



Full Length Article

Inheritance of some Important Agronomic Traits in Hulless Barley

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ABSTRACT

Gene effects for important quantitative traits of two hulless barley crosses (ICNBF93-369 × ICNBF-582 & SB91925 × ICB-102607) were estimated by generation mean and variance analysis. Three-parameter model [m, d, j] provided the best fit for plant height and yield per plant in cross SB91925 × ICB-102607 and number of tillers and days to maturity in both crosses. Five parameter model [m, d, h, j, l] was observed for plant height and grain yield per plant in cross ICNBF93-369 × ICNBF-582 and number of grain per spike in cross SB91925 × ICB-102607 and five-parameters model [m, d, h, i, l] was adequate for number of grains per spike in cross ICNBF93-369 × ICNBF-582. Genetic variance analysis showed that additive gene action in inheritance of plant height, number of tillers and days to maturity. Although in cross ICNBF93-369 × ICNBF-582 the dominance effects had a greater share, in cross SB91925 × ICB-102607 the additive effects played major role in the inheritance of grain yield per plant, since narrow sense heritability of this trait was low. © 2010 Friends Science Publishers

Key Words: Hulless barley; generation mean and variance analysis; Gene effects; Agronomic traits

INTRODUCTION

Barley (*Hordeum vulgare* L.) is one of the principal crops in the world and is classified into hulled and hulless barley according to the grain type. Compared with hulled barley cultivars, hulless cultivars have reduced fiber content and increased starch content due to the absence of the hull. The crude protein of hulless barley typically exceeds that of comparable hulled types and should be 1-3% greater (Griffey, 1999). Hulless barley also has a major advantage over conventional barley in transportation, processing and storage. Removing the hull fraction increases the bulk density compared to conventional barley by about 25% (Bhatty, 1993).

Grain yield is a complex trait made up of the interaction between different yield components and environmental effects. Several studies in the recent past have identified QTLs for yield and its components in barley. Cakir *et al.* (2003) reported three QTLs on chromosomes 2H, 3H and 5H for grain yield in barley. Li *et al.* (2006) reported several QTLs for yield and its components such as number of grains per spike on chromosome 1H. Babb and Muehlbauer (2003) identified major QTL Int 1 on chromosome 3HL and a second QTL cul2 on 6HL for number of tillers. Similarly Mohamadi *et al.* (2005) reported four QTLs on chromosomes 2, 5, 6 and 7 for days to maturity and Chloupek *et al.* (2006) detected plant height QTLs on chromosomes 3H, 4H, 5H and 7H in barley. The choice of an efficient breeding program depends to a large extent on the knowledge of gene action involved in the expression of the character. One of the most appropriate

methods of genetic analysis is the generation mean analysis. In this method, epistatic effects as well as additive and dominance effects can be estimated. Besides gene effects, breeders would also like to know how much of the variation in a crop is genetic and to what extent this variation is heritable. Because efficiency of selection mainly depends on additive genetic variance, influence of the environment and interaction between genotype and environment. The main objective of the present study was to identify genetic architecture of different important traits of hulless barley for further improvement of grain yield.

MATERIALS AND METHODS

The experimental material was composed of four genotypes of hulless barley, all of which had been provided by ICARDA (International Center for Agricultural Research in the Dry Area): ICNBF-582 (6-rowed), ICB-102607 (2-rowed), SB91925 (2-rowed) and ICNBF93-369 (2-rowed). Generation mean analysis was carried out on the six basic generation (the P₁ & P₂ parent cultivars, the F₁ & F₂ first and second filial generations & the BC₁ & BC₂ first & second back crosses) of two combinations of the parental cultivars, ICNBF93-369 × ICNBF-582 and SB91925 × ICB-1026. We used the parents of the respective crosses as the male parent and the F₁ generation as the female parent and effected back crosses to produce the BC₁ (F₁ back crossed to P₁) and BC₂ (F₁ back crossed to P₂) generations and the F₁ hybrids were selfed to obtain F₂ seeds. All these generations were produced during two cropping seasons and as such, all the six generations had to be grown together during the same

cropping season (2007-2008) in a randomized block design with three replications at the Moghan region (Iran). The row-length was always two meters but the number of rows varied as follows: three rows for the non-segregating P₁, P₂ and F₁, 10 rows for the F₂ and 7 rows for the BC₁ and BC₂ generations since the non-segregating generations represent the homogeneous population, while the segregating generations represent the heterogeneous population. The sample size (i.e., number of plants analyzed) varied as follows: 10 plants for the P₁, P₂ and F₁ generations, 70-75 plants for the F₂ generations and 15 plants in the BC₁ and BC₂ generations. The traits assessed were plant height, days to maturity, number of tillers per plant, number of grains per spike and grain yield per plant.

The genetic model that best fit the data was found by the mean of joint scaling test (Mather & Jinks, 1982), and the accuracy of the models was verified by χ^2 -test. Components within each model were evaluated for significance by t-test. The type of epistasis was determined only when dominance [h] and dominance×dominance [I] effects were significant, when these effects had the same sign the effects were complementary, while different signs indicated duplicate epistasis (Kearsey & Pooni, 1996). Broad-sense (h_b^2) and narrow-sense (h_n^2) heritabilities were estimated using the variance component method (Wright, 1968) and variance of F₂ and back cross generations (Warner, 1952), respectively as:

$$h_b^2 = \{VF_2 - [(VP_1 + VP_2 + 2VF_1) / 4]\} / VF_2$$

$$h_n^2 = [VF_2 - (VBC_1 + VBC_2) / 2] / VF_2$$

Response to selection was estimated with 5% selection intensity (i) (selection differential, K= 2.06) as:

$$R = i \times h_n^2 \times \sqrt{VF_2}$$

Variance components (additive, dominance & environment) were estimated as described by Kearsey and Pooni (1996) and Farshadfar (1998), using the following equations:

Additive variance ($V_{[d]} = (2VF_2 - VBC_1 - VBC_2)$), dominance variance ($V_{[h]} = 4 (VF_2 - 1/2V_{[d]} - E)$), environment variance ($V_E = 1/4 (VP_1 + VP_2 + 2VF_1)$) and average degree of dominance $(H/D)^{1/2} = (V_{[h]}/V_{[d]})^{1/2}$.

RESULTS AND DISCUSSION

The result of analysis of variance revealed significant differences for generation for all the characters investigated indicating the presence of genetic variability and possibility of selection for yield and its components (data not shown). Mean comparison between the genotypes (Table I) showed that parents 1 and 3 out performed parents 2 and 4 with respect to plant height, days to maturity, number of tillers and grain yield per plant, but performed almost similar for number of grains per spike.

For cross ICNBF93-369×ICNBF-582, F₁ and F₂ mean performances were greater than the top parent for number of tillers. For this trait BC₂ mean was close to superior parent but F₂ mean was lower than F₁. Also both F₁ and F₂ means for this cross were close to superior parents for plant height and number of grains per spike. But both BC generation means were greater than the top parents for these traits. In this cross all the generation means except BC₂ for days to maturity were close to the earlier maturing parent. However for grain yield per plant all the generation means were greater than or close to the top parent.

For cross SB91925×ICB-102607, F₁, F₂ and BC₁ means for plant height were lower than or close to the superior parent. Also in this cross for days to maturity F₁ and BC₁ means were lower than or close to the earlier maturing parent, however F₂ and BC₂ means were between parental means.

For number of tillers F₁, F₂, BC₁ and BC₂ means were between parental means. However all the generation means exceeded the superior parent for number of grains per spike. Although F₁ mean for grain yield per plant in this cross was close to the top parent, F₂, BC₁ and BC₂ means were between parental means.

In both crosses additive effects were significant for all traits (Table II). But estimates of genetic variance components showed that additive variance was larger than dominance for plant height, days to maturity and number of tillers in both crosses (Table III). The average degree of dominance was less than unity indicating partial dominance gene action for these traits. Also for these traits greater estimates of narrow sense heritability and consequently greater gain from selection were found in both crosses (Table III). Thus selection in a conventional breeding program in the early generation should be effective.

These results in accordance with Islam and Darrah (2005) and Verma *et al.* (2007), who reported that additive and partial dominance genetic effects were important for plant height, number of tillers and days to maturity in hullless and covered barley genotypes, respectively.

Although in cross ICNBF93-369×ICNBF-582, dominance effects were positive and significant for plant height, number of grains per spike and grain yield per plant, the greater ratio of $(H/D)^{1/2}$ from unity indicated over dominance gene action only for number of grains per spike and grain yield per plant. Also in cross SB91925×ICB-102607, dominance effects were significant only for number of grains per spike. However average degree of dominance showed that both additive and non-additive components of genetic variance were involved in governing the inheritance of this trait (Table III). Due to the presence of over dominance type of gene action selection of this trait in early generation will be difficult. As selection based on progeny performance exploits only additive component of genetic variances for this trait bi-parental mating followed by recurrent selection or diallel selective mating, which allows intermating among the selected segregates in the different

Table I: Mean comparison between sub-main plots (genotypes) for various traits of the cross ICNBF93-369 × ICNBF-582 and SB91925 × ICB-102607

Traits	Genotypes					
	P ₁	P ₂	F ₁	F ₂	BC ₁	BC ₂
ICNBF93-369 × ICNBF-582						
Plant height	77.32e	86.82bc	83.2d	85.4cd	92.1a	89.2ab
Days to maturity	203.2a	196.2b	198.3b	196.2b	197.2b	203.4a
Number of tillers	6.41ab	4.51d	6.88a	6.58a	5.81c	6.31b
Number of grains / spike	60.37b	57.06c	58.82bc	59.04bc	65.19a	63.57a
Grain yield / plant	9.71c	8.27d	9.64c	11.3b	11.4ab	12.2a
SB91925 × ICB-102607						
Plant height	79.52d	88.41b	85.2c	88.31b	91.24a	86.41bc
Days to maturity	203.1a	194.4de	195.4cd	197.2bc	192.9e	199.3b
Number of tillers	6.52a	5.02d	6.25b	6.2bc	6.01c	6.3b
Number of grains / spike	59.2d	55.12e	60.12cd	63.11ab	62.13bc	65.04b
Grain yield / plant	9.93a	7.67c	9.98a	8.87b	8.19c	8.96b

Table II: Estimates of genetic components of the mean for various traits studied in cross ICNBF93-369 × ICNBF-582 and SB91925 × ICB-102607

Traits	M	[d]	[h]	[i]	[j]	[l]	χ ²
ICNBF93-369 × ICNBF-582							
Plant height	63.11±15.12**	-4.35±1.16**	73.2±36.31*	-	17.3±5.41**	-51.1±20.11*	3.6 (1)
Days to maturity	182.3±30.11**	3.4±1.05**	-	-	-19.9±5.57**	-	6.74 (3)
Number of tillers	8.84±3.1**	0.97±0.21**	-	-	-2.7±1.01**	-	5.93 (3)
Number of grains / spike	38.15±7.46**	1.95±0.82*	68.3±17.2**	21.36±7.72**	-	-40.91±9.9**	0.06 (1)
Grain yield / plant	6.79±1.2**	0.82±0.17**	14.44±3.16**	-	-3.44±0.74**	-11.8±1.73**	0.18 (1)
SB91925 × ICB-102607							
Plant height	80.1±19.33**	-4.84±1.37**	-	-	19.35±7.62*	-	6.3 (3)
Days to maturity	202.15±25.6**	4.75±1.28**	-	-	-21.1±6.33**	-	5.5 (3)
Number of tillers	5.65±2.11**	0.71±0.19**	-	-	-2.25±0.91*	-	2.7 (3)
Number of grains / spike	54.56±3.35**	2.44±0.33**	24.5±7.39**	-	-9.67±1.79**	-21.36±4.35**	0.6 (1)
Grain yield / plant	9.41±3.12**	1.19±0.33**	-	-	-3.77±1.32**	-	2.9 (3)

M = Mean, [d] = Additive effects, [h] = Dominance effects, [i] = Additive × additive effects, [j] = Additive × dominance effects, [l] = Dominance × dominance effects

*, **: Significant at 5% and 1% level of probability, respectively

Table III: Estimates of variance components and heritability for various traits in cross ICNBF93-369 × ICNBF-582 and SB91925 × ICB-102607

Traits	V _[d]	V _[h]	V _E	(H/D) ^{1/2}	H ² _b	h ² _n	R
ICNBF93-369 × ICNBF-582							
Plant height	28.51	6.19	2.257	0.46	0.87	0.79	7.97
Days to maturity	106.2	6.36	2.05	0.24	0.96	0.93	7.28
Number of tillers	1.41	0.092	0.102	0.25	0.87	0.85	24.16
Number of grains / spike	1.06	3.08	1.36	1.7	0.49	0.2	1.11
Grain yield / plant	0.032	0.078	0.04	1.56	0.47	0.21	1.04
SB91925 × ICB-102607							
Plant height	32.0	7.7	4.37	0.49	0.80	0.72	7.86
Days to maturity	92.62	3.7	3.17	0.20	0.94	0.92	6.82
Number of tillers	0.3	0.12	0.07	0.63	0.72	0.6	9.89
Number of grains / spike	0.52	0.5	0.26	0.98	0.6	0.4	1.05
Grain yield / plant	0.39	0.29	0.262	0.86	0.51	0.37	6.25

V_[d]: Additive variance V_[h]: Dominance variance V_E: Environmental variance (H/D)^{1/2}: Average degree of dominance h²_b: Broad sense heritability h²_n: Narrow sense heritability R: Genetic advance

cycles, would be useful to recover superior homozygote in later generations.

Baghizadeh *et al.* (2003) and Islam and Darrah (2005) found non-additive (non-fixable) type of inheritance for number of grains per spike and grain yield in covered and hulless barley accessions, respectively while Verma *et al.* (2007) reported additive (fixable) gene effects for these traits.

The epistatic types of gene interaction in each cross for different traits were found to be different from each other (Table II). Additive×additive [i] non-allelic interaction was significant only for number of grains per spike in the ICNBF93-369 × ICNBF-582 cross. However additive×dominance gene action effect [j] was significant for plant height, days to maturity, number of tillers and grain

yield per plant in cross ICNBF93-369×ICNBF-582 and for all the traits in cross SB91925×ICB-102607. Non-allelic dominance×dominance [I] interaction was significant for plant height and grain yield per plant in the ICNBF93-369×ICNBF-582 cross and number of grain per spike in both crosses. The signs of dominance [h] and dominance×dominance [I] gene effects were opposite in the case of plant height and grain yield per plant in cross ICNBF93-369×ICNBF-582 and number of grains per spike in both crosses suggesting duplicate type of non-allelic interaction in these traits. This kind of epistasis generally hinders the improvement through selection and hence, a higher magnitude of dominance and [I] type of interaction effects would not be expected. It also indicated that selection should be delayed after several generations of selection (single seed descent) until a high level of gene fixation is attained. Subsequent intermatings between promising lines may be important in accumulating favorable genes. Since none of the signs of [h] were similar to the [I] type of epistasis, it was concluded that no complementary type of interaction was present in the genetic control of the studied traits. Islam and Darrah (2005) showed that non-allelic interaction effects were not important for plant height, number of tillers and days to maturity, while Verma *et al.* (2007) reported additive×dominance and dominance×dominance type of epistasis for grain yield and its component in barley. Kularia and Sharma (2005) showed that duplicate type of interaction was prevalent in cross RD2503×BL2 for days to maturity and in cross RD2508×RD2502 for plant height, number of effective tillers and grain yield per plant. In another study Choo *et al.* (2001) in hullless×covered cross barley using doubled haploid lines, reported additive×additive epistasis for yield and maturity. Although in cross ICNBF93-369×ICNBF-582 the dominance effects had a greater share, in cross SB91925×ICB-102607, the additive effects played major role in the inheritance of grain yield per plant, since heritability of this trait was low.

CONCLUSION

Improving grain yield directly is somehow problematic, because environment has a great contribution in controlling it. Therefore to improve this trait in a given population should be done through improving those traits, which are correlated and less affected by environment. In the population in this study, additive effects formed major part of variability for grain yield component, plant height and number of tillers. Thus, genetic improvement in grain yield would be easier through indirect selection for component traits such as plant height and number of tillers rather than direct selection for grain yield.

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REFERENCES

- Babb, S. and G.J. Muehlbauer, 2003. Genetic and morphological characterization of the barley unicum2 (*cul2*) mutant. *Theor. Appl. Genet.*, 106: 846–857
- Baghizadeh, A., A. Taleai, R. Naghavi and H.Z. Khanaghah, 2003. Evaluation of some quantitative characters in barley using mean generation analysis. *Iranian. J. Agric. Sci.*, 35: 851–857
- Bhatty, R.S., 1993. Physicochemical properties of roller-milled barley bran and flour. *Cereal Chem.*, 70: 397–402
- Cakir, M., D. Poulsen, N.W. Galwey, G.A. Ablett, K.J. Chalmers, G.J. Platz, R.F. Park, R.C.M. Lance, J.F. Panozzo, B.J. Read, D.B. Moody, A.R. Barr, P. Johnston, C.D. Li, W.J.R. Boyd, C.R. Grime, R. Appels, M.G.K. Jones and P. Langridge, 2003. Mapping and QTL analysis of the barley population Tallon × Kaputar. *Australian J. Agric. Res.*, 54: 1155–1162
- Chloupek, O., B.P. Forster and W.T.B. Thomas, 2006. The effect of semi-dwarf genes on root system size in field-grown barley. *Theor. Appl. Genet.*, 112: 779–786
- Choo, T.M., K.M. Ho and R.A. Martin, 2001. Genetic analysis of a hullless×covered cross of barley using doubled-haploid lines. *Crop sci.*, 41: 1021–1026
- Farshadfar, E., 1998. *Application of Biometrical Genetics in Plant Breeding*, Vol. 1, p: 528. Razi University Press, Kermanshah, Iran
- Griffey, C. and R.L. Paris, 1999. Hull-less barley as an improved feed crop. *In: Kentucky Small Grain Growers Association*. <http://www.kysmallgrains.org/research/hullless.html#1999>. Accessed 16 September 2009
- Islam, A.A. and M. Darrah, 2005. Estimation of gene effects for seed yield and component traits in hullless barley. *Turkish J. Field Crops*, 8: 85–92
- Kearsey, M.J. and H.S. Pooni, 1996. *The Genetical Analysis of Quantitative Trait*, p: 381. Chapman and Hall, Inc., London
- Kularia, R.K. and A.K. Sharma, 2005. Generation mean analysis for yield and its component trait in barley (*Hordeum vulgare* L.). *Indian J. Genet.*, 65: 129–130
- Li, J.Z., X.Q. Huang, F. Heinrichs, M.W. Ganai and M.S. Roder, 2006. Analysis of QTLs for yield components, agronomic traits and disease resistance in an advanced backcross population of spring barley. *Genome*, 49: 454–466
- Mather, K. and J.L. Jinks, 1982. *Biometrical Genetics*, p: 396. Chapman and Hall, Inc., London
- Mohammadi, M., A. Taleei, H. Zeinali, M.R. Naghavi, S. Ceccarelli, S. Grandi and M. Baum, 2005. QTL analysis for phonologic traits in doubled haploid population of barley. *Int. J. Agric. Biol.*, 7: 820–823
- Verma, A.K., S.R. Vishwakarma and P.K. Singh, 2007. Genetic architecture for yield and quality component traits over two environments in barley (*Hordeum vulgare* L.). *Barley Genetics Newslett.*, 37: 24–28
- Warner, J.N., 1952. A method for estimating heritability. *Agron. J.*, 44: 427–430
- Wright, S., 1968. *Evolution and the Genetics of Populations*, Vol. 1, pp: 371–420. Genetic and Biometric Foundation, The University of Chicago Press, Chicago

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