components of variance’ and ‘parents-offspring regression’.

Experimental material was planted in to the temporarily beds. Plot size was 3 m x 2 rows (1.2 m²) and 20 cm row space at top of the beds. 4 sampling were practiced in each plot. A base fertilization of 6 kg da⁻¹ pure nitrogen and 6 kg da⁻¹ pure phosphorus in the form of 20.20.0 was applied at sowing. In late joining and early shooting stage in spring, 6 kg da⁻¹ pure nitrogen in the form of Ammonium Nitrate (33%) was applied. Material was irrigated only once in dough stage. Chemical control for broad and narrow leaf weeds was practiced in the experiment.

Heritability estimates utilizing from components of variance (Comstock and Moll, 1963; Yıldırım et al. 1979, Table 2) were preformed. After estimating σ^2_b and σ^2_w values for both parents and offspring, Environmental variation was calculated employing following equations; $[V(E)=\sigma^2_{w(\text{parent})} + \sigma^2_{b(\text{parent})} + \sigma^2_r + \sigma^2_c]$. Then, dominance variance “V(H)”, additive variance “V(D)”, were determined through the equations $\sigma^2_{w(\text{offspring})} - \sigma^2_{w(\text{parent})} = 1/2V(D) + 1/2 V(H)$, $\sigma^2_{b(\text{offspring})} - \sigma^2_{w(\text{parent})} = 1/2V(D) + 1/4 V(H)$. Genotypic variance $[V(G)=V(D)+V(H)]$ and phenotypic variance $[V(P)=V(G)+V(E)]$ were then calculated. The

broad sense heritability was estimated through the equation of $h^2_b = V(G)/V(P)$. The narrow sense heritability was estimated through the equation of $h^2_n = V(D)/V(P)$. Only broad sense heritability in the F_4 generation was calculated utilizing from the mean squares under the presence of only one year and one location data. σ^2_b ve σ^2_e were estimated initially. Then, phenotypic variance (σ^2_f) was estimated through the sum of σ^2_b with σ^2_e . Finally, the broad sense heritability was estimated through the equation of $h^2_b = \sigma^2_b / \sigma^2_p$.

Analyses of covariance (Yıldırım et al., 1979) between maternal, paternal and mid- parent versus offspring in both F_3 and F_4 generation were performed to estimate narrow sense heritability for both characteristics. Then, h^2_n values were estimated through the equations of $h^2_n = b = 2[\text{Cov}(y*x_1)]$ for maternal, $h^2_n = b = 2[\text{Cov}(y*x_2)]$ for paternal and $h^2_n = b = 2[\text{Cov}(y*x)]$ for mid- parent. Family base estimated h^2_n values were averaged for above three methods. Standard deviations for h^2_n estimates were calculated through the equation as follows; Std. dev = $\sqrt{V(b)} = \sqrt{1/(n-2)[V(y)/V(x) - b^2]}$. Family base standard deviations were averaged for these three methods employed for heritability estimates.

Statistical analysis of data was performed by using TARIST statistical software (Açıköz et al., 1994) and MS EXCEL.

Table 2. Sources of variation, degree of freedom, mean and expected mean squares in randomized complete block design with sampling error

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	r-1	MS1	$\sigma^2_w + s \sigma^2_e + st \sigma^2_r$
Family	t-1	MS2	$\sigma^2_w + s \sigma^2_e + sr \sigma^2_b$
Block*Family	(r-1)(t-1)	MS3	$\sigma^2_w + s \sigma^2_e$
Error	rt(s-1)	MS4	σ^2_w
Total	(rts)-1		

r: replication, t: family, s: number of sampling

Results and Discussions

Estimates of heritability through components of variance

ANOVA's of parent and F_3 and F_4 families for number of grain spike⁻¹ were given in Table 3, 4 and 5 respectively.

Table 3. Analysis of variances for grain numbers spike⁻¹ of parents in F_3 and F_4 generations

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	60.500	$\sigma^2_w + 4 \sigma^2_e + 8 \sigma^2_r$
Family	1	22.042	$\sigma^2_w + 4 \sigma^2_e + 12 \sigma^2_b$
Block*Family	2	61.167	$\sigma^2_w + 4 \sigma^2_e$
Error	18	42.125	σ^2_w
Total	23	44.505	

Table 4 Analysis of variances for grain numbers spike⁻¹ of F₃ families

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	60.847	$\sigma_w^2 + 4\sigma_e^2 + 24\sigma_r^2$
Family	5	210.547	$\sigma_w^2 + 4\sigma_e^2 + 12\sigma_b^2$
Block*Family	10	66.914	$\sigma_w^2 + 4\sigma_e^2$
Error	54	45.810	σ_w^2
Total	71	60.807	

Table 5. Analysis of variance for number of grain spike⁻¹ of F₄ families

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	15.542	$\sigma_w^2 + 4\sigma_e^2 + 24\sigma_r^2$
Family	5	162.225	$\sigma_w^2 + 4\sigma_e^2 + 12\sigma_b^2$
Block*Family	10	51.542	$\sigma_w^2 + 4\sigma_e^2$
Error	54	46.171	σ_w^2
Total	71	54.238	

Following components of variance were calculated for number of grain spike⁻¹ in F₃ generation; $\sigma_{w(\text{offspring F}_3)}^2$ was 45.81, $\sigma_{b(\text{offspring F}_3)}^2$ was 11.96, $\sigma_{w(\text{parent})}^2$ is 42.12, $\sigma_{b(\text{parent})}^2$ is 0 and narrow sense heritability of number of grain spike⁻¹ was 11.37 % and broad sense heritability for given characteristic was the same as narrow heritability (11.37 %).

In F₄ generation; $\sigma_{w(\text{offspring F}_3)}^2$ was 46.17, $\sigma_{w(\text{parent})}^2$ was 42.12, σ_g^2 was 9.22 and broad sense heritability for number of grain spike⁻¹ was 16.6 %.

Table 5. Analysis of variance for grain weights r spike⁻¹ of parents

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	0.032	$\sigma_w^2 + 4\sigma_e^2 + 8\sigma_r^2$
Family	1	0.093	$\sigma_w^2 + 4\sigma_e^2 + 12\sigma_b^2$
Block*Family	2	0.032	$\sigma_w^2 + 4\sigma_e^2$
Error	18	0.085	σ_w^2
Total	23	0.076	

Table 6. Results of variance analysis for grain weights per spike of F₃ families

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	0.264	$\sigma_w^2 + 4\sigma_e^2 + 24\sigma_r^2$
Family	5	0.220	$\sigma_w^2 + 4\sigma_e^2 + 12\sigma_b^2$
Block*Family	10	0.176	$\sigma_w^2 + 4\sigma_e^2$
Error	54	0.145	σ_w^2
Total	71	0.158	

Table 7. Results of variance analysis for grain weights per spike of F₄ families

Sources of variation	Degree of freedom	Mean squares	Expected mean squares
Block	2	0.131	$\sigma_w^2 + 4\sigma_e^2 + 24\sigma_r^2$
Family	5	0.590	$\sigma_w^2 + 4\sigma_e^2 + 12\sigma_b^2$
Block*Family	10	0.131	$\sigma_w^2 + 4\sigma_e^2$
Error	54	0.113	σ_w^2
Total	71	0.149	

Following components of variance were calculated for grain weight spike⁻¹ in F₃ generation; $\sigma_{w(\text{offspring F}_3)}^2$ was 0.131, $\sigma_{b(\text{offspring F}_3)}^2$ was 0.114, $\sigma_{w(\text{parent})}^2$ was 0.085, $\sigma_{b(\text{parent})}^2$ was

0.005 and narrow sense heritability for grain weight spike⁻¹ was 35.13 % and broad sense heritability was the same as narrow heritability (35.13 %).

In F₄ generation; $\sigma^2_{w(\text{offspring } F_3)}$ was 0.145, $\sigma^2_{w(\text{parent})}$ was 0.085, σ^2_g was 0.0156 and broad sense heritability for grain weight spike⁻¹ was 32.77 %.

Estimates of narrow sense heritability through analysis of covariance

The h²n estimates for number of grain spike⁻¹ and grain weight spike⁻¹ through b values of parents-offspring regression obtained from analysis of covariance are given in table 8 and 9.

Table 8. h²n estimates of number of grain spike⁻¹ with b values of parents-offspring regression obtained from analysis of covariance

Families	h ² n for F ₃ (%) b=2[Cov(y*x ₁)]	h ² n for F ₃ (%) b=2[Cov(y*x ₂)]	h ² n for F ₃ (%) b=2[Cov(y*x _{mid})]	h ² n for F ₄ (%) b=2[Cov(y*x ₁)]	h ² n for F ₄ (%) b=2[Cov(y*x ₂)]	h ² n for F ₄ (%) b=2[Cov(y*x _{mid})]
1	78.16	0.0	84.36	0.0	41.21	0.0
2	0.0	58.22	20.14	0.0	75.80	32.11
3	0.0	0.0	0.0	0.0	7.37	0.0
4	0.0	61.44	57.10	0.0	36.86	35.59
5	0.0	72.40	13.18	0.0	27.22	0.0
6	73.33	0.0	101.93	0.0	40.08	0.0
Means	75.74±21.74	64.02±35.48	55.34±50.94	0.0	38.09±36.96	33.85±55.67

y: offspring, x₁: first parent, x₂: second parent, x_{mid}: mid parent

Covariance turned out to be negative for some families in F₃ and F₄ generations. H²n for NOGS⁻¹ could not be estimated for those families. In general, narrow sense heritability estimates (h²n) for number of grain spike⁻¹ were found to be higher in F₃ than those of F₄. Average standard deviations for average h²n's were also high in both generations.

Table 9. h²n estimates of grain weight spike⁻¹ with b values of parents-offspring regression obtained from analysis of covariance

Families	h ² n for F ₃ (%) b=2[Cov(y*x ₁)]	h ² n for F ₃ (%) b=2[Cov(y*x ₂)]	h ² n for F ₃ (%) b=2[Cov(y*x _{mid})]	h ² n for F ₄ (%) b=2[Cov(y*x ₁)]	h ² n for F ₄ (%) b=2[Cov(y*x ₂)]	h ² n for F ₄ (%) b=2[Cov(y*x _{mid})]
1	28.74	0.0	0.0	23.86	109.10	144.24
2	0.0	109.37	0.0	213.54	0.0	50.75
3	28.44	0.0	0.0	64.74	0.0	0.0
4	0.0	2.63	2.73	46.50	87.58	125.19
5	35.19	42.24	168.85	225.16	153.99	269.53
6	137.17	0.0	88.35	0.0	117.10	57.49
Means	57.38±37.17	51.41±37.43	86.64±77.54	114.76±87.91	116.94±51.03	129.44±77.86

y: offspring, x₁: first parent, x₂: second parent, x_{mid}: mid parent

Covariance also turned out to be negative for some families and narrow sense heritability could not be estimated for those families. Some of h²n values were found to be

over 100%. Narrow sense heritability estimates were higher in F₄ generation than those of F₃. Standard deviations of heritability estimates were found to be high in both generations.

In general, heritability estimates for number of grain spike⁻¹ through components of variance were quite low for selection in F₃ and F₄ generations. Delay selection is strongly recommended for this characteristic. But the narrow heritability estimates for grain weight per spike⁻¹ through components of variance were partially adequate for selection in those generations.

Parental and mid parent base narrow sense heritability estimates could not be performed due to the presence of negative covariance values for some families. H^2_n values for those families were considered as zero. Narrow sense heritability estimates for number of grain spike⁻¹ through b values of parents-offspring regression in F₃ were higher than those of F₄. The reverse situation might be expected. It was expected that increasing additive effect of mentioned characteristic might result in higher h^2_n value in F₄. This might be due to the presence of some experimental mistakes. It was found that selection can be practiced for this characteristic in F₃. Narrow sense heritability estimates for grain weight spike⁻¹ through b values of parents-offspring regression in both generations (F₃ and F₄) were adequate for selection in early generations giving higher values in latter generation. Selection for grain weight spike⁻¹ can be practiced in F₃ and F₄ generations.

Reliability of h^2_n estimates depend on the fulfillment of all assumptions accepted prior to testing. Experimental design, plot size, number of sampling, plant density, number of replication, genotype x environment interactions are major factors influencing the reliability of heritability estimates. (Yıldırım et al., 1979). One year -one location experiments such as we utilized in components of variance method results in poor estimations for phenotypic variance and heritability respectively. Standard deviation of heritability estimates must be small for more reliability. Falconer (1960) pointed out that parent offspring regression method gave smaller std. deviations contrary to our research findings for heritability estimates. Gilbert (1973) further observed that parent offspring regression method was the more appropriate way to estimate narrow heritability than components of variance method. Some heritability estimates in parent offspring method turned out to be higher than 1 (or 100%). This is weakness of this method. But it can be solved by appropriate transformation prior to analysis.

Conclusion

Heritability estimates might vary due to the method to be employed. Lesser standard deviations of heritability estimates increase the reliability. Narrow heritability estimates for number of grain spike⁻¹ (NOGS⁻¹) in both methods and generations were found to be lower than those of grain weight spike⁻¹ (GWS⁻¹)

It was concluded that selection for GWS⁻¹ can be practiced in F3 and F4 generations whereas, selection can also be practiced for NOGS⁻¹ in same generations with some reservations.

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