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Characteristics of the source material for breeding winter wheat for group resistance to leaf and stem pathogens

Ye. A. Holub*, N. I. Sauliak, O. A. Vasyliev, M. A. Lytvynenko, V. A. Traskovetska, Z. V. Shcherbyna, M. A. Bushulian, Ye. I. Kirchuk

*Plant Breeding and Genetic Institute – National Centre of Seed and Cultivar Investigation, 3 Ovidiopolska doroha St., Odesa, 65036, Ukraine, *e-mail: eva.golub.1979@ukr.net*

Purpose. Investigation of the efficiency of using introgressive lines with group resistance to leaf pathogens as source material in breeding winter wheat (*Triticum aestivum* L.) for the aforementioned trait. **Methods.** Field and laboratory (evaluation of resistance to certain races of leaf rust and powdery mildew at the juvenile growth stage in greenhouses and on light plants); PCR analysis (identification of resistance genes to these diseases in the studied material); statistical analysis; and crossbreeding analysis (study of patterns of inheritance and interaction of resistance genes). **Results.** The original breeding lines of different generations (F_4–F_5), which were created based on the genetics of wild wheat relatives: *Aegilops cylindrica*, *Ae. variabilis*, *Triticum ventricosum*, *Tr. erebuni*, *Tr. tauschi*, *Thinopyrum elongatum*, *Triticosecale* in the PBGI – NCSCI, were studied for group resistance to local populations of leaf diseases and a set of basic agronomic traits. Six lines with effective group resistance genes (*Lr24*, *Lr68*, *Sr15*, *Sr31*, *Sr58*, *Pm38*), as well as their combinations, were identified. These lines provide the selected genotypes with a consistently high level of resistance, excellent grain quality and productivity, regardless of the severity of the infection load. Investigating the genetic basis of the group resistance trait on F_1–F_2 hybrid material, obtained by crossing the studied lines with susceptible local varieties, revealed that its inheritance is determined by the action of two dominant complementary genes. This indicates the possibility of effectively using this material as donors of high resistance. **Conclusions.** As a result of the research, we obtained source material in the form of six lines of winter bread wheat that effectively combine a high level of group resistance to leaf pathogens and a set of basic agronomic traits in their genotype. This makes them valuable breeding material. These lines are included as parental components in the crossbreeding plans of the PBGI – NCSCI and are transferred to leading NAAS of Ukraine scientific breeding centres for use in breeding programmes.

Keywords: *winter wheat; group resistance; resistance genes; leaf and stem diseases; productivity.*

Introduction

Plant breeding plays a crucial role in the modern integrated system for protecting wheat against phytopathogens [1]. Developing and implementing varieties with a genetically determined high level of resistance provides an opportunity to address a number of important issues facing the agricultural sector today, both in our country and abroad [2, 3]. Firstly, the economic aspect must be considered, as genetic protection against numerous pathogens and pests can prevent significant losses in grain yield and deterioration in quality [4]. Cultivating resistant varieties enables us to reduce the

Yevheniia Holub
https://orcid.org/0000-0002-3415-4193
Nadiia Sauliak
https://orcid.org/0000-0001-5164-1105
Oleksii Vasyliev
https://orcid.org/0000-0003-2070-565X
Mykola Lytvynenko
https://orcid.org/0000-0002-8605-6587
Vita Traskovetska
https://orcid.org/0000-0001-6 529-1919
Maryna Bushulian
https://orcid.org/0009-0000-9314-7113
Yevhenii Kirchuk
https://orcid.org/0000-0003-1681-9160

amount of pesticide used to protect plants during the growing process. Developing wheat varieties with group resistance is highly relevant for pesticide-free or minimal-pesticide cultivation technologies, especially for producing clean grain for food intended for children, the sick and the elderly [5].

An analysis of the current state of research on breeding for resistance to phytopathogens has revealed a wide range of innovative developments. These include new methods for identifying sources of resistance containing a complex of genes that ensure long-term stability; modified methodologies; and original schemes enabling the combination of race-specific resistance genes and the creation of genotypes with a high level of race-nonspecific resistance and tolerance [6–8].

Research is also being conducted to improve the efficiency with which pathogen populations are monitored, including species, races, biotypes and strains, as well as changes in their virulence and aggressiveness, in order to adjust breeding programs accordingly [9, 10].

Moreover, the feasibility of incorporating resistant material from different countries is being explored, including genetic sources and donors of new, highly effective resistance genes from wheat's close and distant relatives [11, 12].

Practical experience and analysis of wheat pathogen protection systems demonstrate that resistance to a single pathogen is not a universal solution. A more significant effect is achieved by including varieties with group resistance to several pathogens in breeding programs [13, 14]. Developing such varieties is a complex, long-term process. The success of this type of breeding programs depends primarily on the availability of high-quality source material and donors of highly effective – preferably dominant – resistance genes. The aim of this study is therefore to examine the effectiveness of using introgressive lines with group resistance to leaf and stem pathogens in breeding winter bread wheat.

The research presented is based on scientific work carried out at the Plant Breeding and Genetic Institute – National Centre of Seed and Cultivar Investigation (PBGI – NCSCI) since the 1930s. During this period, the Institute's phytopathologists have conducted extensive research into various aspects of immunity and breeding for this trait. The department has developed immune source material, which is used in various breeding programs at the institution and at leading scientific centers within the National Academy of Agrarian Sciences of Ukraine (NAAS).

The aim of this study is to improve phytopathological evaluation systems and the selection of resistant genotypes at all stages of the breeding process, in controlled and artificially infectious environments.

Materials and Methods

The research was carried out from 2019/20 to 2022/23 on the experimental fields of the Plant Breeding and Genetic Institute – National Centre of Seed and Cultivar Investigation in Odesa, Ukraine. These fields had previously been left uncultivated. This study examined these issues in both the field and the laboratory. When setting up the field trials with plots measuring 10 m^2, the SSFK-7 selection seeder was used. Phenological monitoring, evaluation and harvesting were carried out in accordance with the state strain testing methodology. The plots were harvested using a SAMPO-130 selection harvester.

The research material consisted of lines of winter bread wheat of various generations (F_4–F_5) created using the genetic material of wild wheat relatives: *Aegilops cylindrica* Host., *Aegilops variabilis* var. *typica* Eig., *Triticum ventricosum* (Tausch) Ces., Pass. & Gibelli, *Triticum erebuni* Gandilyan, *Triticum tauschii* (Coss.) Schmalh, *Thinopyrum elongatum* (Host) D.R.Dewey and *Triticosecale* Wittm. & A.Camus. These lines were studied for their resistance to leaf and stem diseases at several stages. Under field conditions and a complex infection background involving a mixture of highly susceptible varieties, the adult plant resistance of the genotypes was examined. Their resistance to individual races of leaf rust and powdery mildew was assessed in greenhouse conditions and under light installations during the juvenile stage of plant development (BBCH 12–13). The racial and biotype composition, as well as the inoculation times, of the pathogens causing leaf and stem diseases are described in the monograph by O. V. Babayants and L. T. Babayants [15]. The resistance of adult plants was evaluated on a 9-point scale: 1–2 = very susceptible; 3 = highly susceptible; 4 = susceptible; 5 = moderately susceptible; 6 = moderately resistant; 7 = resistant; 8 = highly resistant; 9 = immune [16]. The identification of resistance genes to these diseases in the study material was carried out at the PBGI – NCSCI using PCR analysis according to standard methods [17].

The data was statistically processed using Excel software. The limits of the maximum random deviation of the results obtained were determined using the least significant difference (LSD) method. The results of the F_2 segregation were then checked for compliance with the hypothesis using Pearson's correlation coefficient (χ^2) [18].

The genetic analysis was performed using crossing combinations: *Erythrospermum* 57/12 /

'Vatazhok', *Er.* 57/12 / 'Viktoriia Odeska', *Er.* 43/14 / 'Luzanivka', *Er.* 70/14 / 'Odeska Napivkarlykova', *Er.* 2/14 / 'Kuialnyk', *Er.* 67/14 / 'Odeska Napivkarlykova', *Er.* 100/14 / 'Viktoriia Odeska'.

The reliability of the segregation was checked using Pearson's chi-square test (x^2) according to the formula:

$$\chi^2 = \sum \frac{(f - F)^2}{F},$$

where: F – expected; f – observed.

The inheritance patterns and interactions of the resistance genes were determined through hybridological analysis of the F_1–F_2 populations [19].

The protein content of bread wheat grains was determined using a SupNIR-2700 express analyzer. The sedimentation rate was determined using the SDS 30 express method of quality assessment. The flour was evaluated in a bakery using the microbaking method with a no-steam approach. The volume of the bread was determined using 100 g of flour, and the appearance, texture, elasticity and colour of the crumb were assessed. The bread's appearance was assessed based on three criteria: the shape, surface and color of the crust [20].

We followed the State Standards of Ukraine (DSTU) 4138-2002 [21] when calculating the thousand grain weight. The grain bulk density was determined using a one-liter measuring jar (ПХ-1) [22].

Results and Discussion

As part of the methodological research aimed at developing initial material for breeding winter bread wheat with group resistance to leaf and stem diseases, 27 introgressive lines with high levels of resistance to diseases were obtained through complex, stepwise crossings (Table 1).

Table 1

Resistance of introgressive lines of winter bread wheat to leaf and stem disease pathogens (2019/20–2022/23)

Breeding line	Pedigree	Disease resistance, score		
		Leaf rust	Stem rust	Powdery mildew
Lutescens 4/16	('*Amphidipliod* 4' / 'Albatros Odeskyi^{2r}') / (('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Odeska Napivkarlykova') / 'Tira' / 'Amigo'	8 ± 0.50	8 ± 0.50	5 ± 0.38
Erythrospermum 9/16	(('Obrii' / *Triticum erebuni*) / 'Odeska 162') / 'Ukrainka Odeska'/ (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska') / 'Nikoniia'	8 ± 0.38	5 ± 0.01	9 ± 0.02
Erythrospermum 46/16	('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Kuialnyk'	9 ± 0.38	5 ± 0.01	9 ± 0.01
Erythrospermum 47/16	(('Obrii' / *Triticum erebuni*) / 'Odeska 162') / 'Ukrainka Odeska^{2r}'/ (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska') / 'Nikoniia'	8 ± 0.50	8 ± 0.42	4 ± 0.38
Lutescens 48/16	('Kupava' / 'Kuialnyk')	5 ± 0.38	9 ± 0.01	5 ± 0.03
Erythrospermum 53/16	(('Obrii' / *Triticum erebuni*) / 'Odeska 162') / 'Ukrainka Odeska^{2r} / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska') / 'Nikoniia'	8 ± 0.38	8 ± 0.35	5 ± 0.03
Lutescens 64/16	(('Kupava' / *Lutescens* 367/08) / ('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Odeska Napivkarlykova')) / 'Kiriia'	5 ± 0.01	8 ± 0.35	4 ± 0.37
Erythrospermum 72/16	(*Erythrospermum* 5/253-06 / ('Kuialnyk' / MA1*)) / (('Skarbnytsia Odeska^{2r}') / *Erythrospermum* 120/06) / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska') / 'Nikoniia'	9 ± 0.02	5 ± 0.40	8 ± 0.38
Lutescens 112/16	(('Guebon' / 'Kuyalnyk') / *Erythrospermum* 317/06) / (('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Odeska Napivkarlykova') / 'Kiriia'	9 ± 0.38	5 ± 0.35	8 ± 0.37
Erythrospermum 114/16	(('Guebon' / 'Kuialnyk') / *Erythrospermum* 184/06) / ((*Erythrospermum* 5/55-91 / ('Odeska Napivkarlykova' / *Aegilops cylindrica*)) / 'Odeska Napivkarlykova') / *Lutescens* 23397	8 ± 0.01	5 ± 0.01	8 ± 0.02
Erythrospermum 116/16	(('Guebon' / 'Kuialnyk') / *Erythrospermum* 184/06) / ((*Erythrospermum* 5/55-91 / ('Odeska Napivkarlykova' / *Aegilops cylindrica*)) / 'Odeska Napivkarlykova') / *Lutescens* 23397	9 ± 0.36	5 ± 0.35	9 ± 0.32
Erythrospermum 120/16	(('Kniahynia Olha' / *Erythrospermum* 350/06) / (('Obrii' / *Triticum erebuni* / 'Odeska 162')) / 'Ukrainka Odeska^{2r}/ 'Selianka'	8 ± 0.50	5 ± 0.02	4 ± 0.38
Erythrospermum 129/16	(('Kniahynia Olha' / *Erythrospermum* 350/06) / (('Obrii' / *Triticum erebuni*) / 'Odeska 162')) / 'Ukrainka Odeska^{2r} / 'Selianka'	9 ± 0.03	8 ± 0.10	4 ± 0.02
Erythrospermum 130/16	(('Kniahynia Olha' / *Erythrospermum* 350/06) / (('Obrii' / *Triticum erebuni*) / 'Odeska 162')) / 'Ukrainka Odeska^{2r} / 'Selianka'	8 ± 0.50	8 ± 0.37	4 ± 0.38
Erythrospermum 135/16	((('Obrii' / *Triticum erebuni*) / 'Odeska 162') / 'Odeska Napivkarlykova') / 'Antonivka' / 'Amigo'	8 ± 0.00	8 ± 0.38	5 ± 0.00

Continuation table1

Breeding line	Pedigree	Disease resistance, score		
		Leaf rust	Stem rust	Powdery mildew
Erythrospermum 142/16	('Vykhovanka Odeska' / *Erythrospermum* 137/06) / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	8 ± 0.50	8 ± 0.39	4 ± 0.36
Erythrospermum 145/16	('Vykhovanka Odeska' / (*Erythrospermum* 5/258-06 / ('Kuialnyk' / MA1)))	5 ± 0.38	8 ± 0.34	8 ± 0.35
Lutescens 148/16	[RI17091* / Bu1*] / 'Albatros Odeskyi'] / [F13021-12* / 'Ukrainka Odeska']] / (('Donezka Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	9 ± 0.01	4 ± 0.38	9 ± 0.03
Erythrospermum 154/16	(*Erythrospermum* 5/253-06 / ('Kuialnik' / MA1)) / (('Skarbnytsa Odeska²ʳ') / *Erythrospermum* 120/06) / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska') / 'Nikoniia'	8 ± 0.02	4 ± 0.04	4 ± 0.01
Erythrospermum 192/16	(*Erythrospermum* 5/253-06 / ('Kuialnyk' / MA1)) / 'Antonivka' / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska ') / 'Nikoniia'	8 ± 0.01	4 ± 0.03	8 ± 0.32
Erythrospermum 200/16	(('Guebon' / 'Kuialnyk') / *Erythrospermum* 184/06) / ((*Erythrospermum* 5/55-91 / ('Odeska Napivkarlykova' / *Aegilops cylindrica*)) / 'Odeska Napivkarlykova') / *Lutescens* 23397	8 ± 0.37	5 ± 0.01	8 ± 0.38
Erythrospermum 200/16	(('Kupava' / *Erythrospermum* 367/08) / (('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Odeska Napivkarlykova')) / 'Kiriia'	4 ± 0.02	8 ± 0.39	4 ± 0.38
Erythrospermum 57/12	(('Volynska Napivintensyvna' / *Erythrospermum* 186/06) / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	8 ± 0.38	9 ± 0.01	9 ± 0.41
Erythrospermum 2/14	('*Amphidipliod* 4' / 'Albatros²ʳ') / (('Odeska Napivkarlykova' / *Aegilops cylindrica*) / 'Odeska Napivkarlykova') / 'Tira' / 'Amigo'	9 ± 0.01	8 ± 0.37	8 ± 0.38
Erythrospermum 43/14	(('Kupava' / *Erythrospermum* 367/08) / (('Odeska Napivkarlykova' / *Aegilops cylindrica)* / 'Odeska Napivkarlykova')) / 'Kiriia'	9 ± 0.37	8 ± 0.36	9 ± 0.35
Erythrospermum 67/14	(('Raduza' / *Erythrospermum* 138/06) / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	9 ± 0.38	8 ± 0.37	9 ± 0.35
Erythrospermum 100/14	(('Odeska Napivkarlykova' / *Aegilops cylindrica*) / (Bt 12,13*) / 'Poshana' / 'Kiriia' / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	8 ± 0.38	8 ± 0.01	8 ± 0.00
Erythrospermum 70/19	((*Erythrospermum* 5/176-06 / ('Kuialnyk' / MA1)) / (*Erythrospermum* 156/06 / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia' / ((*Erythrospermum* 5/55-91 / 'Odeska Napivkarlykova') / *Lutescens* 23397 / (('Donetska Napivkarlykova' / *Aegilops variabilis*) / 'Ukrainka Odeska')) / 'Nikoniia'	9 ± 0.37	8 ± 0.40	8 ± 0.38
'Odeska Napivkarlykova'	*Erythrospermum* 903/74 / ('Krasnodarskyi Karlyk 1' / 'Odeska 51')	2 ± 0.01	1 ± 0.01	2 ± 0.38

Note. RI17091, Bu1, F13021-12, MA1, Bt 12,13 – original names of collection specimens; 'Albatros Odeskyi²ʳ', 'Ukrainka Odeska²ʳ' – second backcross.

Analysis of this material revealed that wheat genotypes exhibited varying levels of resistance to local races of rust (leaf and stem) and powdery mildew. These levels ranged from moderately susceptible (4–5 points) to highly resistant (8–9 points) (Figure).

Indeed, the largest proportion (33%) of the material under study consisted of genotypes that exhibited high resistance to leaf rust and powdery mildew pathogens under complex infection conditions. Twenty-six per cent of the lines (*Er.* 4/16, *Er.* 47/16, *Er.* 53/16, *Er.* 129/16, *Er.* 130/16, *Er.* 135/16) exhibited high resistance to rust species (scores of 8–9), but were affected by powdery mildew (scores of 4–5). Group resistance to all the studied leaf and stem diseases was observed in 22% of the lines (*Er.* 57/12, *Er.* 43/14, *Er.* 2/14, *Er.* 70/19, *Er.* 67/14, *Er.* 15/14). During extended testing under artificial infection conditions, these lines demonstrated resistance

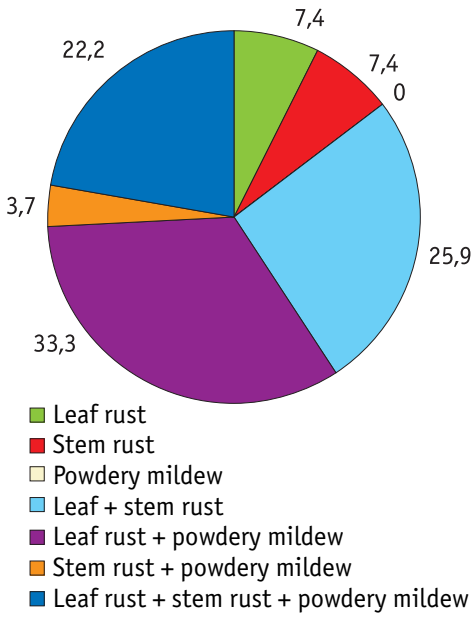

Fig. Percentage of genotypes resistant to individual pathogens and their groups (2019/20–2022/23)

to the studied pathogens at a level of 8–9 points, and they may therefore be valuable sources of effective *Lr*-, *Sr*-, and *Pm*-genes for breeding (Table 2).

Table 2

Assessment of the resistance of selected wheat lines to major disease pathogens (2020/21–2022/23)

Line Name	Leaf rust	Stem rust	Powdery mildew
Erythrospermum 57/12	8 ± 0.35	8 ± 0.39	8 ± 0.39
Erythrospermum 43/14	8 ± 0.01	8 ± 0.35	8 ± 0.41
Erythrospermum 67/14	8 ± 0.02	9 ± 0.37	6 ± 0.40
Erythrospermum 2/14	8 ± 0.38	8 ± 0.40	8 ± 0.38
Erythrospermum 15/14	8 ± 0.36	9 ± 0.01	7 ± 0.38
Erythrospermum 70/19	8 ± 0.32	8 ± 0.02	8 ± 0.01
'Kuialnyk' – Standard	5 ± 0.01	5 ± 0.02	5 ± 0.01

It should be noted that the consistently high level of resistance to leaf and stem diseases in the selected genotypes was due to the presence of a complex of active genes controlling this trait, which were derived from the wild relatives of wheat. The presence of these genes was confirmed by PCR analysis (Table 3).

Notably, a significant proportion of the examined lines were found to be sources of the highly effective resistance genes *Lr24* and *Sr24*, which originate from *Thinopyrum elongatum*. Additionally, genes *Lr26* + *Lr34*, *Lr26* + *Lr21*, *Sr31*, *Pm17*, and Sr^{Amigo} were identified in *Triticosecale* and *Triticum erebuni*. The most effective genes were *Lr24*, *Lr68*, *Sr15*, *Sr31*, *Sr58* and *Pm38*, as well as their combinations. The

Table 3

Identification of effective resistance genes and their groups in the genotypes of introgressive lines selected during the study (2021–2023)

Breeding line	% Homogenies	Genes
Erythrospermum 57/12	1 (≈ 90%)	*Lr21 + Lr24 + Lr^{Amigo}, Sr24 + Sr^{Amigo}, Pm17*
Erythrospermum 43/14	1 (≈ 90%)	*Lr21 + Lr24 + Lr68 + Lr^{Amigo}, Sr24 + Sr^{Amigo}, Pm17*
Erythrospermum 67/14	1 (≈ 90%)	*Lr10 + Lr26 + Lr34 + Lr68, Sr31 + Sr58, Pm3 + Pm8 + Pm38*
Erythrospermum 2/14	1 (≈ 90%)	*Lr10 + Lr20 + Lr21 + Lr26 + Lr68, Sr15 + Sr31, Pm1 + Pm3 + Pm8; Yr9*
Erythrospermum 15/14	1 (> 80%)	*Lr10 + Lr24 + Lr68, Sr24, Pm3*
Erythrospermum 70/19	1 (≈ 90%)	*Lr10 + Lr20 + Lr26 + Lr34 + Lr68, Sr15 + Sr31 + Sr58, Pm1 + Pm3 + Pm38; Yr9 + Yr18, Bdv1*

presence of these genes in the genotypes of the studied lines ensured a consistently high level of resistance to the investigated diseases under artificially created, complex infection conditions throughout the entire growing season.

The study examined the impact of introgressive lines on enhancing the genetically determined level of group resistance to leaf and stem diseases in winter wheat. This was conducted using hybrid material derived from straightforward crosses of parental components that exhibited varying levels of the trait under investigation (Table 4). The resistance of the F_1 hybrids and F_2 populations to these diseases was evaluated in the laboratory for resistance to brown rust and powdery mildew, and in the field for resistance to stem rust, against the infectious background of local races of the studied pathogens.

Through hybrid analysis, we established the inheritance pattern of the trait, the types of gene interaction and the degree of phenotypic dominance.

Analysis of the first generation of hybrids revealed a high level of resistance to leaf and stem pathogens among the studied crossing combinations. This suggests that resistance is controlled by dominant *Lr*-, *Sr*-, and *Pm*-genes.

In the second generation of populations, crossing lines with susceptible varieties such as 'Vatazhok', 'Zysk', 'Odeska Napivkarlykova' and 'Victoria Odeska' produced a reliable correspondence (χ^2 = 0–1.33) between the number of resistant and susceptible plants and the theoretically expected ratio of 9:7. This indicates the action of two dominant complementary *Lr*-, *Sr*-, and *Pm*-genes.

Thus, by utilizing resistance genes from the wild relatives of wheat through interspecific crossbreeding, it is possible to obtain source material for selecting winter bread wheat with complex resistance to the aforementioned pathogens featuring effective resistance genes that control this trait.

A balanced combination of the genetically determined level of resistance to major leaf- and stem-pathogens and a complex of valuable agricultural traits is an important element in creating new breeding material. These traits form the basis for the competitiveness of new varieties.

Therefore, one of the tasks set during the study of the selected genotypes was to determine the genetic productivity level and baking properties of the grain and flour.

The average yield indicators of the introgressive material are presented in Table 5.

The analysis of average yield revealed that the selected lines, based on their group resistance to leaf pathogens, can be effective sources of high productivity, regardless of the infection load during the cultivation period. Under conditions of natural infection, the average productivity of the aforementioned genotypes ranged from 6.0 to

Table 4

The nature of inheritance of resistance to leaf-stem diseases in hybrid F_1–F_2 populations involving introgressive lines with effective resistance genes (2020/21–2021/22)

	F_1 Characteristics			Ratio of Resistant and Susceptible Phenotypes in the F_2 Population						χ^2		
				Actual			Theoretical					
	Leaf rust	Stem rust	Powdery mildew	Leaf rust	Stem rust	Powdery mildew	Leaf rust	Stem rust	Powdery mildew	Leaf rust	Stem rust	Powdery mildew
Erythrospermum 57/12 / 'Vatazhok'	R	R	0	89:61	91:59	50:35	9:7	9:7	9:7	0.58	1.19	0.23
Erythrospermum 57/12 / 'Viktoriia Odeska'	R	R	R	87:63	87:63	309:217	9:7	9:7	9:7	0.19	0.19	1.33
Erythrospermum 43/14 / 'Luzanivka'	R	R	VR	90:60	90:60	86:64	9:7	9:7	9:7	0.86	0.86	0.07
Erythrospermum 70/14 / 'Odeska Napivkarlykova'	R	R	0	86:62	89:59	74:52	9:7	9:7	9:7	0.21	0.91	0.32
Erythrospermum 2/14 / 'Kuialnyk'	R	R	MR	87:63	88:62	87:63	9:7	9:7	9:7	0.19	0.36	0.14
Erythrospermum 67/14 / 'Odeska Napivkarlykova'	R	R	0	85:58	89:62	74:52	9:7	9:7	9:7	0.2	0.8	0.32
Erythrospermum 100/14 / 'Viktoriia Odeska'	R	R	0	83:60	90:61	56:37	9:7	9:7	9:7	0.2	0.9	0.2

Note. Reaction type: 0 – very high resistance, VR – very resistance, R – resistance, MR – moderate resistance.

Table 5

Yield of lines with group resistance to leaf-stem diseases under different infection backgrounds (2020/21–2022/23)

Breeding line	Yield					
	Natural infectious background			Artificial infectious background		
	t/ha	± up to St		t/ha	± up to St	
		t/ha	%		t/ha	%
Erythrospermum 57/12	7.41	0.46	6.20	6.51	1.93	29.61
Erythrospermum 43/14	6.28	–0.66	–10.51	6.22	1.64	26.40
Erythrospermum 67/14	7.62	0.66	8.70	7.49	2.91	38.91
Erythrospermum 2/14	6.22	–0.72	–11.60	6.03	1.45	24.01
Erythrospermum 15/14	6.01	–0.94	–15.72	5.40	0.82	15.20
Erythrospermum 70/19	6.36	–0.58	–9.10	5.34	0.76	14.20
'Kuialnyk' – Standard	6.94	–	–	4.58	–	–
$LSD_{0.05}$	0.33	–	–	0.24	–	–

7.6 t/ha, deviating slightly from the standard 'Kuialnyk' (6.9 t/ha), either increasing or decreasing this indicator. Specifically, some lines showed a significant yield increase of 0.5–0.7 t/ha (lines *Er.* 57/12 and *Er.* 43/14), while four of the genotypes studied (*Er.* 96/14, *Er.* 67/14, *Er.* 2/14 and *Er.* 15/14) produced yields 0.5–0.9 t/ha lower than the standard. The *Er.* 70/19 had a productivity level equal to the standard (6.9 t/ha).

Under conditions of artificial epiphytotic outbreaks of the pathogens of the aforementioned diseases, the yield of the standard variety 'Kuialnyk' decreased significantly from 6.9 t/ha to 4.6 t/ha (see Table 5), resulting in a 34% overall loss in gross harvest. In contrast, despite the presence of infection pressure, the lines with group resistance almost did not reduce their productivity level, with the yield increase compared to the standard varying from 0.7 t/ha (13.2%) to 2.9 t/ha (38.7%). These data convincingly demonstrate that introducing introgressive lines into winter wheat breeding programmes with a focus on group resistance to leaf phytopathogens can significantly stabilise the yield of high-quality grain, regardless of growing conditions.

Analysis of the main quality indicators showed that, in the absence of high infection pressure, the selected lines can produce grain of a quality comparable to that of strong, valuable wheat. In particular, the specific weight and mass of 1000 seeds of the presented material corresponded to the 1st class wheat standard (DSTU 3768:2019 "Wheat. Specifications" [24]). The *Er.* 43/14 and *Er.* 70/19 were particularly valuable in this respect, with specific weights of 800 g/l and 1000-seed weight of 43.7 g and 41.9 g, respectively (Table 6).

A significant proportion of the genotypes studied in terms of their baking properties were of a high quality, with values that varied within

Table 6

Baking properties of grain and flour in winter wheat lines selected during the research (2020/21–2022/23)

Line name	Weight of grain in 1 litre, g/l	1000-grain weight, g	Protein content %	SDS 30, ml	Bread volume, ml	Overall bread score, points
Erythrospermum 57/12	782 ± 0.67	36.9 ± 0.04	10.5 ± 0.22	82 ± 0.45	1260 ± 0.67	4.3 ± 0.04
Erythrospermum 43/14	800 ± 1.32	43.7 ± 0.08	11.9 ± 0.04	89 ± 0.43	1400 ± 0.69	4.9 ± 0.07
Erythrospermum 67/14	777 ± 1.67	36.8 ± 0.09	10.4 ± 0.08	78 ± 0.67	1180 ± 0.42	3.6 ± 0.11
Erythrospermum 2/14	777 ± 0.42	36.2 ± 0.04	10.6 ± 0.04	87 ± 0.69	1340 ± 0.68	4.2 ± 0.06
Erythrospermum 15/14	782 ± 1.56	40.0 ± 0.06	10.6 ± 0.12	68 ± 0.67	1040 ± 0.87	3.2 ± 0.10
Erythrospermum 70/19	800 ± 0.67	41.9 ± 0.07	10.8 ± 0.09	77 ± 0.89	1120 ± 0.67	3.4 ± 0.13
'Kuialnyk' – Standard	785 ± 1.32	40.2 ± 0.11	11.5 ± 0.10	81 ± 0.67	1350 ± 0.44	4.6 ± 0.12

relatively narrow limits (protein content: 10.4–10.8%; sedimentation: 77–87 ml; bread volume: 1040–1340 ml; total baking score: 3.2–4.3 points). The exception was line *Er*. 43/14, which stood out due to its high protein content (11.9%) and its excellent baking properties: bread volume (1400 ml) and total baking score (4.9 points). This increases its breeding value as a genetic source.

Conclusions

The introgressive lines with group resistance to diseases that were created can be effective donors for selecting winter bread wheat for this trait. This source material exhibits a high level of resistance due to the action of genes (*Lr24*, *Lr68*, *Sr15*, *Sr31*, *Sr58* and *Pm38*), which control this trait and were transferred to the wheat genotype from the wild relatives *Thinopyrum elongatum*, *Triticosecale*, and *Tr. erebuni*. The presence of these genes was identified using PCR analysis.

The study of the patterns of inheritance of group resistance in F_1–F_2 hybrid material, obtained by crossing the studied lines *Erythrospermum* 57/12, *Er*. 43/14, *Er*. 2/14, *Er*. 15/14, and *Er*. 70/19 with susceptible varieties of local breeding, showed the dominant nature of inheritance of this trait, which is determined by the action of two complementary genes.

The experimental lines are characterized by consistently high productivity, with yields 13.2–37.8% higher than the standards regardless of the infection load level. Due to the presence of genes from wild wheat relatives in the genotypes of the lines, this material's baking properties met the standard requirements for valuable wheat. This is the case except for the *Er*. 43/14, which is equivalent to high-quality wheat in terms of grain and flour quality, with a protein content of 11.9%, a bread volume of 1400 ml and an overall baking score of 4.9 points.

The resulting source material combines a high level of group resistance to leaf-stem pathogens with a range of economically valuable traits, making it valuable breeding material. These lines have been included as parental components in the crossbreeding plans of the PBGI – NCSCI and transferred to leading scientific breeding centers within the NAAS system of Ukraine for use in breeding programs.

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Голуб Є. А.*, Сауляк Н. І., Васильєв О. А., Литвиненко М. А., Трасковецька В. А., Щербина З. В., Бушулян М. А., Кірчук Є. І. Характеристика вихідного матеріалу для селекції пшениці озимої на групову стійкість проти збудників листостеблових хвороб. *Plant Varieties Studying and Protection*. 2025. Т. 21, № 1. С. 17-24. https://doi.org/10.21498/2518-1017.21.1.2025.327497

*Селекційно-генетичний інститут – Національний центр насіннєзнавства та сортовивчення, вул. Овідіопольська дорога, 3, м. Одеса, 65036, Україна, *e-mail: eva.golub.1979@ukr.net*

Мета. Дослідити ефективність використання інтрогресивних ліній як вихідного матеріалу з груповою стійкістю проти листкових патогенів у процесі селекції пшениці озимої (*Triticum aestivum* L.) за вказаною ознакою. **Методи.** Польовий, лабораторний (оцінювання стійкості проти окремих рас листкової іржі та борошнистої роси на ювенільному етапі росту в тепличних умовах і під світловими конструкціями), ПЛР-аналіз (ідентифікація генів стійкості проти вказаних хвороб у досліджуваному матеріалі), статистичний, аналізувальне схрещування (вивчення закономірностей успадкування та взаємодії генів стійкості). **Результати.** Оригінальні селекційні лінії різних поколінь (F_4–F_5), створені на генетичній основі дикорослих родичів пшениці *Aegilops cylindrica*, *Ae. variabilis*, *Triticum ventricosum*, *Tr. erebuni*, *Tr. tauschi*, *Thinopyrum elongatum*, *Triticosecale*, досліджено в СГІ – НЦНС за основними агрономічними ознаками та ознакою групової стійкості проти локальних популяцій листостеблових хвороб. Шість ліній, що містять ефективні гени групової стійкості (*Lr24*, *Lr68*, *Sr15*, *Sr31*, *Sr58*, *Pm38*) та їхні комбінації, виявилися стабільно стійкими проти листостеблових патогенів, продемонструвавши високу якість зерна та продуктивність незалежно від рівня інфекційного навантаження. Генетичну основу групової стійкості розглянуто на F_1–F_2 гібридному матеріалі, отриманому внаслідок схрещування досліджуваних ліній зі сприйнятливими місцевими сортами. Установлено, що характер успадкування вказаної ознаки визначається дією двох домінантних комплементарних генів, що свідчить про можливість застосування цього матеріалу як донора високої стійкості. **Висновки.** За результатами досліджень одержано вихідний матеріал – шість ліній пшениці озимої, що ефективно поєднують у генотипі високий рівень групової стійкості проти листкових патогенів і набір основних агрономічних ознак, а тому є цінним генетичним матеріалом. Ці лінії (як батьківські компоненти) включено до планів схрещування СГІ – НЦНС та передано до провідних наукових селекційних центрів НААН України для використання у селекційних програмах.

Ключові слова: *пшениця озима; групова стійкість; гени стійкості; хвороби листя та стебла; продуктивність.*

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