



Genotype by year interaction for selected quantitative traits in hybrid lines of *Triticum aestivum* L. with *Aegilops kotschy* Boiss. and *Ae. variabilis* Eig. using the additive main effects and multiplicative interaction model

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Abstract This study estimated the genotype × environment interactions for ten yield associated traits in advanced generation hybrids of several cultivars of common wheat (*Triticum aestivum* L.) with *Aegilops kotschy* Boiss. and *A. variabilis* Eig. using the additive main effects and multiplicative interaction (AMMI) models. Tests were ran over five years at one location in replicated field trials. The AMMI model showed significant genotypic and environmental effects for all analysed traits. A majority of the hybrid lines were less stable in the analysed traits than their parental wheats. The older wheat cultivars, with lower environmental sensitivity, were the most stable. The best total genotype selection index, for all ten traits combined, was observed for the oldest cvs. Gama and Rusałka, and among the hybrid lines, for *Ae. kotschy*/Rusałka//Smuga and *Ae. kotschy*/Rusałka//Muza. The lines *Ae. kotschy*/Rusałka//Smuga, *Ae. kotschy*/

Rusałka//Muza, *Ae. kotschy*/Rusałka//Korweta, *Ae. kotschy*/Rusałka//Begra//Smuga, and *Ae. kotschy*/Rusałka//Begra//Turnia are recommended for inclusion in breeding programmes due to their greater stability and the good average values for the observed traits.

Keywords Adaptability · *Aegilops kotschy* Boiss. · *Aegilops variabilis* Eig. · AMMI · Biplot · Common wheat · Hybrids · Stability · Quantitative traits

Introduction

The global climate is warming. Droughts and high temperatures are the most important limiting factors for crop production in the world (Bansal and Sinha 1991). Yield reduction in wheat under heat stress can be caused by accelerated phasic development (Warrington et al. 1977), increase in respiration (Berry and Bjorkman 1980), reduction in photosynthesis (Blum 1986) and inhibition of starch synthesis in developing kernels (Jenner 1994). Common wheat (*Triticum aestivum* L.) is one of the most important cereals, with an estimated cultivation area of about 200 million ha (Ortiz et al. 2008). With looming negative climate change impacts on crop productivity, there is a need for biological advances in introduction of new

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cultivars—more productive and with more stable yield in changing climate conditions.

The economic value of common wheat is determined by a number of factors, with the most important ones being grain yield, crop quality, and yield stability. Fertility, i.e. the capacity to produce large grain yields, is a complex quantitative trait controlled by a vast number of genes, but breeders know only the role of simple traits, morphological, physiological and anatomical. How these traits are inherited is known (Slafer and Andrade 1993; Kato et al. 1998; Peng et al. 1998; Araki et al. 1999; Keller et al. 1999; Ahmed et al. 2000; Varshney et al. 2000; Li et al. 2002; Hai et al. 2005; Gupta et al. 2006; Houshmand et al. 2007; Kumar et al. 2007). The task of a breeder developing a new cultivar is to combine the largest possible number of alleles contributing to high yield. The more alleles with positive effect on yield a cultivar has, the larger the yield will be. This means it reacts less strongly to environmental changes, producing a similar yield in different growing seasons (Bedó and Láng 2015). Main spike seed set a trait with low heritability, which means that yield levels are significantly influenced by the environment. In common wheat, as in other cereals, the grain yield per land area unit depends mainly on the number of productive tillers, grain number per spike, and grain weight (Novoselovic et al. 2004).

To enrich the common wheat gene pool with new, beneficial traits, it is often hybridized with related species, such as the *Aegilops* species which grow naturally in various parts of Asia (Kimber and Feldman 1987), Molnár-Láng et al. 2015). Such hybrids have resulted in numerous wheat-*Aegilops* introgression lines (with improved tolerance to diseases, nematodes, and insects, as well as to high temperatures and drought (Shimshi et al. 1982; Gorham 1990; Waines 1994; Spetsov et al. 1997; Thiele et al. 2002; Marais et al. 2005; Petersen et al. 2006; Schneider et al. 2007; Coriton et al. 2009).

The need for continuous research on new forms of wheat and the assessment of their practical value is an integral element of wheat breeding. One means of achieving this goal is to learn the relationships among individual yield-affecting traits. Quantitative traits are determined not only by genes but also by environmental factors. Hence, statistical methods are useful in evaluating these relationships. Numerous statistical methods have been developed and used to analyse the

genotype-environment interactions (Becker and León 1988; Singh et al. 1999; Brancourt-Hulmel et al. 2003; Rharrabti et al. 2003; Mohammadi and Amri 2013; Cociu 2018). These methods have helped plant breeders to assess the stability of agronomically important traits and to predict the yield capacity of new genotypes in different environmental conditions. The fact that genotypes react differently in different environments and in different years is regarded as one of the main factors limiting breeding progress, and thus crop production (Esuma et al. 2016; Cuevas et al. 2017). Different reactions in different environments or years make predictions of future yields difficult or impossible (Yan and Kang 2002; Brancourt-Hulmel et al. 2003; Hageman et al. 2012).

The additive main effects and multiplicative interaction (AMMI) model (Zobel et al. 1988; Gauch and Zobel 1990) has been used extensively for analyses of multi-environment yield trials in order to understand complex genotype (G), environment/year (E/Y) and genotype-by-year interactions (GYI). The AMMI model has commonly been used to evaluate the genotype \times environment interactions (Ghaed-Rahimi et al. 2015; Golkari et al. 2016; Paderewski et al. 2016; Shahriari 2018; Rodrigues and Paderewski 2018; Bocianowski et al. 2019b, 2020; Singh et al. 2019).

The aim of this paper was to assess the genotype-by-year interactions (GYI) for ten quantitative grain yield-affecting traits in a set of wheat-*Aegilops* introgression lines and their parents, using the AMMI model. The traits were: productive tillering, the length of the main tiller, the diameter of the second internode from the base, the length of spike rachis, the spikelet number per main spike, main spike density (spikelet number per 10 cm of the spike rachis length), the grain number per main spike, grain weight per main spike, main spike seed set (grain number per spikelet), and the thousand grain weight, in hybrids of *Ae. kotschy* Boiss. and *Ae. variabilis* Eig. with *Triticum aestivum* L. field tested over a period of five years (2010–2014).

Material and methods

Plant material

This study involved 16 hybrid lines of *Triticum aestivum* L. (AABBDD) with *Aegilops kotschy* Boiss. (genomic composition UUSS) and *Aegilops variabilis*

Eig. (*USS*). The wheat cultivars used were Begra, Gama, Korweta, Monopoly, Muza, Piko, Rusalka, Smuga, Turnia and Zyta; original crosses were made in either direction, resulting in some alloplasmic lines (wheat lines with the cytoplasm of *Aegilops*) (Table 1).

The derivation of the materials has been described before (Pražak et al. 2017; Prażak and Molas 2017; Prażak and Krzepiłko 2018). In this study the lines were in generations F_{10-14} and BC_1F_{6-10} . In early generations of line development strong selection was applied for disease resistance, straw stiffness and plant height. The materials were analysed for yield and quality associated traits: plant height, lodging resistance, spike length, weight of grain from the main spike, the thousand grain weight, grain protein and micronutrients content, and resistance to leaf rust.

Field experiments

The field study was carried out over a period of five years, from 2010 to 2014, in an experimental field of University of Life Sciences in Lublin, Poland, located in Zamość (50°42'36.7" N, 23°12'47.3" E) in a randomized complete block design, with two replicates. Plots were sown in a single day between Sept 21 and 26 in different years. The plots were 2.0 × 1.0 m, with 20 × 10 cm row/plant spacing (100 seeds per plot). Soil was brown classified as good wheat

complex and standard recommended cultivation and fertilization practices were applied (NPK = 90–60–90 kg/ha). In each year, seeds for next year's experiment were multiplied on separate, adjacent plots, ensuring purity. For laboratory evaluation, plants were collected from the field at the beginning of August, when fully ripe, and ten quantitative characteristics were analysed in ten plants from each replicate: productive tillering, the main tiller length (cm), the diameter of the second internode from the base (cm), the spike rachis length (cm), the spikelet number per main spike, the main spike density (spikelet number per 10 cm of the spike rachis length), the grain number per main spike, grain weight per main spike (g), grain number per spikelet of the main spike, and the thousand grain weight (g), following the Methodological instructions for conducting varietal experiments, 1978, COBORU, Słupia Wielka). Weather data (Table 2) were obtained from the Meteorological Station in Zamość, Płoskie 1 (50°42'36.7" N, 23°12'47.3" E).

Statistical analysis

Variances and covariances among observed traits were tested. The relationships between the observed traits were estimated using the Pearson's correlation coefficients on the basis of mean values for genotypes. The data were analysed using the additive main effects and

Table 1 Derivation of hybrid lines of *Aegilops kotschy* Boiss. and *Ae. variabilis* Eig. with *Triticum aestivum* L.

Hybrid	Forms
VR5	F_{10-14}^* <i>Ae. variabilis</i> × Rusalka
RV5	F_{10-14} Rusalka × <i>Ae. variabilis</i>
KR4	F_{10-14} <i>Ae. kotschy</i> × Rusalka
RK4	F_{10-14} Rusalka × <i>Ae. kotschy</i>
KRB4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Begra
KRG6	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Gama
KRKo4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Korweta
KRMo4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Monopoly
KRMu4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Muza
KRP4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Piko
KRS4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Smuga
KRT4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Turnia
KRZ4	$BC_1 F_{6-10}$ (<i>Ae. kotschy</i> × Rusalka) × Zyta
KRBP4	$BC_2 F_{5-9}$ [(<i>Ae. kotschy</i> × Rusalka) × Begra] × Piko
KRBS4	$BC_2 F_{5-9}$ [(<i>Ae. kotschy</i> × Rusalka) × Begra] × Smuga
KRBT4	$BC_2 F_{5-9}$ [(<i>Ae. kotschy</i> × Rusalka) × Begra] × Turnia

*Generation since the last cross

Table 2 Rainfalls and temperature according to the Meteorological Station in Zamość

Year	Month				
	April	May	June	July	April–July
<i>Rainfalls (mm)</i>					Sum
2010	18.0	40.9	35.3	20.6	114.8
2011	7.6	8.6	27.0	53.3	96.5
2012	19.6	24.4	36.3	34.4	114.7
2013	15.6	35.6	85.6	63.4	200.2
2014	36.4	147.8	50.2	58.5	292.9
L YM	40.0	66.0	93.0	86.0	285.0
<i>Temperature (°C)</i>					Mean
2010	12.2	17.8	22.1	25.3	19.4
2011	13.1	16.8	22.0	21.7	18.4
2012	12.0	18.4	20.0	24.8	18.8
2013	12.4	20.7	22.6	24.0	19.9
2014	15.0	18.5	20.8	25.2	19.9
L YM	6.9	13.4	15.9	17.1	13.3
L YM—long years mean 1979–1988					

multiplicative interaction (AMMI) model (Gauch and Zobel 1990), for each trait independently. The AMMI model first fits the additive effects for the main effects of genotypes (G) and years (Y), followed by multiplicative effects for GYI by PCA. The results of the AMMI analysis are presented as biplot graphs. The AMMI model (Nowosad et al. 2016) is expressed by the following formula:

$$y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \delta_{en} + Q_{ge},$$

where y_{ge} is the trait mean of a genotype g in year e , μ is the grand mean, α_g is the mean genotype deviation, β_e is the mean year deviation, N is the number of PCA axes retained in the adjusted model, λ_n is the eigenvalue of the PCA axis n , γ_{gn} is the genotype score for the PCA axis n , δ_{en} is the score eigenvector for the PCA axis n , and Q_{ge} is the residual, including the AMMI noise and pooled experimental error. The AMMI stability value (ASV) was used to compare the stability of genotypes as described by Purchase et al. (2000):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1) \right]^2 + (IPCA_2)^2},$$

where SS_{IPCA1} is the sum of squares for $IPCA_1$, SS_{IPCA2} is the sum of squares for $IPCA_2$, and the $IPCA_1$ and $IPCA_2$ scores are the genotype scores in the AMMI model. A lower ASV score indicates a more stable genotype across years (Nowosad et al. 2017).

The genotype selection index (GSI), calculated for each genotype, incorporates both the trait mean and the ASV index in a single criterion (GSI_i), as follows (Farshadfar and Sutka 2003):

$$GSI_i = RM_i + RA_i,$$

where RM_i is the rank of the trait mean [from maximum to minimum for productive tillering, the diameter of the second internode from the base, the length of spike rachis, the spikelet number per main spike, main spike density, the grain number per main spike, grain weight per main spike, main spike seed set (grain number per spikelet) and the thousand grain weight, and from minimum to maximum for the length of the main tiller] for i -th genotype, and RA_i is the rank of the ASV for the i -th genotype. Finally, the total genotype selection index (TGSI) was calculated for each genotype as the sum of the GSIs for all ten traits.

All analyses were conducted using the GenStat v. 18 statistics software.

Results

Variations, covariances and correlations

Variations and covariances between observed traits are presented in Table 3. The variance of the traits ranged from 0.05 (for the spike rachis length) to 458.03 (for the main tiller length) (Table 3). Covariances between productive tillering and other traits were negative and ranged from -123.09 (the main tiller length) to -0.8 (grain number per spikelet of the main spike). Other covariances were positive and ranged from 0.04 (between the spike rachis length and the grain number per spikelet in main spike) to 191.45 (between the main tiller length and the grain number per main spike). All pairs of observed traits were correlated, except for the grain number per spikelet of main spike with: productive tillering, the spikelet number per

Table 3 Variances (diagonal), covariances (above diagonal) and correlation coefficients (below diagonal) between observed traits

Trait	Productive tillering	The length of the main tiller	The diameter of the second internode from the base	The length of spike rachis	The spikelet number per main spike	Main spike density (spikelet number per dm of the spike length)	The grain number per main spike	Grain weight per spike	Main seed set number per spikelet	The 1000-grain weight
Productive tillering	167.4	- 123.09	- 6.86	- 1.39	- 39.37	- 34.7	- 89.12	- 3.64	- 0.8	- 53.21
The length of the main tiller	- 0.81***	458.03	12.67	3.24	77.52	50.26	191.45	7.47	3.64	96.55
The diameter of the second internode from the base	- 0.92***	0.85***	0.82	0.12	3.29	2.62	7.74	0.31	0.13	4.49
The length of spike rachis	- 0.76***	0.86***	0.85***	0.05	0.81	0.16	2.03	0.08	0.04	1.02
The spikelet number per main spike	- 0.93***	0.87***	0.95***	0.83***	23.43	17.85	52.64	1.92	0.77	23.53
Main spike density (spikelet number per dm of the spike rachis length)	- 0.84***	0.59***	0.76***	0.41*	0.83***	24.97	32.99	1.12	0.25	17.05
The grain number per main spike	- 0.81***	0.82***	0.87***	0.77***	0.84***	0.62***	287.28	11.09	10.62	70.55
Grain weight per main spike	- 0.79***	0.78***	0.84***	0.73***	0.75***	0.55**	0.91***	0.6	0.41	4.3
Main spike seed set (grain number per spikelet)	- 0.36	0.45*	0.44*	0.4*	0.35	0.15	0.79***	0.74	0.57	1.77
The 1000-grain weight	- 0.82***	0.71***	0.86***	0.68***	0.74***	0.64***	0.74***	0.88***	0.45*	76.35

*P < 0.05; **P < 0.01; ***P < 0.001

main spike, main spike density (spikelet number per 10 cm of the spike rachis length) and the grain weight per main spike (Table 3).

Analysis of variance

The three sources of variation (genotype, year, and the $G \times Y$ interaction) were highly significant for all ten traits (Table 4) of wheat. In the ANOVA, the sum of squares for the main genotype effect ranged from 20.69% (for the main spike seed set) to 87.77% (for the spikelet number per main spike) of the total trait variation, and this factor had the highest effect on all observed traits except the main spike seed set (Table 4). The differences between years explained from 0.62% (for the spikelet number per main spike) to 16.81% (for grain weight per main spike) of the total trait variation, while GYI explained from 5.09% (for the spikelet number per main spike) to 25.97% (for main spike seed set) (Table 4). Values for the first three principal components were also significant (at the 0.001 level) for all observed traits, together representing from 64.05% (for the diameter of the second internode from the base) to 85.46% (for the main spike density) of the entire effect (Table 4). The first principal component (IPCA 1) accounted for from 38.54% (for grain weight per main spike) to 72.76% (for the main spike density) of variation caused by the interaction (Table 4).

Productive tillering

The numbers of productive tillers per plant ranged from 3.2 (for VR5 in 2012) to 71.0 (for *Ae. variabilis* in 2013), with the average of 15.21 (Table S1). *Ae. variabilis* had the highest average productive tillering (52.56), while cv. Muza had the lowest (10.22). The average productive tillering in individual years ranged from 12.45 in 2011 to 17.30 in 2013 (Table S1). *Ae. variabilis* adapted in environments with similar conditions to these in 2013, and not adapted in 2011 (Fig. S1). VR5 adapted in environments with similar conditions to these in 2014, and not adapted in 2012. KRKo4 and KRMu4 were the most stable, with the ASV of 0.283 and 0.443, respectively, while *Ae. variabilis* (8.269) and *Ae. kotschyi* (7.300) were the least stable (Table S1). Cvs. Piko and Monopoly, with high average productive tillering (13.66 and 13.90, respectively) and the ASV equal to 0.450 and 1.050,

respectively, had the best genotype selection indices (11 and 14, respectively).

The main tiller length

The length of the main tiller ranged from 17.40 cm (for *Ae. kotschyi* in 2010) to 123.10 cm (for KRT4 in 2011) over the the five years, with the average of 89.78 cm (Table S2). The average the length of the main tiller was the highest in KRT4 (117.18 cm) and the lowest in *Ae. kotschyi* (27.54 cm). The average the main tiller length in individual years ranged from 86.99 cm in 2010 to 92.79 cm in 2021. KRP4 adapted in environments with similar conditions to these in years 2012 and 2014, and not adapted in 2010 and 2011 (Fig. S2). The KR4 and KRBP4 adapted in environments with similar conditions to these in 2013, and not adapted in 2011 and 2014. Cv. Zyta and alloplasmic introgression line KRBS4, with the ASV of 0.224 and 0.279, respectively, were the most stable, while KRMo4 (4.467) and KRP4 (3.303) were the least stable (Table S2). RK4, with the average the main tiller length ranging from 66.9 to 76.6 cm and the ASV of 0.374, had the best genotype selection index (6).

The diameter of the second internode from the base

The diameter of the second internode from the base ranged from 0.036 cm (*Ae. kotschyi* in 2012) to 0.508 cm (Begra in 2013) over the five years, with the average of 0.339 cm (Table S3). The average the diameter of the second internode from the base was highest in KRB4 (0.414 cm) and lowest in *Ae. kotschyi* (0.073 cm). The averages individual years ranged from 0.326 cm in 2010 to 0.362 cm in 2011. The stability of parental cultivars as well as euplasmic and alloplasmic introgression lines is illustrated on Fig. S3. *Ae. kotschyi*, KRZ4 and KRP4 adapted in environments with similar conditions to these in 2014, and not adapted in 2011 (Fig. S3). Begra, KRG6, KRMu4 and KRS4 adapted in environments with similar conditions to these in 2013, and not adapted in 2010. Cv. Monopoly and *Ae. variabilis*, with the ASV of 0.132 and 0.174, respectively, were the most stable, cv. Begra (1.547) and euplasmic introgression line RV5 (0.853) were the least stable (Table S3). Cv. Monopoly with the highest average diameter (0.388 cm) and the ASV equal to 0.132, had the best genotype selection index (7) (Table S3).

Table 4 Analysis of variance of main effects and interactions for ten observed traits in hybrid lines of *Aegilops kotschy* Boiss. and *Ae. variabilis* Eig. with *Triticum aestivum* L. and their parental components and variability explained (ve, in %)

Source of variation	Total	Treatments	Genotypes, G	Years, Y	Block	GY Interactions	GY interaction contribution			Error			
							Years, Y	Block	GY Interactions		Residuals		
											IPCA 1	IPCA 2	IPCA 3
Degrees of freedom	1399	139	27	4	45	108	30	28	26	24	1215		
Productive tillering	m.s	167.4	1094.8***	4436.3***	1184.5***	56.4	256.1***	275.1***	107*	74.8	65.4		
	ve (%)	64.98	51.15	2.02	1.08	11.81	55.60	27.85	10.05	6.49			
The length of the main tiller	m.s	458	4198***	19,545***	1438***	74**	464***	686***	303***	126***	44		
	ve (%)	91.07	82.36	0.90	0.52	7.82	39.86	38.34	15.74	6.05			
The diameter of the second internode from the base	m.s	0.819	6.473***	29,617***	5.623***	0.217	0.718***	0.606***	0.572***	0.542***	0.195		
	ve (%)	78.49	69.77	1.96	0.85	6.77	42.14	21.91	19.20	16.75			
The length of spike rachis	m.s	0.051	0.427***	1.9143***	0.7501***	0.0091	0.0432***	0.0747***	0.0273***	0.0229***	0.0095		
	ve (%)	83.20	72.45	4.21	0.57	6.55	47.97	24.84	15.20	11.78			
The spikelet number per main spike	m.s	23.4	220.5***	1065.8***	50.7***	1.3	15.5***	29.4***	11.7***	7.2***	1.7		
	ve (%)	93.48	87.77	0.62	0.18	5.09	52.87	19.70	17.13	10.30			
Main spike density (spikelet number per 10 cm of the spike rachis length)	m.s	25	222.8***	977.2***	192.4***	3.5	35.3***	92.4***	17.3***	11.2***	3.1		
	ve (%)	88.64	75.53	2.20	0.45	10.91	72.76	12.70	7.61	6.93			
The grain number per main spike	m.s	287	2014***	6690***	7317***	117	649***	1237***	567***	480***	96		
	ve (%)	69.66	44.94	7.28	1.31	17.44	52.93	22.64	17.81	6.62			
grain weight per main spike	m.s	0.602	4.191***	11.066***	35.38***	0.268	1.317***	1.826***	0.948***	0.528***	0.203		
	ve (%)	69.21	35.50	16.81	1.43	16.89	38.54	35.23	17.37	8.93			
Main spike seed set (grain number per spikelet)	m.s	0.571	3.168***	6.125***	16.859***	0.384	1.922***	3.893***	1.608***	1.117***	0.697***		
	ve (%)	55.09	20.69	8.43	2.16	25.97	56.26	21.68	14.02	8.04			
The 1000-grain weight	m.s	76.4	597.9***	2347.6***	2897.5***	22.5	75.4***	128.6***	92***	46.1***	18.7		
	ve (%)	77.81	59.34	10.85	0.95	7.62	47.41	31.66	14.72	6.20			

P < 0.01; *P < 0.001

The length of spike rachis

The length of the spike rachis ranged from 2.37 cm (for *Ae. kotschy* in 2013) to 13.8 cm (for KRBT4 in 2010) over the five years, with the average of 8.839 cm (Table S4). It was highest in KRBT4 (12.236 cm) and the lowest in *Ae. kotschy* (3.264 cm). The averages in individual years ranged from 8.156 cm in 2011 to 9.454 cm in 2014. The stability of genotypes can be evaluated on the biplot (Fig. S4). KRZ4, KR4 and RV5 adapted in environments with similar conditions to these in years 2012 and 2013, and not adapted in 2010 (Fig. S4). KRP4, RK4 and VR5 adapted in environments with similar conditions to these in 2014, and not adapted in 2011. Alloplasmic introgression lines KRBS4, KRMo4 and KRS4, with the ASV of 0.017, 0.025 and 0.030, respectively, were the most stable, while KRB4 (0.696) and KRP4 (0.661) were the least stable (Table S4). Cv. Turnia, with a high average spike rachis length (11.186 cm) and the ASV of 0.043, had the best genotype selection index (7).

The spikelet number per main spike

The spikelet number per main spike ranged from 2.7 (for *Ae. kotschy* in 2017) to 23.2 (for KRG6 in 2010) over the five years, with the average of 18.05 (Table S5). Cv. Monopoly had the highest average the spikelet number (22), while *Ae. variabilis* had the lowest (3). The average number in individual years ranged from 17.67 in 2012 to 18.59 in 2014. The stability of the genotypes can be evaluated on the biplot (Fig. S5). Alloplasmic introgression lines VR5, KRG6 and KRMu4 adapted in environments with similar conditions to these in years 2010 and 2014, and not adapted in 2013 (Fig. S5). KR4 adapted in environments with similar conditions to these in 2011, and not adapted in 2012. Cv. Rusalka, with the ASV of 0.068, was the most stable, while introgression lines RV5 (5.402) and VR5 (3.412) were the least stable (Table S5). Cv. Korweta, with the average the spikelet number per main spike of 20.24 and a high ASV (0.249), had the best genotype selection index (11), while introgression lines VR5 and RV5 had the worst genotype selection index (50).

Main spike density

The main spike density of the genotypes ranged from 5.44 (for *Ae. variabilis* in 2013) to 30.83 (for RV5 in 2011) over the five years, with the average of 19.08 (Table S6). Alloplasmic introgression line KRBP4 had the highest average density (25.62), and *Ae. variabilis* had the lowest (6.04). The averages ranged in individual years from 18.35 in 2014 to 20.51 in 2011. The stability of the character is presented on the biplot, Fig. S6. Among the introgression lines KR4 and KRZ4 adapted in environments with similar conditions to these in years 2010 and 2011, not adapted in 2013 and 2014 (Fig. S6). *Ae. variabilis* was the most stable, with the ASV of 0.260, while introgression lines RV5 (15.139) and KR4 (9.528) were the least stable (Table S6). Alloplasmic introgression line KRBP4, with the highest average main spike density (25.62) and the good ASV (0.779), had the best genotype selection index (5), while alloplasmic introgression line KR4 had the worst genotype selection index (50).

The grain number per main spike

The grain number per main spike ranged from 2.6 (for *Ae. kotschy* in 2012) to 60.5 (for KRBS4 in 2013) over the five years, with the average of 35.7 (Table S7). The average the grain number per main spike was highest for the cv. Turnia (47.86) and lowest for *Ae. kotschy* had (4.4). The average the grain number per main spike in individual years ranged from 30.93 in 2010 to 44.39 in 2014. Introgression lines RV5, KR4 and KRG6 adapted in environments with similar conditions to these in years 2011 and 2014, and not adapted in 2013 (Fig. S7). Alloplasmic introgression lines KRB4 and KRMo4 as well as cvs. Zyta and Piko adapted in environments with similar conditions to these in 2012, and not adapted in 2010. Cv. Korweta, with the ASV of 0.197, was the most stable, while introgression lines VR5 (10.949) and RV5 (9.967) were the least stable (Table S7). Alloplasmic introgression line KRMu4, with an the average the grain number per main spike of 47.66 and the ASV of 0.724, had the best genotype selection index (6).

Grain weight per main spike

The grain weight per main spike of the genotypes ranged from 0.019 g (for *Ae. kotschyi* in 2012) to 3.023 g (for KRT4 in 2011) over the five years, with the average of 1.291 g (Table S8). Alloplasmic introgression line KRMu4 had the highest average grain weight per main spike (1.901 g), and *Ae. kotschyi* had the lowest (0.034 g). The average grain weight per main spike in individual years ranged from 1.007 g in 2010 to 1.898 g in 2014. Alloplasmic introgression lines KRP4 and KRMo4, and cvs. Muza and Piko adapted in environments with similar conditions to these in years 2010, 2012 and 2013, and not adapted in 2011 and 2014 (Fig. S8). Cv. Zyta, with the ASV of 0.072, was the most stable, while euplasmic introgression line RV5 (1.128) was the least stable (Table S8). Cv. Zyta, with a high average grain weight per main spike (1.535 g) and the best ASV, had the best genotype selection index (11).

Main spike seed set (grain number per spikelet)

The main spike seed set of the genotypes ranged from 0.307 (for VR5 in 2012) to 3.566 (for *Ae. kotschyi* in 2013) over the five years, with the average of 1.934 (Table S9). Alloplasmic introgression line KRMu4 had the highest average main spike seed set (2.455 g), and alloplasmic introgression line KR4 had the lowest (1.351 g). The average main spike seed set in individual years ranged from 1.663 g in 2010 to 2.318 g in 2014. *Ae. kotschyi* and *Ae. variabilis* adapted in environments with similar conditions to these in 2013, and not adapted in 2011 and 2014 (Fig. S9). Alloplasmic introgression line VR5 adapted in environments with similar conditions to these in 2010, and not adapted in 2012. Cv. Rusalka was the most stable, with the ASV of 0.095, while alloplasmic introgression line KR4 (2.864) was the least stable (Table S9). Cv. Rusalka had the best genotype selection index (7), while *Ae. kotschyi* had the worst (53).

The thousand grain weight (TGW)

The TGW values ranged from 6.95 g (for *Ae. variabilis* in 2011) to 50.21 g (for Rusalka in 2014), with the average of 31.22 g (Table S10). Cv. Rusalka had the highest average TGW (42.81 g), and *Ae.*

kotschyi had the lowest (7.9 g). The average TGW in individual years ranged from 28.75 g in 2011 to 36.63 g in 2014. *Ae. variabilis*, alloplasmic introgression line KRMo4, and cvs. Begra and Smuga adapted in environments with similar conditions to these in years 2012 and 2013, and not adapted in 2011 (Fig. S10). *Ae. kotschyi*, cv. Gama, and alloplasmic introgression lines KR4 and KRBP4 adapted in environments with similar conditions to these in 2010, and not adapted in 2014. The ASV ranged from 0.183 (for alloplasmic introgression line KRKo4) to 3.120 (for alloplasmic introgression line KRP4). The GSI ranged from 8 (for alloplasmic introgression line KRKo4) to 52 (for alloplasmic introgression line KRBP4).

Total genotype selection index

The best total genotype selection index (for all ten traits combined) was observed for cvs. Gama (TGSI = 194), Rusalka (TGSI = 209), and Korweta (TGSI = 223) and for alloplasmic introgression lines KRS4 (TGSI = 222) and KRMu4 (TGSI = 229), and the worst for alloplasmic introgression line KR4 (TGSI = 433). Alloplasmic introgression lines KRMu4, KRS4, KRKo4, KRBS4, and KRBT4 are recommended for further inclusion in breeding programmes due to their better stability in comparison with other lines and the good average values for the observed traits.

Discussion

Crop breeding among others aims at producing new, starting materials for breeding, with desirable levels of resistance to diseases, pests, and unfavourable abiotic conditions. In wheat breeding, the difficulty in achieving these goals is in part a consequence of low genetic variation within the species *Triticum aestivum* L. (Pilch 2011). Wild species related to wheat, e.g. genus *Aegilops*, are a valuable source of alleles for agronomic traits useful in breeding, and their use as source material for cross-breeding significantly increases the gene pool of wheat. The species *Ae. kotschyi* Boiss. and *Ae. variabilis* Eig. are highly resistant to abiotic stressors, including drought, high temperatures, and soil salinity (Shimshi et al. 1982; Kimber and Feldman 1987). For this reason, hybrids of common wheat with these species were chosen to test

the effect of changes in weather conditions in consecutive years on their yield traits.

The experimental field located near Zamość was perfectly suitable for this type of experiment due to its extreme summer and winter conditions. The climate in Zamość area is characterized by dry and hot summers and cold winters. It is also characterized by a large number of sunny days a year (38%) and at times there are up to 60 frost days per year, and with temperature below freezing for up to 130 days. The snow cover time ranges from 60 to 80 days (Reszel 1992). Global warming has resulted in greater variation in weather conditions in recent years, with less frequent rainfall and resulting droughts.

The atmospheric conditions in 2010–2014 were variable (Table 2). In 2010–2013, between April and July, the rainfall deficit was 59.7%, 66.1%, 59.8% and 29.8%, respectively. Only in 2014 did the precipitation total exceed the long-term average, by 2.8%. In all years of the study, the average monthly temperature from April to July exceeded the long-term average, by 6.1 °C in 2010, 5.1 °C in 2011, 5.5 °C in 2012 and 6.6 °C in 2013 and 2014.

For the experiments described here the plots were sown at 20 × 10 cm spacing. This permitted the assessment of tillering, but also promoted it to some degree. However, at times similar experiments are planted at even greater spacing, e.g. 20 × 15 cm (Ćwiklińska et al. 2009). Under these conditions, the tillering of the introgression lines was similar to that of wheat. In both groups, the number of productive tillers were significantly lower than in the *Aegilops* parents. It is clear that selection in early generations removed much of excessive tillering from the introgression lines. Among the latter, *Ae. kotschyi*/Rusałka//Korweta and *Ae. kotschyi*/Rusałka//Muza lines were the most stable in terms of the number of tillers. Cvs. Piko and Monopoly, with the best tillering, had the best genotype selection index. The number of productive tillers per plant is highly variable and largely determined by the environment (Nawracała 2004). Araki et al. (1999) located *QTLs* linked to the tiller number on chromosome arm 4AS of common wheat. Among the introgression lines, the average the length of the main tiller range more widely than among the parental wheat cultivars. The shortest main tillers were in *Ae. kotschyi* Boiss., *Ae. variabilis* Eig. and lines Rusałka/*Ae. kotschyi* and *Ae. kotschyi*/Rusałka//Begra//Piko. Short-straw forms are more resistant to lodging. Keller

et al. (1999) identified nine loci responsible for lodging resistance in wheat, on chromosome arms *1BS*, *2AS*, *2D*, *3AS*, *4AS*, *5AL*, *5BL*, *6BL* and *7BL*. Ahmed et al. (2000) found seven *QTLs* and RFLP markers associated with plant height on chromosomes *1A*, *1D*, *2B*, *2D* and *4B* of common wheat. Genes influencing stem stiffness in wheat have been located on chromosomes *1A*, *1BS*, *3AS*, *4AS*, *5AL*, *3BL*, *5BL*, *2D* (Nawracała 2004; Hai et al. 2005; Houshmand et al. 2007).

The numerical values of morphological features were probably affected by the amount of precipitation during individual growing season. In 2014, when the April to July rainfall total was the highest, the spikes were the longest with the highest numbers of spikelets and grains, grain weight per spike, and the thousand grain weight. Yield traits are influenced by multiple *QTLs* located on most chromosomes. Some of the characters measured are known to be controlled by numerous chromosome regions, scattered over many chromosomes (Kato et al. 1998; Peng et al. 1998; Varshney et al. 2000; Li et al. 2002; Nawracała 2004; Kumar et al. 2006; Nalam et al. 2006). Mollasadeghi et al. (2012) reported that wheat plant height, productive tiller number and grain number showed more genetic variation than other features.

The ASVs indicated that a few alloplasmic introgression lines with *Ae. kotschyi* were the most stable in terms of the all analysed morphological traits, but from parental wheats some were the most stable in the case of some traits such as the length of the main tiller (Zyta), the diameter of the second internode from the base (Monopoly), the spikelet number per main spike (Rusałka), the grain number per main spike (Korweta), the grain weight per main spike (Zyta), the main spike seed set (Rusałka), the thousand grain weight (Turnia, Monopoly).

The alloplasmic introgression lines *Ae. kotschyi*/Rusałka//Piko, *Ae. kotschyi*/Rusałka//Monopoly, and Begra, Gama, Muza, Piko, Smuga parental wheats were adapted in environments with similar conditions to these in 2010, 2012 and 2013, in terms of the grain weight per main spike and thousand grain weight. The alloplasmic introgression line *Ae. variabilis*/Rusałka was adapted in environments with similar conditions to these only in year 2010, in terms of main spike seed set.

The best total genotype selection index for all ten traits combined was observed for the cvs. Gama and

Rusałka, and among hybrid lines, for *Ae. kotschyii* Rusałka//Smuga and *Ae. kotschyii*/Rusałka//Muza. Due to their stability and the good average values for the observed traits, the lines *Ae. kotschyii*/Rusałka//Smuga, *Ae. kotschyii*/Rusałka//Muza, *Ae. kotschyii*/Rusałka//Korweta, *Ae. kotschyii*/Rusałka//Begra//Smuga, and *Ae. kotschyii*/Rusałka//Begra//Turnia can be recommended for further inclusion in breeding programmes.

In a study by Rodrigues and Paderewski (2018), the AMMI analysis was applied to phenotypic data for the location \times management \times year combination (treated as environmental conditions). In wheat cvs. Alcazar, Rapsodia, Boomer, Anthus, Kris and Batuta, the interaction positively affected yield in 2008, but negatively in 2009. The remaining cultivars (Mewa, Legenda, Sukces, Smuga, Turnia, and Zyta) had positive or near-zero interaction effects in 2009, but negative effects in 2008. Ibrahim and Said (2020) assessed 42 genotypes of common wheat in eight environments in Egypt, with two locations and two planting dates in the two growing seasons. They estimated the grain yield, spike number per plant, the thousand grain weight, and plant height. The combined analysis showed that most of the means squares were assigned to environmental effects, indicating that the environments were diverse, with large differences between environmental means causing most of the variation in grain yield and other features. According to the authors, six genotypes, showed better overall adaptability in different environments.

Mohammadi (2017) used the AMMI model to analyse the genotype, year and GYI effects for the grain yield and drought-adaptive traits of 25 wheat genotypes during five seasons. The results showed that GYIs lead to different rankings of genotypes in different environments. According to the author, these breeding lines are unstable because they are more adapted to favourable growing conditions. On the other hand, old wheat cultivars with less sensitivity to environmental conditions were the most stable. Similarly, in our research, the oldest cvs., Rusałka and Gama, were the most stable. Cv. Rusałka, because it crosses well with rye, has long been used in wide hybridization (Stefanowska 1986). Winter cvs. Gama and Begra were placed on the Polish National List of Varieties of Agricultural Plants in 1982, and Korweta in 1997, Zyta in 1999, Turnia in 2001, Piko in 2002, Muza and Smuga in 2004 (COBORU

1982, 1997, 1999, 2001, 2002, 2004). Monopoly it is Canadian wheat cultivar grown in 1990s.

In contrast to the old wheat cultivars, the introgression lines showed less stability, probably due to their hybrid character. The importance of GYIs in plant breeding programmes has been a focus of attention for wheat breeders (Brancourt-Hulmel et al. 2003; Mohammadi and Amri 2013; Farshadfar et al. 2015; Golkari et al. 2016; Paderewski et al. 2016; Semchedinne et al. 2017; Mohammadi 2017; Rodrigues and Paderewski 2018; Roostaei et al. 2018; El-Sherbeny et al. 2019; Singh et al. 2019; Ibrahim and Said 2020; Eltaher et al. 2021).

The frequently used the AMMI model provides a useful tool for diagnosing GEI patterns and improving the accuracy of response estimates (Rharrabti et al. 2003; Paderewski et al. 2016; Fotso et al. 2018; Hassani et al. 2018; Bocianowski et al. 2018, 2019a, 2019c, 2021). The AMMI stability value revealed high stability among the cultivars. According to Yang et al. (2009), a biplot based on the AMMI is a useful visualization technique for identifying similarity or dissimilarity among genotypes or environments. At the same time, Yang et al. (2009) caution against the use of a biplot as more than a visual descriptive tool, as the method utilizes only a sample of the full data set and does not involve any statistical hypothesis testing.

The best total genotype selection index for all ten traits combined was obtained for the cvs. Gama and Rusałka, and among the introgression lines, for KRS4 and KRMu4.

Conclusions

We hypothesized that wheat lines with introgressions from *Aegilops kotschyii* Boiss. and *Ae. variabilis* Eig. would be less sensitive to variable environmental conditions and more stable in terms of the yield traits analysed during the years of the study. However, their responses were varied. For some of these lines, Morphological traits and the genotype selection indexes were higher than or comparable to those of the parental wheats, while for other lines, the values were lower. All of the first group lines have *Ae. kotschi* in the pedigree, used as female in the original cross. Hence, all are alloplasmic lines but at this point, in the absence of reciprocal hybrids, no association between

the cytoplasm and line performance can be made. Regardless, based on the results collected in this study, these lines appear as the most suitable for inclusion in breeding programmes due to their stability and favourable mean values for the observed traits.

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Declarations

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