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ORIGINAL ARTICLE

Evaluation of resistance to diseases of soft winter wheat samples created by hybridization of ecologically and geographically remote forms

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Genetic and breeding improvement of soft winter wheat varieties is one of the most effective methods of increasing yields, resistance against abiotic and biotic environment factors and energy-saving of wheat cultivation. Use of disease-resistant varieties is an economically effective and environmentally safe method of plant protection. The plant's resistance is provided by the existing group of resistance genes, which are specific and act at the first determinant phase of plant and pathogen interaction. In wheat breeding the genes that provide varieties with stable resistance to disease regardless of genetic diversity of pathogens and weather conditions of cultivation are of greatest value. Such genes are often dominant mono- and oligogens. The objective of our research was to identify and select soft winter wheat samples resistant to main diseases and created by hybridization of ecologically and geographically remote forms in order to use them in breeding as donors of resistance. As a result of the research four samples of soft winter wheat 4075, 6151, 3872 and 6254 with complex resistance to diseases (resistance score 8-9) were selected. Created materials showed a significant advantage in resistance to powdery mildew, fusarium and septoria blight in comparison with standard variety Favoritka. Selected samples can be used as donors of resistance genes in the breeding process of high-yielding soft winter wheat varieties.

Keywords: soft winter wheat; resistance; adaptability; genetic control of traits; initial material; donor of genes; ecologically and geographically remote forms; intensity of disease affection

Introduction

Genetic and breeding improvement of agricultural crops is one of the most effective methods of increasing yields, resistance against abiotic and biotic environment factors and energy-saving cultivation of crops, in particular soft winter wheat. Use of disease-resistant varieties is an economically effective and environmentally safe method of plant protection (Lisovyi, 2001).

Plant resistance to biotic stresses is an important component of potential of ontogenetic adaptation. It is evidenced by the fact that annual losses of plant production in the world reach up to 40 % as a result of the affection of agrocenoses by diseases, pests and weeds (Quenouille, et al., 2014). The growing genetic homogeneity of widely distributed varieties and hybrids is one of the reasons for significant affection of agrocenoses. Intensification of agricultural production is accompanied by simplification of agroecological systems at all levels. In general, this tendency inevitably leads to the increase in ecological and in particular genetic vulnerability of agrocenoses. The essence of this tendency lies in the fact that potential of genotypic variability and, as result, ontogenetic adaptation of pathogens significantly exceeds genotypic variability of cultivated plants created by breeding and design of agroecosystems (Mundt, 2014; Goudemand et al., 2013). It is no accident that recombinant plants progeny is more resistant to pathogens than their parental forms. First generation of hybrids are usually characterized by high ontogenetic adaptability to abiotic and biotic factors (Rawat et al., 2016).

Hybridization, mutagenesis and biotechnological methods are most often used in breeding of cereal crops for resistance to phytopathogens. The choice of breeding methods is determined by assigned tasks and goal of the work. But selection of breeding material on infectious backgrounds of pathogens is an obligatory component of this work.

It is considered quite justified to assert that improvement of plant adaptation is ensured in phylogenesis precisely due to recombinogenesis. The main significance of recombinations in evolution and plant breeding has been confirmed, especially from the point of view of creating forms adapted to biotic factors. It should be noted that through meiotic recombination new adaptive genotypes, in particular transgressive according to agronomic-valuable traits and their combinations, appear in wheat.

Numerous examples suggest that specific relationship between genetic systems of ontogenetic and phylogenetic adaptation provides changes in adaptive potential of higher plants. Level and spectrum of recombination variability in the offspring of heterozygotes are due to differences between alleles, loci and blocks of genes in their genomes and also degree of heterozygote adaptability to environmental conditions, which, in comparison with the homozygote has greater flexibility of biochemical processes and consequently breadth of physiological tolerance. The higher this adaptability is, the lower level and spectrum of induced recombinations are in segregating generations.

The aim of our research was to identify and select soft winter wheat samples resistant to main diseases and created by hybridization of ecologically and geographically remote forms in order to use them in breeding as donors of resistance.

Materials and methods

The research was conducted during 2014–2017 on the experimental plots of Uman National University of Horticulture. 119 samples of soft winter wheat obtained from hybridization of ecologically-remote forms were used as the material for research. Phenological observations, evaluations and testing of resistance to diseases (powdery mildew, fusarium blight and septoria blight) were performed on a natural infectious background according to the recommendations of «Ukraine State methodology of agricultural crops testing». Resistance of plants to diseases was determined by the nine-score evaluation system, in which nine scores mean the sample completely resistant to a disease, and one score – fully susceptible.

Results and disscussion

Successful breeding of disease-resistant materials should be based on the fundamental knowledge of genetic nature of a host plant resistance and the virulence of pathogens. Plant resistance is provided by an existing group of resistance genes that are specific and act at the first determinant phase of plant-pathogen interaction. The products of these genes are designed to recognize alien metabolites of the pathogen (Kryuchkova, 2010; French et al, 2016). In wheat breeding the genes that provide varieties with stable resistance to disease, regardless of pathogens genetic diversity and weather conditions of cultivation, are of the greatest value. Such genes are often dominant mono- and oligogens. A number of other resistance genes can only be the stimulants of the main genes (Babayants, 2014).

Use of hybridization can significantly increase genotypic diversity. However, different types of gene interactions, phenomenon of genetic linkage, genetic and physiological correlations significantly limit recombinations of traits in hybrid organisms (Vasilkovskii and Vlasenko, 2002; Dedryver et al., 2009). With joint action of inbreeding and crossbreeding both accumulation of variability and its disclosure are realized in the process of homozygotization of genotype. This intraspecific variability fund determines evolutionary plasticity of the population when relationship between the organism and environmental factors changes.

Powdery mildew, fusarium blight and septoria blight are the most common and harmful diseases of soft winter wheat in Ukraine. The shortage of crops resulting from infection with these diseases in different years can reach from 15 % to 40 %.

Among the materials, created by hybridization, the samples that had a yield of more than 6.0 t/ha were identified. They were evaluated according to the resistance against diseases during the most intensive infection with pathogens. The analysis showed the level of resistance of created samples to diseases.

Powdery mildew is one of the most harmful diseases of soft winter wheat. It can lead to a significant decrease in yield and its quality in different regions of the country. The pathogenic agent of the disease is the fungus Erysiphe graminis f.sp. tritici Em. Marchal., which belongs to the class of Ascomycetes. The harm of the disease manifests in decreasing of leaves assimilative surface, destruction of chlorophyll and other pigments. Decrease in plant bushiness, and under a strong affection by the disease the delay in ear formation, premature death of leaves of affected plants are recorded. Intensive development of the disease may cause decrease in the number and weight of grains per ear and losses of yield from 15 to 36 % (Hospodarenko et al., 2016). The disease develops especially intensively under application of high unbalanced rates of nitrogen fertilizers in agrocenoses. Development of the disease in autumn at the level of 30–75 % causes death of wheat plants up to 40 %.

16 genes with resistance to powdery mildew were identified in soft wheat, eight of them were obtained from other species and genus: Pm2 and Pm6 from T. timopheevii; Pm4a and Mld from T. durum, Pm4b from T. persicum, Pm5 from T. dicoccum, Pm7 and Pm8 — from S. sereale (Chekalin et al, 2008). Main record of the material as to the resistance to powdery mildew was carried out during earing phase which according to BBCH's international classification corresponds to 55–59 phases (Table 1).

The lowest intensity of powdery mildew infection was in the plants of sample 4075 with infection rate of 4.0 %, which is by 9.3 % lower than the same parameter for standard variety Favoritka. Samples 6151, 3872 and 6254 were also significantly more resistant compared to the control variant. Other samples were significantly inferior to the above mentioned forms.

It should be noted also that in 2016 this disease was widespread due to weather conditions. Affection with powdery mildew was observed in autumn on the lower cauline leaves.

Table 1. Resistance to diseases of created soft winter wheat samples, 2014–2017.

Breeding sample	Intensity of plant affection								
	powdery mildew			fusarium blight			septoria blight		
	%	± to standard %	resistance score	%	± to standard %	resistance score	%	± to standard , %	resistance score
Favoritka (st)	13.3	–	7	9.1	–	8	11.5	–	7
4075	4.0	-9.3	9	7.7	-1.4	8	8.0	-3.5	8

6151	4.7	-8.6	9	6.9	-2.2	8	7.3	-4.2	8
3872	6.1	-7.2	8	7.2	-1.9	8	7.0	-4.5	8
6254	7.6	-5.7	8	8.2	-0.9	8	7.8	-3.7	8
3878	15.5	2.2	7	10.3	1.2	7	11.6	0.1	7
2115	17.0	3.7	7	12.1	3.0	7	13.7	2.2	7
1248	16.1	2.8	7	13.7	4.6	7	15.2	3.7	7
1418	16.2	2.9	7	15.6	6.5	6	18.7	7.2	6
547	24.7	11.4	6	25.1	16.0	5	21.7	10.2	6
1325	22.8	9.1	6	27.2	18.1	5	24.1	12.6	6
1678	26.7	13.4	5	27.3	18.2	5	27.6	16.1	5
LSD05	0.7	–	–	0.7	–	–	0.7	–	–

Fusarium ear blight is one of the most common diseases of wheat. It is especially intense in wet years with a lowered temperature in the second half of vegetation period and restrains the maturation of grains.

Infected ears first acquire a pale-pink shade and then pale-pink, orange-red or red pads appear on the scales of spikelets, which gradually merge and form a scab covering entire surface of the ear. Sometimes red pads are formed on the grain. Fusarium blight is easily diagnosed when healthy ears remain green and infected spikelets or entire ear are white. In wet and warm weather small dark-blue or black perithecium appear on affected spikelet.

Fusarium ear blight is caused by incomplete fungi of the genus Fusarium Link, order of Hyphomycetales. More common are Fusarium graminearum Schwabe; F. avenaceum Saccardo. These pathogens form mycelium and conidial sporulation in the form of reddish pads not only on the ears and grains, but also on the scabbard of leaves, nodes and even at the base of a stem during the ripening of cereals. Resistance of plants to Fusarium blight is controlled by the genes Fhb1 and Fhb2 located in chromosomes 3BS and 6BS, respectively (Kolomiets et al., 2001; Kriuchkova, 2007).

Record of the ear infection with fusarium blight was carried out during the phase of milky ripeness, which according to BBCH classification corresponds to 70–75 phases.

The highest resistance to fusarium blight was in the sample 6151. Percentage of infected plants averaged 6.9 %, which is by 2.2 % below the standard. As to their resistance the samples 3872, 4075 and 6254 exceeded variety Favoritka by 1.9 %, 1.4 % and 0.9 % respectively. Resistance of other tested samples was significantly lower than in mentioned materials.

Septoria blight is the disease caused by fungi of the genus Septoria. Most common fungi on winter wheat are Septoria tritici Rob. et Desm., Septoria graminum Desm., which mainly affect leaves and axils of leaves and Septoria nodorum Berk., that affects all above-ground organs, including ears. Septoria blight leads to decrease of assimilation surface, premature drying of leaves and plants, fragility of stems, poor development of ear, premature ripening, decrease in grain yield and deterioration of its technological qualities.

Wheat varieties resistant to septoria blight were not found, but there is a clear differentiation of samples according to resistance against this disease. According to the plant morphotype high- or medium-growing late-ripening forms with awnless ear and intense waxy coating on a plant are resistant to septoria blight. This kind of ecotype is typical for varieties from the north and west of Europe that was used in our hybridization schemes. Short-growing forms with broad leaves are affected by septoria blight much more strongly, because they form the yield at the expense of productive stalks which creates a specific microclimate with high humidity in crops. Damage caused by this disease has been growing lately. The losses of yields can reach up to 40 %.

At present a number genes with resistance to septoria blight — Stb1-Stb12, StbAc1 and StbAc2 — have been identified (Babayants, 2014; Vasilkovsky and Vlasenko, 2002). Sources of resistance to pathogens of common wheat are its related species (Triticale, T. timopheevii, T. fungicidum, T. monococcum, T. boeoticum, T. kiharae, T. urartu, T. zhukovskui, T. tauschii) and wild relatives (Agropyrun elongatum, Aegilops sguarrosa, Ae. Speltoides, Ae. Sharonensis), from which resistance was transferred to cultivars by interspecific and remote hybridization (Kryuchkova, 2007; Lisnevich, et al., 2006).

Main record of plant resistance to septoria blight was carried out during ear formation, and according to BBCH classification this corresponds with 60–69 phases. Wheat varieties totally immune to septoria blight were not found in our research.

Intensity of infection by septoria blight in selected samples was relatively homogeneous. The highest resistance to septoria blight at the level of 7.0 % (8 grades) was in the plants of samples 3872 and 6151. Samples 4075 and 6254 had significantly lower resistance. Other created forms had significantly lower resistance to septoria blight in comparison with mentioned materials and variety Favoritka.

Suchwise samples 4075, 3872, 6151, 6254 have complex resistance to powdery mildew, fusarium and septoria blight. Selected materials are involved into breeding process as donors of resistance genes. Up-to-date methods of molecular genetics were applied to finally identify resistance of breeding material, which allowed to confirm validly the sources of resistance genes.

Conclusion

As a result of the research four samples of soft winter wheat 4075, 6151, 3872 and 6254 created by hybridization of ecologically and geographically remote forms with complex resistance to diseases were selected. Created materials showed a significant advantage in resistance to powdery mildew, fusorium ear blight and septoria blight in comparison with standard variety Favoritka. Selected samples can be used as donors of resistance genes in breeding process for creating high productive wheat varieties.

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