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SELECTION EVALUATION OF INTROGRESSIVE LINES OF SOFT WINTER WHEAT WITH SIGNS OF RESISTANCE TO PHYTOPATHOGENS

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ABSTRACT

Resistance to common diseases has been studied and a selection assessment has been made of improved introgressive lines created by repeated crossing of amphiploids, primitive lines or collection specimens with modern varieties of soft winter wheat. There is a low frequency of combining group stability with high yield and grain quality. It was found that the genetic environment of some introgressive lines is favorable for the positive effect of rye translocation 1BL.1RS on both economically valuable and adaptive traits in the south of Ukraine and the possibility of combining with other resistance genes. There was no correlation of resistance to powdery mildew, leaf and stem rust with yield both in the absence and presence of natural infectious background and a weak positive relationship ($R_{sp} = 0.26^{**}$) yield with resistance to Septoria and yellow rust in only one variant of the experiment. In most cases, there is a weak significant positive correlation between resistance with protein content and weight of 1000 grains, as well as between the resistance of the lines to various diseases, which is obviously a consequence of artificial selection for group resistance. Selected selection lines (E2792_14, AIL1161_16, E218_09, E212_09, AIL1073_16) with foreign polygenic complexes of resistance to rust diseases, high values of weight of 1000 grains, protein content, as well as morphological features; which are characterized by high productivity, adaptability, tolerance to low agrophones, baking quality. The lines are devoid of many negative qualities inherent in wild species, can be a promising source of resistance to these diseases and are of interest for further breeding work in southern Ukraine, provided the preservation of foreign gene complexes.

Keywords: *Triticum aestivum* L., introgressive lines, stability, productivity.

Introduction

One of the factors limiting the yield of high yields of soft winter wheat *Triticum aestivum* L. are diseases, the losses of which can reach 15-30% or more (Soko *et al.*, 2018). Since the selection of plants for immunity to diseases is the most effective means of their protection, a large-scale search for new sources of resistance and the creation of source material, in particular by remote hybridization (Warburton *et al.*, 2006). Much attention is now paid to the study of inheritance of resistance to various diseases of wheat, among which the most common and harmful are fungal, in particular leaf (eg, powdery mildew, rust, leaf Septoria) (Babayants and Babayants, 2014). Harmfulness of these diseases is not only to reduce productivity, but also to worsen the marketable and sowing characteristics of grain (Soko *et al.*, 2017). However, despite the large amount of theoretical research, in practice the situation is only getting worse, especially against the background of climate change (CABI Climate Change Series Lewis *et al.*, 2011).

Powdery mildew (*Blumeria graminis* (DC) Speer f. Sp. Tritici March.) Is widespread in Ukraine, affecting leaves, leaf sheaths, stems, sometimes spikelet's and spines. The

optimal conditions for the development of the fungus are cool temperature and high humidity. With the strong development of the disease, the productive bushiness of the plant decreases, the leaves dry up prematurely. Earing is delayed and emptiness occurs, grain filling deteriorates, which reduces the content of protein, starch and crude gluten (Topchiy and Sandetska, 2017). Powdery mildew is especially dangerous for spreading to the upper tiers of the plant. During 2007-2008 s.-g. year there was a sharp change in the racial composition of the disease in the direction of its greater aggression and virulence (Babayants, and Babayants, 2014).

Wheat rust has three types: leaf (*Puccinia triticina* Erikss. & Henn.), Stem (*Puccinia graminis* sp. Tritici Erikss. & Henn.) And yellow (*Puccinia striiformis* West.), which are considered the most harmful crop diseases globally. In general, the harmfulness of rust diseases is due to metabolic disorders in the affected plant. There is a decrease in the assimilation of CO₂ and chlorophyll content; strengthening of respiration of plants and change of ways of disintegration of substances at breath; the intensity of transpiration deteriorates due to numerous ruptures of the epidermis, the

scarring of which the plant spends a significant supply of energy and plastic substances.

The most common is leaf rust, which affects wheat almost everywhere (Retman *et al.*, 2011). The winter can be affected in the autumn in the phase of germination and tillering, but the greatest damage is caused by the disease in the phase of milk ripeness. During the growing season of wheat, the pathogen forms several generations of urethra with intrasporangia, which explains the intensive increase in the disease before flowering plants. The pathogen is heterogeneous in racial composition, its virulence and aggressiveness depending on the conditions of the year (Babayants and Babayants, 2014). Stem and yellow rust are less common in southern Ukraine, but are considered much more harmful (Soko *et al.*, 2011). Their racial composition is determined and characterized by relative stability over the years (Babayants and Babayants, 2014). Yellow rust becomes important in some years with favorable conditions for the disease (mild winters, cool and humid spring and summer). A characteristic manifestation of the lesion - lemon-yellow oblong stripes in the form of dotted lines, consisting of urethra. Later, dark brown or almost black cells that do not penetrate the epidermis are formed in the affected areas. Currently, yellow rust has adapted to rising temperatures and significantly increased the area of distribution. Moreover, epiphytosis caused by heat-tolerant races is more aggressive, so the stability of varieties is overcome in a short period (Retman *et al.*, 2011). Stem rust, although observed everywhere where wheat is grown, is harmful only in areas with warm and humid climates, where it is considered the most destructive disease of wheat. With the emergence of the extremely dangerous race Ug99, up to 90% of wheat varieties in the world, including those protected by the Sr31 gene, have become susceptible to the pathogen, and thus the disease can cause great harm in a wide range of geographical regions (Soko *et al.*, 2018). In Odessa, stem rust occurs so far, only when artificially infected. In 2019, it was discovered in the field in the Kiev region. The disease manifests itself after flowering on the stems, less often - on the stems of the ear and ear scales in the form of rusty-brown oblong devices, which merge in the form of brown stripes, tearing the epidermis. The flow of nutrients in the stems of the plant is interrupted, the ear is affected, which causes wrinkling of the grain. In addition, infected stems are weakened, and therefore prone to lodging, which leads to further grain loss. In general, the annual yield loss from these diseases is from 15 to 25%, and with epiphytic development up to 40-50%, and the figures increase every year (Soko *et al.*, 2018).

Septoriatrifici Rob. Ex Desm., A disease that has recently progressed with fever, also poses a significant risk to crops. The infection spreads from the lower leaves to the upper tiers of the plant at a relative humidity of 90-100% and a temperature of 12-25 °C; drought during the growing season significantly inhibits or completely stops the development of the fungus. The maximum manifestation of the disease is observed in the phase of milk-wax ripeness, although the disease causes significant damage already in the tubing-flowering phases. Harmfulness is manifested in the reduction of the assimilation surface of the leaves, which dries prematurely, the underdevelopment of the ear, in which the slender grain is formed. With the mass development of

the disease, crop losses reach 30-40% (Retman *et al.*, 2011; O'Driscoll *et al.*, 2014).

Increasing the resistance of wheat to diseases can be achieved due to the genetic resources of closely related wild and cultivated species and genera and artificially created on their basis amphiploids of different genomic structure (Morgounov *et al.*, 2018). The method of remote hybridization in soft wheat was able to transfer useful genes for resistance to diseases (Kovalyshyna and Dmytrenko, 2017) and pests (Bhatta *et al.*, 2018), drought, frost and salt resistance (Reynolds *et al.*, 2007; Ahmadi *et al.*, 2014). The number of results with the successful use of the obtained hybrids indicates the prospects of involving introgressive recombinant variability in the selection of soft winter wheat (Lyfenko *et al.*, 2014). This increases the probability of deriving selection-valuable forms with higher than the standard, real (economic) productivity. In addition, the process of growing a stable material is more environmentally friendly compared to the standard and other common varieties, because the plants, during the growing season, require fewer treatments with chemical protection (Babayants and Babayants, 2014). The most valuable for selection are the forms that have been distinguished by a set of features in the years with the strong development of diseases.

As a result of remote hybridization in the department of general and molecular genetics of Agricultural Institute – Research-scientific Centre of plants breeding (Odessa) were created original primary introgressive lines, characterized by high resistance to phytodiseases (Motsniy and Blagodarova, 2004). Among the disadvantages of the lines - late ripening, low productivity, frost resistance and quality. As a result of 3-8 saturating crosses of the adaptive variety of soft winter wheat Odessa 267 with the best of these lines, as well as collection samples, artificial wheat species and amphiploids with *Aegilops tauschii* Coss., Crossing the variety Selyanka with elite synthetics and subsequent steps hybrids with modern varieties of Agricultural Institute – Research-scientific Centre of plants breeding and 6-8 self-pollinations received 736 improved introgressive lines of soft wheat.

The purpose of the research is to investigate resistance to common diseases and to give a selective assessment of improved introgressive lines created by repeated crossing of low-yielding primary lines, collection samples or amphiploids with the participation of *Aegilops tauschii* Coss with modern varieties of soft winter wheat, identify the links between individual agronomic and economically valuable traits and identify donor lines that combine high productivity with the maximum manifestation of valuable traits of foreign origin and adapted to growing conditions in southern Ukraine.

Materials and Methods

In 2016-2019, introgressive lines of soft winter wheat of different generations, degrees of saturation and origin in the amount of 736 pieces were studied according to the type of selection (SR) and control (KR) nursery. These are mainly derived from crossing a number of soft wheat varieties with 3 recombinant primary and 1 improved introgressive lines, 1 variety, 1 collection specimen and 1 translocant line, 2 original amphiploids with *Elymus sibiricus* L. and 6 amphiploids. tauschii. Most of them are based on spring-winter hybrids. All experimental material was obtained by the Pedigree method as a result of numerous long-term

individual selections on the natural and artificial infectious background of the studied diseases in the presence of foreign signs both during backcrossing and after self-pollination. The selection of elite plants to create lines began with the first generation, which is split, and was carried out without any chemical protection of plants from diseases and pests. When selecting the lines, special attention was paid to their constancy both by individual, including foreign, features, and by their complex.

To obtain improved introgressive wheat lines, intermediate forms were used—42-chromosomal synthetic amphiploids of tetraploid wheat species (*Triticum durum* Desf., *Triticum dicoccum* Schuebl. And *Triticum militinae* Zhuk. Et Migusch.) With *Aegilops tauschii* Coss. Also, saturating crosses were used with the original primary introgressive lines *Erythrosperrum* 200 / 97-2 (E200_97-2), *Hostianum* 242 / 97-1 (H242_97-1), and *Erythrosperrum* 125/03 (E125_03), collection sample H74_90-245 and the original amphiploids ЧЕ1342_98 and ЧЕ1345_98. Lines E200_97-2, H242_97-1 and E125_03 were created by crossing octoploid triticale AD825 (*Gostianum* 237 / rye Voronezh SGI) with winter durum wheat variety Chernomor and re-pollination of F3 hybrids with pollen of collection sample (Motsnyi and Blagodarova, 2004). In addition, several improved lines were obtained with the participation of the Vigen variety derived from hybridization with octoploid NPEA *Elytricum* fertile (Motsnyi *et al.*, 2017), introgressive line E214_09-1 (H242_97-1 / Od.267 * 3 // Kuyalnik F∞) (Motsnyi *et al.*, 2014) or after final crossing of backcrossed hybrids with the MA1 line, which has a modified translocation of 1BL.1RSm in the genetic background of the spring variety Pavon 76 (Lukaszewski, 2000).

Collection samples and amphiploids were obtained from working collections of wild species and amphiploids of the departments of general and molecular genetics and genetic bases of Agricultural Institute – Research-scientific Centre of plants breeding, collected during the years of their existence. Thus, the sample H74_90-245 was created at the Agricultural Institute "Dobrudja" (former IPS), General Toshevo (Bulgaria) from crossing (*T. aestivum* Tom Pouce Blanc / AD (*T. timopheevii* Zhuk. / *Ae. Tauschii* ssp. *Strangulata*) // *T. aestivum* Aurora / 3 / *T. aestivum* Mermaid). In Institute of plant production named V.Ya. Yuriev (Kharkiv), it was introduced under the number IU029995. The spring synthetic amphiploid PEAG (*T. dicoccum* u-244569 / *Ae. Tauschii* k-110, AuBD) was created by MS Letifova on DDS VIRA and received from Ph.D. R.L. Boguslavsky (Institute of plant production named after V.Ya. Yuriev) (catalog № UA0500010). The amphiploid Zhirova

(*T. militinae* / *Ae. Tauschii*, AuGD) was created by E.G. Girov in Scientific centre (Russia) and also received from Institute of plant production named V.Ya. Yuriev (catalog № UA0500016). Amphiploids (genomically-substituted forms, 2n = 42, ABSt) ЧЕ1342_98 and ЧЕ1345_98 was obtained by crossing a variety of durum winter wheat Black Sea with spring octoploid NPEA *Elytricum* fertile and subsequent replacement of genome D genome of soft wheat *E. Spring* elite synthetics (*T. durum* Altar 84 / samples *Ae. Tauschii*, ABD) were created in CIMMYT (Mexico) (Morgounov *et al.*, 2018) and obtained by us from Dr. OI Fishermen (Motsnyi and Rybalka). According to the literature and our preliminary data, all baselines, samples and amphiploids have high resistance to powdery mildew, leaf, yellow and stem rust (Motsnyi and Rybalka, 2011).

The variety of parental forms involved in crossbreeding with varieties of Agricultural Institute–Research-scientific Centre of plants breeding, was classified depending on the source of resistance (Table 1). This division is quite conditional, because the pedigree of the sample H74_90-245, as well as amphiploids PEAG and AD Fat, includes *Ae. tauschii*. However, only derivatives of sample H74_90-245 have wheat-rye translocation (PJT) 1BL.1RS and *T. timopheevii* in the pedigree, and synthetics attributed to the source "*Ae. tauschii* », do not have in the pedigree of other foreign sources of stability, except for various specimens of *Egilops*. The class "Others" includes parental forms that do not have a common origin, due to the small number and statistical insignificance of their derivatives.

Field experiments were established in the crop rotation of the department of selection and seed production of soft winter wheat of Agricultural Institute – Research-scientific Centre of plants breeding according to the generally accepted scheme of the selection process of self-pollinating crops. Predecessor - black steam. In the selection nursery (2016) the material was sown with 1-row plots by manual selection planter SR-1M. Row length 1.15 m, feeding area of an individual plant 30 × 5 cm². To determine the resistance to leaf and stem rust, the material was additionally sown in a field infectious nursery of the Department of Phytopathology and Entomology of Agricultural Institute – Research-scientific Centre of plants breeding on an artificial background of leaf-stem diseases with storage of the accumulator (mixture of highly susceptible varieties, the intensity of which was 1-2 studied). Inoculation with a mixture of leaf and stem rust was performed by the staff of the Department of Phytopathology. Racial composition of rust species, terms and methods of inoculation are given in [Babayants, O.V., Babayants, L.T., 2014].

Table 1 : Classification of parental forms involved in crossbreeding, depending on the sources of stability

Source of stability	Parental forms involved in crossbreeding to obtain introgressive lines
H74_90-245	H74_90-245; E200_97-2; H242_97-1; E125_03; E214_09-1
amphiploids	PEAG; ADZhirova
<i>Ae. tauschii</i>	ES4 (CIGM87.2775, WX193 ¹); ES17 (CIGM87.2760, WX220); ES20 (CIGM87.2761, WX221); ES25 (CIGM86.942, WX224);
Other	CHE1342_98; CHE1345_98; Wigen; MA1

¹Prescription of the combination of crossing and № sample *Ae. tauschii* according to the CYMMIT catalog [Morgounov, A., Abugaliyeva, A., Akan, K., Akın, B., Baenziger, S., Bhatta, M., and Zelenskiy, Y., 2018].

To determine the productivity and individual indicators of grain quality, the selected lines were sown in the control nursery (2017-2019) without repetition. Sowing was carried out with a selection tractor seeder SSFK-7 with a portion apparatus, the plots had seven rows 5 m long, row spacing 15 cm, the estimated area of 5 m² at the rate of 450-500 germinating grains per 1 m² (seeding rate 4.5 million grains ha). Varieties-standards (Antonivka, Kuyalnyk, Lira, Wisdom, Tradition, Nasnaga, etc.) and recurrent form (Odesa 267) were sown every 10 issues in three or four repetitions. Fertilizers were applied according to the technological map of the institute: 1) 150 kg/ha of nitroammophoska were applied for pre-sowing cultivation; 2) early spring fertilization on thawed soil was carried out with ammonium nitrate at a dose of 200 kg/ha using a seeder SZ-3,6; 3) feeding on the leaf was carried out by spraying a tank mixture using urea at a rate of 10-12 kg/ha. The crop grown in a continuous way was harvested with a selection combine "Sampo-130". Plants grown in wide-row sowing were harvested by hand.

As the priority of the study was disease resistance, chemical protection of crops was not performed. Sowing was carried out late - in late November. Therefore, the formed level of yield can be considered the result of the realization of the potential of productivity (adaptability) and genetically determined stability (tolerance) of each line under the influence of a complex of abiotic and biotic negative factors.

The material was evaluated on a number of indicators: the presence of morphological features of alien species, type of development, plant height, yield, grain quality. Phenological observations were made (dates of germination, earing, flowering, grain ripeness was noted). Resistance to most diseases was assessed three times per season: at the stages of earing into the tube, flowering and milk ripeness of grain, to stem rust - at the stages of flowering, milk and full ripeness of grain. The last account was for the period of maximum development of the disease. The degree of plant damage was determined by a 9-point integrated scale (Babayants and Babayants, 2014), developed on the basis of a modified Saar and Precott scale. According to these calculations, the area under the curve of disease resistance (S) was calculated (Babayants and Babayants, 2014), which served as an integral indicator of the resistance of the lines for correlation analysis:

$$S = \sum (Y_i + Y_{i+1}) * (t_{i+1} - t_i) / 2,$$

where: Y - stability assessment (score); t - date of accounting; i - accounting number.

The protein content was determined in whole meal flour according to the Kjeldahl method on the device Kjeltec-Auto 1030 ("FOSS", Sweden) (Kjeldahl, 1983), and the mass of a thousand grains in samples obtained immediately after the combine, according to conventional methods (DSTU 4138-2002) [DSTU 4138-2002 Crop seeds].

Differences between the studied indicators and the values of the standards were legitimized by standard deviation (\pm SD). Empirical and calculated yields, weight of 1000 grains, protein content were combined by the sum of ranks method, as proposed by Lelley *et al.* (Lelley *et al.*, 2004). Initially, the lines were ranked by yield from its highest value to the lowest, and the ranks were assigned starting with 1 in the genotype with the lowest yield. Then

the ranks were adjusted by adding +2 if the line had a yield above the arithmetic mean of the experiment (M) plus SD, +1 if the line had a yield just higher than M and 0 if the line yield was M. Equivalent negative adjustments were also made, if the line yield was lower than M (see Table 5 in (Lelley *et al.*, 2004) for demonstration). The order of adjustment of ranks was repeated concerning other investigated signs; while score assessments of the resistance of lines to disease were considered their ranks. Genotypes that had the highest amount of adjusted ranks for agronomic traits, quality and stability indicators were considered effective for selection by a set of traits.

Correlation analysis was performed by calculating the nonparametric Spearman correlation coefficient (R_{sp}), which does not require the normality of the data distribution (Lakin, 1973). If necessary, the limits of variation (LV), Fisher's criterion (F) and the degree of probability of an indicator, criterion or coefficient (p) were determined. To simplify the presentation of the material in the tables and text of the article are unified common notations of the degree of reliability of our defined or taken from the literature indicators, criteria and coefficients: * - probably at p < 0,05; ** - probably at p < 0,01; *** - probably at p < 0,001. The designations of diseases in the tables and text are given in accordance with the International Catalog of Gene Symbols (McIntosh *et al.*, 2017).

Results and Discussion

In 2016, 736 newly created introgressive lines of different levels of resistance to one or a group of diseases were studied in the Slovak Republic. In general, most lines were severely affected by Septoria, and some of them were also affected by powdery mildew and rust. The vast majority of them have already been selected as constants in the experimental area of the Department of General and Molecular Genetics or in the field infectious nursery of the Department of Phytopathology and Entomology and were the offspring of several plants. Some of the lines were the offspring of individual plants resistant to a particular disease, selected immediately before their transmission to the SR.

Phytopathological evaluation of the lines in breeding nursery and control nursery partially confirmed their level of resistance to these phytodiseases, but the comparison of scores revealed a wide variability in the degree of impression of powdery mildew, leaf rust and *Septoria* over the years. The degree of correlation between estimates of resistance to the same disease obtained on the same lines in different years of their cultivation was calculated using Spearman's rank correlation coefficient. Depending on the sample of lines and years of cultivation, this correlation varied from R_{sp} = 0.40 *** to R_{sp} = 0.45 * for powdery mildew, within R_{sp} = 0.49 *** - 0.82 *** for foliar rust and was R_{sp} = 0.33 *** for *Septoria*. This may be due to changes in the racial composition of pathogen populations, as evidenced by phytopathologists (Babayants and Babayants, 2014), and the presence in the material of unidentified ineffective rasospecific resistance genes.

A slightly different explanation concerns the similar reaction of the material to yellow rust (R_{sp} = 0.17-0.25*), where different scores over the years in the same lines may be due, in addition to the above reason, focal uneven nature of the disease and under infection of individual segments of the field. However, the reaction to stem rust, introgressive

lines differed more depending on the origin of the material than the conditions of the year, and their score was the most constant over the years ($R_{sp} = 0.73^{***} - 0.84^{***}$). The only exception is the correlation between data obtained on a natural background in 2017 and estimates from other years, when surveys were conducted in an infectious nursery ($R_{sp} = 0.37-0.38$). This is obviously due to the presence of an artificial continuous infectious background of the disease with the same infectious load and racial composition in different years and, therefore, in itself can be considered a marker of introgression.

Quite often, lines resistant to stem rust were also resistant to leaf rust but were affected by yellow rust. However, separate lines resistant to all types of rust (E218_09, AIL1073_16, PIL956_16, PIL578PH16, PIL692_18, etc.) have been identified. In this regard, the most effective were the derivatives of crossing octoploid triticale AD825 (parent component) with a variety of winter durum wheat Chernomor (pollinator) and re-pollination of F3 hybrids with pollen of collection sample H74_90-245 from Bulgaria [18] (also indirect H) direct derivatives of the H74_90-245. It is known (Demydov *et al.*, 2019) that in the former by combining foreign resistance genes from different sources, a number of donors of high resistance to rust diseases, especially leaf rust, were created.

In the primary introgressive lines (E200_97-2, H242_97-1) isolated from this combination, wheat-rye translocation (PJT) 1BL.1RS of the Caucasus / Aurora type from sample H74_90-245 (Motsnyi and Blagodarova, 2004) was detected using electrophoresis of spare proteins. inherited by their descendants - advanced lines E214_09-1 (H242_97-1 / Od.267 * 3 // Kuyalnik F ∞), E218_09 (Od.267 / H74 / 90-245 F2 // Od.267*4/3/ Peasant F ∞), E2792_14 (E214_09-1 / Group * 2 F5) (Kozub *et al.*, 2019). As is known (McIntosh *et al.*, 2017), the 1RS arm of this translocation carries the Lr26 / Sr31 / Yr9 / Pm8 gene complex, which is ineffective in modern conditions. Although the effectiveness of these resistance genes is partly lost due to the emergence of new races of pathogens, in particular virulent to Sr31 highly aggressive race of stem rust Ug99 (Saunders *et al.*, 2019), the positive effect of PJT 1BL.1RS on the manifestation of economically valuable and adaptive traits remains and depends on genetic environment, as well as the region of wheat cultivation (Lelley *et al.*, 2003). Thus, the Sr31 gene is still considered effective in Russia (Perschina *et al.*, 2018) and Ukraine (Sauliak *et al.*, 2017). According to our data, lines E218_09, E2792_14 as well as the original forms (H74_90-245, E200_97-2, H242_97-1) are characterized by high stable resistance to stem rust for a long time. Instead, some other lines with identified PZHT 1BL.1RS, which had almost no signs of rust (7-8 points) even in a favorable year for the natural development of the pathogen, with increasing infectious load on a provocative artificial background of the pathogen in the field nursery were affected, although moderate (4-5 points). A similar trend was observed in [Topal, N.N.], when some varieties with PZHT 1BL.1RS on the natural background of stem rust in the south of Ukraine showed high resistance (8-9 points), and on the artificial background were affected by 2-4 points. While other varieties with 1BL.1RS had different levels of resistance (6-8 points). Therefore, the need to introduce other effective Sr genes into the gene pool of Ukrainian selection lines, including those whose stability has

not yet been overcome by races of the local population of the pathogen, is not in doubt.

A possible mechanism for achieving high group stability of these lines may also be a combination with other (including minor, ineffective or overcome) resistance genes. In particular, it is known that in genes (Nikonka, Selyanka, Kuyalnyk, Panna, etc.), which are part of the pedigree of advanced introgressive lines, there is a gene cluster Pm38 / Lr34 / Yr18 (Galaev and Sivolap, 2015). In addition, the recurrent genotype - Odes'ka 267 has a number of overcome ineffective in themselves Lr and Sr genes (Motsnyi and Blagodarova, 2004), which in interaction with foreign genes can enhance their action. Therefore, the interaction of clusters Pm8 / Lr26 / Sr31 / Yr9 and Pm38 / Lr34 / Yr18, under favorable conditions and genetic environments, can provide a certain level of stability. In particular, it is known to increase the resistance to the local population of leaf rust races of the combination Lr26 + Lr34, compared with the corresponding monogens [Galaev, A.V.]. In addition, the resistance donors, the original introgressive lines (E200_97-2, H242_97-1) and the sample H74_90-245 from which they originate, have in their pedigree the amphiploid AD (*T. timopheevii* / *Ae. Tauschii*) from Bulgaria (Motsnyi and Blagodarova, 2004). Therefore, it is likely that some effective resistance genes are derived from its components. For example, monogens Sr36 and Sr37 from *T. timopheevii* provide moderate susceptibility (4-5 points) to stem rust in southern Ukraine (Sauliak *et al.*, 2017). In the literature there is evidence of the effectiveness of combining PJT 1BL.1RS with other foreign genes to achieve high group stability (Babayants *et al.*, 2016).

Indirect confirmation of this assumption can be obtained by obtaining among direct and indirect derivatives of the sample H74_90-245 lines resistant to only one type of rust (AIL375_16, AIL299_16, etc.), as well as lines with different degrees of resistance to a particular pathogen. There are indications in the literature on the different reaction of foreign translocations to the pathogen (from susceptibility to high resistance) depending on the genetic background (Cruz *et al.*, 2016; Cardozo Téllez *et al.*, 2019). These assumptions require further detailed study, in particular involving in-depth phytopathological methods and known races of pathogens to identify introgressed resistance genes.

In the selection nursery, the lines were selected by appearance (overall selection score ≥ 3 points), alignment and constancy by signs of interest (resistance to diseases and plant morphology). As a result of work in the summer of 2016, out of 736 studied lines in the control nursery in 2017 (control nursery -2017), 120 were selected, and in control nursery -2018 - 24. Other lines did not look selectively attractive (overall score 2 points), split by characteristics, or had no signs of interest. Therefore, during 2016-2017, both in the Slovak Republic and in the Kyrgyz Republic, among the material that split but attracted attention, to obtain homozygous lines, an additional individual selection of the best plants (3-5 ears per line) with signs of resistance to common diseases. In 2018, the offspring of these plants were propagated again in the breeding nursery tested for resistance to relevant diseases, and in autumn stable homozygous lines (a total of 142 lines) were sown in the control nursery in 2019 (Table 2). It should be emphasized that in all years of research except 2017 there was a spread of brown rust, in 2015 - yellow, and in 2016 epiphytic of both these diseases

were recorded. In 2017, there was a natural manifestation of spread of powdery mildew and Septoria. stem rust. In addition, in 2016, 2017 and 2019, there was a

Table 2 : Resistance of introgressive lines transferred to the control nursery to common diseases, 2015-2019.

Source of resistance	Disease ¹⁾	N ²⁾	% of lines with reaction (points)					Statistical indicators ³⁾		
			Susceptible			Resistant		M	SD	LV
			1-2	3-4	5	6-7	8-9			
H74_90-245	Pm	77	-	45,5	23,4	31,2	-	4,8	1,32	3-7
	Lr		2,6	50,6	2,6	40,3	3,9	4,8	1,68	2-8
	Yr		-	33,8	6,5	59,7	-	5,7	1,42	3-7
	Sr		1,3	13,0	13,0	58,4	14,3	6,0	1,45	2-8
	Stb		1,3	88,3	9,1	1,3	-	3,8	0,63	2-7
Amphiploids	Pm	57	-	52,6	24,6	22,8	-	4,5	1,15	3-7
	Lr		-	22,8	3,5	38,6	35,1	6,4	1,75	3-8
	Yr		-	61,4	8,8	28,1	1,7	4,7	1,17	3-8
	Sr		1,8	84,2	8,8	5,3	-	3,8	0,82	2-6
	Stb		3,5	91,2	5,3	-	-	3,9	0,48	2-5
<i>Ae. tauschii</i>	Pm	113	3,5	45,1	28,3	21,2	1,8	4,5	1,36	2-8
	Lr		4,4	25,7	8,0	54,9	7,1	5,8	1,71	2-8
	Yr		8,0	32,7	5,3	48,7	5,3	5,3	1,78	2-8
	Sr		18,6	42,5	16,8	18,6	3,5	4,2	1,75	1-8
	Stb		3,5	90,3	4,4	1,8	-	3,6	0,78	2-7
Other	Pm	39	7,7	61,5	20,5	10,3	-	4,0	1,18	1-6
	Lr		10,3	66,7	2,6	20,5	-	4,2	1,29	2-7
	Yr		2,6	56,4	7,7	33,3	-	4,7	1,21	2-7
	Sr		7,7	69,2	10,3	12,8	-	4,0	1,14	2-7
	Stb		7,7	89,7	2,6	-	-	3,7	0,66	2-5

¹⁾Pm, Lr, Yr, Sr, Stb– resistance, respectively, to powdery mildew, leaf, yellow and stem rust and Septoria. ²⁾N– Number of introgressive lines. ³⁾M– the average value of the sign along the lines; SD – standard deviation; LV–limits of variation (min-max).

It should be noted that among the lines of high susceptibility transferred to the control nursery (at the level of drives) was almost not observed; the most vulnerable lines to disease response were mostly almost at the level of standards. This is due to the relatively weak natural background of the studied diseases, a significant number of crosses with modern varieties, as well as the selection carried out in the breeding nursery. In general, the most resistant lines resistant to sheat or yellow rust, reflecting slightly higher average values of scores of resistances (Table 2). This is due to the successful introgression of foreign Lr and Yr genes from all sources involved in hybridization. High long-term resistance to stem rust is observed only among the derivatives of the collection sample H74_90-245. Among the derivatives of amphiploids involving *Ae. tauschii* such lines are very rare; the vast majority of lines that are resistant to stem rust (7-8 points) at the first accounting (flowering phase), gradually lose it during maturation and appear susceptible (2-4 points) during pre-harvest accounting. A similar pattern was observed for Mexican synthetics, which served as the original forms (Motsnyi and Rybalka, 2011).

Few lines resistant to powdery mildew were isolated, and their scoring depended on the conditions of the year, and resistance to Septoria was practically not observed; the best lines showed moderate susceptibility (4-5 points) at the level of standards. Only 3 lines (PIL686R17, PIL688R17 and PIL578PH16) of all studied in the CD (1%) exceeded the standards, and such a reaction to *Septoria* at least two of them most likely has not a genetic but a physiological cause (late maturity) and is not manifested by everyone year. This was reflected in the lower values of statistical indicators M and SD (Tables 2 and 4).

The nature of the distribution of lines in response to a disease suggests that resistance to rust is controlled by major genes, because the whole set of lines, regardless of the source of resistance is more or less clearly divided into two main groups (stable and susceptible), with a relatively low proportion of intermediate forms and is characterized by high SD values. In this case, similarly to (Demydov *et al.*, 2019), except for combinations with Mexican elite synthetics (source "*Ae. Tauschii*"), the response of lines to leaf rust was the most variable compared to other diseases, indicating a radically different level of genetic determination of traits in introgressive lines. Another picture is observed with respect to powdery mildew and especially Septoria (Table 2), where most lines were susceptible (3-4 points), and the distribution is characterized by a high proportion of intermediate forms and low values of SD. Therefore, resistance to these diseases of the most resistant specimens may be due to positive transgression, has a polygenic nature and originates from the so-called minor sources of resistance and, unlike resistance to rust, cannot be easily passed on to offspring by crossing.

Newly created introgressive lines, as a rule, are characterized by a wide range of transgressive variability in grain productivity and quality. The variation of the complex of investigated agronomic features of lines in the Kyrgyz Republic depending on the level of resistance to diseases is characterized. Correlation analysis data (Table 3) showed a weak positive relationship ($R_{sp} = 0.26^{**}$) yield only with resistance to Septoria (in 2017) and yellow rust (in 2019). The absence of a negative correlation between yield and resistance to leaf (2017) or stem (2018) rust, in the absence of infectious load of these diseases, is in itself a positive fact, as it indicates the absence of a strong negative manifestation

of foreign genes. The lack of a similar correlation in other years, in general, corresponds to the literature (Demydov *et al.*, 2019) and is obviously associated with a relatively weak natural background of the studied diseases, because when plants are severely affected by rust diseases (over 60%) grain yield decreases sharply (Demydov *et al.*, 2019).

We also assume the possibility of multidirectional action of genetic determinants of stability. That is, the presence in the genome of lines of foreign genetic material can sometimes cause thinness of the grain. This may explain the trend of negative association of rust resistance with weight of 1000 grains in some cases (Table 3). Note that on an artificial infectious background with a strong infectious load of stem rust, this correlation is usually positive (Fig. 1). In any case, the results of correlation analysis indicate the possibility of combining in one genotype high resistance to the studied diseases and yields at the level of the adaptive norm.

The presence of a weak or even medium positive relationship between resistance and protein content, which is observed in most variants of the experiment (Table 3) and corresponds to the literature (Demydov *et al.*, 2019), due to deteriorating grain filling conditions due to pathogens (Topchiy and Sandetska, 2017) or the possibility of genetic linkage of foreign genes stability with determinants of high protein content in grain (Gpc factors) (Uauy *et al.*, 2005). Instead, the negative correlation ($R_{sp} = -0.48^*$) between resistance to Septoria and protein content in 2018 may be caused by grain tenderness in severely affected lines, which is evidenced by the positive correlation ($R_{sp} = 0.30$) between resistance to Septoria and weight of 1000 grains. Significant positive correlation between the indicators of resistance of lines to different diseases, which is observed in most variants of the experiment (Table 3), is obviously a consequence of artificial selection for group resistance. However, we also do not rule out the possibility of genetic linkage between individual Lr and Sr genes in the parental lines (Motsnyi and Blagodarova, 2004).

Table 3 : The results of correlation analysis of traits in introgressive lines

Year of harvest	Pairs of signs (R_{sp})							
	Resistance to	Yield	protein content	weight of 1000 grains	Resistance to diseases ¹⁾			
					Pm	Lr	Yr	Sr
2017 (120)	Pm	0,04	0,22*	-0,00				
	Lr	0,05	0,00	0,00	-0,10			
	Yr	-0,10	0,03	0,17	0,44***	0,25**		
	Sr	0,02	0,30**	-0,09	0,31***	0,21*	0,15	
	Stb	0,26**	-0,15	-0,09	-0,09	0,14	-0,29**	-0,08
2018 (24) ²⁾	Pm	-0,13	0,29	0,52**				
	Lr	-0,13	0,46*	-0,16	0,39*			
	Yr	-0,18	0,39	-0,17	0,46*	0,61***		
	Sr	-0,02	0,05	-0,30	0,37	0,48*	0,74***	
	Stb	-0,18	-0,48*	0,30	-0,06	-0,14	-0,26	-0,19
2019 (142)	Pm	-0,04	0,06	0,15				
	Lr	-0,12	-0,04	0,27*	0,06			
	Yr	0,26**	0,31***	0,20*	0,25**	0,00		
	Sr	-0,03	0,25**	-0,21*	-0,16	-0,07	-0,01	
	Stb	0,15	0,10	0,08	-0,15	0,17*	0,17*	0,08

* –probably at $p < 0,05$; ** –probably at $p < 0,01$; *** –probably at $p < 0,001$. ¹⁾Pm, Lr, Yr, Sr, Stb– resistance, respectively, to powdery mildew, leaf, yellow and stem rust and Septoria. ²⁾The number of introgressive lines is indicated in parentheses.

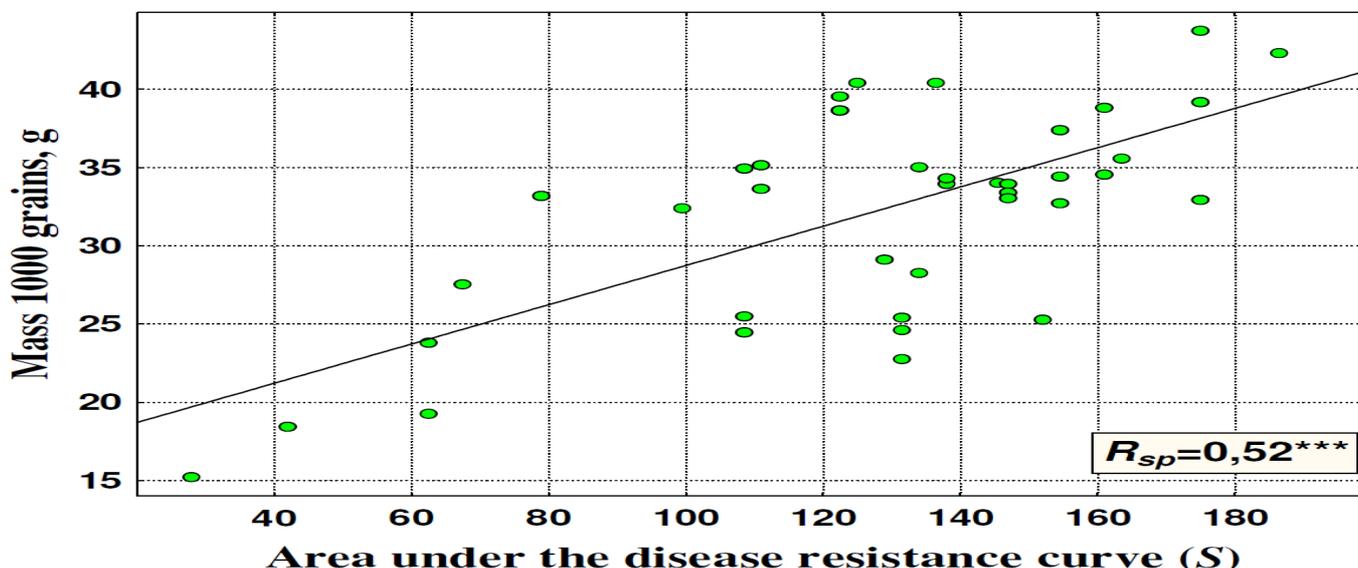


Fig. 1. Relationship between the mass of a thousand grains and the resistance index (S [4]) of introgressive wheat lines on an artificial background of stem rust in a field infectious nursery (wide-row sowing)

It so happened that the conditions of the experiment in the control nursery in 2017-2019 were different in terms of impact on plant development and unfavorable for wheat, in particular due to too late sowing, as well as a combination of agronomic and meteorological factors. This was manifested in the relatively low yield of standards ($M = 62.7$ c / ha; $LV = 40.8-83.5$ c / ha), compared to previous years (Motsniy et al., 2019), and in the presence of a probable impact of year

conditions on their yield. ($F = 29.0$ ***). In the Kyrgyz Republic, selection evaluation showed that in the vast majority, lines with high resistance to several diseases were characterized by low yields, protein content or fine grain. However, the obtained lines with fairly high weight of 1000 grains or protein content, which retained a set of target features of group stability (Tables 4, 5).

Table 4 : Characteristics of the best lines with group resistance to disease

Line ¹⁾	Year of harvest	Resistance to (score) ²⁾					Yield c/ha	Protein, %	weight of 1000 grains, g ³⁾
		Pm	Lr	Yr	Sr	Stb			
PIL939_16	2017	7	7-8	8	4	4	57,1	12,6	38,2
E218_09		6	7	7	8	4	50,5	12,9	37,9
AIL1073_16		5-6	6-8	6-7	7	4	64,1	11,9	40,4
E2792_14		6	8;7	4-7	7	4	60,9	12,0	34,6
PIL686R17		7	6-7	7	3	7	34,4	9,1	43,8
AIL1049_16		5	6-7	4-7	5-6	4	58,1	12,2	40,9
AIL229_16		4	7	5	6	5	57,4	12,6	34,4
AIL1161_16		5	6-8	4	7-8(6)	4	75,4	12,6	35,7
AIL375_16		6	7-8	4	4	5	49,2	12,0	39,6
PIL956_16		2-3	7	6	5-7	2	40,5	12,6	43,2
PIL856_16		5	5-7	7	4	3	54,0	11,0	39,3
AIL213_16		5	6-7	5-7	4	4	51,4	12,3	40,7
AIL379_16		6	4-8	4-7	4	4	58,6	11,5	36,9
AIL299_16		6	7-8	4-5	3-4	4	60,5	12,8	36,4
St ⁴⁾		3	3-4	3-5	3-4	3-4	56,1	11,0	38,7
M ⁴⁾		4,6	5,4	5,2	4,2	3,7	48,2	11,5	39,0
SD ⁴⁾		1,3	1,9	1,5	1,4	0,7	9,9	0,9	3,4
AIL381_18	2018	4-6	6;4-7	5-7	7-8	3	60,4	10,2	35,9
E196_09		6-7;6	3-5	7	6-7(5)	2	68,8	11,0	41,8
AIL1047_16		5-6	7	4-7	4-6	4	70,3	10,8	42,5
AIL1050_16		5-6	7	3-7	4-6	4	69,0	10,7	40,7
AIL334_17		3-5	5-7	4	4-7	4	71,0	10,5	38,8
St ⁴⁾		3-6	3-4	4-6	2-3	3-4	66,3	10,4	40,8
M ⁴⁾		4,7	4,5	5,6	4,1	3,7	64,6	10,5	37,1
SD ⁴⁾		1,3	1,5	1,3	1,8	0,6	11,8	0,6	3,2
PIL768_16	2019	6-7	7-9	7-8	3	4-5	46,0	11,6	47,0
PIL578PH16		6-8	7-8	6-7	7	3-7	46,2	13,6	23,4
PIL692_18		4-5	7-8	7	7	4	71,0	10,8	39,0
PIL451PH18		5-8	5-8	5-8	3	4-5	78,4	12,3	35,0
PIL702_18		3-5	7-8	7	6	4	63,0	10,1	37,7
E212_09		7-8	5-7;6	6-7	6-7	3-4	70,6	10,6	44,5
AIL72PH18		3-5	7-8	5-6	6	4-5	66,6	10,3	35,5
PIL687_18		4-5	7-8	6-7	3	4-5	71,6	10,5	42,4
AIL76PH18		3-5	7-8	5-6	6	3-4	72,4	10,9	34,3
AIL341/18		4-6	6(4)-7	4-7	7	4-5	70,6	12,7	35,4
PIL355PH18		4	6-7	7	3	5	73,0	12,0	40,1
St ⁴⁾		3-6	3-5	4-6	2-4	3-5	72,4	10,1	38,6
M ⁴⁾		4,3	6,0	5,1	4,8	4,4	63,9	10,6	37,1
SD ⁴⁾		1,3	1,7	1,7	2,0	0,8	9,2	0,8	3,2

¹⁾Lines are ranked by the sum of stability points within each year. Impressions of infection accumulators and indicators of high susceptibility to diseases (Odessa semi-dwarf) - 1-2 points each year. ²⁾The notation 3-7 means the scope of variation of scores over the years of the study, 7, 3 - splitting, 7 (3) - among the mostly stable plants are rarely susceptible. ³⁾MTS - mass of 1000 grains. ⁴⁾St- values of standards, M- is the average value of the sign according to the experiment; SD - standard deviation.

Table 5 : The origin of the best lines with group resistance to disease

Line name ¹⁾	Origin ²⁾
E196_09	Od.267/E200/97-2//Od.267 ^{*2} /3/Panna F _∞
E212_09	H242/97-1/Od.267 ^{*3} // Kuyalnik F _∞
E218_09	Od.267/H74_90-245 F ₂ //Od.267 ^{*4} /3/Peasant F _∞
AIL229_16	Od.267/H74_90-245 F ₂ //Od.267 ^{*11} /3/MA1 F ₄

AIL334_17	Od.267/AD Zhirova//Od.267 ^{*8} /3/ Leader F ₅
AIL375_16, AIL379_16	Od.267/AD Zhirova//Od.267 ^{*8} /3/Куяльник F ₄
AIL72PH18, AIL76PH18	Od.267/AD Zhirova//Od.267 ^{*8} /3/Change F ₅
AIL299_16	Change/3/Od.267/AD Zhirova//Od.267 ^{*8} F ₄
AIL1161_16, AIL341/18 AIL213_16, AIL381_18	Kuyalnik/4/(Od.267/H74_90-245 F ₂ //Od.267 ^{*4} /3/ Peasant F ₄) F ₅
PIL768_16	Sergeant // PEAG / Peasant F ₆
PIL451PH18	Peasant/ES4 F ₂ //Od.267 F ₄ /3/Borvius F ₄
PIL856_16	Peasant/ES17 F ₂ // Peasant F ₄ /3/Kuyalnik F ₆
PIL939_16	Peasant/ES20 F ₂ // Peasant F ₇
PIL687_18	Peasant/ES20 F ₂ //Od.267 F ₄ /3/Ватажок F ₄
PIL692_18	Peasant/ES20 F ₂ //Od.267 F ₄ /3/Wigen F ₄
PIL702_18, PIL355PH18	Peasant/ES20 F ₂ //Od.267 F ₅ /3/Group F ₄
PIL686R17	Peasant/ES25 F ₂ // Peasant F ₇
PIL956_16	Peasant/ES25 F ₂ //Od.267 F ₆
E2792_14, AIL1049_16, AIL1047_16, AIL1050_16	E214_09-1/Group ^{*2} F ₅
AIL1073_16	E214_09-1/Group //Zhayvir F ₆
PIL578PH16	CS ϕ 1b / E125/03 // CS ϕ 1b F _{∞}

¹⁾ E – Erythrospermum, PIL– primitive introgressive line, AIL– advanced introgressive line, PH – line from field infectious nursery of phytopathology and entomology department.

²⁾ E200/97-2, H242/97-1 and E125/03– triticales AD825/T. durum BlackSea F₃ //H74/90-245; H74/90-245 – Tom Pouce Blanc/AD(T. timopheevii/Ae. tauschii ssp. strangulata)//Aurora /3/Mermaid; AD Zhirova– AD(T. militinae/Ae. tauschii), PEAG – AD(T. dicoccum/Ae. tauschii), ES4, ES17, ES20 and ES25 –T. durum Altar 84/samples Ae. tauschii WX224, E214_09-1 (H242_97-1/Od.267^{*3} //Kuyalnik F _{∞}).

At the same time, lines with a low frequency were distinguished every year, which in these conditions exceeded the standards on individual grounds or their complex. As a rule, such lines were characterized by moderate resistance to one or two diseases and moderate susceptibility to others. Thus, in terms of yield, which is of first interest to the producer, the average values of the standards exceeded the following lines: AIL1161_16 - 75.4 c / ha (2017); AIL334_17 - 71.0 c / ha (2018); PIL451PH18 - 78.4 c / ha (2019). According to the absolute values of the complex of traits (yield, protein content, weight of 1000 grains), respectively, the lines were distinguished (Table 4): AIL1073_16 - 64.1 c / ha, 11.9%, 40.4 g, AIL1049_16 - 58.1 c / ha, 12.2%, 40.9 g (2017); E196_09 - 68.8 c / ha, 11.0%, 41.8 g, AIL1047_16 - 70.3 c / ha, 10.8%, 42.5 g (2018); PIL692_18 - 71.0 c / ha, 10.8%, 39.0 g, PIL355PH18 - 73.0 c / ha, 12.0%, 40.1 g (2019).

The disadvantages of the vast majority of selected introgressive lines are their late ripening, sometimes tallness, xeromorphic structure of the plant, heavy threshing of grain and instability to lodging. Thus, 21% of all studied lines (mainly from the source "Ae. Tauschii") were poorly threshed by the combine, although the degree of manifestation of this deficiency was different. And the most productive in 2017-line AIL1161_16 was characterized by a tendency to lodging, and also sprouted in the conditions of the experiment 3-4 days later than the standards, which in the onset of typical early summer drought can lead to grain inflammation, reduced yields and quality. In general, late ripening is a problem of remote hybridization, but in this case, it is mainly due to the wide involvement in crossing relatively late-ripening recurrent variety Odes'ka 267. To overcome late ripening, it is advisable to cross individual disease-resistant lines with the most early-ripening modern ones.

Some lines were split during reseeding by plots on the basis of resistance, although in the infectious nursery they were selected as constant (Table 4). In addition, heterogeneity was observed with respect to morphological features - leaf

and ear pubescence, stem color, ear and spines, as well as with respect to individual agronomic features (e.g. bush shape, plant height, ear date, ear habitus) or their complex, even if constancy of lines on resistance to a certain disease. It is possible that the presence of foreign genetic material in large quantities adversely affects the cytological stability and fertility of these lines. Therefore, they lose the acquired symptoms due to aneuploidy or re-pollination. Genetic instability of lines against the background of their cytological stability also seems probable, which may be due to suppression of foreign genes (Boyd *et al.*, 2001), their interaction with each other (Galaev, 2016) or with the genetic environment (Cardozo Téllez *et al.*, 2019), placement near heterochromatin segments of chromosomes, spontaneous mutations during gametogenesis. (Kozub *et al.*, 2019), intrachromosomal rearrangements (Antonyuk *et al.*, 2013), transposon movement or epigenetic variability (Antonyuk *et al.*, 2013; Shpylchyn *et al.*, 2013). Another reason may be clogging of the material during sowing or threshing. However, lines characterized by constancy and combining resistance to three types of rust and powdery mildew were identified (Table 4).

In general, a significant disadvantage of high-performance introgressive lines is the lack of yield stability in different conditions (Motsnyi *et al.*, 2014). Marked, as a rule, is inherent in the derivatives of ecologically remote hybrids. Obviously, this pattern extends to interspecific hybridization, which, to some extent, is also ecologically remote. It should be noted that in our study in the control nursery each year, mainly, other lines were studied. However, in the case of re-sowing of some lines next year or a year later, there is a discrepancy in the results of the studied indicators, depending on the year of seed harvest. So, for example, the line AIL1073_16 in 2017 surpassed, and in 2018 conceded to the standard on productivity. Line AIL1161_16, which stood out in the breeding nursery in 2017 in terms of yield and protein content (Table 4), was mediocre in these respects in 2019. Conversely, line AIL1047_16, which in 2017 was

significantly inferior to the standard in terms of yield (47.3 c/ha), in 2018 exceeded it in absolute values of all studied features. The line E2792_14 highlighted in the current study was included in the best set of traits also in our previous study (Motsnyi *et al.*, 2019), as it showed high yields in arid conditions in 2016. However, the line is characterized by heterogeneity in the presence of PJT 1BL.1RS (Kozub *et al.*, 2019), and in 2019 it yielded to the yield standard and showed signs of clogging. Also, in 2018 and 2019, in contrast to 2017, the recurrent variety (Odessa 267) on average exceeded the yield standards. Obviously, the advantages of the genotype, resistant to late sowing, low agrophones and harsh growing conditions were manifested here.

The results of tests in the Kyrgyz Republic in 2017-2019 showed that the material selected by a set of traits in the breeding nursery of the department of selection and seed production of soft winter wheat from splitting families is generally better in productivity than constant lines selected for individual foreign traits, in the Department of General and Molecular Genetics. The higher yields achieved in this way in 2018 and 2019, primarily among introgressive lines (Table 4), is due to the selection among them, including resistance to disease, which reduces the overall infectious load in the biocenosis. At the same time, the lines of early generations constant in terms of stability (individual selections from F₂-F₄ populations) isolated and transmitted to the Kyrgyz Republic were more split by a set of agronomic traits. However, it is from such lines that it is sometimes possible to distinguish highly productive biotypes of later generations. In particular, among the numerous selections, two (E2792_14-1 and E2792_14-2) made from the line E2792_14 make a good impression. Instead, all constant lines turned out to be low-performance. Obviously, the low efficiency of selections in the early generations (F₂-F₃) is explained by the presence of a high degree of heterozygosity and the manifestation of competitive heterosis, which gradually subsides in subsequent generations. On the other hand, selection in later generations, especially with intensive technologies, is often subject to natural negative selection, when low-yielding extensive but better adapted to medium and low agrophones biotype has lower potential productivity, but higher in these conditions reproduction rate (small grain), which allows it to successfully compete with high-yielding biotype and prevail in later generations (Orlyuk *et al.*, 1987).

Note that when using parental forms with significant differences in origin (genetically or ecologically distant hybrids), the efficiency of selection of high-yielding genotypes among stable hybrid populations increases both in higher backcrosses (BC_{5,6}) and in later generations. Thus, among the studied combinations, the highest yield of high-yielding genotypes was obtained among the improved lines derived from sample H79_90-245 (Tables 4, 5). Instead, there were more forms with group stability among the primary lines. Obviously, resistance to each of the diseases and especially productivity are polygenic traits, in addition, their inheritance is controlled by additional both genotypic and exogenous factors, which leads to long-term cleavage in hybrid populations. Therefore, for remote hybrids, the beginning of intensive individual selections in the breeding nursery to identify high-yielding biotypes that can already be considered donors of resistance, it is desirable to start with 5-6 generations, to which the material must be brought by Pedigree with permanent selection on the basis of interest.

From our data it turns out that the genetic background of individual introgressive lines, direct or indirect derivatives of the sample H74_90-245 (Table 5), is favorable for the implementation of the positive effect of PJT 1BL.1RS on both economically valuable and adaptive traits in the Odessa region. The role of WRT as a donor of wheat resistance to yellow and stem rust in Ukrainian selection should not be underestimated. However, the presence of the 1RS chromosome in breeding lines does not guarantee resistance to these diseases. Given that new pathotypes of *P. graminis* are able to overcome the resistance of translocation (Saunders *et al.*, 2019), the search for additional sources of resistance is becoming increasingly urgent. The role of so-called secondary sources in the creation of the genetic environment is becoming more important and requires further exploitation. Therefore, the search for new effective genes in the gene pool of wild relatives, as well as a detailed study of small sources of resistance to wheat rust and their combination is an important prerequisite for achieving high long-term resistance.

In contrast to the derivatives of sample H74_90-245, none of the derivatives of the MA1 line with modified WRT 1BL.1RSm (Lukaszewski, 2000) has not yet entered the best in terms of disease resistance or agronomic characteristics (Table 5). This contradicts the data (Babayants *et al.*, 2016), which states the creation of such a line (Phyto43 / 14) in the combination Kuyal'nik / MA1. This line is characterized by group resistance to six diseases, yield and quality at the level of the standard zone (Kuyal'nik), although 10-15 cm higher than it (Babayants *et al.*, 2016). It is possible that in our study for this translocation has not yet created a suitable genetic background on which it could show its advantages, or in the south of Ukraine WRT 1BL.1RSm is inferior to the positive impact on economically valuable and adaptive traits of intact translocation 1BL.1RS through lack of proximal segment of rye chromatin with strong QTL on root system development, drought resistance and productivity (Howell *et al.*, 2014).

The results of the study of introgressive lines E2792_14, E218_09, E212_09, AIL1073_16 showed their moderate resistance to powdery mildew. In comparison with the standard varieties susceptible to rust species, these lines also showed group resistance to local populations of brown, yellow and stem rust (Table 4). At the same time, introgressive lines approached yield standards and exceeded them in terms of weight of 1000 grains or protein content in grain. It should be emphasized that when using in the hybridization of varieties of the laboratory of selection of intensive varieties of soft wheat (Table 5), the increase in material productivity is often accompanied by grain grinding. This contradicts some trends in world selection (Wang *et al.*, 2012), when increasing yields are achieved, including through grain enlargement (weight of 1000 grains up to 50 g or more).

According to the results of tests in the Kyrgyz Republic in 2017 and 2019, medium-early short-stemmed introgressive line E2792_14 was identified as the most productive and widely involved in crossing with modern varieties and promising lines of Agricultural Institute – Research-scientific Centre of plants breeding as a donor of stability. From its individual selections for use in the further selection process are carried out. Medium-ripe introgressive line AIL1161_16 is involved in crossing with precocious modern varieties to overcome late ripening and tendency to lodging. Late-

maturing lines E218_09, E212_09 and AIL1073_16 is limitedly involved in the selection process as donors of group resistance to rust diseases and powdery mildew.

Conclusions

Therefore, as a result of crossing the original primary introgressive lines, collection samples, amphiploids with the participation of *Ae. tauschii* and other sources with modern varieties of wheat obtained several breeding lines with foreign polygenic complexes of disease resistance, high values of weight of 1000 grains, protein content and morphological characteristics, which, by 8-10 backcross with highly adaptive to local conditions variety Odes'ka 267, deprived negative qualities inherent in wild species (xeromorphic structure of the plant, fragility and spontaneous shedding of the ear during ripening, poor threshing of grain, stiffness of spikelet's and flower scales, etc.). In addition, similarly [30, 32, 34, 35], shows the effectiveness of using derivatives of the collection sample H74_90-245, to obtain improved introgressive lines that combine genes for resistance to fungal pathogens, localized in WRT 1BL.1RS, with complexes of effective resistance genes from other sources. Also, there is a tendency to increase productivity in lines with translocation 1BL.1RS, compared with other introgressive lines.

The lines are characterized by group resistance to powdery mildew and types of rust of various degrees, high adaptability to growing conditions in the south of Ukraine, drought and winter hardiness, tolerance to low and hard agrophones, high quality. In terms of productivity, the lines reach the zone standard or exceed it in harsh conditions and technological deviations in some years and already belong to the category of sustainability donors. These lines need to be tested for productivity on high agrophones and improved in terms of yield stability and early ripening, and can be used without any restrictions as a starting material for wheat breeding. It should be borne in mind that when crossing them with the best varieties or promising lines and subsequent selection for productivity, foreign gene complexes will "fall apart" if they are not specifically controlled.

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References

- Antonyuk, M.Z.; Shtefyuk, T.V. and Ternovska, T.K. (2013). Common wheat introgressive line polymorphism for microsatellite locus alleles, *Factors in experimental evolution of organisms*, Kyiv, Logos, vol. 12, pp. 97–101 (in Ukrainian).
- Antonyuk, M.Z.; Shpylchyn V.V. and Ternovska, T.K. (2013). Permanent genetic variability in the introgressive lines and amphidiploids of *Triticinae*, *Cytol. Genet.*; vol. 47, no. 4, pp. 242–251.
- Ahmadi, J.; Pour-Aboughadareh, A.; Ourang, S.F. (2018). Mehrabi, A.A. and Siddique, K.H.M.; Wild relatives of wheat: *Aegilops-Triticum* accessions disclose differential antioxidative and physiological responses to water stress, *Acta Physiol. Plant.*; vol. 40, no. 5, pp. 90–104, doi:10.1007/s11738-018-2673-0.
- Arabbeigi, M.; Arzani, A.; Majidi, M.M.; Kiani, R.; Tabatabaei, B.E.S. and Habibi, F. (2014). Salinity tolerance of *Aegilops cylindrica* genotypes collected from hyper-saline shores of Uremia Salt Lake using physiological traits and SSR markers, *Acta Physiol. Plant.*; vol. 36, no. 8, pp. 2243–2251, doi: 10.1007/s11738-014-1602-0.
- Babayants, O.V.; Babayants, L.T. (2014). Bases of breeding and methodology of assessments of wheat resistance to pathogens, Odessa: VMV, (in Russian).
- Bhatta, M.; Morgounov, A.; Belamkar, V.; Yorgancilar, A. and Baenziger, P. S. (2018). Genome-wide association study reveals favorable alleles associated with common bunt resistance in synthetic hexaploid wheat, *Euphytica*, vol. 214, no. 11, pp. 200–209, doi: 10.1007/s10681-018-2282-4.
- Babayants, O.V.; Sauliak, N.I.; Babayants, L.T.; Ternovyi, K.P. and Galaev, O.V. (2016). The new initial breeding material of wheat (*Triticum aestivum* L.) for selection to complex resistance to phytopathogenes, *Coll. PBGI-NCSCI*, Odessa, vol. 68, no. 28, pp. 68–75 (in Russian).
- Boyd, L.; Minchin, P. (2001). Wheat mutants showing altered adult plant disease resistance. *Euphytica*, vol. 122, no. 2, pp. 361–368, doi: 10.1023/A:1012948702416.
- Cruz, C.D.; Peterson, G.L.; Bockus, W.W.; Kankanala, P.; Dubcovsky, J.; Jordan, K.W.; Akhunov, E.; Chumley, F.; Baldeomar, F.D. and Valent, B. (2016). The 2NS translocation from *Aegilops ventricosa* confers resistance to the *Triticum* pathotype of *Magnaportheorizae*, *CropSci.*; vol. 56, no. 3, pp. 990–1000, doi: 10.2135/cropsci2015.07.0410.
- Climate change and crop production, *CABI Climate Change Series*, 2011, vol. 1, pp. 292.
- Cardozo Téllez, L.; Chavez, A.; Bobadilla, N.; Pérez-Estigarribia, P. and Kohli, M. (2019). Variable resistance of bread wheat (*Triticum aestivum*) lines carrying 2NS/2AS translocation to wheat blast, *Pl. Breed.*; vol. 138, no. 1, pp. 62–68, doi: 10.1111/pbr.12661.
- Soko, T.; Bender, C.M.; Prins, R. and Pretorius, Z.A. (2018). Yield loss associated with different levels of stem rust resistance in bread wheat, *Plant Disease*, vol. 102, no. 12, pp. 2531–2538, doi: 10.1094/PDIS-02-18-0307-RE.
- Morgun, V.V.; Topchiiy, T.V. (2016). The search for new sources of winter wheat resistance to the main pathogens of fungal diseases, *Plant Physiology and Genetics*, vol. 48, no. 5, pp. 393–400 (in Ukrainian).
- Topchiiy, T.V.; Sandetska, N.V. (2017). Formation of the productivity of winter wheat varieties with various degree of resistance under the influence of fungal diseases, *Plant Varieties Studying and Protection*, vol. 13, no. 4, pp. 416–422, doi: 10.21498/2518-1017.13.4.2017.117751 (in Ukrainian).
- Lewis, C.M.; Persoons, A.; Beber, D.P.; Kigathi, R.N.; Maintz, J.; Findlay, K.; et al. (2018). Potential for re-emergence of wheat stem rust in the United Kingdom, *Commun. Biol.*; vol. 1, Art. no. 13, pp. 1–9, doi: 10.1038/s42003-018-0013-y.
- Retman, S.V.; Shevchuk, O.V. and Gorbacheva, N.P. (2011). Diseases of leaves and ear, *Quarantine and plant protection*, vol. 4, pp. 25–27 (in Ukrainian).
- O'Driscoll, A.O.; Kildea, S.; Doohan, F.; Spink, J. and

- Mullins, E. (2014). The wheat-*Septoria* conflict: a new front opening up?, *Trends Plant Sci.*; vol. 19, no. 9, pp. 602–610, doi: 10.1016/j.tplants.2014.04.011.
- Morgounov, A.; Abugalieva, A.; Akan, K.; Akin, B.; Baenziger, S.; Bhatta, M. and Zelenskiy, Y. (2018). High-yielding winter synthetic hexaploid wheats resistant to multiple diseases and pests, *Pl. Genet. Res.*; vol. 16, no. 3, pp. 273–278, doi: 10.1017/S147926211700017X.
- Kovalyshyna, H.M.; Dmytrenko, Yu.M. (2017). Sources of resistance to brown rust pathogen and their use in the development of soft wheat varieties, *Plant Varieties Studying and Protection*, vol. 13, no. 4, pp. 379–386, doi: 10.21498/2518-1017.13.4.2017.117742 (in Ukrainian).
- Reynolds, M.; Dreccer, F. and Trethowan, R. (2007). Drought adaptive traits derived from wheat wild relatives and landraces, *J. Exp. Bot.*; vol. 58, no. 2, pp. 177–186, doi: 10.1093/jxb/erl25.
- Lyfenko, S.Ph.; Nargan, T.P. and Nakonechny, N.Ju. (2014). Problematic but prospective direction of breeding: introgressions into genome of winter bread wheat different donors, *Breeding and seed production*, no. 105, pp. 39–50, doi: 10.30835/2413-7510.2014.42043(in Ukrainian).
- Motsnyi, I.I.; Blagodarova, E.M. (2004). Inheritance of resistance to diseases and morphological characters in the hybrids of common wheat with introgression lines, *Coll. PBGI-NCSCI*, Odessa, vol. 46, no. 6, pp. 179–193 (in Ukrainian).
- Motsnyi, I.I.; Narhan, T.P.; Yeryniak, M.I. and Liphenko, S.F. (2017). Application of derivatives of incomplete wheat-wildrye amphiploid (WWRA) *Elytricum fertile* in selection of winter soft wheat, *News of agrarian sciences*, vol. 8, pp. 45–50 (in Ukrainian).
- Motsnyi, I.I.; Narhan, T.P.; Lyfenko, S.Ph. and Yerynyak, N.I. (2014). Involvement of introgression lines for winter bread wheat breeding, *Bulletin of Kharkiv National Agrarian University. Series: Biology*, vol. 31, no. 1, pp. 79–90 (in Ukrainian).
- Lukaszewski, A. (2000). Manipulation of the 1BL.1RS translocation in wheat by induced homoeologous recombination, *Crop Sci.*; vol. 40, no. 1, pp. 216–225, doi: 10.2135/cropsci2000.401216x.
- Motsnyi, I.I.; Rybalka O.I. (2011). Variability of Mexican amphiploids and their hybrids to winter wheat for morphological characters and disease resistance, *Coll. PBGI-NCSCI*, Odessa, vol. 57, no. 17, pp. 45–53 (in Ukrainian).
- Kjeldahl, J. (1983). Neue Methode zur Bestimmung des Stickstoffs in organischen Körpern" (New method for the determination of nitrogen in organic substances), *Zeitschrift für analytische Chemie*, vol. 22, no. 1, pp. 366–383.
- DSTU 4138-2002 Crop seeds. Methods of quality determination / Kindruk, M.O.; et al.; *Derzhspozhyvstandart of Ukraine*, Kyiv, 2003, p.17–18, https://www.studmed.ru/dstu-4138-2002-nasnnya-slskogospodarskih-kultur-metodi-viznachennya-yakost_e073265435f.html (in Ukrainian).
- Lelley, T.; Eder, C. and Grausgruber, H. (2004). Influence of 1BL.1RS wheat-rye chromosome translocation on genotype by environment interaction, *J. Cer. Sci.*; vol. 39, pp. 313–320, doi: 10.1016/j.jcs.2003.11.003.
- Lakin, G.F. (1973). *Biometrics. Textbook for universities and pedagogical institutes*, Moscow, Higher School, 343 p.
- McIntosh, R.A.; Dubcovsky, J.; Rogers, W.J.; Morris, C.F.; Appels, R. and Xia, X.C. (2017). Catalogue of gene symbols for wheat: Supplement.
- Demydov, O.A.; Volohdina, H.B.; Voloshchuk, S.I.; Humeniuk, O.V.; Kyrylenko, V.V. and Khomenko, S.O. (2019). Parent material for breeding winter wheat with high disease resistance under environments of forest-steppe of Ukraine, *Factors in experimental evolution of organisms*, Kyiv, vol. 24, pp.63–69, doi: 10.7124/FEEO.v24.1080 (in Ukrainian).
- Saunders, D.G.O.; Pretorius, Z.A. and Hovmoller, M.S. (2019). Tackling the re-emergence of wheat stem rust in Western Europe, *Commun. Biol.*; vol. 2, Art. no. 51, pp. 1–3, doi: 10.1038/s42003-019-0294-9.
- Pershina, L.A.; Belova, L.I.; Trubacheeva, N.V.; Osadchaya, T.S.; Shumny, V.K.; Belan, I.A.; Rosseeva, L.P.; Nemchenko, V.V. and Abakumov S.N. (2018). Alloplasmic recombinant lines (*H. vulgare*)-*T. aestivum* with 1RS.1BL translocation: initial genotypes for production of common wheat varieties, *Vavilov Journal of Genetics and Breeding*, vol. 22, no. 5, pp. 544–552, doi: 10.18699/VJ18.393 (in Russian).
- Sauliak, N.I.; Ternovyi, K.P.; Babayants, O.V.; Vasyli'iev, O.A. and Galaev, O.V. (2017). The efficiency of wheat (*Triticum aestivum* L.) genes resistance to *Puccinia graminis* Pers. f. sp. *tritici* Erikss et Henn under Ukraine environments, *Coll. PBGI-NCSCI*, Odessa, vol. 70, no. 30, pp. 61–69 (in Ukrainian).
- Topal, N.N. (2014). Adaptive properties and productivity of varieties and lines with wheat-rye translocations in the south of Ukraine, *Collection of PBGI – NCSCI*, Odessa, is. 23 (63), pp. 88–99.
- Galaev, A.V.; Sivolap, Yu.M. (2015). Description of the soft wheat varieties of Ukrainian and Russian breeding by alleles of locus csLV34 closely connected with multipathogen resistance gene *Lr34/Yr18/Pm38*, *Cytol. Genet.*; vol. 49, no. 1, pp. 13–19, doi: 10.3103/S0095452715010041.
- Galaev, A.V. (2016). Effectiveness of different resistance genes to leaf rust and their combinations in interline hybrids of spring bread (*Triticum aestivum* L.) in South Ukraine, *Coll. PBGI-NCSCI*, Odessa, vol. 68, no. 28, pp. 109–122 (in Ukrainian).
- Hurni, S.; Brunner, S.; Stirnweis, D.; Herren, G.; Peditto, D.; McIntosh, R.A. and Keller, B. (2014). The powdery mildew resistance gene *Pm8* derived from rye is suppressed by its wheat ortholog *Pm3*, *The Plant Journal*, vol. 79, no. 6, pp. 904–913, doi: 10.1111/tpj.12593.
- Uauy, C.; Brevis, J.-C.; Chen, X.; Khan, I.; Jackson, L.; Chicaiza, O.; Distelfeld, A.; Fahima, T. and Dubcovsky, J. (2005). High-temperature adult-plant (HTAP) stripe rust resistance gene *Yr36* from *Triticum turgidum* ssp. *dicoccoides* is closely linked to the grain protein content locus *Gpc-B1*, *Theor. Appl. Genet.*; vol. 112, no. 1, pp. 97–105, doi 10.1007/s00122-005-0109-x.
- Motsnyi, I.I.; Litvinenko, N.A.; Molodchenkova, O.O.; Sokolov, V.M.; Fayt, V.I. and Sechnyak, V.Ye. (2019). Development of winter wheat starting material using interspecific crossing for breeding for increased protein content, *Cytol. Genet.*; vol. 53, no. 2, pp. 113–123.
- Kozub, N.A.; Sozinov, I.A.; Bidnyk, H.Ya.; Demianova,

- N.A.; Sozinova, O.I.; Karelov, A.V. and Blume, Ya.B. (2019). Mutants at gliadin loci on the basis of the common wheat cultivar Bezostaya 1, *Factors in experimental evolution of organisms*, Kyiv, vol. 24, pp. 109–114, doi: 10.7124/FEEO.v24.1088 (in Ukrainian).
- Shpylchyn V.V.; Mykhailyk, S.Yu. and Ternovska, T.K. (2016). Transposons activity as a factor of loss *Iw2(T)* gene function in the off springs of artificial *Triticinae* amphidiploids, *Factors in experimental evolution of organisms*, Kyiv, Logos, vol. 19, pp. 51–54 (in Ukrainian).
- Orlyuk, A.P.; Basaliy, V.V. and Lavrynenko, U.O. (1987). Variability of the genetic structure of hybrid populations of spring wheat when reseeded, *Genetika*, vol. 23, no. 3, pp. 464–472 (in Russian).
- Howell, T.; Hale, I.; Jankuloski, L.; Bonafede, M.; Gilbert, M. and Dubcovsky, J. (2014). Mapping a region within the 1RS.1BL translocation in bread wheat affecting grain yield and canopy water status, *Theor. Appl. Genet.*; vol.127, no. 12, pp. 2695–2709, doi: 10.1007/s00122-014-2408-6.
- Wellings, C.R. (2011). Global status of stripe rust: a review of historical and current threats, *Euphytica*, vol. 179, no. 1, pp. 129–141, doi: 10.1007/s10681-011-0360-y.
- Warburton, M.L.; Crossa, L.; Franco, J.; Kazi, M.; Trethowan, R.; Rajaram, S.; Pfeiffer, W.; Zhang, P.; Dreisigacker, S. and van Ginkel, M. (2006). Bringing wild relatives back into the family: recovering genetic diversity in CIMMYT improved wheat germplasm, *Euphytica*, vol. 149, no. 3, pp. 289–301, doi: 10.1007/s10681-005-9077-0.
- Wang, L.; Ge, H.; Hao, C.; Dong, Y. and Zhang, X. (2012). Identifying loci influencing 1,000-kernel weight in wheat by microsatellite screening for evidence of selection during breeding, *PLoS ONE*, vol. 7, no. 2, e29432, pp. 1–10, doi: 10.1371/journal.pone.0029432.