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Research Article

Multi-environment trials of spring barley genotypes (*Hordeum vulgare* L.) in the final stage of breeding process

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Abstract

Spring barley genotypes (cultivars and advanced breeding lines) have been tested in three environmental zones of Ukraine (Central Forest-Steppe, Northern Steppe and Polissia). The ANOVA has revealed reliable contributions from all three source of the variation: genotype, environment and genotype–environment interaction, but with their different ratio depending on the test conditions and studied genotypes. For spring barley cultivars the contribution of genotype–environment interaction was 22.55%, but for the advanced breeding lines it was only 10.56%. To establish patterns of genotype–environment interaction and genotypes ranking the GGE biplot model has been used. Both the change in the contribution of genotype to the total variation depending on environmental conditions and the dependence of characteristics of test environments on the genotypes studied have been revealed that in general, the combination of different ecological and year conditions of trial contributed to the identification of "the best of the best" genotypes in the final stage of breeding work. Spring barley cultivar MIP Bohun and breeding lines Deficiens 5005, Nutans 4855, and Nutans 4941 with optimal combination of yield performance and stability have been selected.

Key words

Spring barley, cultivar, breeding line, multi-environment trial, genotype–environment interaction, stability

Introduction

Increasing crop adaptability to provide stable level of yield remains the central objective of plant breeding theory and practice (Macholdt and Honermeier. 2016). One of the main problems in this aspect is genotype–environment interaction (Hill. 1975). The genotype–environment interaction is a part of phenotypic variation that occurs as a result of non-compliance between genetic and environmental effects (Malosetti *et al.* 2013). Phenotypic level of trait expression is the result of multiple interactions between genetic system of the plant organism and environment. It leads to the fact that selecting genotypes under certain conditions may not provide advantage of these genotypes in other conditions. Nowadays, due to strong competitions between breeding companies, it is necessary to create and release new cultivars as quickly as possible. Therefore, the comprehensive assessment of breeding lines at the competitive strain testing to decide on transfer them as new cultivars to the State Strain Testing should not be extended to several years. At the same time, the breeding lines need thorough testing of the main agronomic and adaptive traits. Multi–environment trial is effective for assessing genotype-environment interaction and selection of promising genotypes. To interpret the experimental data of multi–environment trial, it is necessary to use the most appropriate statistical models. Van Eeuwijk *et al.* (2016) report that high-quality analysis of this phenomenon underlies the progress of any breeding program. The GGE (genotype plus genotype–environment interaction) biplot model makes it possible to visually characterize all aspects of genotype–environmental trial data: 1) mega–environment analysis; 2) ranking environments by discriminating ability and representativeness; 3) assessment and selection of both specifically adapted genotypes and ones with the optimal combination of yield performance and stability (Yan *et al.* 2007). The interpretation of experimental data from multi-environment barley trials using GGE biplot has been conducted in Ukraine (Solonechnyi *et al.* 2018), India (Sarkar *et al.* 2014), and Iran (Mohammadi *et al.* 2015).

The aim of the research is to reveal genotype–environment interaction under the same conditions, but with different set of genotypes and to identify the best breeding lines with combination yield performance and stability.

Materials and Methods

The experiment included two blocks of genotypes: the first 10 spring barley cultivars bred in leading domestic institutions and foreign companies; the second 9 spring barley advanced breeding lines and the standard cultivar Vzirets. The breeding lines have been selected in competitive strain tasting at the V. M. Remeslo Myronivka Institute of Wheat of NAAS (MIW) in 2015. In 2015–2017, the study was carried out through three environmental zones. 1) MIW (Central Forest-Steppe, Latitude – 49°64', Longitude – 31°08', Altitude – 153 m). 2) Nosivka Plant Breeding and Experimental Station of the V. M. Remeslo MIW of NAAS (NPBES) (Polissia, Latitude – 50°93', Longitude – 31°69', Altitude – 126 m). 3) Institute of Agriculture of Steppe of NAAS (IAS) (Northern Steppe, Latitude – 48°56', Longitude – 32°32', Altitude – 171 m). Thus, for three years of competitive strain testing, genotypes were tested in seven environments. At the same time, the conditions of the MIW as an ecological site where breeding lines had been developed were more frequently presented in the general mega-environment. The trial was laid out with complete randomized blocks in three replications in each ecological zone. GGE biplot analysis was performed using non-commercial software GEA-R Version 4.1. Software review is provided in the publication (Frutos *et al.* 2014).

Results and Discussion.

The levels of yield performance and variation of spring barley cultivars are shown in Table 1. The highest grand mean yield in the experiment was obtained in the environment M15 (6.72 t/ha), the lowest one was in K17 (4.30 t/ha). The largest variation range between cultivars was observed in M16 (2.45 t/ha), the smallest in K17 (1.09 t/ha). In the block of breeding lines the variation of mean yield between environments was 3.21 t/ha, with the highest value in M15 (7.51 t/ha), and the lowest in K17 (4.30 t/ha) (Table 2). The difference between the maximum and minimum limits of the yield of breeding lines ranged from 2.49 t/ha in M16 to 1.02 t/ha in K17. It was significantly higher than LSD_{05} (0.19–0.46 t/ha). Consequently, significant differences in the yield performance among the genotypes were detected in each year. Analysis of variance (ANOVA) revealed reliable contributions from all three source of the variation: genotype, environment, and genotype–environment interaction in both blocks (Table 3). The largest variation range was related to environmental conditions (69.62 %), followed by genotype–environment interaction (22.55 %) and genotype (7.83 %). In the block of breeding lines, contribution of environmental conditions was significantly higher (83.95 %), but effects of genotype–environment interaction (10.56 %) and genotype (5.49 %) were lower. The obtained results indicated a strong contrast of the environmental zones and the conditions of years, which significantly influenced the breeding lines yield. In our opinion, small values of contribution genotype and genotype–environment interaction in total variation is associated with previously selected the best breeding lines which were included into trial. At the same time, such combination of environmental and weather (in different years) conditions contributed to the comprehensive assessment and allocation "the best of the best" genotypes. Comparing the results of analysis of variance for both blocks of genotypes, we can note that if the trial held in the same conditions, but with different sets of genotypes, the ratio of the components of variation will be significantly changed. In GGE biplot, represents differentiation ability and representativeness of test environments is given in fig 1. In the block of spring barley cultivars, the first two main components of the GGE biplot model accounted for 63.74 % of the genotype–environment interaction. K17 and M17 environments were the most representative, K16 and N17 were the least representative. The highest differentiating ability was observed in M16 and K16. The environment M15 combined high differentiating ability and representativeness. K16 and N17 were the most distant from each other. M17 and K17 were the similar, as well as M15 and N16. In the block of breeding lines, the first two main components of the GGE biplot model explain higher percentage of the genotype–environment interaction as compared to the cultivars (76.0 %). The N16 environment combined high representativeness and differentiation ability. The highest differentiating ability was observed in the environment M16, the lowest in K17. M15 and K17 were the most remote from each other. It should be noted the distance between M15 and M16, which were the most productive – 7.51 t/ha and 6.89 t/ha, respectively. Thus, not only the value of yield variation in the environment characterized their similarity or difference, but also the rank of the genotypes. At the same time, there were indicative the similarities between different environmental conditions in different years (M17 and K17, M15 and N17) and the differences in the same environmental conditions, but in different years (K16 and K17, M15 and M17). The peculiarities we have revealed testified considerable variability of conditions and the response of the studied genotypes both in spatial (ecological) and temporal (years) gradients. This confirmed the effectiveness of their combination for assessment and identification of promising genotypes. The GGE biplot visualizations also indicated that the response of genotypes in particular environmental conditions can significantly modify their characteristics.

The "which-won-where" GGE biplot polygon view is effective for visualizing the interaction between genotypes and environments (Fig. 2). In the block of spring barley cultivars the environments are divided into three sectors. The first sector integrates the M15, M16, M17, N16, K17 environments into a mega-environment. K16 is the second environment, and N17 is the third environment. The cultivar MIP Bohun (G1) had significant advantage over the other genotypes in the first mega-environment, the cultivar Helios (G5) had in K16, the cultivar Shakira (G9) had in N17. In the block of breeding lines another three mega-environments have been observed: the first was formed with the M16, K16 and N16 environments; the second was formed with the M15 and N17; the third was formed with the M17 and K17. For the breeding lines Deficiens 5005 (G4), Nutans 4941 (G6) and Nutans 4855 (G8), the first mega-environment was preferred. The breeding line Nutans 4983 (G2) had specific adaptability to the second mega-environment. No winners have been found in the third mega-environment. GGE biplot average-environment coordination for yield and stability is given in fig 3). In the block of cultivars, MIP Bohun (G1) had the highest yield. Stability was noted for the cultivars Luka (G4) and Skif (G8). However, in terms of yield, they were inferior to the grand mean in the trial. Among the cultivars with higher than mean yield, Sviatomykhailivskyi (G3) was the most stable. The three cultivars Helios (G5), Skarb (G6) and Shakira (G9) had equal levels of yield, but were significantly differed in response to the environments. The first two cultivars (G5 and G6) responded strongly to the K16 conditions. The variety Shakira (G9) had specific adaptation to the N17. In the block of breeding lines the maximum yield in descending order was noted for Nutans 4941 (G6), Nutans 4855 (G8), and Deficiens 5005 (G4). The variety Vzirets (G1) and breeding line Nutans 4855 (G8) had higher stability than other genotypes. The breeding lines Nutans 5006 (G5) and Pallidum 5023 (G10) were the most variable.

The genotypes ranking with respect to the "ideal" genotype is depicted in fig 4. In the block of cultivars, MIP Bohun (G1) was much closer to it in comparison with others. In the block of breeding lines, Nutans 4855 (G8) was the closest to the "ideal" genotype. Breeding lines Nutans 4941 (G6) and Deficiens 5005 (G4) lines should be also highlighted. Thus, the scheme of multi-environment trials and analysis of experimental data with GGE biplot have been theoretically substantiated and practically implemented. They contributes to thorough evaluation of adaptive potential of genotype and selection of "the best of the best" spring barley breeding lines in the final stage of breeding process. At the same time, a different ratio of constituent variations depending on the test conditions and studied genotypes has found. Also, GGE biplot visualizations indicate that the response of the genotypes studied under certain conditions significantly affects at the characteristics of the environments themselves. Therefore, the identified patterns of genotype-environment interaction and genotype stability are relevant only for the genotypes studied in particular conditions.

References

Frutos E, Galindo M. P. and Leiva V. 2014. An interactive biplot implementation in R for modeling genotype-by-environment interaction. *Stoch. Environ. Res. Risk. Assess.* **28**: 1629–1641.

Hill J. 1975. Genotype-environment interaction – a challenge for plant breeding. *J. Agric. Sci.* **85**(3): 477–493.

Macholdt J. and Honermeier B. 2016. Impact of climate change on cultivar choice: adaptation strategies of farmers and advisors in German cereal production. *Agronomy*. **6**(40): doi: 10.3390/agronomy6030040

Malosetti M., Ribaut J.-M. and van Eeuwijk F. A. 2013. The statistical analysis of multi-environment data: modeling genotype-by-environment interaction and its genetic basis. *Front. Physiol.* **4**: 44. doi: 10.3389/fphys.2013.00044

Mohammadi M., Noorinia A. A., Khalilzadeh G. R. and Hosseinpoo T. 2015. Application of GGE biplot analysis to investigate GE interaction on barley grain yield. *Curr. Opin. Agric.* **4**(1): 25–32.

Sarkar B., Sharma R. C., Verma R. P. S. *et al.* 2014. Identifying superior feed barley genotypes using GGE biplot for diverse environments in India. *Indian J. Genet.* **74**(1): 26–33.

Solonechnyi P., Kozachenko M., Vasko N. *et al.* 2018. AMMI and GGE biplot analysis of yield performance of spring barley (*Hordeum vulgare L.*) varieties in multi environment trials. *Agriculture & Forestry.* **64**(1): 121–132.

Van Eeuwijk F. A., Bustos-Korts D. V. and Malosetti M. 2016. What should students in plant breeding know about the statistical aspects of genotype × environment interactions? *Crop Sci.* **56**(5): 2119–2140.

Yan W., Kang M. S., Ma B. *et al.* 2007. GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Sci.* **47**(2): 641–653.

Table 1. Grain yield of spring barley cultivars in the multi-environment trial, t/ha

Code	Cultivars	Environmental condition (site) and year of trial (code)						
		MIW			NPBES		IAS	
		2015	2016	2017	2016	2017	2016	2017
		M15	M16	M17	N16	N17	K16	K17
G1	MIP Bohun	7.34	7.21	5.45	6.18	6.66	5.68	4.63
G2	Imidzh	5.74	5.92	4.53	6.27	6.90	4.77	3.63
G3	Sviatomykhailivskyi	7.08	5.95	4.06	6.08	5.91	5.77	4.53
G4	Luka	6.43	4.76	5.08	5.10	6.00	4.46	4.53
G5	Helios	7.13	5.31	4.63	5.72	6.19	6.29	4.33
G6	Skarb	6.93	5.08	4.99	6.11	7.09	6.13	4.72
G7	Veles	6.62	6.03	4.29	5.95	6.43	4.91	4.34
G8	Skif	6.70	5.01	4.43	6.24	7.00	5.05	3.74
G9	Shakira	7.48	6.52	4.21	5.33	7.07	4.31	4.55
G10	Brusefield	5.78	4.92	4.29	5.10	5.95	6.37	3.97
Mean		6.72	5.67	4.60	5.81	6.52	5.37	4.30
LSD_{05}		0.27	0.35	0.29	0.46	0.29	0.19	0.37

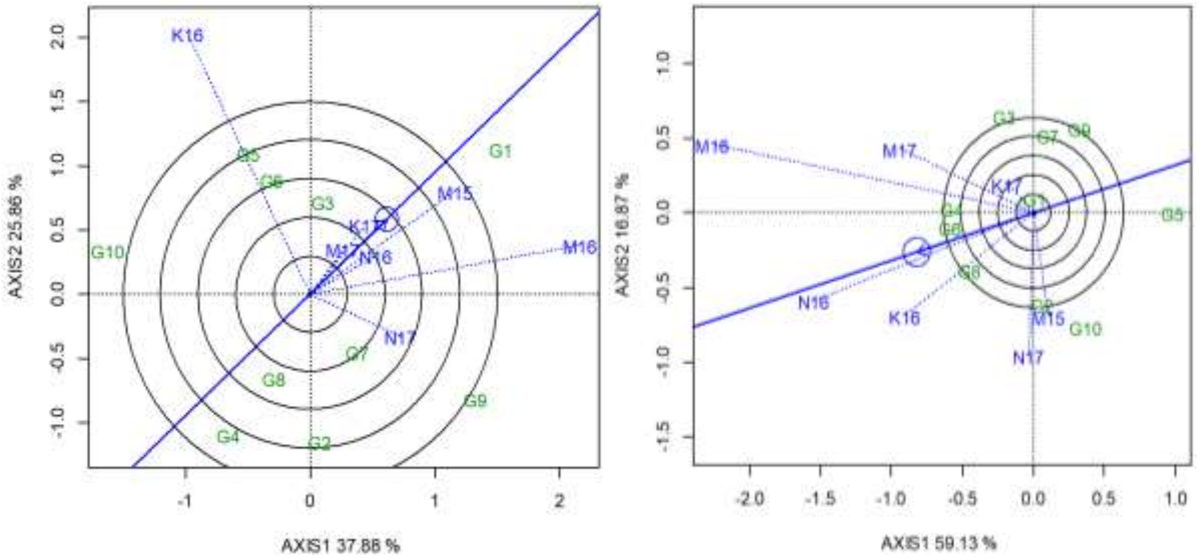
Table 2. Grain yield of spring barley breeding lines in the multi-environment trial, t/ha

Code	Standard cultivar, breeding lines	Environmental condition (site) and year of trial (code)						
		MIW			NPBES		IAS	
		2015	2016	2017	2016	2017	2016	2017
		M15	M16	M17	N16	N17	K16	K17
G1	Vzirets	7.02	6.88	4.66	6.01	6.61	5.73	4.53
G2	Nutans 4983	7.32	6.32	4.56	6.70	7.06	5.67	4.73
G3	Nutans 4890	7.35	7.59	5.27	6.01	6.38	5.21	4.32
G4	Deficiens 5005	7.63	7.88	5.20	6.73	6.55	5.66	4.20
G5	Nutans 5006	7.67	5.39	4.56	5.20	7.03	4.28	4.22
G6	Nutans 4941	7.74	7.78	5.42	7.07	7.01	5.16	4.56
G7	Nutans 4693	7.12	6.74	4.75	6.28	6.01	4.99	4.26
G8	Nutans 4855	7.57	7.41	5.37	6.80	7.15	5.69	4.12
G9	Nutans 4867	7.34	6.52	4.92	5.65	6.23	4.86	4.36
G10	Pallidum 5023	8.35	6.34	4.25	5.85	6.87	5.59	3.71
Mean		7.51	6.89	4.90	6.23	6.69	5.28	4.30
LSD_{05}		0.23	0.31	0.33	0.45	0.22	0.19	0.41

Table 3. Analysis of variance of the grain yield in spring barley, 2015–2017

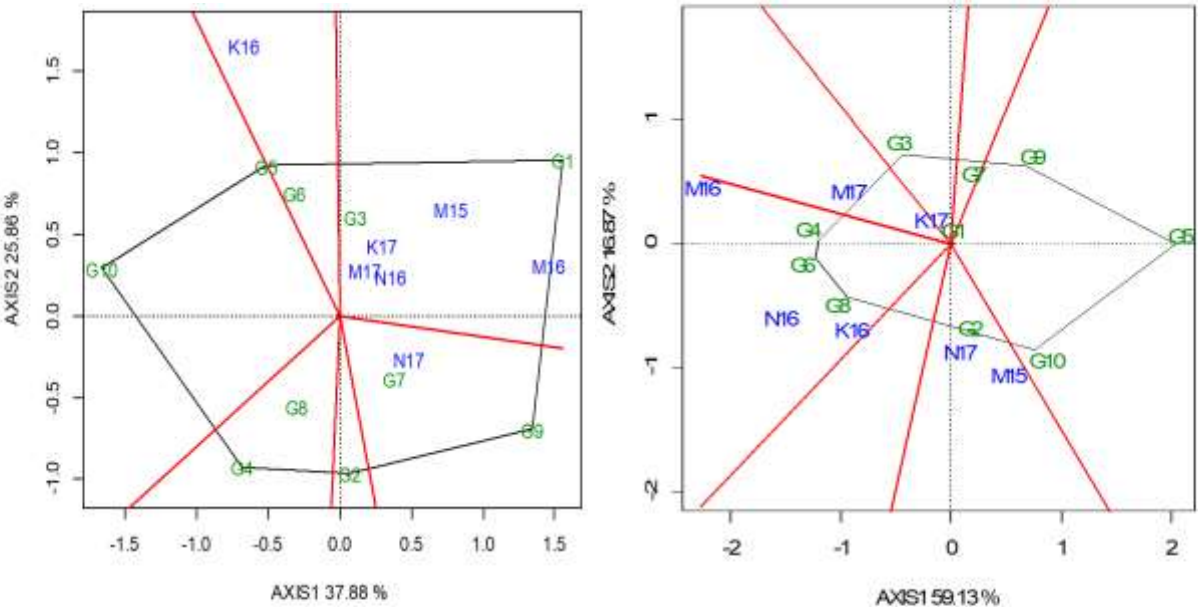
Source	Sum of squares	Degree of freedom	Mean square	Percentage relative to the sum of squares
Spring barley cultivars				
Genotype (G)	16.47	9	1.83*	7.83
Environment (E)	146.44	6	24.41*	69.62
G x E	47.44	54	0.88*	22.55
Spring barley breeding lines				
Genotype (G)	16.09	9	1.79*	5.49
Environment (E)	246.03	6	41.00*	83.95
G x E	30.95	54	0.57*	10.56

* significant at 1 % level of a probability



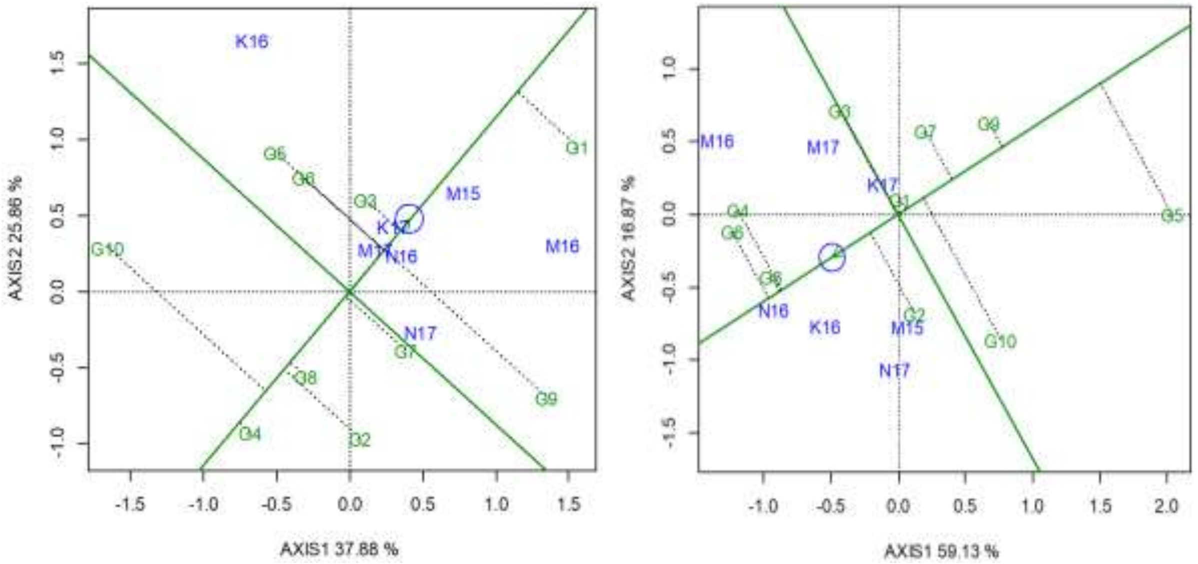
a – spring barley cultivars б – spring barley breeding lines

Fig. 1.The GGE biplot of discriminating ability against representativeness of test environments, 2015–2017



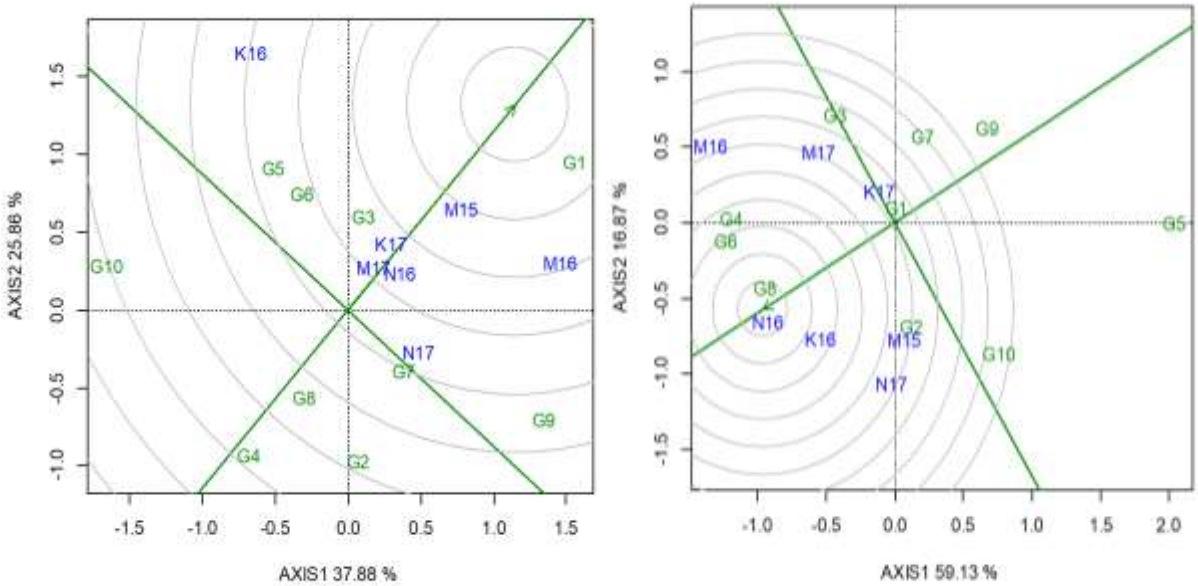
a – spring barley cultivars б – spring barley breeding lines

Fig. 2. The «which-won-where» polygon view of GGE biplot, 2015–2017



a – spring barley cultivars б – spring barley breeding lines

Fig. 3. The average-environment coordination view of the GGE biplot «mean yield against stability», 2015–2017



a – spring barley cultivars б – spring barley breeding lines

Fig. 4. The GGE biplot ranking genotypes based on both mean performance and stability respectively to the «ideal» genotype, 2015–2017