

Evaluation of grain yield performance and its stability in various spring barley accessions under condition of different agroclimatic zones of Ukraine

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Two extremely urgent problems of biological and agronomic research nowadays are ensuring an optimal balance between usage of natural resources to meet rapidly growing needs for food production and preservation of biodiversity. It is also important to extend the genetic diversity of the main crop varieties in agroecosystems. At the same time, modern varieties should be characterized by a combination of high yield and preserving yield stability under variable conditions. Solving the outlined tasks requires comprehensive research and involvement in breeding process of the genetical diversity concentrated in genebanks of the world. Barley (*Hordeum vulgare* L.) is one of the most important crops that satisfy the various needs of humanity. In respect to this, in 2020–2022, a multi-environment trial was conducted in three agroclimatic zones of Ukraine (Forest-Steppe, Polissia, and Northern Steppe). We studied 44 spring barley collection accessions of different ecological and geographical origin, different subspecies and groups of botanical varieties which were obtained from the National Center for Plant Genetic Resources of Ukraine. Statistical indices (Hom, Sc) and graphical models (GGE biplot, AMMI) were used to interpret the yield performance and its stability. Both individual ecological sites in different years and combinations of different sites and years of trials were characterized for productivity, discriminating power and representativeness. The environments differed quite strongly among themselves in terms of these indicators. It was established that most of the genotypes were characterized by higher adaptability to individual environmental conditions (stability in different years), compared to adaptability for all agroclimatic zones (wide adaptation). A strong cross-over genotype by environment interaction was found for most studied accessions. Nevertheless, both genotypes with very high stability in only one agroclimatic zone (Amil (UKR), Gateway (CAN)) and genotypes with a combination of high adaptability to one or two ecological niches and relatively higher wide adaptability (Stymul (UKR), Ly-1064 (UKR), Rannij (KAZ), Shedevr (UKR), and Arthur (CZE)) were identified. There were also the accessions which did not show maximum performance in the individual sites, but had relatively higher wide adaptability (Ly-1059 (UKR), Ly-1120 (UKR), Diantus (UKR), and Danielle (CZE)). In general, the naked barley genotypes were inferior to the covered ones in terms of yield potential and wide adaptability, but at the same time, some of them (CDC ExPlus (CAN), CDC Gainer (CAN), and Roseland (CAN)), accordingly to the statistical indicators, had increased stability in certain ecological sites. Among naked barley accessions relatively better wide adaptability according to the graphical analysis was found in the accession CDC McGwire (CAN), and by the statistical parameters CDC ExPlus (CAN) was better than standard. The peculiarities of yield manifestation and its variability in different spring barley genotypes in the multi-environment trial revealed in this study will contribute to the complementation and deepening of existing data in terms of the genotype by environment interaction. Our results can be used in further studies for developing spring barley variety models both with specific and wide adaptation under conditions of different agroclimatic zones of Ukraine. The distinguished accessions of different origin and botanical affiliation are recommended for creating a new breeding material with the aim of simultaneously increasing yield potential and stability, as well as widening the genetic basis of spring barley varieties.

Keywords: *Hordeum vulgare* L.; genotype by environment interaction; variability; adaptability; homeostaticity; GGE biplot; AMMI.

Introduction

Today's agricultural production faces a large number of difficult challenges, some of which are unprecedented in human history. Among them, we should highlight the constant growth of the global population, which requires a significant increase in the production of key food products

(Godfray et al., 2010; Foley et al., 2011). Another threat is the global climate change (increased air temperature and CO₂ concentration) which causes fluctuations in meteorological factors and can lead to a significant decrease in yield or the complete impossibility of producing certain agricultural products in some regions (Moore & Lobell, 2015; Ummenhofer & Meehl, 2017; Ramonet et al., 2020). According to most forecasting

models, the impact of climate change on crop yield will worsen unless adequate measures are taken to prevent it (Ingvordsen et al., 2015; Yawson et al., 2016). The vulnerability and fragility of global food supply chains was once again pointed out by brutal war waged by Russia against Ukraine (Bentley, 2022). Thus, most of the abovementioned problems are directly or indirectly related to irresponsible human activity (Tilman & Clark, 2014; Dietz, 2017; Poore & Nemecek, 2018). One of the aspects of a careless attitude towards the natural environment, which can have very serious consequences on a planetary scale, is the loss of biodiversity (Cardinale et al., 2012). At the current rate of population growth, this problem may become much more complicated (Simkin et al., 2022). Therefore, significant attention is paid to various measures aimed at preserving biodiversity all over the world (Visseren-Hamakers & Kok, 2022). Successfully solving this problem requires a deep understanding of many complex processes and systemic approaches (Gavin et al., 2018; Wu et al., 2022). It is necessary to find an optimal balance between usage of natural resources and their preservation (Schneiderhan-Opel & Bogner, 2019; Zabel et al., 2019).

Along with preserving the biodiversity of wild species in natural conditions, it is extremely important to have the widest possible diversity in agroecosystems (Balzan et al., 2020; Cappelli et al., 2022; Wilson et al., 2022). One aspect of this is maintaining the genetic diversity of cultivated crop varieties (Ebert & Engels, 2020; Ramirez-Villegas et al., 2022). This can significantly mitigate the negative impact of abiotic and biotic factors on agricultural production and help improve the provision of humanity with quality food products in sufficient volume. The narrowing of the genetic diversity of crop varieties due to the intensification of agricultural production is called genetic erosion (van de Wouw et al., 2010; Khoury et al., 2022). Its most characteristic manifestation is the narrowing of diversity due to the replacement of a wide range of diverse forms (e. g. landraces) by commercial varieties only from the so-called elite gene pool (Tesfaye & Sime, 2022). Genetic erosion significantly reduces adaptive responses of agricultural crops to various stress factors (Bijlsma & Loeschke, 2011).

Genebanks of plant resources play a fundamental role in preserving biological and genetic diversity (Mascher et al., 2019; Breman et al., 2021). Therefore, in most countries of the world, considerable attention is paid to the formation and preservation of genetic collections (Singh et al., 2019; Weise et al., 2020; Lennon et al., 2021). One of the most famous seed storages in the world is the Svalbard Global Seed Vault, which contains more than one million accessions (Asdal & Guarino, 2018). It should be emphasized that collection accessions are the genetic basis of successful plant breeding, as they are sources of various traits (Piechota et al., 2020; Zahn et al., 2020; Pan et al., 2022). Therefore, a comprehensive study of collection accessions concentrated in genebanks is important for their practical usage (Singh et al., 2018; Halewood et al., 2020; König et al., 2020).

Table 1
Spring barley (*Hordeum vulgare* L. sensu lato) collection accessions panel

Code	Accession	Origin	Subspecies	Botanical variety	Type of spike	Type of kernel
G1	Vzirets (Standard)	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G2	Stymul	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G3	Kontrast	UKR	<i>distichon</i> (L.) Koern.	<i>inerme</i> Koern.	two-rowed	covered
G4	Shedevr	UKR	<i>vulgare</i> L.	<i>rikotense</i> Regel.	six-rowed	covered
G5	Harant Premium	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G6	Berkut	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G7	Amil	UKR	<i>vulgare</i> L.	<i>pallidum</i> Ser.	six-rowed	covered
G8	Diantus	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G9	Krasen	UKR	<i>distichon</i> (L.) Koern.	<i>inerme</i> Koern.	two-rowed	covered
G10	Ly-1110	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G11	Ly-1114	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G12	Ly-1120	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G13	Ly-1059	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G14	Ly-1064	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G15	Ly-1078	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G16	Ly-1089	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G17	Ly-1091	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G18	Ly-1096	UKR	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G19	Polygena	SRB	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered
G20	Trebon	SRB	<i>distichon</i> (L.) Koern.	<i>mutans</i> Schübl.	two-rowed	covered

Barley (*Hordeum vulgare* L.) is one of the most important agricultural crops that satisfy the various needs of humanity (Mastanjević et al., 2017; Habschied et al., 2021). The genetic diversity of barley is greatly wide (Milner et al., 2019; Jayakodi et al., 2020; Hill et al., 2021). Despite this, a rather limited number of botanical varieties of barley are used in agricultural production (Kompanets & Kozachenko, 2017). At the same time, as an example, naked barley varieties have an advantage over traditional covered varieties due to the increased content of protein and other valuable nutrients (Vasko et al., 2018). In the aspect of widening the genetic base of new varieties comprehensive assessment and involvement in breeding process of collection accessions not only of different botanical varieties but also of different ecological origins are of practical importance (Kumar et al., 2018).

Due to the climate and weather fluctuations, there is a very urgent need for developing climate-resilient varieties (Dhankher & Foyer, 2018; Reynolds et al., 2021; Zhou et al., 2022). Genetic sources of increased adaptive potential are the basis for breeding such varieties (Galluzzi et al., 2020). It should be noted that in different environmental conditions, the same genotypes can have different value, which depends on the availability of natural resources (soil fertility, air temperature, precipitation, solar insolation, etc.) and the manifestation of a number of abiotic and biotic stressful factors. This is due to the fact that the accessions differ in their ability to utilize resources and withstand stresses (Tanaka & Nakano, 2019; Bauer & von Wirén, 2020).

Based on the above, the study of collection accessions of different origins, different subspecies and botanical varieties is relevant for the selection of both genotypes specifically adapted to certain environmental conditions and the genotypes with relatively wide adaptability, which provide the formation of a stable yield under different environmental conditions. The involvement of the selected genotypes in the breeding process will contribute to widening the genetic base of spring barley varieties and increase their adaptive potential. The obtained experimental data will contribute to the deepening of existing ideas about the genotype by environment interaction and the peculiarities of the yield manifestation level of various barley genotypes in different environmental conditions.

Materials and methods

The objects of the study were 44 spring barley collection accessions of different geographical origin and botanical varieties (Table 1). The accessions were obtained from the National Center for Plant Genetic Resources of Ukraine (Plant Production Institute named after V. Y. Yuriev of National Academy of Agrarian Sciences of Ukraine). Spring barley variety Vzirets (UKR) (G1) was used as a standard. The trial was laid out with randomized complete blocks in three replications. The size of elementary plot was 1 m².

Code	Accession	Origin	Subspecies	Botanical variety	Type of spike	Type of kernel
G21	Tobol	KAZ	<i>distichon</i> (L.) Koern.	<i>nutans</i> Schübl.	two-rowed	covered
G22	Velikan	KAZ	<i>distichon</i> (L.) Koern.	<i>nutans</i> Schübl.	two-rowed	covered
G23	Monolit	KAZ	<i>vulgare</i> L.	<i>parallellum</i> Koern.	six-rowed	covered
G24	Rannij	KAZ	<i>distichon</i> (L.) Koern.	<i>submedicatum</i> Schubl.	two-rowed	covered
G25	Karabalykskij 85	KAZ	<i>distichon</i> (L.) Koern.	<i>medicum</i> Koern.	two-rowed	covered
G26	Celinnij	KAZ	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G27	Arthur	CZE	<i>distichon</i> (L.) Koern.	<i>nutans</i> Schübl.	two-rowed	covered
G28	Danielle	CZE	<i>distichon</i> (L.) Koern.	<i>deficiens</i> (Steud.) Koern.	two-rowed	covered
G29	Inari	CZE	<i>distichon</i> (L.) Koern.	<i>deficiens</i> (Steud.) Koern.	two-rowed	covered
G30	Shuffle	CZE	<i>distichon</i> (L.) Koern.	<i>nutans</i> Schübl.	two-rowed	covered
G31	Gateway	CAN	<i>vulgare</i> L.	<i>rikotense</i> Regel	six-rowed	covered
G32	Hysky	CAN	<i>vulgare</i> L.	<i>rikotense</i> Regel.	six-rowed	covered
G33	Trail	CAN	<i>vulgare</i> L.	<i>pallidum</i> Ser.	six-rowed	covered
G34	CDC Hilose	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G35	Roseland	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G36	CDC ExPlus	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G37	CDC Gainer	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G38	CDC Freedom	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G39	Lico	CAN	<i>vulgare</i> L.	<i>pallidum</i> Ser.	six-rowed	covered
G40	Erie	CAN	<i>distichon</i> (L.) Koern.	<i>medicum</i> Koern.	two-rowed	covered
G41	CDC Clear	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G42	CDC Lophy-1	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G43	CDC McGwire	CAN	<i>distichon</i> (L.) Koern.	<i>nudum</i> L.	two-rowed	naked
G44	Clipper	AUS	<i>distichon</i> (L.) Koern.	<i>nutans</i> Schübl.	two-rowed	covered

The multi-environment trial was conducted in 2020–2022 at three scientific institutions of the National Academy of Agrarian Sciences of Ukraine, which are located in three different agroclimatic zones. The V. M. Remeslo Myronivka Institute of Wheat of the National Academy of Agrarian Sciences of Ukraine (MIW) is located in the Central part of the Ukrainian Forest-Steppe (latitude 49°64', longitude 31°08', altitude 153 m). Soils are deep, little humus, slightly leached chernozem. Humus content 3.8%, alkaline hydrolysed nitrogen (N) – 59.0 mg/kg, P₂O₅ – 220.1 mg/kg, K₂O – 96.0 mg/kg, pH = 5.8. Nosivka Plant Breeding and Experimental Station of the V. M. Remeslo MIW of NAAS (NPBES) is located in the Ukrainian Polissia (latitude 50°93', longitude 31°69', altitude 126 m). Soils are modal, have little humus, leached chernozem.

Humus content 2.6%, N – 85.0 mg/kg, P₂O₅ – 122.0 mg/kg, K₂O – 75.0 mg/kg, pH = 4.6. The Institute of Agriculture of Steppe of NAAS (IAS) is located in the Nothem Steppe of Ukraine (latitude 48°56', longitude 32°32', altitude 171 m). Soils are deep, middle humus, clayic loamic chernozem. Humus content 4.6%, N – 120.0 mg/kg, P₂O₅ – 116.0 mg/kg, K₂O – 118.0 mg/kg, pH = 5.4.

The hydrothermal regime of the 2020–2022 growing seasons of spring barley is presented in the Table 2. In all ecological niches there was found an increased monthly air temperature in June and July as compared to the long-term data, with the exception at the NPBES in July 2022. The monthly amount of precipitation in different agroclimatic zones fluctuated significantly in different years and months.

Table 2

The hydrothermal regime during spring barley growing seasons in different agroclimatic zones of Ukraine

Institution (agroclimatic zone)	Year (growing season)	Code of the environment	Monthly air temperature, °C				Monthly precipitation, mm			
			April	May	June	July	April	May	June	July
MIW (Forest-Steppe)	2022	M22	8.4	14.6	20.7	20.4	86.0	29.3	20.7	20.4
	2021	M21	7.7	14.5	20.2	23.3	47.2	87.0	100.4	111.2
	2020	M20	9.5	12.8	21.7	21.7	47.5	91.6	57.1	21.4
	Long-term	-	8.8	15.0	18.0	19.7	42.1	51.2	85.2	86.5
NPBES (Polissia)	2022	N22	7.4	13.2	19.8	19.7	76.8	31.6	79.6	71.8
	2021	N21	7.6	14.3	20.0	23.3	51.6	58.6	51.1	62.8
	2020	N20	8.9	13.6	23.4	22.2	24.2	94.9	124.3	38.3
	Long-term	-	7.9	15.0	18.4	20.2	35.6	45.1	64.5	73.0
IAS (Nothem Steppe)	2022	K22	10.2	15.3	23.2	23.0	37.5	49.1	53.7	15.9
	2021	K21	9.2	16.7	21.6	26.4	52.0	86.7	109.0	78.2
	2020	K20	10.8	14.8	23.7	25.3	6.0	91.6	20.0	41.2
	Long-term	-	8.9	15.3	18.6	20.0	36.0	45.0	66.0	72.0

Note: MIW – the V. M. Remeslo Myronivka Institute of Wheat of National Academy of Agrarian Sciences of Ukraine, NPBES – Nosivka Plant Breeding and Experimental Station of the V. M. Remeslo MIW of NAAS, IAS – Institute of Agriculture of Steppe of NAAS.

For statistical analysis of the experimental data we used homeostaticity (Hom) and breeding value (Sc) indices (Khangildin, & Litvinenko, 1981). They were calculated with formulae: $Hom = x^2/\sigma$ and $Sc = x * x_{lim} / x_{opt}$, where x is the mean yield of genotype, σ is the standard deviation, x_{lim} is the minimum yield of genotype, x_{opt} is the maximum yield of genotype. To visualize the genotype by environment interaction, the accessions were ranked accordingly to the performance level in each environment. The 1 rank corresponds to the highest yield value, and rank 44 to the lowest one. For the purpose of the evaluation of the genotype by environment interaction we applied additive main effects and multiplicative interaction (AMMI) and genotype main effects plus genotype by environment interaction (GGE biplot) graphical models (Gauch, 1988; Yan & Tinker, 2006). The AMMI and GGE biplot analyses were performed with non-commercial software GEA-R, version 4.1 (CIMMYT, Mexico). Analysis of variance of the AMMI was conducted according to the approach described by Gollob (1968). The results are given in Tables 3 and

4 as $x \pm SE$ (mean \pm standard error). Differences among the values of the experimental variants were calculated using ANOVA with Bonferroni correction and were considered significant at $P < 0.05$. Computer program Statistica 12 (TIBCO, USA) was used for calculations.

Results

The yield performance of spring barley accessions in each ecological location in 2020–2022 is shown in the Table 3. At the MIW in 2020 (M20), 15 spring barley accessions in terms of yield exceeded the standard Vzirets (UKR) (G1) (500 g/m²) or were on the same level (unreliably exceeded). These are accessions Amil (UKR) (G7), CDC McGwire (CAN) (G43), Arthur (CZE) (G27), Rannij (KAZ) (G24), Ly-1114 (UKR) (G11), Stymul (UKR) (G2), Trail (CAN) (G33), Gateway (CAN) (G31), Shedevr (UKR) (G4), Ly-1059 (UKR) (G13), Monolit (KAZ) (G23), Ly-1089 (UKR) (G16), CDC Gainer (CAN) (G37), Ly-1078

(UKR) (G15), and Ly-1096 (UKR) (G18) (507–558 g/m²) (Table 3). In 2021 (M21) eight spring barley accessions (Danielle (CZE) (G28), She-devr (UKR) (G4), Diantus (UKR) (G8), Amil (UKR) (G7), Krasen (UKR) (G9), Stymul (UKR) (G2), Ly-1091 (UKR) (G17), and CDC ExPlus (CAN) (G36)) had higher or the same yield as the standard (330–390 g/m²). In 2022 (M22) yield was higher than the standard (518 g/m²) in nine accessions Ly-1089 (UKR) (G16), Arthur (CZE) (G27), Ly-1059 (UKR) (G13), Ly-1064 (UKR) (G14), Krasen (UKR) (G9), Stymul (UKR) (G2), Amil (UKR) (G7), Harant Premium (UKR) (G5), and Ly-1120 (UKR) (G12) (527–632 g/m²).

At the NPBES in 2020 (N20), only two accessions Stymul (UKR) (G2) (490 g/m²) and CDC ExPlus (CAN) (G36) (465 g/m²) had higher yield than the standard Vzirets (UKR) (G1) (455 g/m²). The accessions Arthur (CZE) (G27), Roseland (CAN) (G35), Diantus (UKR) (G8), She-devr (UKR) (G4), Ly-1064 (UKR) (G14), CDC Gainer (CAN) (G37), and Ly-1110 (UKR) (G10) had yield lower than standard (432–442 g/m²), but they were comparatively better than other ones. In 2021 (N21), the highest yield was in the standard Vzirets (UKR) (G1) (872 g/m²). Relatively better than others (672–767 g/m²) were accessions Ly-1064 (UKR) (G14), Rannij (KAZ) (G24), Ly-1120 (UKR) (G12), Ly-1078 (UKR) (G15), Ly-1059 (UKR) (G13), Clear (CAN) (G41), CDC Gainer (CAN) (G37), She-devr (UKR) (G4), Ly-1110 (UKR) (G10), Stymul (UKR) (G2), and CDC McGwire (CAN) (G43). In 2022 (N22),

yield was higher than 1000 g/m² in the accession Rannij (KAZ) (G24) (1037 g/m²) and the standard Vzirets (UKR) (G1) (1008 g/m²). The accessions Arthur (CZE) (G27), Stymul (UKR) (G2), Ly-1064 (UKR) (G14), Krasen (UKR) (G9), Celinnyj (KAZ) (G26), and Inari (CZE) (G29) were inferior to the two mentioned above (925–978 g/m²), but they were superior to most others.

At the IAS in 2020 (K20), higher yield than in the standard (440 g/m²) was in 15 accessions Ly-1078 (UKR) (G15), Rannij (KAZ) (G24), Ly-1064 (UKR) (G14), Amil (UKR) (G7), Ly-1059 (UKR) (G13), She-devr (UKR) (G4), Monolit (KAZ) (G23), Clipper (AUS) (G44), CDC Hilose (CAN) (G34), CDC Gainer (CAN) (G37), Danielle (CZE) (G28), Ly-1091 (UKR) (G17), Diantus (UKR) (G8), Trail (CAN) (G33), and Ly-1120 (UKR) (G12) (453–536 g/m²). In 2021 (K21), yields better than the standard (517 g/m²) were in 16 accessions Ly-1120 (UKR) (G12), She-devr (UKR) (G4), Kontrast (UKR) (G3), Ly-1110 (UKR) (G10), Ly-1114 (UKR) (G10), Monolit (KAZ) (G23), Rannij (KAZ) (G24), Ly-1059 (UKR) (G13), Ly-1096 (UKR) (G18), Harant Premium (UKR) (G5), Clipper (AUS) (G44), Arthur (CZE) (G27), Amil (UKR) (G7), Ly-1091 (UKR) (G17), Diantus (UKR) (G8), Celinnyj (KAZ) (G26) (534–606 g/m²). In 2022 (K22), six accessions Arthur (CZE) (G27), Ly-1110 (UKR) (G10), I nari (CZE) (G29), Ly-1064 (UKR) (G14), Stymul (UKR) (G2), and CDC Lophy-1 (CAN) (G42) had yield higher or close to the standard (425–507 g/m²).

Table 3

Grain yield performance of spring barley accessions in all (three sites and three years) environments ($\bar{x} \pm SE$, $n = 3$, g/m²)

Code	MIW			NPBES			IAS		
	M20	M21	M22	N20	N21	N22	K20	K21	K22
G1	500±3	330±36	518±39	455±118	872±18	1008±15	440±37	517±22	425±34
G2	548±38*	336±26	540±4	490±15	679±22*	962±33*	435±25	501±2	427±35
G3	463±26*	287±24*	482±22	337±12	428±23*	727±21*	378±42*	598±41*	396±76
G4	541±11*	380±28*	453±17*	437±45	703±54*	827±20*	486±55*	599±42*	348±58*
G5	425±10*	194±32*	531±38	312±24*	502±68*	880±5*	417±31	558±41*	331±78*
G6	427±12*	218±20*	415±30*	367±28	408±20*	762±21*	426±15	507±9	396±15
G7	558±21*	354±25	532±33	415±52	475±25*	845±25*	510±20*	546±3*	377±56*
G8	499±28	362±20	442±23*	438±42	645±30*	812±16*	457±15	538±45	415±29
G9	483±33	337±24	554±7	397±81	522±18*	948±21*	426±17	478±29*	320±18*
G10	499±96	272±16*	450±18*	432±20	697±21*	840±18*	419±18	585±74*	468±20*
G11	551±34*	218±12*	358±22*	390±36	590±18*	878±25*	437±24	576±38*	396±58
G12	483±19	304±24	527±22	387±58	732±10*	808±8*	453±8	606±30*	392±31
G13	533±6*	269±22*	560±12*	360±20	723±20*	855±13*	493±15*	566±28*	359±39*
G14	481±30*	281±27*	559±16*	433±101	767±25*	960±23*	516±16*	501±9	439±14
G15	510±34	300±24	447±26*	405±67	730±26*	773±25*	536±29*	516±36	362±37*
G16	526±12*	221±28*	632±20*	390±18	565±35*	740±23*	434±28	437±26*	411±11
G17	456±27*	332±28	345±13*	363±50	537±25*	688±10*	457±21	539±14	339±26*
G18	507±45	289±19*	441±51*	353±13	535±23*	745±15*	409±15	562±39*	345±54*
G19	367±15*	300±23	488±20	243±38*	453±38*	685±30*	270±11*	370±25*	376±45*
G20	390±33*	273±19*	484±10	363±45	538±28*	728±19*	403±11	461±14*	331±53*
G21	360±10*	178±13*	337±12*	357±19	597±52*	737±29*	339±24*	490±41*	397±24
G22	433±11*	299±31	449±42*	330±26*	490±18*	757±18*	373±7*	448±12*	370±52*
G23	529±15*	258±16*	432±36*	380±35	575±30*	802±3*	483±24*	572±27*	404±42
G24	552±14*	256±17*	378±19*	345±54	378±19*	750±28*	525±4*	571±44*	379±63*
G25	419±35*	211±19*	446±5*	247±14*	538±66*	752±13*	308±8*	482±11*	339±37*
G26	477±28*	242±20*	486±8	413±15	605±35*	942±16*	357±16*	534±55	341±50*
G27	554±16*	219±30*	587±13*	442±46	622±33*	978±21*	438±16	551±8*	507±32*
G28	425±35*	390±16*	492±20	383±25	600±23*	812±10*	467±15	502±11	384±29*
G29	450±25*	329±27	428±30*	395±80	647±24*	925±20*	418±31	486±14*	447±50
G30	375±10*	278±27*	465±24*	318±28*	645±39*	853±6*	385±26*	450±31*	395±29
G31	542±31*	319±27	509±23	267±33*	556±24*	718±15*	428±28	476±18*	327±27*
G32	416±35*	174±26*	353±12*	373±8	418±18*	778±23*	425±43	468±65*	335±35*
G33	545±23*	155±20*	256±13*	278±16*	253±28*	615±30*	456±32	513±40	385±46*
G34	394±24*	301±19	362±9*	405±22	655±38*	712±24*	471±39	440±33*	359±55*
G35	499±27	273±24*	415±37*	442±77	650±28*	768±23*	351±10*	468±32*	422±26
G36	482±19	330±18	428±17*	465±44	582±8*	652±21*	437±26	512±26	381±58*
G37	525±32	240±12*	390±15*	433±48	708±20*	708±18*	468±32	470±5*	421±22
G38	459±17*	226±27*	475±28	388±46	568±13*	727±21*	361±21*	489±16*	359±36*
G39	378±37*	179±30*	363±15*	347±40	275±33*	535±28*	355±13*	457±29*	297±21*
G40	419±13*	247±21*	349±13*	398±23	645±28*	587±26*	346±8*	480±5*	274±57*
G41	482±5*	280±26*	343±17*	367±28	712±8*	790±5*	363±25*	503±67	366±11*
G42	423±26*	238±25*	457±18*	332±38*	632±28*	825±13*	325±14*	432±21*	425±17
G43	557±37*	310±30	455±23*	372±20	672±30*	868±25*	393±14*	434±26*	364±53*
G44	344±30*	174±10*	246±12*	288±20*	377±25*	552±24*	477±26	554±37*	303±32*

Note: the accession code according to the Table 1, institution abbreviation and the environment code according to the Table 2, * – significantly differs from the standard Vzirets (G1) at $P < 0.05$ according to ANOVA with Bonferroni correction.

In general, yield level of the spring barley accessions significantly varied and depended on both ecological conditions and years of trial. The change in the yield ranks indicated a strong cross-over genotype by environment interaction in most accessions, both in the individual ecologi-

cal niches in different years and in a certain year through different agroclimatic zones (Fig. 1). However, the genotype by environment interaction was significantly higher when analyzing yield ranks in three agroclimatic zones and in three years altogether.

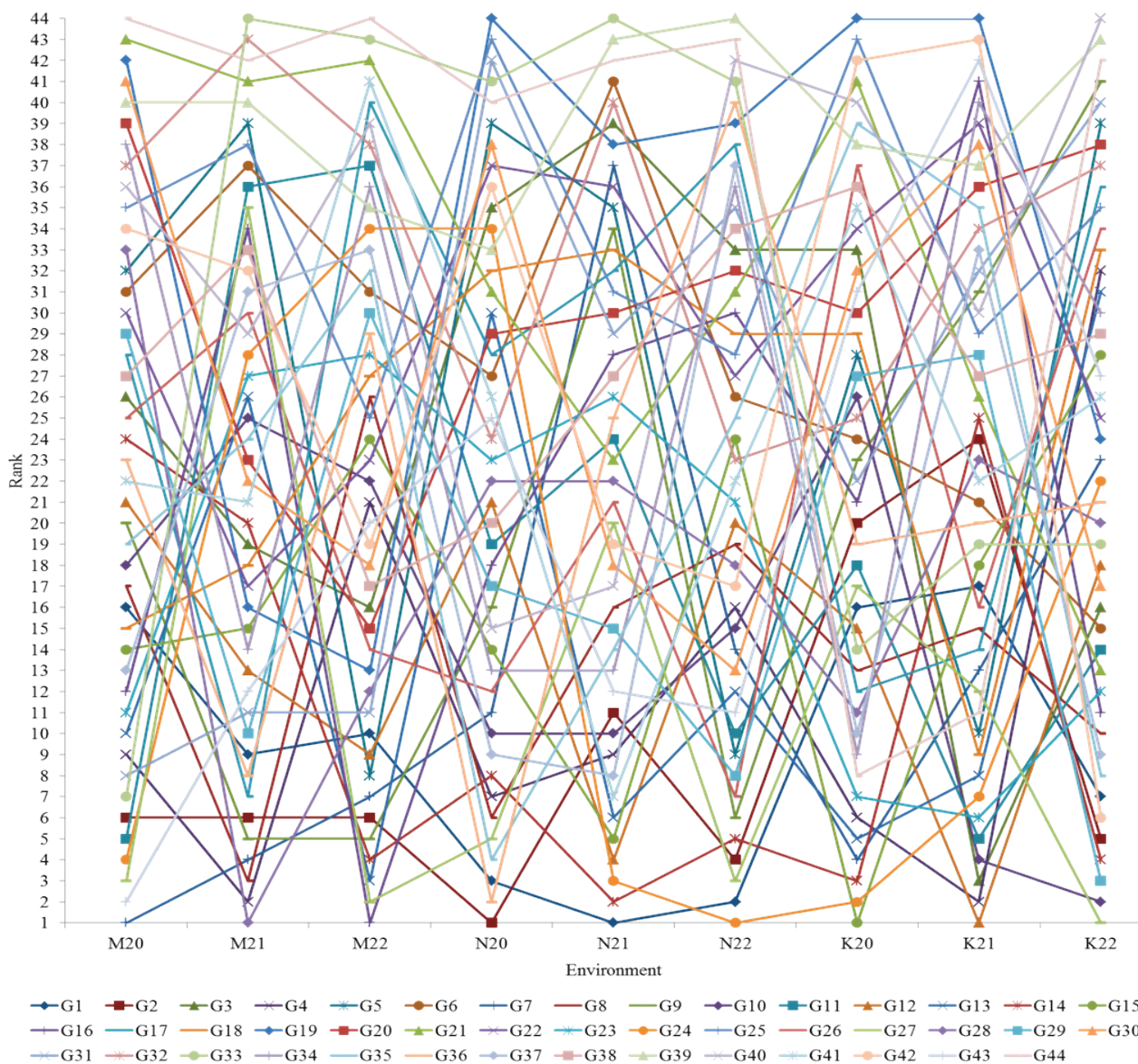


Fig. 1. Genotype by environment interaction view in terms of changing ranks in yield performance of spring barley accessions under condition of different environments (sites and years): accession code (G1...G44) according to the Table 1, environment code (M20...K22) according to the Table 2, the 1 rank corresponds to the highest yield value, and rank 44 to the lowest one

At the MIW, the largest cross-over genotype by environment interaction in different years (differences between the highest and the lowest ranks were 29–37) was found in accessions Trail (CAN) (G33), Ly-1089 (UKR) (G16), Ly-1091 (UKR) (G17), Arthur (CZE) (G27), Ly-1114 (UKR) (G11), Danielle (CZE) (G28), Harant Premium (UKR) (G5), Rannij (KAZ) (G24), and Polygena (SRB) (G19). Only the accession Stymul (UKR) (G2) did not have the cross-over interaction (sixth rank in all three years). The accessions Tobol (KAZ) (G21), Clipper (AUS) (G44), Gateway (CAN) (G31), Lico (CAN) (G39), Berkut (UKR) (G6), Amil (UKR) (G7), and Hysky (CAN) (G32) had a very low cross-over interaction (differences between ranks were 2–6). However, only the accession Amil (UKR) (G7) had a fairly high yield (481 g/m²). In the accessions Clipper (AUS) (G44), Tobol (KAZ) (G21), Lico (CAN) (G39), Hysky (CAN) (G32), and Berkut (UKR) (G6) yield was very low (255–353 g/m²).

At the NPBES, the largest genotype by environment interaction between years (differences between ranks were 29–38) was found in the accessions CDC ExPlus (CAN) (G36), Rannij (KAZ) (G24), Harant

Premium (UKR) (G5), and CDC Gainer (CAN) (G37). The accessions Vzirets (UKR) (G1), Trebon (SRB) (G20), Clipper (AUS) (G44), Trail (CAN) (G33), Danielle (CZE) (G28), Ly-1096 (UKR) (G18), Ly-1110 (UKR) (G10), Monolit (KAZ) (G23), Ly-1064 (UKR) (G14), Kontrast (UKR) (G3), and Polygena (SRB) (G19) had relatively low cross-over interaction (differences between ranks were 2–6). However, only standard Vzirets (UKR) (G1) (778 g/m²) and the accession Ly-1064 (UKR) (G14) (720 g/m²) had high yield performance. The accessions Trail (CAN) (G33), Clipper (AUS) (G44), Kontrast (UKR) (G3), and Polygena (SRB) (G19) had very low yield for this ecological niche (382–461 g/m²).

At the IAS, the largest variability between yield ranks (differences of 29–37 ranks) in different years was in the accessions CDC Lophy-1 (CAN) (G42), Clipper (AUS) (G44), Roseland (CAN) (G35), CDC Hilose (CAN) (G34), Ly-1089 (UKR) (G16), Kontrast (UKR) (G3), Shedevr (UKR) (G4), and Harant Premium (UKR) (G5). The accessions CDC ExPlus (CAN) (G36), Diantus (UKR) (G8), Trial (CAN) (G33), Monolit (KAZ) (G23), and Lico (CAN) (G39) had the lowest shifts between ranks (differences of 2–6 ranks). Among them, the accession Mo-

nolit (KAZ) (G23) was relatively better than others in yield (486 g/m²). We have also analyzed the genotype by environment interaction depending on different agroclimatic zones in each of the years. In 2020, the highest cross-over interaction (differences of 29–36 ranks) across three ecological sites was found in the accessions Clipper (AUS) (G44), Roseland (CAN) (G35), Gateway (CAN) (G31), Trail (CAN) (G33), Rannij (KAZ) (G24), CDC Hilose (CAN) (G34), and CDC McGwire (CAN) (G43). The accessions Polygena (SRB) (G19), Shedevr (UKR) (G4), CDC Gainer (CAN) (G37), and Ly-1120 (UKR) (G12) had the lowest variability (differences between ranks were 2–6). Along with that, the accession Polygena (SRB) (G19) was the poorest in yield (294 g/m²) in this year.

In 2021, the largest shifts in ranks (differences of 29–36 ranks) were found in the accessions Kontrast (UKR) (G3), Amil (UKR) (G7), Clipper (AUS) (G44), Ly-1114 (UKR) (G11), CDC McGwire (CAN) (G43), Harant Premium (UKR) (G5), and Krasen (UKR) (G9). The lowest shifts in ranks (difference of 6 ranks) were found in the accessions Lico (CAN) (G39) and CDC Freedom (CAN) (G38). But it should be mentioned that the accession Lico (CAN) (G39) had the lowest yield (304 g/m²) among studied genotypes.

In 2022 the highest variability in yield ranks (differences of 29–36 ranks) was found in the accessions Krasen (UKR) (G9), Rannij (KAZ) (G24), Harant Premium (UKR) (G5), Gateway (CAN) (G31), Tobol (KAZ) (G21), and Ly-1089 (UKR) (G16). The accessions Ly-1064 (UKR) (G14), Arthur (CZE) (G27), and Stymul (UKR) (G2) combined low changes in ranks and high level of average yield (643–691 g/m²). The accessions Clipper (AUS) (G44), Velikan (KAZ) (G22), Ly-1078 (UKR) (G15), Ly-1091 (UKR) (G17), Shuffle (CZE) (G30), Erie (CAN) (G40), Ly-1096 (UKR) (G18), and CDC Hilose (CAN) (G34) also had relatively low cross-over genotype by environment interaction in 2022, but their yield performance was not great.

There were no accessions with a small difference between the lowest and the highest yield ranks when determining their performance in the trial in general (three agro-climatic zones and three years). Thus, all accessions had a cross-over genotype by environment interaction, but each of them with a different magnitude. The difference between the marginal ranks (the lowest and the highest) varied from 11 to 40 points. The accession Lico (CAN) (G39) had the lowest difference between ranks (difference of 11 ranks). However, it also had the lowest yield (354 g/m²). That is, it was consistently poor in yield. The accessions Ly-1089 (UKR) (G16), CDC McGwire (CAN) (G43), CDC ExPlus (CAN) (G36), Trail (CAN) (G33), CDC Lophy-1 (CAN) (G42), Clipper (AUS) (G44), Kontrast (UKR) (G3), Krasen (UKR) (G9), Amil (UKR) (G7), and Roseland (CAN) (G35) were characterized by the greatest shifts in ranks (differences of 35–40 ranks).

The identification of the accessions with a combination of high yield and its relative stability in different conditions is of practical importance. At the MIW, the higher average yield in 2020–2022 in comparison to the standard Vzirets (UKR) (G1) (449 g/m²) was in the accessions Amil (UKR) (G7), Stymul (UKR) (G2), Ly-1089 (UKR) (G16), Krasen (UKR) (G9), Shedevr (UKR) (G4), Gateway (CAN) (G31), Ly-1059 (UKR) (G13), and Arthur (CZE) (G27) (453–481 g/m²). Five accessions (Danielle (CZE) (G28), Diantus (UKR) (G8), Shedevr (UKR) (G4), Inari (CZE) (G29), and Amil (UKR) (G7)) were better than the standard in terms of homeostaticity (Hom = 2090–3679) and breeding value (Sc = 294–346). In the standard Vzirets (G1) (UKR) the values of these indices were Hom = 1947 and Sc = 286. Three accessions (CDC Hilose (CAN) (G34), CDC ExPlus (CAN) (G36), and Ly-1091 (UKR) (G17)) were superior over the standard only in terms of homeostaticity (Hom = 2089–2639). The accession Stymul (UKR) (G2) had higher breeding value (Sc = 291) than Vzirets (G1) (UKR). Thus, the accessions Amil (UKR) (G7) and Shedevr (UKR) (G4) prevailed over the standard in terms of yield, homeostaticity and breeding value indices. The accession Stymul (UKR) (G2) was better than Vzirets (G1) (UKR) in terms of yield and breeding value.

At the NPBS, the highest average yield over three years was in the standard Vzirets (UKR) (G1) (778 g/m²). There were four accessions (CDC ExPlus (CAN) (G36), CDC Gainer (CAN) (G37), Roseland (CAN) (G35), and Stymul (UKR) (G2)) which had higher homeostaticity (Hom = 2125–3399) and breeding value (Sc = 362–404) than the standard

(Hom = 2102; Sc = 351). Among them the accession Stymul (UKR) (G2) had relatively higher yield (710 g/m²). Another four accessions (Erie (CAN) (G40), Shedevr (UKR) (G4), CDC Hilose (CAN) (G34), and Diantus (UKR) (G8)) were better than the standard only in terms of homeostaticity (Hom = 2133–2290).

At the IAS, in 2020–2022, 12 accessions (Arthur (CZE) (G27), Rannij (KAZ) (G24), Ly-1110 (UKR) (G10), Monolit (KAZ) (G23), Ly-1064 (UKR) (G14), Ly-1120 (UKR) (G12), Shedevr (UKR) (G4), Amil (UKR) (G7), Ly-1059 (UKR) (G13), Ly-1078 (UKR) (G15), Diantus (UKR) (G8), and Ly-1114 (UKR) (G11)) had better yield performance (470–499 g/m²) than Vzirets (G1) (UKR) (461 g/m²). Six accessions (Ly-1089 (UKR) (G16), CDC Gainer (CAN) (G37), Inari (CZE) (G29), Ly-1064 (UKR) (G14), Stymul (UKR) (G2), and Arthur (CZE) (G27)) were superior (Hom = 4350–12803; Sc = 387–412) over standard (Hom = 4290; Sc = 379) by both statistical indices. Two accessions were better than Vzirets (G1) only by homeostaticity index. They are Shuffle (CZE) (G30) (Hom = 4815) and CDC McGwire (CAN) (G43) (Hom = 4434). Therefore, two accessions (Arthur (CZE) (G27) and Ly-1064 (UKR) (G14)) combined high level of yield with high level of homeostaticity and breeding value indices.

In the trial in general the highest average yield was in the standard Vzirets (UKR) (G1) (563 g/m²). The accessions Ly-1064 (UKR) (G14), Stymul (UKR) (G2), Arthur (CZE) (G27), Rannij (KAZ) (G24), and Shedevr (UKR) (G4) were statistically on the same level as the standard (530–548 g/m²), since their yield was within the limits of reliability. Two of mentioned accessions were superior to Vzirets (UKR) (G1) in terms of homeostaticity and breeding value indices (Hom = 1413; Sc = 184). These are accessions Stymul (UKR) (G2) (Hom = 1637; Sc = 191) and Shedevr (UKR) (G4) (Hom = 1803; Sc = 224). Only in homeostaticity were the following accessions better than standard; Ly-1064 (UKR) (G14) (Hom = 1500) and Arthur (CZE) (G27) (Hom = 1469).

The accessions CDC ExPlus (CAN) (G36), Danielle (CZE) (G28), Diantus (UKR) (G8), Ly-1091 (UKR) (G17), Amil (UKR) (G7), Ly-1078 (UKR) (G15), Ly-1120 (UKR) (G12), and CDC Hilose (G34) were inferior to the standard in average yield Vzirets (UKR) (G1), but they surpassed it in both statistical indices (Hom = 1496–2284; Sc = 193–240). There were also 12 accessions with a homeostaticity index higher than in the standard (Hom = 1420–1599). Among them, relatively better yield performance was found in the accessions Ly-1110 (UKR) (G10) (518 g/m²) and Ly-1059 (UKR) (G13) (524 g/m²).

The AMMI and GGE biplot models were used for in-depth analysis of the genotype by environment interaction, characterization and comparison of different test environments, as well as differentiation of accessions and selection among them of the best genotypes in terms of yield performance and its stability. The analysis of variance of the AMMI model for yield is given in the Table 5. Experimental data from each ecological site in different years were analyzed separately, as well as generalized data in the trial in general. The highest part of sum square for the genotype (25.2%) and for the genotype by environment interaction (23.8%) was found at the IAS. The largest percentage of year conditions was at the NPBS (72.9%). In the trial in general, the significance of the environment (sites and years) was the highest (76.6%). The contribution of the genotype by environment interaction was estimated as 14.3%. Despite the lowest value of the genotype (9.1%) it was statistically reliable. The data obtained pointed to the huge variability of environmental conditions (combination of different ecological niches and years) and strong cross-over genotype by environment interaction. At the same time it highlighted that in the studied panel of accessions there were genotypes with a different reaction to different ecological and year conditions. Respectively it gives the possibility for identification of the accessions with desirable yield performance.

The pattern of distribution of spring barley accessions in the two-component space of the AMMI1 biplot, which formed by the first principal component (Factor 1) and mean yield (Yield), is shown in Figure 2. There are represented values of individual accession mean yield (labeled as G1...G44) and the productivity of the environments (mean yield in the whole accession panel in the particular ecological niche and in the particular year) (labeled as M20...K22).

Table 4Spring barley accessions mean yield in different environments and parameters of homeostaticity and breeding value, 2020–2022 ($\bar{x} \pm SE$, $n = 3$)

Code	MIW			NPBES			IAS			General		
	mean	Hom	Sc	mean	Hom	Sc	mean	Hom	Sc	mean	Hom	Sc
G1	449 ± 26	1947	286	778 ± 50	2102	351	461 ± 31	4290	379	563 ± 36	1413	184
G2	475 ± 23	1878	291	710 ± 23*	2125	362	454 ± 21	5057	387	546 ± 22	1637	191
G3	410 ± 24*	1568	244	497 ± 18*	1212	230	457 ± 53	1710	289	455 ± 32*	1524	180
G4	458 ± 19	2611	322	656 ± 40*	2156	346	478 ± 52	1820	278	530 ± 37	1803	224
G5	383 ± 27*	852	140	565 ± 32*	1102	200	435 ± 50	1652	258	461 ± 36*	1088	102
G6	353 ± 21*	1060	180	512 ± 23*	1209	247	443 ± 13	3394	345	436 ± 19*	1318	125
G7	481 ± 26*	2090	306	578 ± 34*	1436	284	478 ± 26	2557	329	512 ± 29*	1809	215
G8	434 ± 24	2736	315	632 ± 29*	2133	341	470 ± 29	3525	362	512 ± 27*	1891	228
G9	458 ± 21	1897	279	622 ± 40*	1338	260	408 ± 22*	2073	273	496 ± 28*	1315	168
G10	407 ± 43*	1387	222	656 ± 20*	2078	337	491 ± 37	2826	352	518 ± 33*	1599	168
G11	376 ± 22*	844	148	619 ± 26*	1563	275	470 ± 40	2344	323	488 ± 30*	1264	121
G12	438 ± 21	1619	252	642 ± 25*	1836	307	484 ± 23	2121	313	521 ± 23*	1631	196
G13	454 ± 13	1279	218	646 ± 18*	1628	272	473 ± 28	2126	300	524 ± 20*	1488	165
G14	440 ± 24	1352	221	720 ± 50*	1946	325	485 ± 13	5747	412	548 ± 29	1500	161
G15	419 ± 28*	1628	246	636 ± 40*	2010	333	471 ± 34	2342	319	509 ± 34*	1640	197
G16	459 ± 20	989	160	565 ± 25*	1824	298	427 ± 22*	12803	402	484 ± 22*	1544	144
G17	378 ± 23*	2089	275	529 ± 28*	1724	279	445 ± 20	1968	280	451 ± 24*	1678	217
G18	412 ± 38*	1518	235	544 ± 17*	1512	258	439 ± 36	1727	270	465 ± 30*	1549	180
G19	385 ± 19*	1552	236	461 ± 35*	960	164	339 ± 27*	1933	243	395 ± 27*	1155	140
G20	383 ± 20*	1385	216	543 ± 31*	1617	271	399 ± 26*	2445	286	442 ± 26*	1450	166
G21	292 ± 12*	855	144	563 ± 33*	1652	273	409 ± 30*	2191	283	421 ± 25*	1077	101
G22	394 ± 28*	1877	262	526 ± 21*	1281	229	397 ± 24*	3534	327	439 ± 24*	1432	173
G23	406 ± 22*	1202	198	586 ± 23*	1625	278	486 ± 31	2807	343	493 ± 25*	1577	158
G24	395 ± 17*	1050	183	710 ± 37*	1452	236	492 ± 37	2415	327	533 ± 30	1180	131
G25	359 ± 20*	1002	170	512 ± 31*	1035	168	376 ± 19*	1529	241	416 ± 23*	1040	117
G26	402 ± 19*	1168	200	653 ± 22*	1596	287	411 ± 40*	1574	262	489 ± 27*	1182	126
G27	453 ± 19	1011	170	681 ± 34*	1696	307	499 ± 18*	4350	396	544 ± 24	1469	122
G28	436 ± 24	3679	346	598 ± 19*	1672	283	451 ± 18	3338	345	495 ± 20*	1772	234
G29	402 ± 27*	2510	294	656 ± 41*	1621	280	451 ± 32	5980	388	503 ± 34*	1402	179
G30	372 ± 20*	1483	223	606 ± 24*	1360	226	410 ± 29*	4815	351	463 ± 24*	1189	151
G31	456 ± 27	1728	268	514 ± 24*	1153	191	410 ± 24*	2211	282	460 ± 25*	1491	171
G32	314 ± 25*	785	131	523 ± 16*	1234	251	409 ± 48*	2461	293	416 ± 29*	1078	93
G33	319 ± 18*	502	91	382 ± 25*	723	157	451 ± 39	3176	339	384 ± 27*	938	97
G34	353 ± 17*	2639	270	591 ± 28*	2137	336	423 ± 42*	3111	323	455 ± 29*	1496	193
G35	396 ± 29*	1373	217	620 ± 42*	2324	356	414 ± 23*	2909	310	476 ± 31*	1510	169
G36	414 ± 18*	2224	283	566 ± 24*	3399	404	443 ± 37	2979	329	474 ± 26*	2284	240
G37	385 ± 20*	1037	176	617 ± 29*	2395	377	453 ± 20	7431	406	485 ± 23*	1577	164
G38	386 ± 24*	1072	184	561 ± 27*	1860	300	403 ± 24*	2189	296	450 ± 25*	1420	140
G39	307 ± 27*	846	145	386 ± 34*	1107	198	370 ± 21*	1683	240	354 ± 27*	1219	118
G40	338 ± 16*	1322	199	543 ± 25*	2290	336	367 ± 23*	1283	209	416 ± 21*	1289	159
G41	369 ± 16*	1312	214	623 ± 14*	1722	289	411 ± 34*	2112	297	467 ± 21*	1243	166
G42	373 ± 23*	1178	194	596 ± 26*	1430	240	394 ± 17*	2581	296	454 ± 22*	1168	131
G43	441 ± 30	1564	245	637 ± 25*	1623	273	397 ± 31*	4434	332	492 ± 29*	1349	176
G44	255 ± 17*	763	129	406 ± 23*	1229	212	444 ± 31	1538	243	368 ± 24*	1012	116

Note: accession code according to the Table 1, institution abbreviation according to the Table 2, mean – mean yield in three years (g/m^2), Hom – homeostaticity index, Sc – breeding value index, * – significantly differs from the standard Vzirets (G1) at $P < 0.05$ according to ANOVA with Bonferroni correction.

Table 5

Analysis of variance of the AMMI model (Golob's test) for grain yield in the spring barley accessions and sum of squares decomposition of the genotype by environment interaction

Source of variation	MIW			NPBES			IAS			General		
	SS	df	%	SS	df	%	SS	df	%	SS	df	%
Genotype (G)	1007810.2	43	20.2	2763173.1	43	17.5	570450.8	43	25.2	2795152.5	43	9.1
Environment (E)	3144025.4	2	63.1	11503243.1	2	72.9	1151583.5	2	50.9	23655779.7	8	76.6
G × E interaction	831674.8	86	16.7	1502799.8	86	9.5	538309.9	86	23.8	4419066.0	344	14.3
Factor 1	502347.7	44	60.4	768405.0	44	51.1	338428.5	44	62.9	1681186.4	50	38.0
Factor 2	329327.1	42	39.6	734394.7	42	48.9	199881.4	42	37.1	929377.8	48	21.0
Factor 3	0.0	40	0.0	0.0	40	0.0	0.0	40	0.0	629788.9	46	14.3
Factor 4	-	-	-	-	-	-	-	-	-	316412.7	44	7.2
Factor 5	-	-	-	-	-	-	-	-	-	273253.4	42	6.2
Factor 6	-	-	-	-	-	-	-	-	-	228086.3	40	5.2
Factor 7	-	-	-	-	-	-	-	-	-	197572.9	38	4.5
Factor 8	-	-	-	-	-	-	-	-	-	163387.7	36	3.7
Factor 9	-	-	-	-	-	-	-	-	-	0.0	34	0.0
Residuals	168884.0	264	0.0	299245.3	264	0.0	301638.7	264	0.0	769768.0	792	0.0

Note: Factor 1...9 – principal components, SS – sum of squares, df – degree of freedom, % – percent of contribution of the particular source in general variation, institution abbreviation according to the Table 2.

A graphical analysis was conducted for individual sites (agroclimatic zones) in different years and for the trial in general (three sites and three years). At the MIW the highest yield was in 2020 (M20) (472 g/m^2) and

the lowest yield was in 2021 (M21) (272 g/m^2) (Fig. 2a). At the NPBES the highest yield was produced in 2022 (N22) (793 g/m^2) and the lowest one was in 2020 (N20) (376 g/m^2) (Fig. 2b). At the IAS the highest yield

was produced in 2021 (K21) (508 g/m²) and the lowest one was in 2022 (K22) (378 g/m²) (Fig. 2c). It is noticeable that in the different agroclimatic zones yield had its highest manifestation level in different years. Characterising all nine environments (three sites in three years) it should be mentioned that the highest productivity (793 g/m²) in the trial in general was in the environment N22 (at the NPBES in 2022) and the lowest (272 g/m²) was in the environment M21 (at the MIW in 2021) (Fig. 2d). According to AMMI model the most desirable are genotypes with a combination of high yield on the Yield axis and the closest localization to zero point on the Factor 1 axis. Thus, the accessions Amil (UKR) (G7), Stymul (UKR) (G2), and Gateway (G31) should be highlighted at the MIW. At the

NPBES optimal performance was found in the accession Ly-1064 (UKR) (G14). More shifted than the mentioned one from zero point was the standart Vzirets (UKR) (G1), as well as the accessions Stymul (UKR) (G2) and Rannij (KAZ) (G24). The accession Ly-1064 (UKR) (G14) had such characteristics at the IAS. In the trial in general, among accessions with combination of high yield and closer location to zero on Factor 1 axis were the accessions Shedevr (UKR) (G4) and Diantus (UKR) (G8). A number of accessions (Stymul (UKR) (G2), Ly-1078 (UKR) (G15), Ly-1110 (UKR) (G10), Ly-1120 (UKR) (G12), Athrur (CZE) (G27), Ly-1059 (UKR) (G13), Ly-1064 (UKR) (G14) etc.) were more dislocated from zero point than two mentioned above, but they were better than the standard.

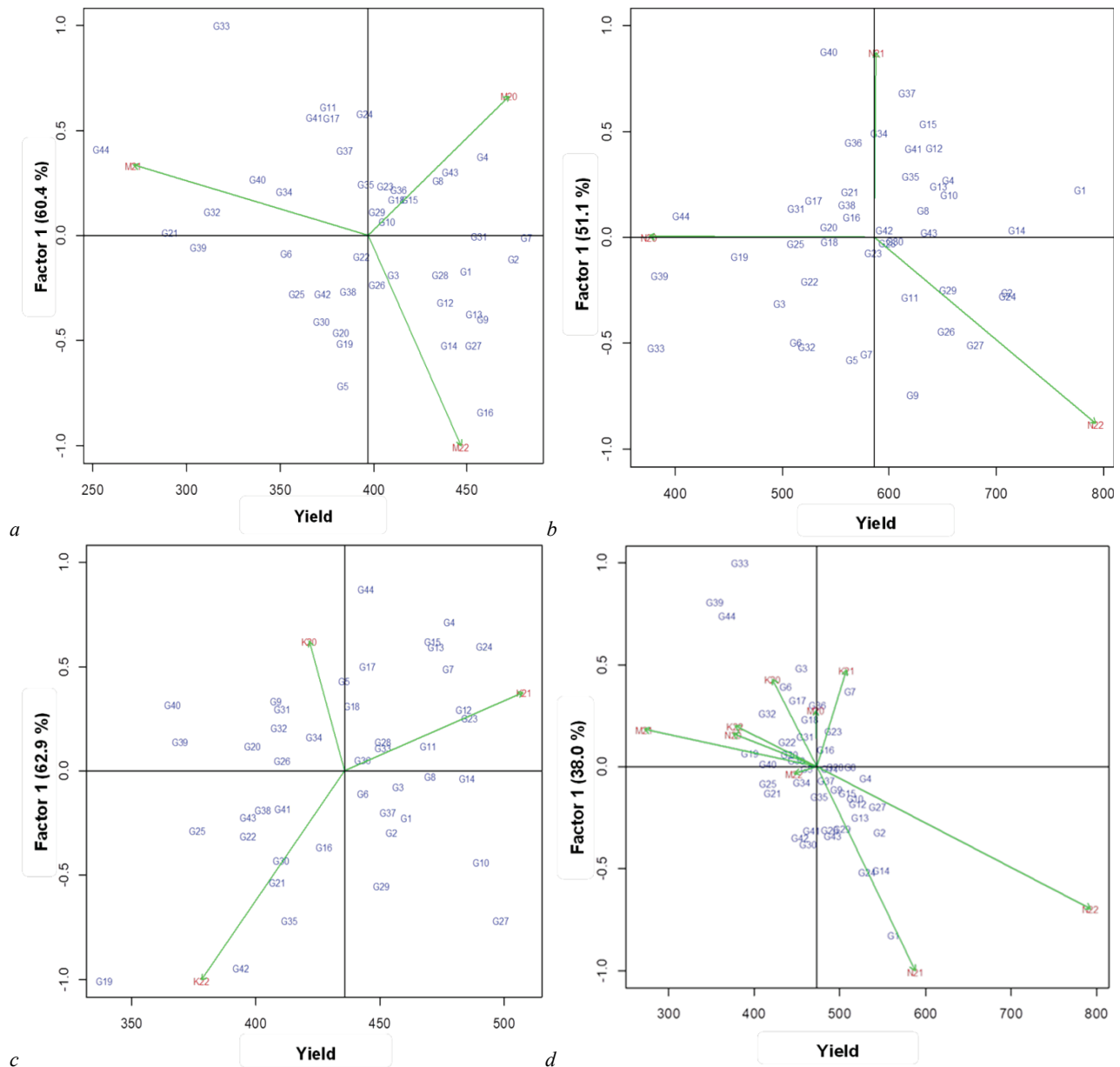


Fig. 2. The AMMI1 biplot dispersion of spring barley accessions and test environments in coordinates of mean yield (Yield) and the first principal component (Factor 1): *a* – MIW, *b* – NPBES, *c* – IAS, *d* – the trial in general, accession code according to the Table 1, environment code according to the Table 2

The AMMI2 biplot is formed by the first (Factor 1) and second (Factor 2) principal components (Fig. 3). Peculiarities in distribution of the environments and the accessions also confirmed that conditions of individual years in given ecological sites and adaptive reactions of genotypes to them significantly differed (Fig. 3a–c). It is shown by localization of the environments in different sectors. In the trial in general three environments (N21, N22, and M22) fell in three different sectors (Fig. 3d). Two environments (N20 and M21) were located in one sector and formed a mega-

environment. A second mega-environment was formed with three other environments (M20, K21, and K22). In this sector, but practically on the line which separates it from the first mega-environment, there was placed vector of the environment K20. On the angles of the polygonal figures there were located accessions with the highest reaction to the conditions of the particular environment (mega-environment) if the latter is in the same sector. The accessions which lay closer to the center of the AMMI2 biplot had lower reaction to the conditions of the particular environments.

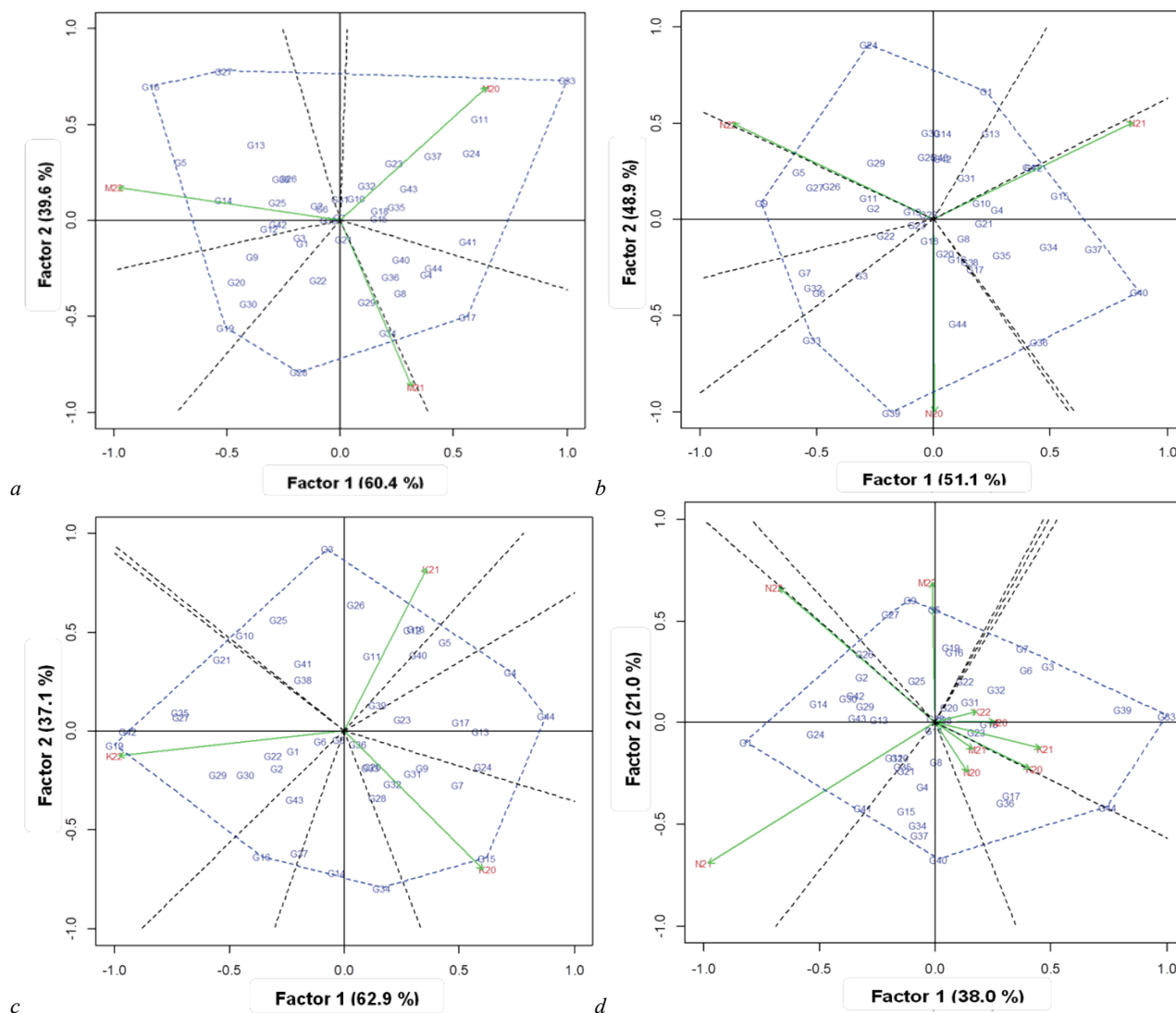


Fig. 3. The AMMI2 biplot dispersion of spring barley genotypes and test environments in coordinates of the first two principal components (Factor 1 vs Factor 2): *a* – MIW, *b* – NPBES, *c* – IAS, *d* – the trial in general, accession code according to the Table 1, environment code according to the Table 2

The GGE biplot discriminating power and representativeness of the test environments also indicate differences in peculiarities of yield manifestation level both in the individual ecological niches in the different years and in the trial in general (Fig. 4). At the MIW the most distant from each other were vectors of the environments (years) M20 and M22 (Fig. 4a). At the same time, the environment M22 had the greatest discriminating power. The environment M21 was the most representative. At the NPBES the vectors of the environments N20 and N21 (Fig. 4b) were very close to each other. On the other hand, they were quite different in terms of discriminating power. The environments N21 and N22 had the greatest distance between their vectors, but both had high discriminating power. At the IAS vectors of the environments K20 and K21 were close to each other and had small differences in discriminating power (Fig. 4c). The vector of the environment K22 was significantly remote from the two abovementioned. In the trial in general the greatest discriminating power was found in the environments N21 and N22 (Fig. 4d). The environment M22 was slightly inferior to them in discriminating power. At the same time, the environments N21 and M22 were the most distant from each other. The other environments were inferior to those mentioned above in terms of discriminating power. The environments K21 and K22 were the nearest to the average environment axis (AEA) and, accordingly, were the most representative.

The peculiarities of the test environments discussed above are quite clearly visible on the GGE biplot “which-won-where” view (Fig. 5). At the MIW, the environments were separated into different sectors (Fig. 5a). In the sector with the environment M22 on the angle of the polygon was located accession Ly-1089 (UKR) (G16). According to GGE biplot mod-

el it was the best in the conditions of the environment M22. The other accessions located in this sector also had relatively better performance in the environment M22 as compared to the two other environments (M20 and M21). In the sector with the environment M21 the accessions Amil (UKR) (G7) and Shedevr (UKR) (G4) were better than the others, since these accessions are located on the angles of the polygonal figure. The accessions Stymul (UKR) (G2) and CDC McGwire (CAN) (G43) were close to the two mentioned above. The environment M20 placed on the dividing line between the sector with the environment M21 and the sector without environments and accessions. At the NPBES two environments (N20 and N21) fell into one sector (Fig. 5b). In this sector standard Vzires (UKR) (G1) and the accession Rannij (KAZ) (G24) were superior to the others. The accessions Arthur (CZE) (G27) and Celinnyj (KAZ) (G26) were placed on the line which separated this sector from the sector with the environment N22. At the IAS the environments K20 and K21 fell into one sector (Fig. 5c). On the top of the polygon in this sector there were placed the accessions Rannij (KAZ) (G24) and Shedevr (UKR) (G4). In the sector with the environment K22 on the top of the polygon was the accession Arthur (CZE) (G27). Two mega-environments were found when analysis was performed for the trial in general (Fig. 5d). The first mega-environment included environments M21, N21, N20, K20, K21, and K22.

Thus, it was formed by all years at the IAS, two years at the NPBES and one year at the MIW. However, it should be mentioned that the environment K22 was placed very close to the dividing line between two mega-environments, and the environment K21 was located practically in the origin of the biplot.

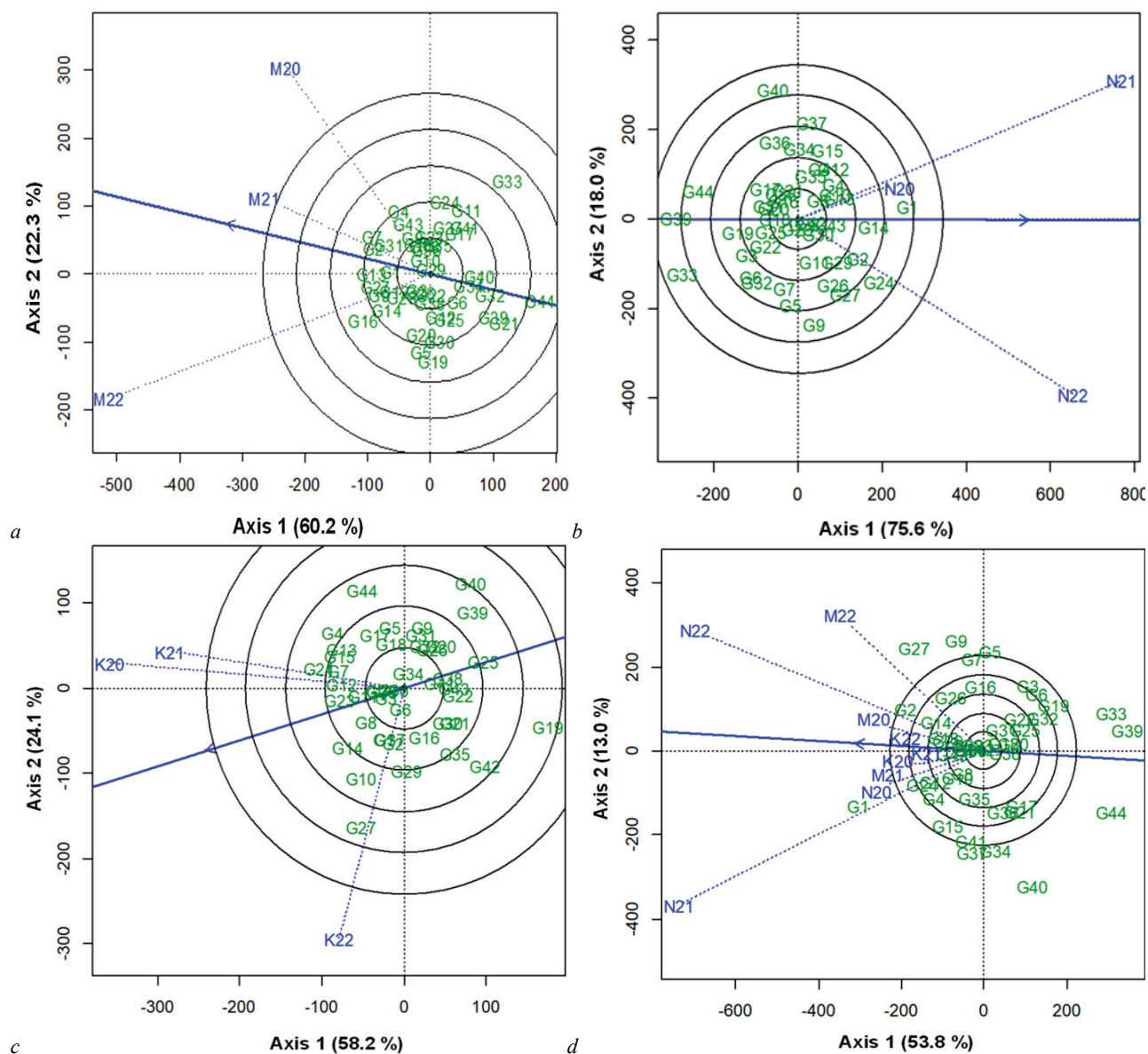


Fig. 4. The GGE biplot discriminating power and representativeness of test environments:

a–MIW, *b*–NPBES, *c*–IAS, *d*–the trial in general, accession code according to the Table 1, environment code according to the Table 2

The second mega-environment was formed by environments M22, M20, and N22. At the same time, these environments were placed not far from dividing line between two mega-environments. The undisputed winner in the first mega-environment was Vzirets (UKR) (G1). There was the accession Krasen (UKR) (G9) in the second mega-environment on the oblique angle. There was the accession Arthur (CZE) (G27) on the dividing line between two mega-environments and very close to the environment N22. The accession Celinyj (KAZ) (G26) was placed on the same line but more close to the origin of the GGE biplot. The accessions which fell into the sectors which contained mega-environments had better performance than the other ones which were in the sectors without environments.

On the GGE biplot “mean yield against stability” view, in the direction indicated with the arrow on the AEA, the accessions were placed according to their mean performance in all studied environments (Fig. 6). The ranking is performed in values of two first principal components. The vertical line which intersected the origin of the GGE biplot represents a mean performance of all accessions in all environments. At the MIW the best was the accession Amil (UKR) (G7) and the worst was the accession Clipper (AUS) (G44) (Fig. 6a). The accession Amil (UKR) (G7) was placed on the AEA, which points to its optimal yield performance among studied accessions panel at the MIW in each of three years of trial. The accession displacements from AEA corresponds to their significant

reaction to conditions of individual environments. This happens when performance of one or another accession in a particular environment significantly differs from the general trend of all accessions in the trial. For example, the accession Trail (CAN) (G33) was the most displaced in the direction towards the environment M20. The accessions Ly-1089 (UKR) (G16) and Harant Premium (UKR) (G5) were shifted towards the environment M22. The accessions Stymul (UKR) (G2) and Gateway (CAN) (G31) combined fairly yield and good stability. The accessions Ly-1110 (UKR) (G10) and Inari (CZE) (G29) also had good stability but lower than in two mentioned above ones. The accessions Berkut (UKR) (G6), Lico (CAN) (G39), and Tobol (KAZ) (G21) had very high stability, but very poor yield performance. At the NPBES the best in yield performance was standard Vzirets (UKR) (G1), and the worst was the accession Lico (CAN) (G39) (Fig. 6b). Along with that, both genotypes had high stability. That is, the first was consistently high-yielding, the latest was consistently low-yielding. The combination of fair yield and high stability was demonstrated by the accession Ly-1064 (UKR) (G14). At the IAS the accessions with the highest mean performance were significantly shifted from AEA (Fig. 6c). The accession Rannij (KAZ) (G24) was displaced towards the environments K20 and K21, and the accession Arthut (CZE) (G27) was towards the environment K22. The accession Ly-1064 (UKR) (G14) had slightly lower average performance than them, but it had a high stability.

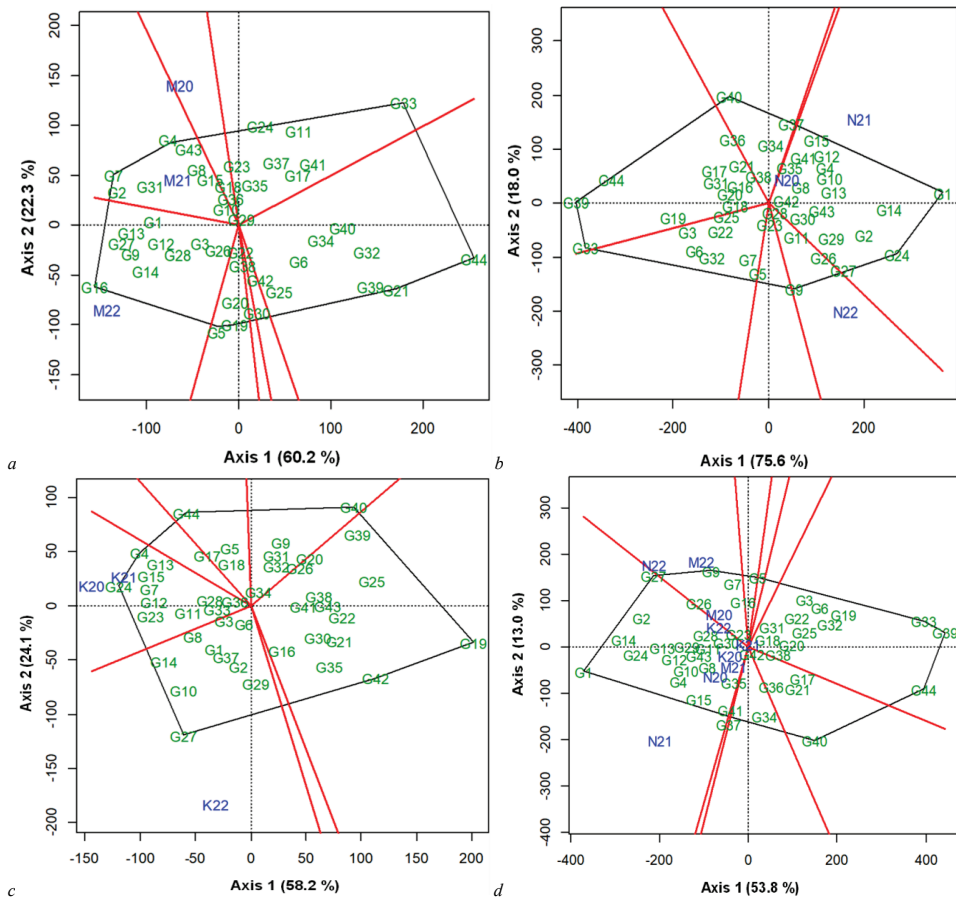


Fig. 5. The GGE biplot “which-won-where” view: *a*–MIW, *b*–NPBES, *c*–IAS, *d*–the trial in general, accession code according to the Table 1, environment code according to the Table 2

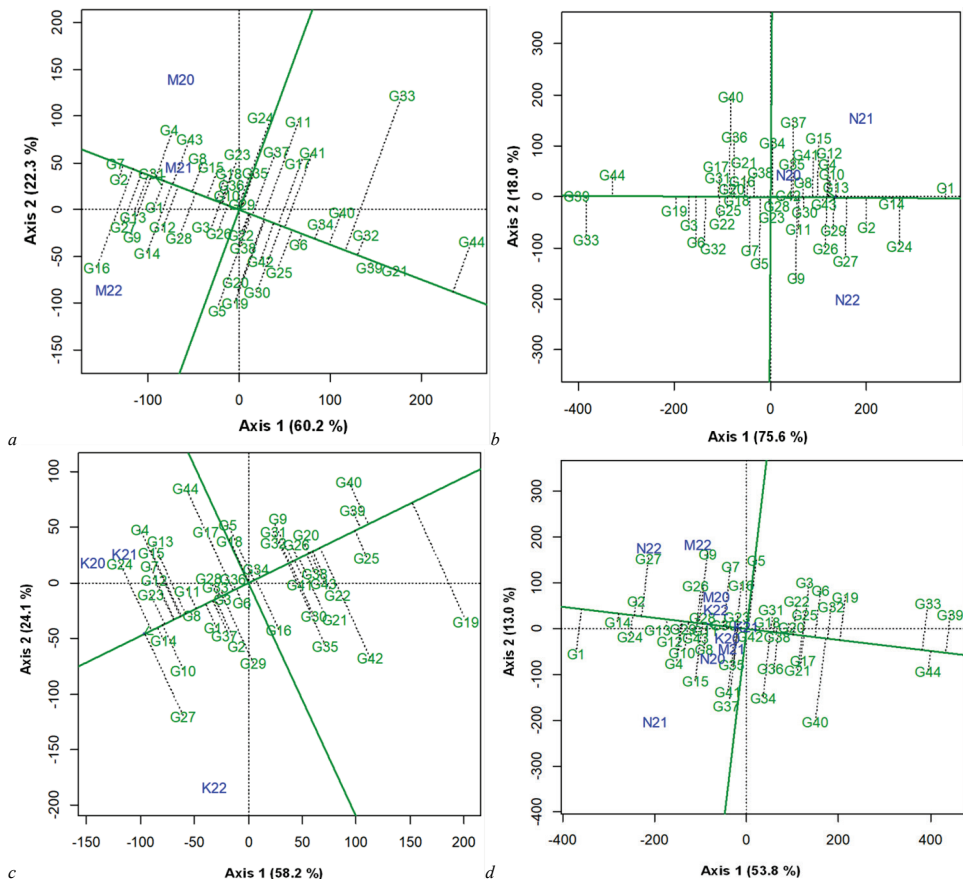


Fig. 6. The average-environment coordination view of the GGE biplot “mean yield against stability”: *a*–MIW, *b*–NPBES, *c*–IAS, *d*–the trial in general, accession code according to the Table 1, environment code according to the Table 2

The accessions Ly-1110 (UKR) (G10) and Monolit (KAZ) (G23) were characterized by lower yield than Rannij (KAZ) (G24) and Arthut (CZE) (G27) but by better stability than them. A high stability was found in the accession Diantus (UKR) (G8). The worst in terms of yield and its stability was the accession Polygena (SRB) (G19). In the trial in general the highest mean yield was in the standard Vzirets (UKR) (G1) (Fig. 6d). The accessions Ly-1064 (UKR) (G14), Stymul (UKR) (G2), and Rannij (KAZ) (G24) were slightly inferior to it in yield but better in stability. The accessions Lico (CAN) (G39), Clipper (AUS) (G44), and Trail (CAN) (G33) had the poorest yield performance.

The considered peculiarities of the accessions in terms of the yield manifestation level and its relative stability over the environments determined their ranking with reference to the “ideal genotype” (Fig. 7). The latest theoretically should be located in the centre of the central circles. At the MIW the accession Amil (UKR) (G7) localization was exactly matched with the “ideal genotype” (Fig. 7a). The accessions Stymul (UKR) (G2) and Gateway (CAN) (G31) were also very close to it. At the NPBES the best was standard Vzirets (UKR) (G1) (Fig. 7b). In addition to the mentioned, the accession Ly-1064 (UKR) (G14) should

also be highlighted, as well as the accessions Stymul (UKR) (G2) and Rannij (KAZ) (G24). At the IAS all accessions were quite remote from the “ideal genotype” as they were located even outside the entire set of central circles (Fig. 7c). The accession Ly-1064 (UKR) (G14) could be highlighted as relatively better than the others. In the trial in general closer than others to the “ideal genotype” was the accession Ly-1064 (UKR) (G14) (Fig. 7d). Not far from it, but in the second circle were the accessions Stymul (UKR) (G2), Rannij (KAZ) (G24), and Ly-1059 (UKR) (G13). The accession Arthur (CZE) (G27) was placed between the second and the third circles but more remote from the AEA. The standard Vzirets (UKR) (G1) was superior to these accessions in average yield but was more displaced than them from the AEA. In addition, we should also highlight the accessions Inari (CZE) (G29), Danielle (CZE) (G28), Ly-1120 (UKR) (G12), CDC McGwire (CAN) (G43), Ly-1110 (UKR) (G10), Ly-1114 (UKR) (G11), Shedevr (UKR) (G4), Celinnyj (KAZ) (G26), and Diantus (UKR) (G8), which were in the third circle and relatively near to the AEA. The accessions that were on “the other side” of the vertical demarcation line have no practical interest for further study in terms of yield and stability at all.

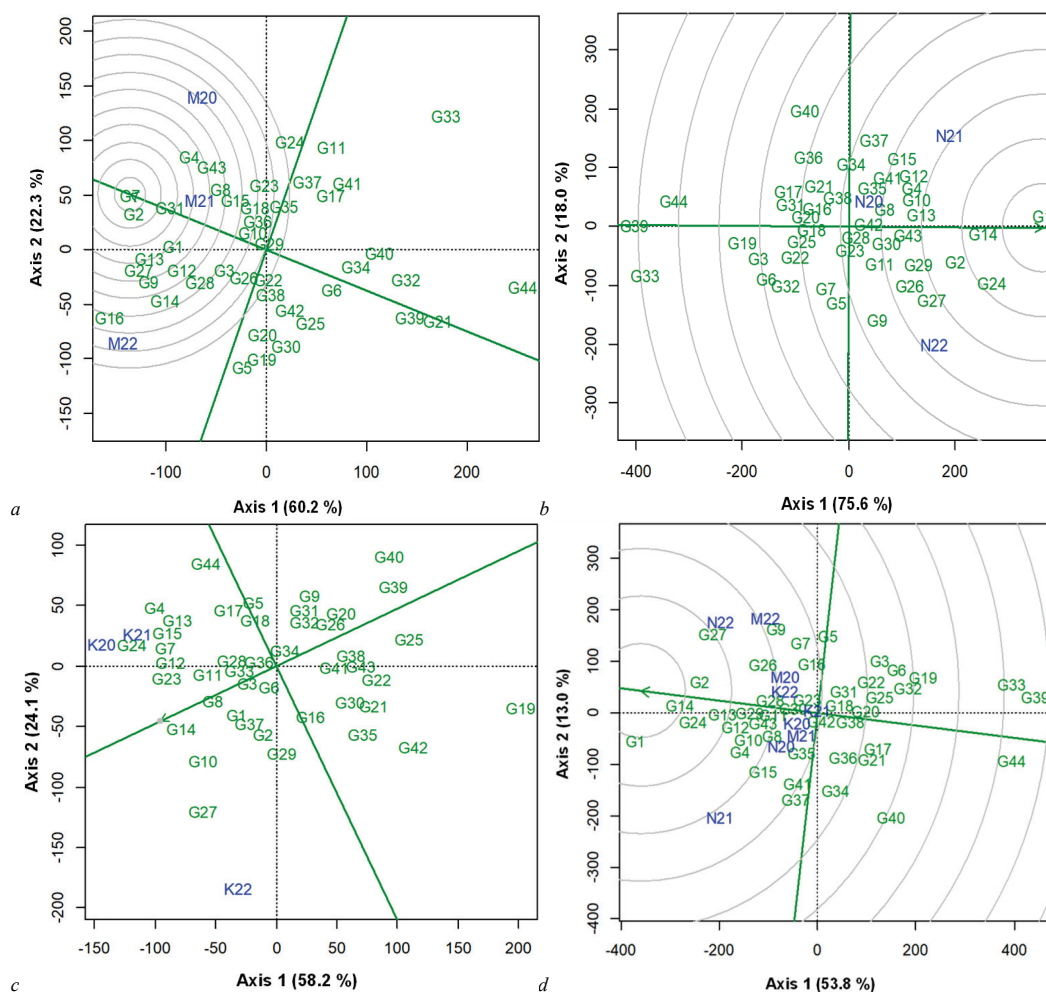


Fig. 7. The GGE biplot ranking spring barley accessions based on both mean performance and stability with reference to the “ideal genotype”: a – MIW, b – NPBES, c – IAS, d – the trial in general, accession code according to the Table 1, environment code according to the Table 2

Discussion

There are many studies aimed at evaluating the genetic diversity of barley based on both molecular and genetic levels and agro-morphological traits (Taibi et al., 2019; Kumar et al., 2020; Brbaklić et al., 2021). For example, only in recent years were results published of assessment of barley genetic diversity in Algeria (Rahal-Bouziene et al., 2015), Oman (Al Lawati et al., 2021), Tunisia (Marzougui et al., 2020), Tibet (Li et al., 2020), Jordan (Al-Abdallat et al., 2017), Pakistan (Khan et al., 2021), Iraq (Lateef et al., 2021), Kazakhstan (Almerekova et al., 2021), Brasil (Monteiro et al., 2020), India (Kaur, 2022), Ethiopia (Jalata et al., 2020; Gadissa

et al., 2021; Angassa & Mohammed, 2022; Teklemariam et al., 2022), China (Memon et al., 2021), Palestine (Shtaya & Abdallah, 2021). Thus, it should be mentioned that even in the era of modern molecular technologies, studying genetic diversity by phenotypic traits has not lost its value. This is due to the fact that most economically valuable characteristics, including yield, are quantitative, and therefore their manifestation level depends significantly on environmental conditions. That is, when studying genotypes in different conditions, there are changes in ranks of the traits’ manifestation level as a result of their reaction to the environmental conditions. One of the main reasons for this is the genotype by environment interaction (Hill, 1975; Saltz et al., 2018). Despite the successful results of

deciphering the genomes of major crops (Mascher et al., 2017; IWGSC, 2018) and further thorough research (Hussain et al., 2022), the question of complete capture of the phenotype at the genomic level still remains open. This is due to the fact that, in addition to the genetic determination of traits, epigenetic regulation plays an important role in the adaptive responses of plant organisms (Pan et al., 2016; Thiebaut et al., 2019; Guarino et al., 2022). However, for a systemic biological understanding of the complex plant phenotype, in addition to genomics and epigenetics, it is also necessary to consider the transcriptome, proteome, and metabolome (Varshney et al., 2021). Thus, the phenotype formation is associated with the complex interaction of various systems and pathways of the organism (genotype) in response to the pressure (magnitude, duration, etc.) of different environmental factors (King, 2015; Li et al., 2018; Cammarano et al., 2021; Vandermeulen & Cullen, 2022). As a result, the genotype by environment interaction is quite difficult to study. At the same time, a qualitative statistical analysis of this phenomenon is necessary for successful breeding (Malosetti et al., 2013; Mühleisen et al., 2014; van Eeuwijk et al., 2016). Thereby, to evaluate the genotype by environment interaction a number of parametric and non-parametric statistical methods (Eberhart & Russel, 1966; Lin & Binns, 1988; Huehn, 1990), as well as graphical models (Yan et al., 2007; Gauch et al., 2008; Hongyu et al., 2014) have been developed. For example, there are numerous studies devoted to the analysis of the genotype by environment interaction and the selection of stable genotypes of a wide range of agricultural crops using different statistical approaches. In particular, for wheat (Buenrostro-Rodríguez et al., 2019; Bishwas et al., 2021; Bosi et al., 2022), cucumber (Dia et al., 2018), finger millet (Anuradha et al., 2022), maize (Katsenios et al., 2021; Hudson et al., 2022), pigeon pea (Yohane et al., 2021), sorghum (Enyew et al., 2021; Silva et al., 2022), cowpea (Kindie et al., 2021), lettuce (Lafra et al., 2021), groundnut (Khan et al., 2021). Such studies in barley have been conducted in Bulgaria (Dyulgerova & Dyulgerov, 2019), Turkey (Kendal et al., 2019; Öztürk 2020), Algeria (Guendouz et al., 2022), Jordan (Al-Sayaydeh et al., 2019), Ethiopia (Shibeshi & Mekiso, 2022), India (Verma et al., 2019), Serbia (Pržulj et al., 2015), and Ukraine (Hudzenko et al., 2020; Kozachenko et al., 2022). However, for an in-depth elucidation of all aspects of the genotype by environment interaction, it is important to characterize not only genotypes, but also environments (Yan et al., 2021). In this context, it is necessary to determine the productivity of the environments (mean yield of all studied genotypes), their discriminating power and representativeness. This makes it possible to determine to which target populations of environment a certain genotype is adapted (Bustos-Korts et al., 2019).

We have found a strong variability in yield manifestation level of spring barley accessions in both temporal (in a certain ecological site in different years) and spatial (across different ecological sites) gradients. For example, at the MIW, the difference in productivity between years was 200 g/m^2 with variation from 472 g/m^2 in 2020 to 272 g/m^2 in 2021. At the IAS, the difference in yield between years was the least (130 g/m^2) among three ecological sites and varied from 508 g/m^2 in 2021 to 378 g/m^2 in 2020. At the NPBES, such a difference was the greatest (417 g/m^2) with the highest limit 793 g/m^2 in 2022, and the lowest limit 376 g/m^2 in 2020. Despite the greatest yield variability between years at the NPBES its level was the highest among all environments in the relatively favourable year 2022. At the same time, the minimal yield in the worst year in this site was practically on the same level as minimal yield at the IAS and even 104 g/m^2 higher than minimal yield at the MIW. It is important to highlight that the maximum and minimum yield levels in different ecological niches were formed in different years. Thus, at the MIW, the highest yield on average in three years was in 2020, but at the NPBES it was in 2022, and at the IAS in 2021. The lowest yield levels for these sites were in 2021, 2020 and 2022, respectively. Thereby, in addition to the general difference between three sites in terms of ecological, soil and climatic conditions, the weather conditions in the years of research, and, accordingly, the combinations of certain unfavourable abiotic and biotic factors, were quite different.

According to the analysis of variation of the AMMI model, significant changes in the percentage of contribution to the total variation for environmental conditions were found (from 72.9% at the NPBES to 50.9% at the IAS). The genotype by environment interaction also varied

significantly from 9.5% at the NPBES to 23.8% at the IAS. The percentage for the genotype varied from 17.5% at the NPBES to 25.2% at the IAS. Thus, in individual ecological niches, the contribution of the genotype to the total variation over the years was quite high. Another obvious fact that should be emphasized was that the same genotypes in different agroclimatic zones responded differently to a combination of site and year conditions. When analyzing the genotypes yield in the trial in general (three zones and three years), the percentage for the genotype was significantly lower (9.1%), although statistically reliable. In general, environmental conditions had the greatest significance – 76.6%. On the one hand, it emphasizes the significant contrast between three agroclimatic zones, which is strengthened by the variability over the years of research. On the other hand, the obtained data indicate that in this panel of accessions most of the genotypes were characterized by a better adaptability to certain ecological conditions, as compared to adaptability to all agroclimatic zones (wide adaptation). In this case, combining all environmental conditions (sites and years) was decisive in the variation. Despite this, in all variants (both in individual ecological locations and in the trial in general) all three factors of variation (genotype, environment and their interaction) were statistically reliable, and therefore from a given panel of genotypes it is possible to select individuals with relatively different adaptive reactions. This is evidence of the complexity of developing varieties with wide adaptation, which is consistent with the results of another authors (Ceccarelli, 1989). At the same time, the validity of the genotype contribution to the general variation does not completely exclude such a possibility. Further systematic conducting of such multi-environment trials with different genotypes will contribute to the developing varieties with a relatively wide adaptation. However, breeding genotypes with high adaptation to specific ecological conditions (with high yield stability over the years) will be much easier and more successful.

According to the AMMI analysis, the first two principal components for individual sites of trial covered 100% of the genotype by environment interaction. The main differences between the sites were in the ratio of the values of the first and the second principal components. In the trial in general the first two principal components covered only 59.0% of the variability. According to the GGE biplot model, the first two principal components had slightly lower values than in the AMMI model and were different for each site. In particular, in the MIW, the value of the principal components was 82.5%, at the NPBES it was 93.6%, and in the IAS it was 82.3%. However, in the trial in general there was a slightly higher percentage of the first two components of the GGE biplot (66.8%) as compared to AMMI.

When analyzing individual sites of trial by discriminating power and representativeness of the GGE biplot model, a high discriminating power was established in two out of three years in the conditions of the MIW and the NPBES. In the conditions of IAS all three years were characterized by a high discriminating power. Relatively higher representativeness was found only in one year in the conditions of MIW. Thus, in each ecological site, the conditions of most years differed significantly. In turn, the genotypes had different reactions to these changes. Therefore, the selection of stable genotypes over the years in the individual sites of trial has significant practical importance. When characterizing the environments all together (years and sites), it was established that superior discriminating power was present in two years at the NPBES (N21 and N22) and in one year in the MIW (M22). At the same time, the environments M22 and N21 were the most distant from each other. Significantly lower discriminating power, but the greatest representativeness was found in the IAS (K20, K21, and K22).

Hence, the conditions of the NPBES were relatively better for the formation of a higher yield level of spring barley accessions as compared to the other two sites of trial. Therefore, in the conditions of NPBES there is a possibility to identify the genotypes with increased productive potential. At the same time, the conditions of MIW and IAS contribute to the selection of genotypes with a higher tolerance to the pressure of environmental factors. The assessment of the accessions in all these sites over different years contributes to the selection of genotypes with an optimal combination of yield potential and its relative stability. In other words, it will contribute to the identification of genotypes with a relatively wide adaptive potential and increased resilience to a number of stressful factors.

According to the graphical models and statistical indices, the accessions most adapted to the conditions of MIW were Amil (UKR) (G7), Shedevr (UKR) (G4), and Stymul (UKR) (G2). The accession Gateway (CAN) (G31) is only noteworthy by graphical analysis. The accession Stymul (UKR) (G2) and standard Vzirets (UKR) (G1) had the greatest adaptability to the conditions of NPBS. The accessions Ly-1064 (UKR) (G14) and Rannij (KAZ) (G24) are noteworthy only by graphical analysis. The naked barley accessions CDC ExPlus (CAN) (G36), CDC Gainer (CAN) (G37), and Roseland (CAN) (G35) had high homeostaticity index, but significantly lower yield. At the IAS, we should highlight as relatively better than others the accessions Ly-1064 (UKR) (G14) and Arthur (CZE) (G27). The accessions Ly-1064 (UKR) (G14) and Stymul (UKR) (G2) were characterized by a relatively wide adaptation. Apart from them, we should point out, only by statistical parameters, the accession Arthur (CZE) (G27), as well as only by graphical analysis the accessions Ranni (KAZ) (G24) and Ly-1059 (UKR) (G13). A number of accessions that were inferior to the mentioned ones but prevailed over the others according to the results of graphical analysis and statistical indices (Ly-1120 (UKR) (G12), Diantus (UKR) (G8), Ly-1110 (UKR) (G10), Shedevr (UKR) (G4), and Danielle (CZE) (G28)) or accessions which were relatively better only by graphical analysis (Inari (CZE) (G29), Ly-1114 (UKR) (G11), and CDC McGwire (CAN) (G43), also have some practical value for further studies.

Thus, both the accessions with very strong adaptability in only one site of trial (Amil (UKR) (G7) and Gateway (CAN) (G31)) and the genotypes with a combination of high adaptability in one or two ecological niches and increased wide adaptability (Stymul (UKR) (G2), Ly-1064 (UKR) (G14), Rannij (KAZ) (G24), Shedevr (UKR) (G4), and Arthur (CZE) (G27)) have been identified. The accessions Ly-1059 (UKR) (G13), Ly-1120 (UKR) (G12), Diantus (UKR) (G8), and Danielle (CZE) (G28) did not have the best performance in the individual sites of trial, but were characterized by a relatively high wide adaptability. The standard Vzirets (UKR) (G1) combined a high adaptability to the conditions of NPBS with a relatively high wide adaptability. In general, the naked barley accessions were inferior to the covered ones in terms of yield potential, however, some of them (CDC ExPlus (CAN) (G36), CDC Gainer (CAN) (G37), and Roseland (CAN) (G35)) had increased stability according to the statistical indices, in particular in the conditions of NPBS. Among naked barley accessions relatively better wide adaptability according to the graphical analysis was found in the accession CDC McGwire (CAN) (G43) while the accession CDC ExPlus (CAN) (G36) was superior to the standard by statistical parameters. However, it should be noted that even the best accessions in terms of yield and stability differed among themselves in reactions to the conditions of different ecological niches and years of trials according to the graphical and statistical tools. The characteristics of a number of accessions according to graphical (GGE biplot, AMMI) and statistical (Hom, Sc) approaches were different. In our opinion, this may be due to the fact that the statistical indices used characterize only the value and variability of the yield (standard deviation or limits of variation) in an individual genotype. The graphical models take into account how much the reaction of particular genotype is relative to the change in the mean value of the whole panel of accessions in certain environments. In other words, the applied statistical and graphical tools capture somewhat different aspects regarding the peculiarities of the yield manifestation level and its variation in genotypes. Thus, the use of statistical or graphical tools with different mathematical principles is appropriate for a thorough assessment of such a complex phenomenon as the genotype by environment interaction and the selection of genotypes with the optimal combination of high yield and its stability.

Our results complement and extend the existing experimental data revealed by other researchers regarding the peculiarities of the manifestation of the genotype by environment interaction. It can be used to develop models of spring barley varieties with specific or wide adaptation under conditions of different agro-climatic zones of Ukraine. Selected collection accessions of various botanical varieties and different origin with increased yield and its stability have practical importance for use in the breeding process with the aim of widening the genetic base of new spring barley varieties.

Conclusion

The peculiarities of yield manifestation level and its variability in spring barley accessions of different origins and botanical varieties depending on conditions of different agroclimatic zones and different years have been revealed. The yield level of spring barley accessions varied significantly depending on both different ecological conditions and years of trial. The change in yield ranks indicate a strong cross-over genotype by environment interaction in most accessions, both in the individual ecological niches in different years and in a certain year through different agroclimatic zones. However, the genotype by environment interaction was significantly higher when analyzing yield ranks in three agroclimatic zones and in three years altogether. The results of characterization of the test environments indicate that in the conditions of NPBS (Ukrainian Polissia) there is a greater possibility to identify genotypes with increased productive potential. The conditions of MIW (Ukrainian Forest-Steppe) and IAS (Northern Steppe of Ukraine) give more opportunities to select genotypes with a higher tolerance to the complex of environmental stress factors. The assessment of accessions in three agroclimatic zones in different years makes it possible to determine genotypes with an optimal combination of yield potential and its stability. When using statistical and graphical tools, spring barley accessions were selected with a combination of increased yield and its stability in different ecological niches in different years. In the conditions of the MIW the most adapted were the accessions Amil (UKR), Shedevr (UKR), Stymul (UKR), and Gateway (CAN). At the NPBS we should highlight the accessions Stymul (UKR), Ly-1064 (UKR), Rannij (KAZ) and standard Vzirets (UKR). In the conditions of IAS relatively better were accessions Ly-1064 (UKR) and Arthur (CZE). The accessions Ly-1064 (UKR), Stymul (UKR), Arthur (CZE), Rannij (KAZ) and Ly-1059 (UKR) were characterized by relatively higher wide adaptability in three ecological niches over three years. The accessions Danielle (CZE), Ly-1120 (UKR), Diantus (UKR), Ly-1110 (UKR), and Shedevr (UKR), which were inferior to the abovementioned accessions in terms of wide adaptability but prevailed in it over the other ones, are of practical interest too. The naked barley accessions in general had lower yield potential than covered ones, but some of them (CDC ExPlus (CAN), CDC Gainer (CAN), and Roseland (CAN)) had a high value of homeostaticity index in the conditions of NPBS. The accessions CDC McGwire (CAN), and CDC ExPlus (CAN) could be pointed out as relatively better among the studied naked barley accessions in terms of wide adaptability. In a number of accessions, the characteristics of stability according to the graphical (GGE biplot, AMMI) and statistical (Hom, Sc) tools differed to some extent. In order to comprehensively evaluate the genotype by environment interaction and select genotypes with an optimal combination of yield and stability, it is advisable to combine statistical or graphical models that differ in mathematical calculation principles. The distinguished accessions of different origin and botanical affiliation are recommended to be used in further studies to create new breeding material with the aim at simultaneously increasing yield and stability, as well as widening the genetic basis of breeding programs. The identified peculiarities of the genotype by environment interaction complement the available data on the yield performance in spring barley collection accessions depending on spatial (ecological sites) and temporal (years) gradients and their combination. It can be used to develop models of spring barley varieties with specific or wide adaptation under conditions of different agro-climatic zones of Ukraine.

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References

- Al Lawati, A. H., Nadaf, S. K., AlSaady, N. A., Al Hinai, S. A., Almamari, A. R., & Al Maawali, A. A. (2021). Genetic diversity of Omani barley (*Hordeum vulgare* L.) gemplasm. *Open Agriculture*, 6(1), 628–639.

- Al-Abdallat, A. M., Karadshah, A., Hadadd, N. I., Akash, M. W., Ceccarelli, S., Baum, M., Hasan, M., Jighly, A., & Abu Elenein, J. M. (2017). Assessment of genetic diversity and yield performance in Jordanian barley (*Hordeum vulgare* L.) landraces grown under Rainfed conditions. *BMC Plant Biology*, 17, 191.
- Almerekova, S., Genievskaya, Y., Abugalieva, S., Sato, K., & Turuspekoy, Y. (2021). Population structure and genetic diversity of two-rowed barley accessions from Kazakhstan based on SNP genotyping data. *Plants*, 10, 2025.
- Al-Sayaydeh, R., Al-Bawalize, A., Al-Ajlouni, Z., Akash, M. W., Abu-Elenein, J., & Al-Abdallat, A. M. (2019). Agronomic evaluation and yield performance of selected barley (*Hordeum vulgare* L.) landraces from Jordan. *International Journal of Agronomy*, 2019, 9575081.
- Angassa, D., & Mohammed, J. (2022). Agro-morphological variability study of Ethiopian barley (*Hordeum vulgare* L.) accessions for their important agronomical traits at Hadiya zone, Southern Ethiopia. *Journal of Plant Sciences*, 10(1), 19–25.
- Anuradha, N., Patro, T. S. S. K., Singamsetti, A., Sandhya Rani, Y., Triveni, U., Nirmala Kumari, A., Govanakoppa, N., Lakshmi Pathy, T., & Tonapi, V. A. (2022). Comparative study of AMMI- and BLUP-based simultaneous selection for grain yield and stability of finger millet [*Eleusine coracana* (L.) Gaertn.] genotypes. *Frontiers in Plant Science*, 12, 786839.
- Asdal, Å., & Guarino, L. (2018). The Svalbard global seed vault: 10 years – 1 million samples. *Biopreservation and Biobanking*, 16(5), 391–392.
- Balzan, M. V., Sadula, R., & Scalvenzi, L. (2020). Assessing ecosystem services supplied by agroecosystems in Mediterranean Europe: A literature review. *Land*, 9(8), 245.
- Bauer, B., & von Wirén, N. (2020). Modulating tiller formation in cereal crops by the signalling function of fertilizer nitrogen forms. *Scientific Reports*, 10, 20504.
- Bentley, A. (2022). Avert global wheat crisis due to invasion of Ukraine. *Nature*, 603, 551.
- Bijlsma, R., & Loeschcke, V. (2011). Genetic erosion impedes adaptive responses to stressful environments. *Evolutionary Applications*, 5, 117–129.
- Bishwas, K. C., Poudel, M. R., & Regmi, D. (2021). AMMI and GGE biplot analysis of yield of different elite wheat line under terminal heat stress and irrigated environments. *Heliyon*, 7, e07206.
- Bosi, S., Negri, L., Fakaros, A., Oliveti, G., Whittaker, A., & Dinelli, G. (2022). GGE biplot analysis to explore the adaptation potential of Italian common wheat genotypes. *Sustainability*, 14(2), 897.
- Brbakčić, L., Trkulja, D., Mikić, S., Mirosavljević, M., Momčilović, V., Dudić, B., Procházková, L., & Aćin, V. (2021). Genetic diversity and population structure of Serbian barley (*Hordeum vulgare* L.) collection during a 40-year long breeding period. *Agronomy*, 11, 118.
- Breman, E., Ballesteros, D., Castillo-Lorenzo, E., Cockel, C., Dickie, J., Faruk, A., O'Donnell, K., Offord, C. A., Pironon, S., Sharrock, S., & Ulian, T. (2021). Plant diversity conservation challenges and prospects – the perspective of Botanic Gardens and the Millennium Seed Bank. *Plants*, 10, 2371.
- Buenrostro-Rodríguez, J. F., Solís-Moya, E., Gámez-Vázquez, A. J., Raya-Pérez, J. C., Mandujano-Bueno, A., Cervantes-Ortiz, F., & Covarubias-Prieto, J. (2019). Yield performance and GGE biplot analysis of wheat genotypes under two irrigation treatments at El Bajío, Mexico. *Chilean Journal of Agricultural Research*, 79(2), 234–242.
- Bustos-Korts, D., Malosetti, M., Chenu, K., Chapman, S., Boer, M. P., Zheng, B., & van Eeuwijk, F. A. (2019). From QTLs to adaptation landscapes: Using genotype-to-phenotype models to characterize G×E over time. *Frontiers in Plant Science*, 10, 1540.
- Cammarano, D., Ronga, D., Francia, E., Akar, T., Al-Yassin, A., Benbelkacem, A., Grando, S., Romagosa, I., Stanca, A. M., & Pecchioni, N. (2021). Genetic and management effects on barley yield and phenology in the Mediterranean basin. *Frontiers in Plant Science*, 12, 655406.
- Cappelli, S. L., Domegno-Horta, L. A., Loaiza, V., & Laine, A.-L. (2022). Plant biodiversity promotes sustainable agriculture directly and via belowground effects. *Trends in Plant Science*, 27(7), 674–687.
- Cardinale, B., Duffy, J., Gonzalez, A., Hooper, D. U., Perrings, C., Venail, P., Narwani, A., Mace, G. M., Tilman, D., Wardle, D. A., Kinzig, A. P., Daily, G. C., Loreau, M., Grace, J. B., Larigauderie, A., Srivastava, D. S., & Naeem, S. (2012). Biodiversity loss and its impact on humanity. *Nature*, 486, 59–67.
- Ceccarelli, S. (1989). Wide adaptation. How wide? *Euphytica*, 40(3), 197–205.
- Dhankher, O. P., & Foyer, C. H. (2018). Climate resilient crops for improving global food security and safety. *Plant, Cell and Environment*, 41(5), 877–884.
- Dia, M., Wehner, T. C., Elmstrom, G. W., Gabert, A., Motes, J. E., Staub, J. E., Tolla, G. E., & Widders, I. E. (2018). Genotype x environment interaction for yield of pickling cucumber in 24 U.S. environments. *Open Agriculture*, 3, 1–16.
- Dietz, T. (2017). Drivers of human stress on the environment in the twenty-first century. *Annual Review of Environment and Resources*, 42, 189–213.
- Dyulgerova, B., & Dyulgerov, N. (2019). Genotype by environment interaction for grain yield of barley mutant lines. *Agriculture (Polnohospodárstvo)*, 65(2), 51–58.
- Eberhart, S. A., & Russel, W. A. (1966). Stability parameters for comparing varieties. *Crop Science*, 6(1), 36–40.
- Ebert, A. W., & Engels, J. M. M. (2020). Plant biodiversity and genetic resources matter! *Plants*, 9(12), 1706.
- Enyew, M., Feyissa, T., Geleta, M., Tesfaye, K., Hammenhag, C., & Carlsson, A. S. (2021). Genotype by environment interaction, correlation, AMMI, GGE biplot and cluster analysis for grain yield and other agronomic traits in sorghum (*Sorghum bicolor* L. Moench). *PLoS One*, 16(10), e0258211.
- Foley, J. A., Ramankutty, N., Brauman, K. A., Cassidy, E. S., Gerber, J. S., Johnston, M., Mueller, N. D., O'Connell, C., Ray, D. K., West, P. C., Balzer, C., Bennett, E. M., Carpenter, S. R., Hill, J., Monfreda, C., Polasky, S., Rockström, J., Sheehan, J., Siebert, S., Tilman, D., & Zaks, D. P. M. (2011). Solutions for a cultivated planet. *Nature*, 478(7369), 337–342.
- Gadisa, F., Abebe, M., & Bekele, T. (2021). Agro-morphological traits-based genetic diversity assessment in Ethiopian barley (*Hordeum vulgare* L.) landrace collections from Bale highlands, Southeast Ethiopia. *Agriculture and Food Security*, 10, 58.
- Galluzzi, G., Seyoum, A., Halewood, M., Noriega, I. L., & Welch, E. W. (2020). The role of genetic resources in breeding for climate change: The case of public breeding programmes in eighteen developing countries. *Plants*, 9(9), 1129.
- Gauch, H. G. (1988). Model selection and validation for yield trials with interaction. *Biometrics*, 44(3), 705–715.
- Gauch, H. G., Piepo, H.-P., & Annicchiarico, P. (2008). Statistical analysis of yield trials by AMMI and GGE: Further consideration. *Crop Science*, 48(3), 866–889.
- Gavin, M. C., McCarter, J., Berkes, F., Mead, A. T. P., Sterling, E. J., Tang, R., & Turner, N. J. (2018). Effective biodiversity conservation requires dynamic, pluralistic, partnership-based approaches. *Sustainability*, 10(6), 1846.
- Godfray, H. C. J., Beddington, J. R., Crute, I. R., Haddad, L., Lawrence, D., Muir, J. F., Pretty, J., Robinson, S., Thomas, S. M., & Toulmin, C. (2010). Food security: The challenge of feeding 9 billion people. *Science*, 327(5967), 812–818.
- Gollob, H. F. (1968). A statistical model which combines feature of factor analytic and analysis of variance techniques. *Psychometrika*, 33, 73–115.
- Guarino, F., Cicitelli, A., Castiglione, S., Agius, D. R., Orhun, G. E., Fragkostefanakis, S., Leclercq, J., Dobránszki, J., Kaiserli, E., Lieberman-Lazarovich, M., Sömera, M., Sarmiento, C., Vettori, C., Paffetti, D., Poma, A. M. G., Moschou, P. N., Gašparović, M., Yousefi, S., Vergata, C., Berger, M. M. J., Gallusci, P., Miladinović, D., & Martinelli, F. (2022). An epigenetic alphabet of crop adaptation to climate change. *Frontiers in Genetics*, 13, 818727.
- Guendouz, A., & Bendada, H. (2022). Stability analysis for the grain yield of some barley (*Hordeum vulgare* L.) genotypes growing under semi-arid conditions. *International Journal of Bio-Resource and Stress Management*, 13(2), 172–178.
- Habschied, K., Lalić, A., Krstanović, V., Dvojković, K., Abičić, I., Šimić, G., & Mastanović, K. (2021). Comprehensive comparative study of the malting qualities of winter hull-less and hulled barley (2016–2019). *Fermentation*, 7(1), 8.
- Halewood, M., Jamora, N., Noriega, I. L., Anglin, N. L., Wenzl, P., Payne, T., Ndjiondjop, M.-N., Guarino, L., Kumar, P. L., Yazbek, M., Muchugi, A., Azevedo, V., Tchamba, M., Jones, C. S., Venuprasad, R., Roux, N., Rojas, E., & Lusty, C. (2020). Germplasm acquisition and distribution by CGIAR genebanks. *Plants*, 9(10), 1296.
- Hill, C. B., Angessa, T. T., Zhang, X.-Q., Chen, K., Zhou, G., Tan, C., Wang, P., Westcott, S., & Li, C. (2021). A global barley panel revealing genomic signatures of breeding in modern Australian cultivars. *The Plant Journal*, 106, 419–434.
- Hill, J. (1975). Genotype-environment interaction – a challenge for plant breeding. *The Journal of Agricultural Science*, 85(3), 477–493.
- Hongyu, K., Garcia-Pena, M., de Araujo, L. B., & dos Santos Dias, C. T. (2014). Statistical analysis of yield trials by AMMI analysis of genotype x environment interaction. *Biometrical Letters*, 51(2), 89–102.
- Hudson, A. I., Odell, S. G., Dubreuil, P., Tixier, M.-H., Praud, S., Runcie, D. E., & Ross-Ibarra J. (2022). Analysis of genotype-by-environment interactions in a maize mapping population. *G3 Genes, Genomes, Genetics*, 12(3), 13.
- Hudzenko, V., Polishchuk, T., Demydov, O., Sardak, M., Buniak, N., & Ishchenko, V. (2020). Identification of spring barley breeding lines with superior yield performance and stability. *Acta Universitatis Agriculturae Silviculturae Mendelianae Brunensis*, 68(6), 947–958.
- Huehn, M. (1990). Nonparametric measures of phenotypic stability. Part 1: Theory. *Euphytica*, 47(3), 189–194.
- Hussain, B., Akpmar, B. A., Alaux, M., Algharib, A. M., Sehgal, D., Ali, Z., Aradotir, G. I., Batley, J., Bellec, A., Bentley, A. R., Cagirici, H. B., Cattivelli, L., Choulet, F., Cockram, J., Desiderio, F., Devaux, P., Dogramaci, M., Dorado, G., Dreisgackner, S., Edwards, D., El-Hassouni, K., Eversole, K., Fahima, T., Figueroa, M., Gálvez, S., Gill, K. S., Govta, L., Gul, A., Hensel, G., Hernandez, P., Crespo-Herrera, L. A., Ibrahim, A., Kilian, B., Korzun, V., Krugman, T., Li, Y., Liu, S., Mahmoud, A. F., Morgounov, A., Muslu, T., Naseer, F., Ordon, F., Paux, E., Perovic, D., Reddy, G. V. P., Reif, J. C., Reynolds, M., Roychowdhury, R., Rudd, J., Sen, T. Z., Sukumaran, S., Ozdemir, B. S., Tiwari, V. K., Ullah, N., Unver, T., Yazar, S., Appels, R., & Budak, H. (2022). Capturing wheat phenotypes at the genome level. *Frontiers in Plant Science*, 13, 851079.
- Ingvordsen, C. H., Backes, G., Lyngkjær, M. F., Peltonen-Sainio, P., Jensen, J. D., Jalli, M., Jahoor, A., Rasmussen, M., Mikkelsen, T. N., Stockmarr, A., & Jørgensen, R. B. (2015). Significant decrease in yield under future climate conditions: Stability and production of 138 spring barley accessions. *European Journal of Agronomy*, 63, 105–113.

- International Wheat Genome Sequencing Consortium (IWGSC). (2018). Shifting the limits in wheat research and breeding using a fully annotated reference genome. *Science*, 361, eaar7191.
- Jalata, Z., Garoma, B., & Nandeshwar, B. C. (2020). Evaluation of genetic divergence among barley genotypes based on agro-morphological characters. *Current Journal of Applied Science and Technology*, 39(36), 102–110.
- Jayakodi, M., Padmarasu, S., Haberer, G., Bonthala, V. S., Gundlach, H., Monat, C., Lux, T., Kamal, N., Lang, D., Himmelbach, A., Ens, J., Zhang, X.-Q., Angessa, T. T., Zhou, G., Tan, C., Hill, C., Wang, P., Schreiber, M., Boston, L. B., Plott, C., Jenkins, J., Guo, Y., Fiebig, A., Budak, H., Xu, D., Zhang, J., Wang, C., Grimwood, J., Schmutz, J., Guo, G., Zhang, G., Mochida, K., Hirayama, T., Sato, K., Chalmers, K. J., Langridge, P., Waugh, R., Pozniak, C. J., Scholz, U., Mayer, K. F. X., Spannagl, M., Li, C., Mascher, M., & Stein, N. (2020). The barley pan-genome reveals the hidden legacy of mutation breeding. *Nature*, 588, 284–289.
- Katsenios, N., Sparangis, P., Chanioti, S., Giannoglou, M., Leonidakis, D., Christopoulos, M. V., Katsaros, G., & Efthimiadou, A. (2021). Genotype – environment interaction of yield and grain quality traits of maize hybrids in Greece. *Agronomy*, 11, 357.
- Kaur, V., Aravind, J., Manju, Jacob, S. R., Kumari, J., Panwar, B. S., Pal, N., Rana, J. C., Pandey, A., & Kumar, A. (2022). Phenotypic characterization, genetic diversity assessment in 6,778 accessions of barley (*Hordeum vulgare* L. ssp. *vulgare*) germplasm conserved in national genebank of India and development of a core set. *Frontiers in Plant Science*, 13, 771920.
- Kendal, E., Karaman, M., Tekdal, S., & Doğan, S. (2019). Analysis of promising barley (*Hordeum vulgare* L.) lines performance by AMMI and GGE biplot in multiple traits and environment. *Applied Ecology and Environmental Research*, 17(2), 5219–5233.
- Khan, A., Ihsan, M., Nisar, M., Hazrat, A., Ali, M., Ul-Haq, R., Khan, K., Gul, K., & Faisal, S. (2021). Evaluation of genetic diversity in barley landraces through agro-morphological and biochemical characterization. *Sarhad Journal of Agriculture*, 37(3), 984–992.
- Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., & Mamun, M. A. (2021). AMMI and GGE biplot analysis for yield performance and stability assessment of selected Bambara groundnut (*Vigna subterranea* L. Verdec) genotypes under the multi-environmental trials (METs). *Scientific Reports*, 11, 22791.
- Khangildin, V. V., & Litvinenko, N. A. (1981). Gomeostaticnost i adaptivnost sortov ozimoy pshenitsi [Homeostaticity and adaptability of winter wheat varieties]. *Nauchno-Tekhnicheskii Byulleten VSGL*, 39, 8–14 (in Russian).
- Khoury, C. K., Brush, S., Costich, D. E., Curry, H. A., de Haan, S., Engels, J. M. M., Guarino, L., Hoban, S., Mercer, K. L., Miller, A. J., Nabhan, G. P., Perales, H. R., Richards, C., Riggins, C., & Thormann, I. (2022). Crop genetic erosion: Understanding and responding to loss of crop diversity. *New Phytologist*, 233, 84–118.
- Kindie, Y., Tesso, B., & Amsalu, B. (2021). Genotype x environment interaction and yield stability in early-maturing cowpea (*Vigna unguiculata* (L.) Walp.) landraces in Ethiopia. *Advances in Agriculture*, 2021, 3786945.
- King, G. J. (2015). Crop epigenetics and the molecular hardware of genotype × environment interactions. *Frontiers in Plant Science*, 6, 968.
- Kompanets, K. V., & Kozachenko, M. R. (2017). Selektivna tsinnist ta efektyvnist vykorystannia v selektsii bezostykh ta ostytykh sortiv yachmeniu yaroho [Breeding value and efficiency of use of awny and awnless barley cultivars in breeding]. *Plant Breeding and Seed Production*, 112, 56–67 (in Ukrainian).
- König, P., Beier, S., Basterrechea, M., Schüller, D., Arend, D., Mascher, M., Stein, N., Scholz, U., & Lange, M. (2020). BRIDGE – a visual analytics web tool for barley genebank genomics. *Frontiers in Plant Science*, 11, 701.
- Kozachenko, M. R., Solonechnyi, P. M., Zymohliad, O. V., Vasko, N. I., Vazhenina, O. Y., Naumov, O. H., Kobyzeva, L. N., & Kolomatska, V. P. (2022). Value of *Hordeum vulgare* L. genotypes in terms of yield and its stability. *Žemės Ūkio Mokslai, Agricultural Sciences*, 29(1), 20–27.
- Kumar, P., Banjarey, P., Malik, R., Tikle, A. N., & Verma, R. P. S. (2020). Population structure and diversity assessment of barley (*Hordeum vulgare* L.) introduction from ICARDA. *Journal of Genetics*, 99, 70.
- Kumar, P., Pratap, S., Verma, R. P. S., Tikle, A. N., & Malik, R. (2018). Diversity assessment of hulled barley (*Hordeum vulgare* L.) accessions of ICARDA in Indian condition using cluster analysis. *Indian Journal of Agricultural Research*, 52(4), 429–433.
- Lafia, A., Sandoya, G., & Mou, B. (2021). Genetic variation and genotype by environment interaction for heat tolerance in crisphead lettuce. *HortScience*, 56(2), 126–135.
- Lateef, D., Mustafa, K., & Tahir, N. (2021). Screening of Iraqi barley accessions under PEG-induced drought conditions. *All Life*, 14(1), 308–332.
- Lennon, J. T., den Hollander, F., Wilke-Berenguer, M., & Blath, J. (2021). Principles of seed banks and the emergence of complexity from dormancy. *Nature Communications*, 12, 4807.
- Li, X., Guo, T., Mu, Q., Li, X., & Yu, J. (2018). Genomic and environmental determinants and their interplay underlying phenotypic plasticity. *Proceedings of the National Academy of Sciences of the United States of America*, 115(26), 6679–6684.
- Li, Z., Lhundrup, N., Guo, G., Dol, K., Chen, P., Gao, L., Chermi, W., Zhang, J., Wang, J., Nyema, T., Dawa, D., & Li, H. (2020). Characterization of genetic diversity and genome-wide association mapping of three agronomic traits in qingke barley (*Hordeum vulgare* L.) in the Qinghai-Tibet Plateau. *Frontiers in Genetics*, 11, 638.
- Lin, C. S., & Binns, M. R. (1988). A superiority measure of cultivar performance for cultivar x location data. *Canadian Journal of Plant Science*, 68(1), 193–198.
- Malosetti, M., Ribaut, J.-M., & van Eeuwijk, F. A. (2013). The statistical analysis of multi-environment data: Modeling genotype-by-environment interaction and its genetic basis. *Frontiers in Physiology*, 4, 44.
- Marzougui, S., Kharat, M., & ben Younes, M. (2020). Assessment of genetic diversity and population structure of Tunisian barley accessions (*Hordeum vulgare* L.) using SSR markers. *Acta Agrobotanica*, 73(4), 7343.
- Mascher, M., Gundlach, H., Himmelbach, A., Beier, S., Twardziok, S. O., Wicker, T., Radchuk, V., Dockter, C., Hedley, P. E., Russell, J., Bayer, M., Ramsay, L., Liu, H., Haberer, G., Zhang, X.-Q., Zhang, Q., Barrero, R. A., Li, L., Taudien, S., Groth, M., Felder, M., Hastie, A., Šimkova, H., Staňkova, H., Vrana, J., Chan, S., Munoz-Amatriain, M., Ounit, R., Wanamaker, S., Bolser, D., Colmsee, C., Schmutzer, T., Aliyeva-Schnorr, L., Grasso, S., Tanskanen, J., Chailyan, A., Sampath, D., Heavens, D., Clissold, L., Cao, S., Chapman, B., Dai, F., Han, Y., Li, H., Li, X., Lin, C., McCooke, J. K., Tan, C., Wang, P., Wang, S., Yin, S., Zhou, G., Poland, J. A., Bellgard, M. I., Borisjuk, L., Houben, A., Doležel, J., Ayling, S., Lonardi, S., Kersey, P., Langridge, P., Muehlbauer, G. J., Clark, M. D., Caccamo, M., Schulman, A. H., Mayer, K. F. X., Platzer, M., Close, T. J., Scholz, U., Hansson, M., Zhang, G., Braumann, I., Spannagl, M., Li, C., Waugh, R., Stein, N. (2017). A chromosome conformation capture ordered sequence of the barley genome. *Nature*, 544, 427–433.
- Mascher, M., Schreiber, M., Scholz, U., Graner, A., Reif, J. C., & Stein, N. (2019). Genebank genomics bridges the gap between the conservation of crop diversity and plant breeding. *Nature Genetics*, 51, 1076–1081.
- Mastanjević, K., Lenart, L., Šimić, G., Lalić, A., & Krstanović, V. (2017). Malting quality indicators of Croatian dual-purpose barley varieties. *Croatian Journal of Food Science and Technology*, 9(2), 145–151.
- Memon, S., Yang, S., Liu, X., He, X., Memon, S., Khaskheli, M. I., & Feng, Z. (2021). Assessment of genetic diversity in Chinese hulless barley accessions for qualitative traits. *Bioscience Journal*, 37, e37046.
- Milner, S. G., Jost, M., Taketa, S., Mazón, E. R., Himmelbach, A., Oppermann, M., Weise, S., Knüppfer, H., Basterrechea, M., König, P., Schüller, D., Sharma, R., Pasam, R. K., Ruttgen, T., Guo, G., Xu, D., Zhang, J., Herren, G., Müller, T., Krattinger, S. G., Keller, B., Jiang, Y., González, M. Y., Zhao, Y., Habekuß, A., Färber, S., Ordon, F., Lange, M., Bömer, A., Graner, A., Reif, J. C., Scholz, U., Mascher, M., & Stein, N. (2019). Genebank genomics highlights the diversity of a global barley collection. *Nature Genetics*, 51, 319–326.
- Monteiro, V. A., Amabile, R. F., Spehar, C. R., Faleiro, F. G., Vieira, E. A., Peixoto, J. R., Junior, W. Q. R., & Montalvão, A. P. L. (2020). Genetic diversity among 435 barley accessions based in morpho-agronomical characteristics under irrigation in the Brazilian savannah. *Australian Journal of Crop Science*, 14(9), 1385–1393.
- Moore, F. C., & Lobell, D. B. (2015). The fingerprint of climate trends on European crop yields. *Proceedings of the National Academy of Sciences of the United States of America*, 112(9), 2670–2675.
- Mühlaisen, J., Piepho, H.-P., Maurer, H. P., Zhao, Y. S., & Reif, J. C. (2014). Exploitation of yield stability in barley. *Theoretical and Applied Genetics*, 127(9), 1949–1962.
- Öztürk, İ. (2020). Yield stability and physiological parameters of barley (*Hordeum vulgare* L.) genotypes under rainfed conditions. *International Journal of Innovative Approaches in Agricultural Research*, 4(4), 473–487.
- Pan, H., Holbrook, J. D., Kamani, N., & Kwok, C. K. (2016). Gene, environment and methylation (GEM): A tool suite to efficiently navigate large scale epigenome wide association studies and integrate genotype and interaction between genotype and environment. *BMC Bioinformatics*, 17, 299.
- Pan, Y., Zhu, J., Hong, Y., Zhang, M., Lv, C., Guo, B., Shen, H., Xu, X., & Xu, R. (2022). Screening of stable resistant accessions and identification of resistance loci to Barley yellow mosaic virus disease. *PeerJ*, 10, e13128.
- Piechota, U., Czembor, P. C., & Czembor, J. H. (2020). Evaluating barley landraces collected in North Africa and the Middle East for powdery mildew infection at seedling and adult plant stages. *Cereal Research Communications*, 48, 179–185.
- Poore, J., & Nemecek, T. (2018). Reducing food's environmental impacts through producers and consumers. *Science*, 360, 987–992.
- Pržulj, N., Miroslavljević, M., Čanak, P., Zorić, M., & Bočanski, J. (2015). Evaluation of spring barley performance by biplot analysis. *Cereal Research Communication*, 43(4), 692–703.
- Rahal-Bouziane, H., Berkani, S., Merdas, S., Nait, M. S., & Abdelguerfi, A. (2015). Genetic diversity of traditional genotypes of barley (*Hordeum vulgare* L.) in Algeria by pheno-morphological and agronomic traits. *African Journal of Agricultural Research*, 10(31), 3041–3048.

- Ramirez-Villegas, J., Khoury, C. K., Achicanoy, H. A., Diaz, M. V., Mendez, A. C., Sosa, C. C., Kehel, Z., Guarino, L., Abberton, M., Aunario, J., Al Awar, B., Alarcon, J. C., Amri, A., Anglin, N. L., Azevedo, V., Aziz, K., Capilit, G. L., Chavez, O., Chebotarov, D., Costich, D. E., Debouck, D. G., Ellis, D., Falalou, H., Fiu, A., Ghanem, M. E., Giovannini, P., Goungoulou, A. J., Gueye, B., El Hobyb, A. I., Jamnadass, R., Jones, C. S., Kpeki, B., Lee, J.-S., McNally, K. L., Muchugi, A., Ndjiondjop, M.-N., Oyatomi, O., Payne, T. S., Ramachandran, S., Rossel, G., Roux, N., Ruas, M., Sansaloni, C., Sardos, J., Setiyono, T. D., Tchamba, M., van den Houwe, I., Velazquez, J. A., Venuprasad, R., Wenzl, P., Yazbek, M., & Zavala, C. (2022). State of ex situ conservation of landrace groups of 25 major crops. *Nature Plants*, 8, 491–499.
- Ramonet, M., Ciais, P., Apadula, F., Bartyzel, J., Bastos, A., Bergamaschi, P., Blanc, P. E., Brunner, D., di Torchiarolo, L. C., Calzolari, F., Chen, H., Chmura, L., Colomb, A., Conil, S., Cristofanelli, P., Cuevas, E., Curcoll, R., Delmotte, M., di Sarra, A., Emmenegger, L., Forster, G., Frumau, A., Gerbig, C., Gheusi, F., Hammer, S., Haszpra, L., Hatakka, J., Hazan, L., Heliasz, M., Henne, S., Hensen, A., Hermansen, O., Keronen, P., Kivi, R., Kominková, K., Kubistin, D., Laurent, O., Laurila, T., Lavric, J. V., Lehner, I., Lehtinen, K. E. J., Leskinen, A., Leuenberger, M., Levin, I., Lindauer, M., Lopez, M., Myhre, C. L., Mammarella, I., Manca, G., Manning, A., Marek, M. V., Marklund, P., Martin, D., Meinhardt, F., Mihalopoulos, N., Mölder, M., Morgui, J. A., Necki, J., O'Doherty, S., O'Dowd, C., Ottosson, M., Philippon, C., Piacentino, S., Pichon, J. M., Plass-Duelmer, C., Resovsky, A., Rivier, L., Rodó, X., Sha, M. K., Scheeren, H. A., Sferlazzo, D., Spain, T. G., Stanley, K. M., Steinbacher, M., Trisolino, P., Vermeulen, A., Vitková, G., Weyrauch, D., Xueref-Remy, I., Yala, K., & Yver Kwok, C. (2020). The fingerprint of the summer 2018 drought in Europe on ground-based atmospheric CO₂ measurements. *Philosophical Transactions of the Royal Society B*, 375, 20190513.
- Reynolds, M. P., Lewis, J. M., Ammar, K., Basnet, B. R., Crespo-Herrera, L., Crossa, J., Dhugga Dreisigacker, S., Juliana, P., Karwat, H., Kishii, M., Krause, M. R., Langridge, P., Lashkari, A., Mondal, S., Payne, T., Pequeno, D., Pinto, F., Sansaloni, C., Schulthess, U., Singh, R. P., Sonder, K., Sukumaran, S., Xiong, W., & Braun, H. J. (2021). Harnessing translational research in wheat for climate resilience. *Journal of Experimental Botany*, 72(14), 5134–5157.
- Saltz, J. B., Bell, A. M., Flint, J., Gomulkiewicz, R., Hughes, K. A., & Keagy, J. (2018). Why does the magnitude of genotype-by-environment interaction vary? *Ecology and Evolution*, 8, 6342–6353.
- Schneiderhan-Opel, J., & Bogner, F. X. (2019). Between environmental utilization and protection: Adolescent conceptions of biodiversity. *Sustainability*, 11(17), 4517.
- Shibeshi, S., & Mekiso, M. (2022). Performance evaluation and yield stability test of released food barley (*Hordeum vulgare* L.) varieties in highland areas of Siltie and Gurage Zones. *Advances in Agriculture, Food Science and Forestry*, 10(2), 12–23.
- Shtaya, M. J. Y., & Abdallah, J. M. (2021). Assessment of phenotypic diversity of barley genotypes through cluster and principal component analyses. *Journal of Animal and Plant Sciences*, 31(5), 1345–1351.
- Silva, K. J., da Menezes, C. B., de Teodoro, P. E., Teodoro, L. P. R., Santos, C. V., dos Campos, A. F., de Carvalho, A. J., & Barbosa, E. da S. (2022). Multi-environmental evaluation of sorghum hybrids during off-season in Brazil. *Pesquisa Agropecuária Brasileira*, 57, e02628.
- Simkin, R. D., Seto, K. C., McDonald, R. I., & Jetz, W. (2022). Biodiversity impacts and conservation implications of urban land expansion projected to 2050. *Proceedings of the National Academy of Sciences of the United States of America*, 119(12), e2117297119.
- Singh, N., Wu, S., Raupp, W. J., Sehgal, S., Arora, S., Tiwari, V., Vikram, P., Singh, S., Chhuneja, P., Gill, B. S., & Poland, J. (2019). Efficient curation of genebanks using next generation sequencing reveals substantial duplication of germplasm accessions. *Scientific Reports*, 9, 650.
- Singh, S., Vikram, P., Sehgal, D., Burgueño, J., Sharma, A., Singh, S. K., Sansaloni, C. P., Joyson, R., Brabbs, T., Ortiz, C., Solis-Moya, E., Govindan, V., Gupta, N., Sidhu, H. S., Basandrai, A. K., Basandrai, D., Ledesma-Ramires, L., Suaste-Franco, M. P., Fuentes-Dávila, G., Moreno, J. I., Sonder, K., Singh, V. K., Singh, S., Shokat, S., Arif, M. A. R., Laghari, K. A., Srivastava, P., Bhavani, S., Kumar, S., Pal, D., Jaiswal, J. P., Kumar, U., Chaudhary, H. K., Crossa, J., Payne, T. S., Imtiaz, M., Sohu, V. S., Singh, G. P., Bains, N. S., Hall, A., & Pixley, K. V. (2018). Harnessing genetic potential of wheat germplasm banks through impact-oriented-prebreeding for future food and nutritional security. *Scientific Reports*, 8, 12527.
- Taibi, W., Belletreche, A., Kharsi, M., & Gaouar, S. B. S. (2019). Phenotypic diversity for quantitative and qualitative characters of barley (*Hordeum vulgare*) accession from Algeria. *Biodiversitas*, 20(12), 3794–3803.
- Tanaka, R., & Nakano, H. (2019). Barley yield response to nitrogen application under different weather conditions. *Scientific Reports*, 9, 8477.
- Teklemariam, S. S., Bayissa, K. N., Matros, A., Pillen, K., Ordon, F., & Wehner, G. (2022). The genetic diversity of Ethiopian barley genotypes in relation to their geographical origin. *PLoS One*, 17(5), e0260422.
- Tesfaye, S., & Sime, B. (2022). Review on genetic erosion of barley (*Hordeum vulgare* L.) in the highlands of Ethiopia. *EAS Journal of Biotechnology and Genetics*, 4(2), 24–30.
- Thiebaut, F., Hemerly, A. S., & Ferreira, P. C. G. (2019). A role for epigenetic regulation in the adaptation and stress responses of non-model plants. *Frontiers in Plant Science*, 10, 246.
- Tilman, D., & Clark, M. (2014). Global diets link environmental sustainability and human health. *Nature*, 515, 518–522.
- Ummenhofer, C. C., & Meehl, G. A. (2017). Extreme weather and climate events with ecological relevance: A review. *Philosophical Transaction of the Royal Society B*, 372(1723), 20160135.
- van de Wouw, M., Kik, C., Van Hintum, T., Van Treuren, R., & Visser, B. (2010). Genetic erosion in crops: Concept, research results and challenges. *Plant Genetic Resources*, 8(1), 1–15.
- van Eeuwijk, F. A., Bustos-Korts, D. V., & Malosetti, M. (2016). What should students in plant breeding know about the statistical aspects of genotype × environment interactions? *Crop Science*, 56(5), 2119–2140.
- Vandermeulen, M. D., & Cullen, P. J. (2022). Gene by environment interactions reveal new regulatory aspects of signaling network plasticity. *PLoS Genetics*, 18(1), e1009988.
- Varshney, R. K., Bohra, A., Roorkiwal, M., Barmukh, R., Cowling, W. A., Chitikeni, A., Lam, H.-M., Hickey, L. T., Croser, J. S., Bayer, P. E., Edwards, D., Crossa, J., Weckwerth, W., Millar, H., Kumar, A., Bevan, M. W., & Siddique, K. H. M. (2021). Fast-forward breeding for a food-secure world. *Trends in Genetics*, (37)12, 1124–1136.
- Vasko, N. I., Kozachenko, M. R., Pozdniakov, V. V., Naumov, O. G., Solonechnyi, P. M., Vazhenina, O. E., Solonechna, O. V., Zymogliad, O. V., Sheliakina, T. A., Ilchenko, N. K., Antsyferova, O. V., Suprun, O. G., & Serik, M. L. (2018). Stvorennia holozemykh sortiv ta linii yachmeniu yaroho z vysokymy kharchovymy yakostiamy [Creation of naked varieties and lines of spring barley with high food qualities]. *Plant Breeding and Seed Production*, 114, 25–38 (in Ukrainian).
- Verma, A., Kumar, V., Kharab, A. S., & Singh, G. P. (2019). AMMI model to estimate G × E for grain yield of dual purpose barley genotypes. *International Journal of Current Microbiology and Applied Sciences*, 8(5), 1–7.
- Visseren-Hamakers, I. J., & Kok, M. T. J. (Ed.). (2022). *Transforming biodiversity governance*. Cambridge University Press, Cambridge.
- Weise, S., Lohwasser, U., & Oppermann, M. (2020). Document or lose it – on the importance of information management for genetic resources conservation in Genebanks. *Plants*, 9(8), 1050.
- Wilson, S., Alavi-Shoushtari, N., Pouliot, D., & Mitchell, G. W. (2020). Similarity between agricultural and natural land covers shapes how biodiversity responds to agricultural expansion at landscape scales. *Agriculture, Ecosystems and Environment*, 30, 107052.
- Wu, S., Chen, Y., Hao, C., Liu, K., Zhang, W., & Zhang, L. (2022). Promoting biodiversity conservation requires a better understanding of the relationships between ecosystem services and multiple biodiversity dimensions. *Frontiers in Ecology and Evolution*, 10, 891627.
- Yan, W., & Tinker, N. A. (2006). Biplot analysis of multi-environment trial data: Principles and applications. *Canadian Journal of Plant Science*, 86(3), 623–645.
- Yan, W., Kang, M. S., Ma, B., Woods, S., & Cornelius, P. L. (2007). GGE biplot vs. AMMI analysis of genotype-by-environment data. *Crop Science*, 47(2), 641–653.
- Yan, W., Mitchell-Fetch, J., Beattie, A., Nilsen, K. T., Pageau, D., DeHaan, B., Hayes, M., Mountain, N., Cumiskey, A., & MacEachern, D. (2021). Oat mega-environments in Canada. *Crop Science*, 61(2), 1141–1153.
- Yawson, D. O., Ball, T., Adu, M. O., Mohan, S., Mulholland, B. J., & White, P. J. (2016). Simulated regional yields of spring barley in the United Kingdom under projected climate change. *Climate*, 4(4), 54.
- Yohane, E. N., Shimelis, H., Laing, M., Mathew, I., & Shayanowako, A. (2021). Genotype-by-environment interaction and stability analyses of grain yield in pigeonpea [*Cajanus cajan* (L.) Millspaugh]. *Acta Agriculturae Scandinavica, Section B – Soil and Plant Science*, 71(3), 145–155.
- Zabel, F., Delzeit, R., Schneider, J. M., Seppelt, R., Mauser, W., & Václavík, T. (2019). Global impacts of future cropland expansion and intensification on agricultural markets and biodiversity. *Nature Communication*, 10, 2844.
- Zahn, S., Koblenz, B., Christen, O., Pillen, K., & Maurer, A. (2020). Evaluation of wild barley introgression lines for agronomic traits related to nitrogen fertilization. *Euphytica*, 216, 39.
- Zhou, R., Jiang, F., Niu, L., Song, X., Yu, L., Yang, Y., & Wu, Z. (2022). Increase crop resilience to heat stress using omic strategies. *Frontiers in Plant Science*, 13, 891861.