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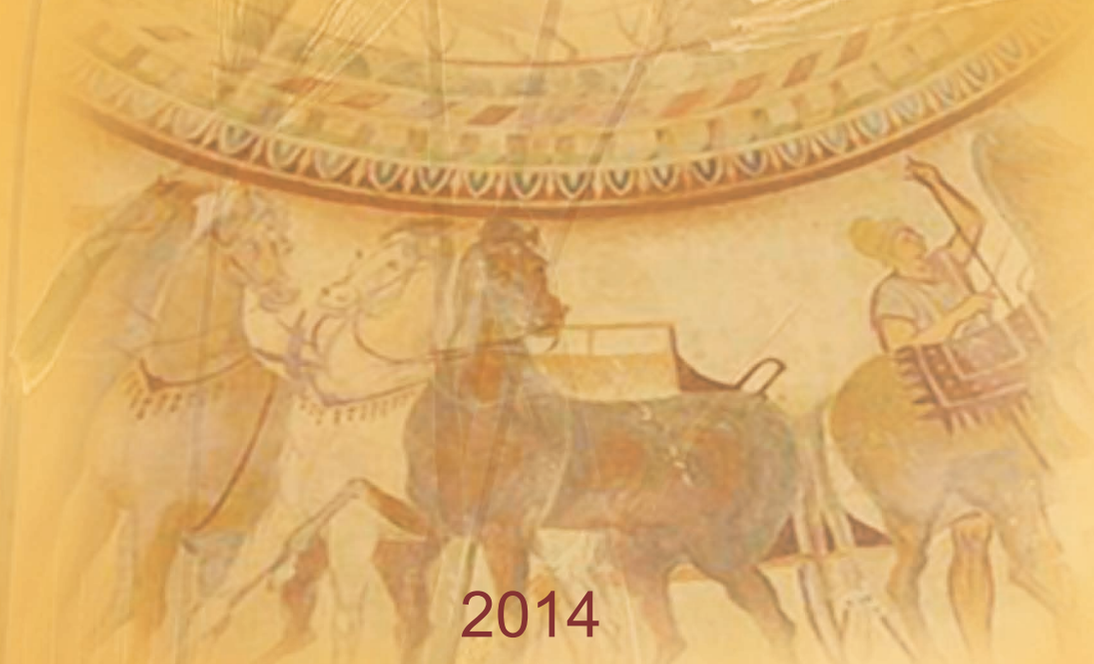

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Genetic variability in two-rowed spring barley

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Abstract. *A total of 23 varieties of 2-rowed spring barley were grown in two successive seasons of 2011 and 2012 to study variability, heritability and genetic advance for 5 characters - spike length, spikelet number per spike, grain number per spike, grain weight per spike and 1000 grains weight. Significant differences were observed among the varieties regarding all the traits studied. Genotypic and phenotypic coefficients of variability were higher in 1000 grains weight than other traits. Estimates of heritability ranged from 66.62% for grain number per spike to 89.35% for 1000 grains weight. Heritability coupled with high genetic advance was observed for 1000 grains weight and spikelet number per spike indicating the importance of these traits in selection and crop improvement.*

Keywords: barley, variability, heritability, genetic advance

Introduction

One of the main objectives of any breeding program is to produce high-yielding and better-quality lines for release as cultivars. The prerequisite to achieve this goal is to find sufficient amount of variability, in which desired lines have to be selected for further manipulation to achieve the target. Identification of better genotypes with desirable traits and their subsequent use in a breeding program and the establishment of suitable selection criteria can be helpful for the successful varietals improvement program. Analysis of variability among the traits would be of great importance in planning a successful breeding program (Kahrizi et al., 2010; Muñoz-Amatriaín et al., 2014).

Development of high-yielding cultivars requires a thorough knowledge of the existing genetic variation for yield and its components. A major factor limiting the progress in plant breeding has been low heritability of quantitative traits. Broad-sense heritability estimates the ratio of total genetic variance, including additive, dominance and epistatic variance of the phenotypic variance (Falconer, 1996; Acquaah, 2007). The most important function of heritability in studies of quantitative traits is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Singh and Chaudhary, 1985; Falconer, 1989). Characters not greatly influenced by the environment usually have high heritability. This may determine the choice of a selection procedure used by the plant breeder (Acquaah, 2007). The magnitude of the components of variances has been obtained from analysis of variance to estimate the different genetic parameters as described by Singh and Chaudhary (1985), Falconer (1989). Estimates of heritability alone do not provide an idea about the expected gain in the next generation, but have to be considered in conjunction with estimates of genetic advance, the change in the mean value among successive generations (Shukla et al., 2006).

The objective of the present study was to evaluate the genetic variability of barley germplasm based on spike traits.

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Material and methods

Plant Materials

The materials used in the present study included 23 varieties of two-rowed spring barley – Hocky, Cameo, Tun, Escort, Flute, Oasis, Flare, Flare from England, Makomako, Kuaka from New Zealand, MFB 102 from Hungary, Kervana from France, Birka from Sweden, Creemore, Winthrop, AC Metcalfe from Canada, Prominant, Beta Abert, Wirde from Denmark, Tetonia, Craft, Haxby, Sublette from USA.

Field Experimental Setup

This research was conducted in the 2011 and 2012 growing seasons in the experimental field of the Institute of Agriculture, Karnobat, Southeastern Bulgaria. The experiments were organized in a Randomized Complete Block Design with 3 replications. Each plot consisted of five 110 cm rows, 30 cm apart. Sowing was performed by hand in March. Standard agronomic and plant protection practices were used.

Weather Conditions

The long-term average precipitation for this region was 203.1 mm per growing season. The amount of precipitation in the first year growing period was lower (141.1 mm) than that in the second year (193.4 mm).

Characters Studied

The characters studied included spike length (cm), spikelet number per spike, grain number per spike, grain weight per spike (g) and 1000 grains weight (g) measured on ten plants sampled from the middle of the plot of each genotype in each replication.

Genetic Parameters Estimates

Broad-sense heritability (h^2) was estimated according to Falconer (1989):

$$h^2 = \frac{\sigma^2 g}{\sigma^2 ph}$$

where $\sigma^2 g$ is genotypic variance and $\sigma^2 ph$ is phenotypic variance. Genotypic ($\sigma^2 g$) and phenotypic variances ($\sigma^2 ph$) were obtained from the analysis of variance table according to Comstock and Robinson (1952). The mean values were used for genetic analyses to determine phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV), according to Singh and Chaudhury (1985):

$$GCV\ (\%) = \frac{\sqrt{\sigma^2 g}}{x} .100$$

$$PCV\ (\%) = \frac{\sqrt{\sigma^2 ph}}{x} .100$$

where $\sigma^2 g$ is genotypic variance, $\sigma^2 ph$ is phenotypic variance, X is sample mean.

Genetic advance (GA) was calculated with the method suggested by Allard (1960) and Singh and Chaudhury (1985):

$$GA = K.\sqrt{\sigma^2 ph} .h^2$$

where K is constant = 2.06 at 5% selection intensity, $\sigma^2 ph$ is phenotypic variance, h^2 is broad-sense heritability.

Statistical analysis

Analysis of variance, using randomized complete block design, was computed for all the traits evaluated using the computer software system of SPSS 16.00 for Windows 16.0 (SPSS Inc., 2007).

Results and discussion

The results from analyses of variance over two years for the investigated characteristics are presented in Table 1. Effect of genotype and interaction of genotype by year were found to be significant for all the traits. Effect of year was significant for grain number per spike and grain weight per spike.

Table 1. Mean squares for spike traits for 23 spring barley genotypes (2011 – 2012)

Traits	Genotype	Year	Interaction
Spike length	4.18***	0.16^{ns}	0.98***
Spikelet number per spike	20.52***	1.29^{ns}	3.89***
Grain number per spike	19.52***	26.13***	6.52***
Grain weight per spike	0.09***	0.03*	0.02***
1000 grains weight	85.57***	1.48^{ns}	9.11***

*Significant at 5% level of probability, *** Significant at 0.5% level of probability, ns – non-significant

The mean values of the traits studied are shown in Table 2. Spike length ranged from 8.28 to 11.70 cm. Maximum spikelet number per spike of 33.70 was exhibited by variety Winthrop whereas minimum spikelets per spike of 24.68 was recorded for the genotype Oasis. Grain number per spike ranged from 21.23 to 30.59. Grain weight per spike varied from 1.04 for variety Oasis to 1.50 g for variety Winthrop. Data for 1000-grain weight ranged between 39.99 and 54.32 g, maximum 1000-grain weight was recorded for variety Kuaka, whereas minimum one was recorded for variety Tun.

Table 2. Means for spike traits for 23 spring barley genotypes (2011 – 2012)

Genotypes	Spike length, cm	Spikelet number per spike	Grain number per spike	Grain weight per spike, g	1000 grains weight, g
Tetonia	8.99	30.55	27.19	1.36	51.77
Prominant	9.19	29.25	25.07	1.12	43.83
Craft	9.86	30.96	27.77	1.50	53.79
Haxby	10.41	28.68	25.60	1.35	52.36
Sublette	9.72	28.98	26.09	1.28	48.31
Beta Abert	10.27	32.33	28.23	1.26	44.20
Hocky	9.05	29.24	26.23	1.31	50.67
Cameo	10.11	30.63	27.55	1.27	48.01
Birka	10.62	31.88	27.52	1.38	49.49
Tun	9.99	29.52	27.08	1.10	39.99
Escort	8.41	28.67	25.42	1.12	43.99
Kervana	10.50	31.65	28.26	1.17	41.53
Flute	9.35	29.94	26.43	1.17	45.41
Wirde	9.99	31.20	27.34	1.19	44.01
Oasis	8.28	24.68	21.23	1.04	47.91
Flare	9.91	28.17	29.23	1.40	52.47
Makomako	9.13	30.77	27.53	1.31	46.76
Kuaka	11.70	30.49	25.22	1.43	54.32
Creemore	10.78	32.19	28.28	1.30	45.50
Vista	8.99	27.75	24.81	1.21	48.20
MFB 102	9.00	29.55	26.37	1.30	48.48
Winthrop	10.18	33.70	30.59	1.50	47.96
AC Metcalfe	9.29	31.39	26.98	1.32	47.06
Mean	9.73	30.09	26.78	1.28	47.65
Minimum	8.28	24.68	21.23	1.04	39.99
Maximum	11.70	33.70	30.59	1.50	54.32

The estimates of heritability and genetic advances are important preliminary steps in any breeding program as they provide information needed in designing the most effective breeding program and the relative practicability of selection. Genotypic variance, phenotypic variance, GCV, PCV, broad sense heritability, GA and genetic advance expressed as percentage of mean (GAM) for 5 spike traits are presented in Table 3. The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. In all traits a large portion of the phenotypic variance was accounted for by the genetic component. As expected, phenotypic coefficient of variation was greater than genotypic coefficient of variation for all the characters. Phenotypic coefficient of variation and genotypic coefficient of variation were the highest for 1000 grains weight (PCV=9.41%; GCV=8.31%), followed by spike length (PCV=8.62%; GCV=7.55%). Low variability was recorded for spikelet number per spike and grain number per spike.

Heritability is the proportion of genetic variance in phenotypic variance, expressed as percentage. In the present study heritability was high (above 70%) for all the characters except grain weight per

Table 3. Estimates of variance and genetic parameters for spike traits in 23 spring barley genotypes

Traits	σ^2g	σ^2ph	h^2, %	GCV, %	PCV, %	GA	GAM
Spike length	0.533	0.696	77.00	7.55	8.62	1.10	11.41
Spikelet number per spike	2.772	3.419	81.06	5.53	6.15	5.71	18.98
Grain number per spike	2.168	3.253	66.62	5.50	6.74	4.47	16.68
Grain weight per spike	0.011	0.014	77.98	8.31	9.41	0.02	1.82
1000 grains weight	12.743	14.262	89.35	7.47	7.90	26.25	54.94

σ^2g – genotypic variance, σ^2ph – phenotypic variance, h^2 – broad-sense heritability, GCV – genotypic coefficient of variation, PCV – phenotypic coefficient of variation, GA – genetic advance, GAM – GA as % of mean

spike. The low heritability recorded for this trait indicates that direct selection for the trait will be ineffective. The highest estimate of heritability was observed for 1000 grains weight (89.3%), followed by spikelet number per spike (81.1%). High heritability indicated that the characters were less influenced by the environment. High heritability for different characters in barley was also reported by Vimal and Vishwakarma (1998), El-Bawab (2003), Wang et al. (2006) and Al-Tabbal and Al-Fraihat (2012).

Since high heritability does not always indicate high genetic gain, heritability with genetic advance considered together should be used in predicting the ultimate effect for selecting superior varieties (Ali et al., 2002). Genetic advance expressed as percentage of mean was the highest for 1000 grains weight (54.94%). Other characters showed moderate genetic advance except grain weight per spike which had low genetic advance. 1000 grains weight and spikelet number per spike showed high heritability coupled with high genetic advance. Vimal and Vishwakarma (1998) observed high heritability along with high genetic advance for length of spike, spikelets per spike and grain yield per plant in barley. Panse (1957) stated that high heritability coupled with high genetic advance indicates the additive gene effects while high heritability coupled with low genetic advance indicates the non-additive gene effects for control of the particular character. The present study indicated that 1000 grains weight and spikelet number per spike showing high heritability and high genetic advance are important characters to be considered for selection and improvement of spring two-rowed barley.

Conclusion

Significant differences were observed among the varieties regarding all the characters studied. The results revealed considerable phenotypic and genotypic variances among the genotypes for the traits under consideration. Genotypic and phenotypic coefficients of variability were higher in 1000 grains weight than other traits. Estimates of heritability ranged from 66.62% for grain number per spike to 89.35% for 1000 grains weight, while grain weight per spike showed 77.98% heritability. Heritability coupled with high genetic advance was observed for 1000 grains weight and spikelet number per spike indicating the importance of these traits in selection and crop improvement.

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Review

Genetics and Breeding

Nutrition and Physiology

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Papers shall be submitted at the editorial office typed on standard typing pages (A4, 30 lines per page, 62 characters per line). The editors recommend up to 15 pages for full research paper (including abstract references, tables, figures and other appendices)

The manuscript should be structured as follows: Title, Names of authors and affiliation address, Abstract, List of keywords, Introduction, Material and methods,Results, Discussion, Conclusion, Acknowledgements (if any), References, Tables, Figures.

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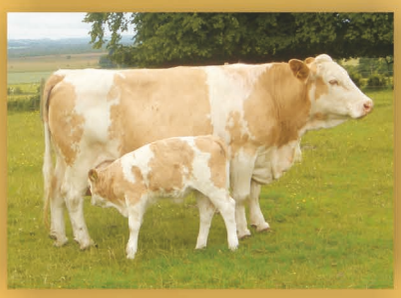

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