CHARACTERIZATION OF Aegilops kotschyi Boiss. x Triticum aestivum L. HYBRID LINES

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Received: 22.04.2013

A b s t r a c t

A study of four F₅ and one BC₁F₁ Aegilops kotschyi Boiss. x Triticum aestivum L. hybrid lines was conducted to determine their quantitative morphological and qualitative features as well as a molecular investigation was carried out. Observations of ten quantitative traits showed that the F₅ hybrid lines exhibited intermediate values between Aegilops kotschyi Boiss. and Triticum aestivum L., or had similar traits to one of the parents. These hybrid lines had a significantly lower number and weight of grains per main spike, main spike fertility and 1000-grain weight than T. aestivum L. cv. ‘Rusalka’. The BC₁F₁ hybrid line was characterized by wheat-like fertility and phenotype. The F₅ hybrid lines were characterized by much higher variability of the analysed morphological traits than T. aestivum L. cv. ‘Rusalka’. Grains of the hybrid lines had higher protein and micronutrient (iron and zinc) content than wheat grains.

The presence of DNA fragments specific to Aegilops kotschyi Boiss. in the genotypes of the hybrid lines was confirmed by seven ISSR (Inter Simple Sequence Repeats) molecular markers. Two ISSR markers – ISSR23690 and ISSR33650 – were the most effective for germplasm analysis of the hybrid lines. The analysed lines can become a source material for improvement of common wheat T. aestivum L. in crossing programs.

K e y w o r d s: Aegilops kotschyi Boiss., morphological traits, PCR ISSR, iron, zinc, protein, Triticum aestivum L.

I n t r o d u c t i o n

Intergeneric hybrids are interesting materials from a theoretical point of view and have the potential to increase genetic variation in common wheat breeding. The goal of distant hybridization is to introduce to breeding materials genes from wild species that code resistance to non-favourable agricultural conditions as well as high grain protein and micronutrient content. Aegilops species are often used as sources of desirable agronomic characters that can be introduced into wheat cultivars [1,2,3,4,5,6,7,8,9,10,11,12].

Aegilops kotschyi Boiss. (2n = 4x = 28, UUSS) is a species of particular interest for genetic and breeding research as an important gene donor for complex disease resistance [6,8,13,14,15], drought, heat and salt tolerance [4,16,17,18], because its grains have a high protein and lysine content [19,20,21]. Moreover, its cytoplasm is a potential basis for inducing cytoplasmic male sterility [22] and haploidy [23]. Aegilops kotschyi Boiss. has higher iron and zinc content than T. aestivum L. and an efficient genetic system for uptake/translocation of the micronutrients, which could be effectively used for biofortification of wheat cultivars [24,25].

Wheat breeding programs have been directed towards factors such as grain yield and quality. An ideal cultivar for high grain yield or for any other desirable traits needs to express genetic potential with a low value of variance in different environmental factors of growing. Traits such as, for example, number of productive tillers, grain number and grain weight per spike, fertility of main spike, and 1000-grain weight were positively correlated with grain yield [17,26]. High temperature stress during the grain-filling period is one of the major environmental constraints limiting the grain yield of wheat in many countries in the world [27,17]. Aegilops kotschyi Boiss. is the most xerophytic of the wild wheat relatives. Its genes can be used for genetic improvement of common wheat [28].

The basis of plant breeding is the selection of specific plants with desirable traits. Selection typically involves evaluating a breeding population for one or
more traits in field or glasshouse trials (e.g. agronomic traits, disease resistance or stress tolerance), or with chemical tests (e.g. grain quality). The goal of plant breeding is to assemble more desirable combinations of genes in new varieties. In a commonly used pedigree breeding method, selecting desirable plants begins in early generations for traits of higher heritability. However, for traits of low heritability, selection is often postponed until later generations (F3 or F4). Selection of superior plants involves visual assessment for agronomic traits or resistance to stresses as well as laboratory tests for quality or other traits [29].

The aim of this study was to indicate diagnostic traits for the F1 and BC1, *Ae. kotschyi* Boiss. × *T. aestivum* L. hybrid lines which can be used in breeding programs for improvement of wheat yield and quality. Our interest focused on some agronomic characters such as morphological traits and yield components as well as grain protein, iron and zinc contents, and on the identification of genes of *Ae. kotschyi* Boiss. in the genotypes of the hybrid lines using the Inter Simple Sequence Repeats (ISSR) technique.

**MATERIALS AND METHODS**

A set of four F1, *Aegilops kotschyi* Boiss. × *Triticum aestivum* L. cv. ‘Rusalka’ hybrid lines (KR3, KR4, KR6, KR9) and one BC1, F1 (*Ae. kotschyi* Boiss. × *T. aestivum* L. cv. Rusalka) × *T. aestivum* L. cv. ‘Begra’ hybrid line (KRB) originating from the crosses of *Ae. kotschyi* Boiss. no. AE 120/78 (seeds from the Institute of Plant Breeding in Cambridge, Great Britain) with *T. aestivum* L. cv. ‘Rusalka’ and *T. aestivum* L. cv. ‘Begra’ (seeds from the Institute of Genetics, Plant Breeding and Biotechnology, University of Life Sciences in Lublin, Poland) were used in this study. The ‘Rusalka’ cultivar was chosen for intergeneric crosses because it had good crossability with *Secale cereale* L.

The hybrid lines and their parental forms were cultivated under field conditions. 100 seeds of each hybrid line and cv. ‘Rusalka’ were sown manually in 1 m² plots, with 20 cm space between 2 m long rows and 10 cm distance between each seed in a row. The experiment was performed using a low seeding rate so that the hybrid lines could express their maximum genetic potential for tillering and other components. The fields were prepared with standard production practices. During the vegetation period, phenological observations were performed (emergence stage, tillering stage, winterhardiness, heading stage, flowering stage, maturity stage).

**Analysis of quantitative morphological traits**

For the analysis of morphological traits, 20 plants of each form at the full maturity stage were used. The following features were measured: productive tillering, length of the main tiller, diameter of the basal stem (the second internode from the bottom to the top of the plant), length of spike rachis, number of spikelets in the main spike, main spike density (the number of spikelets per 1 dm of spike rachis), grain number and weight per main spike, fertility of main spike (number of grains per spikelet), and 1000-grain weight.

Means and range of variation of agronomic characters were calculated. The significance of differences between the agronomic characters analysed were verified by Tukey’s test at p = 0.05. The results are presented in Tables 1–2 and Figures 1–3.

**Analysis of grain protein and micronutrient content**

The protein content in grains of wheat and hybrid forms was determined by the Kjeldahl block digestion method [30]. For micronutrient analysis, the dried grain material was digested using a diacid (HNO3-HClO4) mixture. After dilution of the digests, they were processed for zinc (Zn) and iron (Fe) analysis using an atomic absorption spectrophotometer (AAS). The analysis of protein and micronutrient contents in grains was carried out in the Central Agro-Ecological Laboratory of the University of Life Sciences in Lublin.

**Molecular analysis**

DNA extraction from lyophilized leaves into a microfuge tube (1.5 mL) was done as in the modified Milligan [31] procedure. PCR ISSR analysis was performed by a modified procedure based on Ziętkiewicz et al. [32] for two DNA probes of each genotype, with a control reaction without DNA matrix performed at the same time. The 15 μL reaction volume contained 1 x PCR buffer (10 mM Tris-HCl pH 8.8, 50 mM KCl, 0.08% Nonidet P40, Fermentas, Lithuania), 130 μM of each dNTP, 470 pM of each primer, 1.5 mM MgCl2, 0.5 unit of *Taq* DNA polymerase, and 60 ng template DNA. Of sixteen primers tested, seven were chosen for PCR ISSR analysis: ISSR 6: 5’–(GT)8C - 3’, ISSR 14: 5’–(GA)7YG – 3’, ISSR 16: 5’–(GA)8C – 3’, ISSR 17: 5’–(GA)8YC– 3’, ISSR 23: 5’–(CA)3GC – 3’, ISSR 33: 5’–(AG)3T – 3’, and ISSR 35: 5’–(TC)3CG – 3’.

DNA amplification reactions were performed in a thermocycler (Whatman-Biometra model T1) programmed as follows: an initial denaturation step at 95°C for 7 minutes followed by amplification for 38 cycles with denaturation at 95°C for 30 s, annealing the first 3 cycles at 54°C for 45 s, the following 3 cycles at 53°C for 45 s and 32 cycles at 52°C for 45 s, and extension at 72°C for 2 minutes with a final extension step at 72°C for 7 minutes. The amplified products were separated by electrophoresis in 2.5% agarose gel in 1 x TBE
buffer, containing 0.01% ethidium bromide, in the presence of size markers. GeneRuler™ 100 bp DNA Ladder Plus (Fermentas, Lithuania) was used to determine the size of the products. DNA bands were photographed under ultra violet light, using a photo documentation system (version 3.03 of DNAfrag).

RESULTS

In eastern Poland conditions, the F₂ and BC₁F₁ Ae. kotschyi Boiss. x T. aestivum L. hybrid lines were characterized by winter hardiness and growing season length similar to those of cv. Rusalka.

Analysis of quantitative morphological traits

Table 1 contains means and range of variation of some morphological traits and yield components of the parental wheat T. aestivum L. cv. ‘Rusalka’ and the Ae. kotschyi Boiss. x T. aestivum L. hybrids lines. Cv. ‘Rusalka’ was distinguished by lower tillering in comparison to the hybrid forms, except the KR 9 hybrid line. Cv. ‘Rusalka’ had a shorter length of main shoot and spike rachis than the studied hybrid lines. Some spikes of the KR3 hybrids were very long (1.8 dm) (Table 1, Fig. 1). The hybrid lines were distinguished by significantly lower main spike compactness in comparison to cv. ‘Rusalka’.

The diameter of the second internode was similar in the case of all analysed forms. Only the KR3 hybrid line had a significantly lower number of spikelets in the main spike in comparison to cv. ‘Rusalka’. Spikes of the hybrids were less dense than those of wheat. The F₂ hybrid lines (KR3, KR4, KR6, KR9) had a significantly lower number and weight of grains per main spike as well as lower main spike fertility and 1000-grain weight than cv. ‘Rusalka’. In the case of 1000-grain weight of the KR 6 hybrid strain, this difference was not statistically significant. The KRB hybrid line had significantly lower grain weight per main spike and 1000-grain weight than wheat. But the number of grains per main spike and main spike fertility were similar to the wheat (Table 1).

In most of the F₂, Ae. kotschyi Boiss. x T. aestivum L. cv. ‘Rusalka’ hybrid lines, much higher variability of the analysed morphological traits was observed than in wheat cv. ‘Rusalka’ (Table 1). Grain number per spike is one of the most important yield components. The grain weight per main spike of the hybrid plants reached 4.6 g and the grain number reached 135. Grains of the F₃ and BC₃F₁ hybrid lines, despite their small weight, were characterized by rather good filling (Fig. 2).

Analysis of grain protein and micronutrient content

The grain protein content in the Ae. kotschyi Boiss. x T. aestivum L. hybrid strains varied from 17.6 to 23.5%, so it was higher than that in T. aestivum L. cv. ‘Rusalka’ (15.7%) (Table 1).

The grain iron and zinc concentrations in the hybrid lines were also analyzed and compared with T. aestivum L. cv. ‘Rusalka’ (Table 1). All the hybrids had higher iron and zinc content than wheat. The grain iron content in the Ae. kotschyi Boiss. x T. aestivum L. hybrid lines varied from 46.5 to 54.0 mg × kg⁻¹ DW, whereas in the case of zinc – from 39.8 to 57.8 mg × kg⁻¹ DW. It was more than in the case of grains of T. aestivum L. cv. ‘Rusalka’ (41.7 mg × Fe kg⁻¹ DW and 23.6 mg × Zn kg⁻¹ DW, respectively).

Molecular analysis

The hybrid nature of the Ae. kotschyi Boiss. x T. aestivum L. lines was confirmed through DNA analysis. The presence of markers specific for Ae. kotschyi Boiss. in the genotypes of the Ae. kotschyi x T. aestivum L. cv. ‘Rusalka’ and (Ae. kotschyi Boiss. x T. aestivum L. cv. ‘Rusalka’) x T. aestivum L. cv. ‘Begra’ hybrid lines was confirmed using the PCR ISSR method.

In our study, based on electrophoresis of PCR amplification products, the presence of Ae. kotschyi Boiss. ISSR markers was proved in the case of all Ae. kotschyi Boiss. x T. aestivum L. hybrids (Table 2, Fig. 3). The ISSR23690 and ISSR33650 markers were detected in eight hybrids and ISSR33380 in six. The ISSR23690 marker was detected in all eight hybrids and ISSR33380 in six. The ISSR699 and ISSR33650 polymorphic bands were observed in four hybrids, and ISSR35200 and ISSR35260 in three. The remaining markers were present in one or two hybrid lines. The biggest number of ISSR markers was found in the F₂ KR 3 and F₂ KR 4 hybrid lines (9 markers). Slightly fewer ISSR polymorphic bands appeared in the F₂ KR 3 (6 markers), F₂ KR 6 (5 markers), F₂ KR 4 (4 markers) and F₂ KRB lines (4 and 3 markers). One polymorphic band specific for Ae. kotschyi Boiss. was noted in the F₂ KR 6 and F₂ KR 9 lines. No markers were detected in case of the F₃ KR 9 line.
Table 1
Mean values and range of variation of some morphological traits and protein, iron and zinc contents in the grains of F5 and BC1F1 Aegilops kotschyi Boiss. x Triticum aestivum L. hybrid lines and Triticum aestivum L. cv. ‘Rusalka’

<table>
<thead>
<tr>
<th>Forms analysed</th>
<th>Productive tillering</th>
<th>Length of main shoot (cm)</th>
<th>Diameter of 2nd bottom internode (mm)</th>
<th>Length of main rachis (dm)</th>
<th>No. of spikelets in main spike</th>
<th>Main spike compactness</th>
<th>No. of grains per main spike</th>
<th>Weight of grains per main spike (g)</th>
<th>Main spike fertility</th>
<th>1000-grain weight (g)</th>
<th>Total protein content (%)</th>
<th>Iron content (mg × kg(^{-1}) DW)</th>
<th>Zinc content (mg × kg(^{-1}) DW)</th>
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<tbody>
<tr>
<td>KR 3</td>
<td>Ae. kotschyi x Rusalka</td>
<td>29.6* (8.0-50.0)</td>
<td>95.5* (460.0-120.0)</td>
<td>4.2</td>
<td>1.2* (07.1-18)</td>
<td>17.2* (150.1-19.0)</td>
<td>13.6* (9.1-19.0)</td>
<td>9.1* (1.0-26.0)</td>
<td>0.3* (0.01-1.2)</td>
<td>0.5* (0.06-1.37)</td>
<td>25.0* (11.0-40.8)</td>
<td>23.5</td>
<td>54.0</td>
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<td>KR 4</td>
<td>Ae. kotschyi x Rusalka</td>
<td>20.1* (4.0-41.0)</td>
<td>88.7* (490.0-111.0)</td>
<td>4.5</td>
<td>1.1</td>
<td>18.3* (140.1-26.0)</td>
<td>16.5* (13.1-23.8)</td>
<td>20.9* (0.0-58.0)</td>
<td>0.7* (0.0-2.4)</td>
<td>1.1* (0.0-3.2)</td>
<td>28.3* (0.0-43.0)</td>
<td>23.0</td>
<td>47.8</td>
</tr>
<tr>
<td>KR 6</td>
<td>Ae. kotschyi x Rusalka</td>
<td>19.0* (6.0-34.0)</td>
<td>97.5* (620.0-131.0)</td>
<td>4.2</td>
<td>1.1</td>
<td>19.8* (180.0-22.0)</td>
<td>17.9* (14.8-21.0)</td>
<td>17.0* (8.0-25.0)</td>
<td>0.6* (0.2-1.0)</td>
<td>0.8* (0.4-1.4)</td>
<td>28.2* (19.3-37.4)</td>
<td>21.7</td>
<td>50.4</td>
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<tr>
<td>KR 9</td>
<td>Ae. kotschyi x Rusalka</td>
<td>7.7* (5.0-12.0)</td>
<td>80.7* (73.0-86.0)</td>
<td>4.7</td>
<td>0.9</td>
<td>17.0* (150.0-20.0)</td>
<td>17.2* (15.0-19.0)</td>
<td>5.0* (0.0-14.0)</td>
<td>0.2* (0.0-0.7)</td>
<td>0.3* (0.0-0.7)</td>
<td>12.8* (0.0-26.5)</td>
<td>18.5</td>
<td>46.5</td>
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<tr>
<td>KRB (Ae.kotschyi x Rusalka) x Begra</td>
<td>19.3* (14.0-24.0)</td>
<td>96.3* (910.0-103.0)</td>
<td>5.3</td>
<td>1.2*</td>
<td>22.3</td>
<td>18.0</td>
<td>47.3</td>
<td>1.3*</td>
<td>2.25</td>
<td>24.4*</td>
<td>17.6</td>
<td>48.6</td>
<td>39.8</td>
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<tr>
<td>KRB (Ae.kotschyi x Rusalka) x Begra</td>
<td>12.7* (5.0-22.0)</td>
<td>77.5* (640.0-94.0)</td>
<td>4.5</td>
<td>0.88</td>
<td>19.1</td>
<td>21.0</td>
<td>38.1</td>
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* - result significantly different in relation to the wheat at p=0.05

Table 2
Specification of presence in the genotypes of Ae. kotschyi Boiss. x T. aestivum L. cv. Rusalka (KR) and (Ae. kotschyi Boiss. x T. aestivum L. cv. ‘Rusalka’) x T. aestivum L. cv. Begra (KRB) hybrid lines specific for Ae. kotschyi Boiss. ISSR markers

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* - base pairs
Characterization of *Aegilops kotschyi* Boiss. × *Triticum aestivum* L. hybrid lines

Fig. 1. Spikes (from the left): 1–7, 11–12 F₃ hybrid lines of *Ae. kotschyi* Boiss. × *T. aestivum* L. cv. ‘Rusalka’, 8–10 BC₁ hybrid line of (*Ae. kotschyi* Boiss. × *T. aestivum* L. cv. ‘Rusalka’) × *T. aestivum* L. cv. ‘Begra’, *Ae. kotschyi* Boiss., *T. aestivum* L. cv. ‘Rusalka’

Fig. 2. Grains (from the left): upper row 1–3 F₃ hybrid lines of *Ae. kotschyi* Boiss. × *T. aestivum* L. cv. ‘Rusalka’, lower row 1–3 BC₁ hybrid line of (*Ae. kotschyi* Boiss. × *T. aestivum* L. cv. ‘Rusalka’) × *T. aestivum* L. cv. ‘Begra’, *T. aestivum* L. cv. ‘Rusalka’
DISCUSSION

Among the evaluated F1 hybrids, the most distinguished was the KR3 *Ae. kotschyi* Boiss. × *T. aestivum* L. cv. ‘Rusalka’ line due to the highest length of spike rachis, and grain protein and micronutrient content. In this line, the largest number of ISSR markers specific for *Ae. kotschyi* Boiss. was found (9 markers).

Generally, the *Ae. kotschyi* × *T. aestivum* L. hybrid lines were characterized by more productive tillers, longer shoots and spike rachises as well as lower main spike compactness, number and weight of grain per main spike, fertility, and 1000-grain weight in comparison to cv. ‘Rusalka’. The values of the quantitative traits in the F1 hybrid lines varied and these lines were characterized by much higher variability of the analyzed morphological traits than cv. ‘Rusalka’. This research is in agreement with previously published papers which also found high variability in yield components of *Aegilops* L. × wheat hybrids. In the studies conducted by Stefanońska...
Aegilops L. x Triticum L. hybrids were characterized by high variability of the analyzed morphological traits in comparison to common wheat. The length of the main shoot of Ae. juvenalis (Thell.) Eig. and Ae. ventricosa Boiss. with Triticum sp. hybrids ranged from 65.4 to 118.8 cm, the diameter of the second internode from 2.5 to 4.4 mm, the number of spikelets in the main spike from 9.9 to 23.0, and 1000-grain weight from 21.6 to 52.1 g. In the present study, the length of the main shoot of the Ae. kotschyi Boiss. x T. aestivum L. hybrid lines ranged from 80.7 to 97.5 cm, the diameter of the second internode from 4.2 to 5.3 mm, the number of spikelets in the main spike from 17.0 to 22.3, and 1000-grain weight from 12.8 to 28.3 g. Pilch and Głowacz [10] found 28 spikelets in the main spike of Ae. speltoides Tausch. x T. aestivum L. hybrids. These authors also reported that some of the hybrid forms significantly exceeded wheat with respect to number and weight of grains per main spike. Aegilops L. x Triticum L. hybrid lines selected by Pilch and Głowacz [35] were characterized by long spikes with large grains, much bigger than those of wheat T. aestivum L. cv. ‘Chinese Spring’.

In the present study, spikes of the F2 Ae. kotschyi Boiss. x T. aestivum L. hybrid lines were less different in density, awning, shape, and length of spike rachis than spikes of the F2 hybrids [36].

Bültner and Schumann [19] reported that the grain protein content in Ae. kotschyi Boiss. was 27.70%. RAWat et al. [25] noted that BC2 and BC1F2 plants from interspecific crosses between ‘Chinese Spring’ CS (Ph’) wheat and Ae. kotschyi Boiss. had a higher level of grain iron and zinc concentrations (26.8–79.8 and 22.1–55.2 mg kg1 DW, respectively), similarly to our study. Cakmak et al. [37] also indicated lower iron and zinc content among T. aestivum cultivars as compared to wild and primitive Triticum species. The wild relatives of wheat, especially Ae. kotschyi Boiss., and other S genome Aegilops species are a promising source for enriching cultivated wheats to obtain a high Fe and Zn content [24]. Ae. kotschyi Boiss. is easily crossable with hexaploid wheat and thus can be used for transferring high Fe and Zn content to cultivated wheats through the induction of homoeologous pairing [24]. In addition to the S genome, some other genomes (U, M) of Aegilops species also control high iron and zinc content, which can be exploited for biofortification. Biofortification is a method of breeding crops to increase their nutritional value [37].

DNA markers are used to select and identify desirable forms, to assess the adjustment of breeding material, to confirm crossbreeding efficiency, and to identify the genes which determine important functional traits [38]. In the present study, ISSR markers were used to identify the genes of Ae. kotschyi Boiss. in the genotypes of the hybrids lines. In our study, the ISSR23690 and ISSR33650 markers were detected in the largest number of the hybrids (8 and 6).

The inter simple sequence repeats (ISSR) are a kind of molecular marker involving PCR amplification of DNA by a single primer 16–18 bp long composed of a repeated sequence anchored at the 3’ or 5’ end by 2–4 arbitrary nucleotides [32]. They are easy to handle, highly informative and repeatable. Since repeated sequences are abundant throughout the genome, SSR primers anneal in several regions, typically giving a complex amplification pattern in which fragments are often polymorphic between different individuals. Among the various available molecular markers, microsatellites have been shown to be superior to other DNA-based markers because of their higher level of polymorphism and informativeness in hexaploid wheat [39, 40, 41]. Microsatellite markers were used for germplasm analysis and estimation of the genetic relationship between accessions of Ae. tauschii Coss. [42]. Microsatellite analysis of germplasm is also useful in molecular investigations of Aegilops species and their hybrids. Gała et al. [43] detected the introgression of genome elements of the Ae. cylindrica Host into the T. aestivum L. genome by ISSR analysis. Grącz et al. [44] estimated the genetic similarity in triticale (6x) hybrids with Ae. crassa (4x) Boiss and confirmed the existence of DNA fragments of the wild species in the triticale (6x) hybrid strains background. In the analyses, fourteen ISSR selected primers were used. Huguet-Robert et al. [45] used microsatellite markers to locate the gene Ph 1 for resistance to eyespot in the resistant Ae. ventricosa Tausch. x T. durum Desf. cv. Creso recombination lines. Kuroparty et al. [9] analysed wheat-alien translocation, with leaf rust and stripe rust resistance genes Lr57 and Yr40 transferred from Ae. geniculata Roth., using physically mapped ESTs. Microsatellite markers linked to the Pm gene of Ae. tauschii Coss. introgressed into common wheat were identified by Miranda et al. [46].

CONCLUSIONS

1. Most of the Aegilops kotschyi Boiss. x T. aestivum L. hybrid lines were observed to have more productive tillers, longer shoots and longer, more loose spikes as well as lower number and weight of grains per main spike, fertility and 1000-grain weight than cv. ‘Rusalka’.

2. The majority of the hybrid lines were characterized by much higher variability of the analysed morphological traits than the wheat cultivar ‘Rusalka’.
4. The hybrid lines contained in grains more protein and micronutrients – iron and zinc – in comparison to the ‘Rusalka’ cultivar. Among the hybrid lines, KR3 Ae. kotschyi Boiss. x T. aestivum L. cv. ‘Rusalka’ was distinguished by the highest grain protein, iron and zinc content.

5. The PCR ISSR method confirmed the presence of markers specific for Ae. kotschyi Boiss. in the hybrid genotypes. Among the ISSR markers analysed, the most successful were ISSR23690 and ISSR33650.

Acknowledgments

This work was financially supported by the Subdepartment of Plant Biology, Faculty of Agricultural Sciences in Zamość, University of Life Sciences in Lublin.

Authors’ contributions

The following declarations about authors’ contributions to the research have been made: study conception: RP; collecting data: RP; morphological data analysis and interpretation: RP; protein and micronutrients analyses – data interpretation: RP; molecular analysis and data interpretation: EP-G; writing the manuscript, table and figure arrangement: RP, EP-G.

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Charakterystyka linii mieszańcowych

Aegilops kotschyi Boiss. x Triticum aestivum L.

S t r e s z c z e n i e


W liniach mieszańcowych potwierdzono obecność prążków specyficznych dla Ae. kotschyi Boiss. za pomocą siedmiu markerów molekularnych ISSR (Inter Simple Sequence Repeats – polimorfizm odcinków DNA pomiędzy mikrosatelitami). Dwa markery ISSR – ISSR23690 i ISSR33650 – okazały się najbardziej efektywne w analizie genomów linii mieszańcowych. Badane linie mogą zostać wykorzystane w programach hodowlanych mających na celu ulepszenie pszenicy zwyczajnej.

Handling Editor: Elżbieta Weryszko-Chmielewska

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