The Interrelationships of Agronomic Characters in a Doubled Haploid Population of Wheat

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Abstract: A doubled haploid (DH) population consisting of 157 lines derived from a cross between Fukuho-kumogi and Oligoculm was evaluated for agronomic characters in this study. Highly significant differences were detected among DH lines for all of the characters investigated, including grain yield and its components. Estimation of phenotypic and genetic coefficients of variation indicated that peduncle length, spikes/m^2, plant height, grains/spike and grain weight/spike had higher variation than the other characters. The narrow sense heritability ranged from 63% for grain yield to 99% for plant height. Grain yield correlated positively with each of biological yield, spikes/m^2, harvest index and grain weight/spike. There was no correlation between grain yield and heading date or maturity. Based on regression analysis, the most important components for grain yield were recognized as grain weight/spike, spikes/m^2 and spikletes/spike, which contributed to 64.2%, 28.4% and 0.5% of its variation, respectively. Path analysis revealed that grains/spike had the largest direct and positive effect on grain yield. The lowest direct and positive effect on grain yield was found for 1000-grain weight. The largest indirect and negative effect on grain yield was related to spikes/m^2 via grains/spike. These results implies that grain yield of this population can be improved by improvement of the spikes/m^2 and grains/spike.

Keywords: doubled haploid; genetic variation; heritability; path-analysis; yield components; bread wheat

Bread wheat (*Triticum aestivum* L.) is the most widely cultivated and important food crop in the world. The development of high yielding wheat cultivars is the major objective of breeding programs. The genetic variation for the trait under selection and a higher heritability are necessary to have response to selection (Falconer & Mackay 1996).

Knowledge of the genetic association between grain yield and its components can help the breeders to improve the efficiency of selection. Therefore, it is important to study the relationships among the characters and to find their direct and/or indirect effects on grain yield. Although the relationship between yield and other agronomic characters in wheat has been studied by a number of workers (Singh & Stoskpof 1971; Ehdaie & Waines 1989; Moghaddam *et al.* 1997), it is not fully understood (Campbell *et al.* 2003). In the studies conducted by Bhatt (1973), Jaimini *et al.* (1974), and Sinha and Sharma (1979), grain yield was positively correlated with number of heads per plant, number of grains per head and grain weight. The positive direct effects of number of heads per plant, number of grains per head, grain weight and harvest index on grain yield has been reported in wheat (Ehdaie & Waines 1989).

The objective of this work was to investigate the genetic variation, estimate the heritabilities, and study the relationships among the characters, including grain yield and its components, in a wheat DH population.

MATERIALS AND METHODS

A DH population of bread wheat (157 lines), which was developed from a cross between a Japanese wheat cultivar Fukuho-komugi and a breeding line Oligoculm (Atsmon & Jacobs 1977) with their parents were evaluated in this study. The DH lines were produced by wheat × maize crosses (Suenaga 1991). The Fukuho-komugi had a normal spike size and spike number, while the Oligoculm showed extremely large spikes with restricted spike number (Atsmon & Jacobs 1977). The experiment was carried out in 2003, at the Isfahan University of Technology Research Farm, using a randomized complete block design with three replications. Each experimental unit consisted of four rows, each 2m long and with 20 cm between rows. The data for heading date (HD), spike length (SL), spikelets/spike (S/S), spikelet compactness (SC), plant height (PH), peduncle length (PL), maturity (M), spikes/m^2 (S/m^2), biological yield/m^2 (BY), grain yield/m^2 (GY), grain weight/spike (GW/S), grains/spike (G/S), 1000-grain weight (TGW) and harvest index (HI) were recorded for each experimental unit.

The variance components, phenotypic and genetic coefficient of variation (PCV and GCV) were computed as suggested by Burton and DeVane (1953). Genetic correlation coefficients were estimated based on the formula of Miller *et al.* (1958), using the genetic variance and covariance components. Since, the genetic variances among DH lines consists of $2\sigma^2_A$ (additive variance), the estimated heritabilities were considered as narrow-sense (Halluer & Miranda 1998). Stepwise regression analysis (Montgomery & Peck 1992) was used to find the important characters contributing to grain yield variation. Path coefficients analysis (Dewey & Lu 1959) using genetic correlation coefficient was performed to determine the direct and indirect effects of grain yield components on grain yield.

RESULTS

Highly significant differences were observed among the genotypes for all the characters, indicating that there was genetic variation for these characters (Table 1). The genetic coefficient of variation (GCV) was high for peduncle length, plant

Table 1. Phenotypic (PCV) and genetic coefficient of variation (GCV), components of variance, coefficient of variation (CV) and narrow-sense heritability (H_n%) of the characters

Character	Mean squares of genotypes	Estimates of variance components[a]			Mean	CV (%)	PCV (%)	GCV (%)	H_n (%)
		σ^2_{ph}	σ^2_g	σ_e^2/r					
Heading date (days)	80.1**	26.6	25.4	1.2	148.9	3.47	3.4	3.3	95
Maturity (days)	22.49**	7.4	5.7	1.7	198.1	1.38	1.3	1.2	77
Plant height (cm)	977.1**	324.9	322.0	2.9	86.54	20.85	20.8	20.7	99
Peduncle length (cm)	201.3**	67.0	65.6	1.4	35.93	22.80	22.8	22.5	97
Spike length (cm)	13.9**	4.56	4.1	0.46	17.67	12.19	12.2	11.5	89
Spikletes/spike	6.6**	2.28	1.9	0.29	19.30	7.70	7.7	7.1	83
Spiklete compactness	0.06**	0.011	0.01	0.001	1.11	13.9	9.4	9.0	90
Spikes/m^2	52 210**	19 735	13 541	6 194	702.8	19.99	20.3	19.9	68
Grains/spike	499**	149.5	138.7	10.8	61.7	19.82	19.8	19.1	92
Grain weight/spike (g)	0.66**	0.22	0.19	0.02	2.40	19.59	19.6	18.4	86
Biological yield/m^2 (g)	36 855**	122 842	81 572	41 277	2 114.7	16.57	16.5	13.5	66
Grain yield/m^2 (g)	72 427**	24 142	15 449	8 693	907.2	17.13	17.1	13.7	63
Harvest index (%)	0.007*	0.0023	0.002	0.0003	0.43	17.13	11.8	10.4	86

[a]σ^2_{ph}, σ^2_g and σ_e^2 indicate the phenotypic, genetic and error variance, respectively

Table 2. Genetic correlation coefficients among the characters of heading date (HD), maturity (M), plant height (PH), peduncle length (PL), spike length (SL), spikletes/spike (S/S) , spikelet compactness (SC), spikes/m^2 (S/m^2) , grains/spike (G/S), 1000-grain weight (TGW), grain weight/spike(GW/S), biological yield/m^2 (BY), grain yield/m^2 (GY) and harvest index (HI)

Character	HD	M	PH	PL	SL	S/S	SC	S/m^2	G/S	TGW	GW/S	BY	GY	HI
HD	1.00	0.79	0.08	0.03	0.63	0.44	–0.31	–0.37	0.49	–0.56	0.23	0.13	–0.12	–0.37
M		1.00	–0.22	–0.26	0.46	0.42	–0.17	–0.34	0.61	–0.58	0.30	0.05	–0.04	–0.15
PH			1.00	0.96	0.33	–0.35	–0.52	0.21	–0.35	0.29	–0.15	0.53	0.08	–0.65
PL				1.00	0.28	–0.35	–0.47	0.20	–0.36	0.29	–0.16	0.46	0.04	–0.63
SL					1.00	0.21	–0.85	–0.23	0.35	–0.32	0.26	0.42	0.06	–0.53
S/S						1.00	0.39	–0.35	0.65	–0.56	0.33	–0.06	0.05	0.14
SC							1.00	0.02	0.04	–0.03	–0.05	–0.44	–0.02	0.61
S/m^2								1.00	–0.65	0.07	–0.71	0.41	0.40	0.01
G/S									1.00	–0.51	0.77	0.01	0.20	0.27
TGW										1.00	0.12	0.18	0.18	0.18
GW/S											1.00	0.14	0.33	0.27
BY												1.00	0.75	–0.29
GY													1.00	0.39
HI														1.00

height, spike/m^2, grains/spike, grain weight/spike and grain yield and it was moderate for spike length, biological yield, grain yield, grain weight and harvest index (Table 1). However, the heading date and maturity had the lowest GCV among the genotypes. The narrow-sense heritability ranged from 63% for grain yield to 99% for plant height (Table 1). High heritabilities were estimated for all the characters, except for maturity, spikes/m^2 and both biological and grain yield which had relatively moderate heritabilities (Table 1).

The heading date and maturity were positively and highly correlated. Maturity had relatively high and positive correlation with grains/spike and moderately correlated with spikelets/spike and spike length (Table 2). No considerable genetic correlation was observed between maturity and each of grain yield, harvest index and biological yield. However, the genetic correlation between maturity and 1000-grain weight was moderate and negative. Plant height showed positive correlation with biological yield, but it was negatively correlated with harvest index and spiklete compactness. Grain yield was positively correlated with biological yield, spikes/m^2, harvest index and grain weight/spike. Grains/spike had positive correlation with grain weight/spike, spikletes/spike, spike length, heading date and maturity. The results of regression analysis for grain yield as dependent variable and other characters as independent variables were presented in Table 3. Based on the partial coefficients of determination (R^2), spikes/m^2 and grain weight/spike contributed approximately 28.4% and 64.2% in grain yield variation, respectively. However, spikletes/spike had the lowest, but significant contribution in grain yield variation.

The path analysis showed that grains/spike, spikes/m^2 and 1000-grain weight had positive

Table 3. Results of regression analysis for grain yield as dependent variable

Independent variable	Coefficient	Partial R^2	Model R^2	Prob. > F
Spikes/m^2	1.344	0.2840	0.2841	0.0001
Grain weight/spike	339.056	0.6420	0.9260	0.0001
Spikletes/spike	8.484	0.0058	0.9318	0.0004

Table 4. Direct and indirect effects of yield components on grain yield via grain/spike, spike/m^2 and 1000-grain weight

Character	Direct effect	Indirect effect			Genetic correlation
		grains/spike	sipkes/m^2	1000-grain weight	
Grains/spike	1.333	–	–0.727	–0.397	0.20
Sipkes/m^2	1.172	–0.827	–	0.054	0.40
1000 grain weight	0.778	–0.681	0.082	–	0.18

direct effects on grain yield (Table 4). Large direct effects on grain yield were observed for grains/spike (1.333) and spikes/m^2 (1.172). However, 1000-grain weight had the lowest direct effect on grain yield. Although grains/spike had the largest and positive direct effect on grain yield, but it showed large and negative indirect effects via spikes/m^2 and 1000-grain weight resulted in a low genetic correlation between this charter and grain yield. Spikes/m^2 had negative indirect effect on grain yield only via the grains/spike and it showed higher genetic correlation with grain yield than the spikes/m^2 and 1000-grain weight. Positive direct effect of 1000-grain weight on grain yield was cancelled by its negative indirect effects via grains/spike, resulted in having a very low genetic correlation with grain yield.

DISCUSSION

Phenotypic and genetic coefficients of variation showed that there was high genetic variation among the DH lines for all of the characters, except for maturity and heading date. The existing genetic variation indicates that the population has high genetic potential for improvement of the characters by selection programs. Selection efficiency for a character is dependent on the magnitude of its heritability and genetic variation (Falconer & Mackay 1996). High heritabilities for most of the characters in this study indicate that they can be successfully improved by selection. The lowest heritability for grain yield in this study was in agreement with the results of the others (Sidwell *et al.* 1976; Ehdaie & Waines 1989; Belay *et al.* 1993; Moghaddam *et al.* 1997). The lower heritability for grain yield than the yield components and also the existing positive genetic correlation between this character and its components suggest that selection based upon the yield components may be more effective to improve grain yield. The results of this study showed that grains/spike and spikes/m^2 had more contribution in grain yield variation and they can be considered as selection indices for grain yield improvement. No considerable association between grain yield and each of plant height, maturity and heading date indicate that simultaneous improvement of earliness, dwarfness and grain yield in this population is possible.

References

Atsmon D., Jacobs E. (1977): A newly bred gigas form of bread wheat (*Triticum aestivum* L.): Morphological features and thermo-photoperiodic responses. Crop Science, **17**: 31–35.

Belay G., Tesemma T., Becker H.C., Merker A. (1993): Variation and interrelationships of agronomic traits in Ethiopian tetraploid wheat land races. Euphytica, **71**: 181–189.

Bhatt G.M. (1973): Significance of path coefficient analysis in determine the nature of character association. Euphytica, **22**: 338–343.

Burton G., Devane E.H. (1953): Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. Agronomy Journal, **45**: 478–481.

Campbell B.T., Baenziger P.S., Gill K.S., Eskridge K.M., Budak H., Erayman M., Dweikat I., Yen Y. (2003): Identification of QTLs and environmental interactions associated with agronomic traits on chromosome 3A of wheat. Crop Science, **43**: 1493–1505.

Dewey D.R., Lu R.H. (1959): A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agronomy Journal, **51**: 515–518.

Ehdaie B., Waines J.G. (1989): Genetic variation, heritability and path-analysis in landraces of bread wheat from southwestern, Iran. Euphytica, **41**: 183–190.

Falconer D.S., Mackay T.F.C. (1996): Introduction to quantitative genetics. Longman, Harlow, U.K.

Halluer A.R., Miranda J.B. (1998): Quantitative Genetic in Maize Breeding. Iowa State University Press, Ames, Iowa, USA.

Jaimini S.N., Goyal S.N., Tikka B.S. (1974): Estimation of correlations and path–coefficient analysis of some biometric characters in wheat. Indian Journal of Agriculture Science, **44**: 201–203.

Miller P.A., Williams J.C., Robinson H.F., Comstock R.E. (1958): Estimates of genotypic and environmental variances and covariances in upland cotton and their implications in selection. Agronomy Journal, **50**: 126–131.

Moghaddam M., Ehdaie B., Waines J.G. (1997): Genetic variation and interrelationships of agronomic characters in landraces of bread wheat from southeastern Iran. Euphytica, **95**: 361–369.

Montgomery D.C., Peck E.A. (1992): Introduction to Linear Regression Analysis. John Wiley & Sons, New York, USA.

Sidwell R.J., Smith E.L., Mcnew R.W. (1976): Inheritance and interrelationships of grain yield and selected yield related traits in hard red winter wheat cross. Crop Science, **16**: 650–654.

Singh I.D., Stoskopf N.C. (1971): Harvest index in cereals. Agronomy Journal, **63**: 224–226.

Sinha G.C.P., Sharma N.N. (1979): Correlation, regression and path analysis studies in wheat varieties. Indian Journal of Agronomy, **25**: 225–229.

Suenaga K. (1991): An effective method of production of haploid wheat (*Triticum aestivum* L.) plants by wheat and maize (*Zea mays* L.) crosses. In: Adachi A. (ed.): International Colloqium for overcoming breeding barrier. Miyozaki, Japan: 195–200.