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The degree of dominance of resistance trait against pathogens in F_1 winter wheat

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Abstract. One of the most effective and at the same time environmentally friendly measures of integrated protection of wheat against diseases is the development of resistant varieties through breeding adapted to specific agroclimatic conditions. The purpose of the present study was the phytopathological evaluation of winter wheat collection samples on artificial infection backgrounds

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in the field and to determine the dominance of resistance of F_1 hybrids to *Puccinia recondita* and *Tilletia caries*. The study was conducted during 2023, 2024 in a selection crop rotation on natural and artificial infection backgrounds and in the laboratory of the winter wheat breeding laboratory of the V.M. Remeslo Myronivka Institute of Wheat of the National Academy of Agrarian Sciences of Ukraine according to generally accepted methods. 189 collection numbers of winter wheat were studied against artificial infectious backgrounds of brown rust and stinking smut. The study found that the varieties protected by resistance genes Arthur 71 (*Lr9*), McNair 2203 (*Lr9*), Agrus (*Lr19*), Century (*Lr24 + Lr42*), TAM-200 (*Lr24 + Lr43*), V1275 (*Lr19*), VR89Bo22 (*Lr19*) were immune to the pathogen *Puccinia recondita*; immunity to *Tilletia caries* was reflected by winter wheat varieties Rada (SVK), Famulus (DEU), SHARK/F4. 105W21 (USA), Reia (UKR), Eksprompt, Erythrospermum 24210, and Line 46 (UKR). When studying the composition of the population of *Puccinia recondita*, it was found that the average efficiency was shown by genes *Lr10*, *Lr13*, *Lr25*, and *Lr34* (gene of age resistance) at the 5-10% degree of damage to the lines. The genes *Lr9* and *Lr19* stably maintained strong resistance and continued to be highly effective. In terms of resistance to *Puccinia recondita*, superdominance (heterosis) was found in five (14.72% of the total number of hybrid combinations) hybrid combinations Beres/Blueboy II, Beres/TAM-200, Matuo/TAM-200, Tobarzo/TAM-200, Matuo/Blueboy II. It was noted that the local population of the pathogen *Tilletia caries* is avirulent or slightly virulent to resistance genes: Bt6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21. The study of the genetics of resistance to this disease showed that among F_1 hybrid combinations, 41.63% showed partial positive dominance (PPD). No overdominance to the pathogen of stinking smut was found

Keywords: brown rust; resistance gene; variety; line; stinking smut of wheat; background

Introduction

Development of high-yielding varieties of soft winter wheat *Triticum aestivum* L. is a major task of modern breeding. These varieties should be capable of demonstrating maximum grain yields, effectively utilising their genetic potential in various agroecological conditions. At the same time, minimising the gap between biological (potential) and economic (actual) productivity caused by adverse biotic factors continues to be a vital task. Fungal diseases are a substantial source of crop losses, which can reach 15-50% depending on the virulence of the pathogen and specific weather conditions. These diseases have a particularly strong impact on wheat varieties susceptible to them, causing severe damage to producers (Topko *et al.*, 2021; Kayim *et al.*, 2022). M. Lunzer *et al.* (2023) noted that among the common and harmful diseases of wheat, the most significant are powdery mildew (*Erysiphe graminis* DC. f. sp. *tritici* Em. Marchal), stinking smut (*Tilletia caries*

Tul.), brown rust (*Puccinia recondita* Rob. et Desm. f. sp. *tritici* Eriks.), and leaf septoriosiis (*Septoria tritici* Rob. et Desm.). L.A. Murashko *et al.* (2022) noted that in certain epiphytotic years in Ukraine, crop damage led to a decrease in yield by 25-30% or more.

A.G. Bashlay & V.A. Vlasenko (2020) noted that *Tilletia caries*, which causes the emergence of a black mass instead of grain, reduces seed germination and crop density due to the death of affected plants, is most evident in late winter crops and early spring wheat crops. E. Ritzer *et al.* (2021) identified several specialised forms of smut that affect only some wheat species: *Tilletia vulgaris* – affects *Triticum aestivum* (*vulgare*), weakly – *Triticum compactum* and very weakly – *Triticum durum*, *Triticum dicoccum*, *Triticum monococcum*, and *Triticum timopheevi*; *Tilletia dicaccus* – affects *Triticum diccicum*, *Triticum aestivum*. The pathogen *Puccinia recondita* is an obligate parasite capable of forming infectious urediniospores, provided that

the affected leaf tissues stay viable. T. Krępski *et al.* (2024) found that uredinospores are dispersed by air currents, infecting host plants even at considerable distances, which can reach hundreds of kilometres from the initial focus.

O.E. Markovska *et al.* (2021) found that brown leaf rust, caused by the fungus *Puccinia recondita* f. sp. tritici Rob. ex Desm, is the most widespread rust disease affecting wheat. Under Ukrainian conditions, the pathogen develops according to a shortened vegetation cycle with the involvement of plants of the genus *Thalictrum* spp. as an intermediate host. N.I. Sauliak *et al.* (2024) proved that this disease most intensively affects the leaves of winter wheat, and less often its leaf sheaths and stems. A. Palamarchuk *et al.* (2018) noted that the pathogen overwinters as a mycelium, whose spores can effectively withstand low temperatures during the winter period.

The study of the heritability of wheat resistance to certain diseases is a key task of breeding. M.O. Samoilik (2024) found that breeding experts annually review and update the list of genotypes used as basic material for further selection. The data on the resistance of these genotypes to various diseases has a dual significance: it not only contributes to solving current practical problems in the field of breeding but also serves as a key tool for predicting its effectiveness in the longer term. It is the systematic analysis and use of such data that ensures the development of varieties that can meet the growing demands of agronomy and successfully adapt to new environmental challenges.

According to H. Lisova *et al.* (2023), data on the donor properties of individual varieties that are used once, repeatedly, or permanently as parental forms are particularly valuable. This information, as well as information on the structural composition of existing hybrid populations in terms of their resistance or susceptibility to various diseases, including *Puccinia recondita* and *Tilletia caries*, can substantially contribute to the efficiency of breeding resistant winter durum wheat varieties.

The purpose of the present study was to conduct phytopathological evaluation of winter soft wheat collection samples under artificial infection load caused by pathogens in the field environment. Furthermore, the task was to determine the level of dominance of resistance to *Puccinia recondita* and *Tilletia caries* in first-generation hybrids under artificial infection with pathogens.

Materials and Methods

Experimental studies were conducted during 2023-2024 in breeding crop rotations on a natural background, artificial infection environment, and in laboratory conditions. The study was conducted at the Winter Wheat Breeding Laboratory of the V.M. Remeslo Myronivka Institute of Wheat of the National Academy of Agrarian Sciences of Ukraine (MIW). To achieve maximum efficiency in fulfilling productivity objectives and optimising the selection and accounting processes, a sparse sowing method was used. Specifically, the intervals between plants in a row were 5 cm, the inter-row distance was 30 cm, and the length of each row was 1 metre. The object of research included collection samples of winter bread wheat obtained from the National Centre of Plant Genetic Resources of Ukraine and other breeding centres. In the collection nurseries, 189 collection accessions of winter soft wheat were studied using artificial infectious backgrounds of *Puccinia recondita* and *Tilletia caries*. The artificial infection background of the brown rust pathogen was used to study 78 collection samples. The composition of the *Puccinia recondita* population was studied on a series of isogenic lines of spring wheat variety Thatcher. In the collection nursery of resistant forms to *Tilletia caries*, 111 cultivar samples were studied.

In August and November 2023, the average monthly air temperatures exceeded the long-term average by 1.2° C and 1.7°C, respectively, while in September and October they were lower by 1.6°C and 0.5°C, respectively, which contributed to the development of stinking smut. Excessive precipitation during this period (84.4 mm

in August and 117.5 mm in September) led to waterlogging of the topsoil. In 2022, winter wheat plants stopped growing on 15 November at an average daily air temperature of +4.0°C, which gradually decreased to 3.8°C (16.11); 1°C (17.11); -0.6°C (18.11). In November, there was 80.9 mm of precipitation, which was 40.8 mm greater than the long-term average. The resumption of winter crops vegetation in 2024 was noted on 21 March at an average daily air temperature of +9.0°C with a subsequent gradual increase. In the spring-summer wheat growing season, the average monthly temperatures were 0.5-0.2°C below the long-term average, with only 0.4°C higher in June.

In April, an excessive moisture supply was observed, the excess of precipitation from the norm was 40.0 mm, which contributed to the growth of brown rust, and then during the period from May to June a rather acute shortage of precipitation was observed, especially in May – only 21.0 mm (the long-term average was 51.4 mm). The spring (April-June) period favoured the development of the brown rust pathogen. Accordingly, the level of hydrothermal coefficient (HTC) was low: April – 0.89, May – 0.46, June – 0.67. Winter wheat was infected with the pathogen *Puccinia recondita* in the booting phase of the plant according to the method (Babayants & Babayants, 2014). To create an artificial infection background, the local population of the pathogen was used, and the Myronivska 10 cultivar was used as an infection accumulator.

The artificial infection background of *Tilletia caries* was created according to the method of seed inoculation a few days before sowing. The Polka cultivar (HUN) was used as a susceptible variety, and sowing was conducted in the beginning of the first decade of October (Demidov *et al.*, 2023). The resistance of winter wheat plants to pathogens was assessed according to generally accepted methods (Tribel *et al.*, 2010; Demidov *et al.*, 2023). The degree of phenotypic dominance in hybrid combinations for this quantitative trait was calculated according to the following formula (Griffing, 1950):

$$h_p = (F_1 - MP)/(BP - MP), \quad (1)$$

where h_p is the degree of dominance, F_1 is the average value of the indicator for first generation hybrids, MP is the average value of the indicator for both parental forms, BP is the average value of the parental form with a more pronounced development of the trait. The value of the degree of dominance (h_p) can range from $-\infty$ to $+\infty$ (Tribel *et al.*, 2010). For ease of analysis, the data were classified according to the scale (Beil & Atkins, 1963):

- positive overdominance (heterosis) (PD) ($h_p > +1$),
- partial positive dominance (PPD) ($+0.5 < h_p \leq +1$),
- intermediate inheritance (II) ($-0.5 \leq h_p \leq +0.5$),
- partial negative inheritance (PNI) ($-1 \leq h_p < -0.5$),
- negative dominance (depression) (ND) ($h_p < -1$).

The study was conducted following the Convention on Biological Diversity (1992). The study included an analysis of the presence of effective resistance genes and their role in the formation of plant immunity. Genetic control of resistance was determined using a series of crosses and assessment of phenotypic dominance of the trait.

Results

The average development of *Puccinia recondita* over two years was 15.9%, and the development of the pathogen ranged within 0-80%. The varieties protected by the known resistance genes Arthur 71 (*Lr9*), McNair 2203 (*Lr9*), Agrus (*Lr19*) Century (*Lr24 + Lr42*), TAM-200 (*Lr24 + Lr43*), V1275 (*Lr19*) (USA), VR89Bo22 (*Lr19*) (FRA) were immune to brown rust (Table 1). High resistance (2-5%) against brown rust was found in 24 (30.8%) samples: Osage (2%), Agrus (3%), Blue-boy II (5%) (USA), Bu 22 (CZE), and others.

The genes *Lr10*, *Lr13*, *Lr25*, and *Lr34* (age resistance gene) showed average efficiency – the degree of damage to the lines was 5-10%. The genes *Lr9* and *Lr19* stayed stable and highly effective (Table 2). The resistance genes found in winter wheat varieties showed high efficiency: Rendezvous (*Lr37*) (ANG), Century (*Lr42*), TAM-200 (*Lr43*), Arthur-71, McNair 2203, Flex (USA), VR89Bo 22 (CZE), and others.

Table 1. Donors of resistance against *Puccinia recondita* with known resistance genes

Sample	Origin	Resistance genes	Damage intensity, %
Myronivska 10 (vulnerable cultivar)	UKR	-	80
Arthur 71	USA	<i>Lr9</i>	0
McNair 2203	USA	<i>Lr9</i>	0
Agrus	USA	<i>Lr19</i>	3
Flex	USA	<i>Lr19</i>	0
V1275	USA	<i>Lr19</i>	0.5
Osage	USA	<i>Lr24</i>	2
Blueboy II	USA	<i>Lr10, Lr24</i>	5
VR89Bo22	FRA	<i>Lr19</i>	0
Rendezvous	ANG	<i>Lr37</i>	0
Bu 22	CZE	<i>Lr3, Lr26</i>	5
203-238	BOL	<i>Lr9, Lr26</i>	0
Century	USA	<i>Lr42+Lr24</i>	0
TAM-200	USA	<i>Lr43+Lr24</i>	0

Source: developed by the authors of this study

Table 2. Intensity of *Puccinia recondita* *Lr* infection in spring wheat Thatcher series lines

Line series resistance gene	Type of seedling immunity in laboratory conditions, %	Degree of damage in the field phase of milk ripeness, %
<i>Lr1</i>	0.5	8.5
<i>Lr2a</i>	0	45.1
<i>Lr2c</i>	0	50.7
<i>Lr3</i>	0	51.2
<i>Lr3bg</i>	1	15.4
<i>Lr3ka</i>	0.5	25.1
<i>Lr9</i>	1	45.7
<i>Lr10</i>	1	40.6
<i>Lr11</i>	0.5	50.5
<i>Lr12</i>	0.5	0
<i>Lr13</i>	1	52.1
<i>Lr14</i>	0.5	50.9
<i>Lr14a</i>	0.5	62.1
<i>Lr14b</i>	0	60.3
<i>Lr19</i>	0	46.1
<i>Lr23</i>	0.5	63.4
<i>Lr24</i>	0	53.7
<i>Lr25</i>	1	8.1
<i>Lr26</i>	0	60.5
<i>Lr29</i>	0.5	63.8
<i>Lr30</i>	0	46.1
<i>Lr32</i>	1	45.3
<i>Lr34</i>	0	40.7
<i>LrEch</i>	0	8.2

Source: developed by the authors of this study

The following genes were found to be ineffective: *Lr1, Lr2a, Lr2c, Lr3, Lr3bg, Lr3ka, Lr11, Lr12, Lr14, Lr14a, Lr14b, Lr23, Lr26, Lr29, Lr30, Lr32, LrEch*. The degree of damage to Thatcher

lines with the above genes in the years of study was 15-60%. To investigate the genetic control of resistance traits against *Puccinia recondita* and *Tilletia caries* in winter wheat varieties, a series of crosses was conducted in 2023. To determine the genetics of the resistance trait in a series of sources of resistance to *Puccinia recondita* (Beres,

Matyo, Tobarzo, Polka), a series of crosses were conducted: donors with the vulnerable cultivar Myronivska 65, donors with each other and test varieties carrying effective resistance genes Arthur 71 (*Lr9*), Flex (*Lr19*), Blueboy II (*Lr10*, *Lr24*), Century (*Lr24+Lr42*), TAM 200 (*Lr24+Lr43*) (USA), Rendezvous (*Lr 37*) (ANG) (Table 3).

Table 3. The degree of phenotypic dominance of resistance trait against *Puccinia recondita* in F_2 , 2024

Cross	Intensity of plant damage, %			Degree of phenotypic dominance (h_p)/type of dominance
	♀	F_1	♂	
Beres / MYR 65	0	1.0	40.0	0.95 / PPD
Matuo / MYR 65	0	10.0	35.0	0.4 / II
Tobarzo / MYR 65	0	8.0	30.0	0.5 / PPD
Polka / MYR 65	1.0	30.0	40.0	-0.48 / II
Beres / Matuo	0	0.5	0.5	-1.3 / D
Beres / Tobarzo	0	1.0	0	0.15 / II
Beres / Polka	0	2.0	0	0.35 / II
Beres / Arthur-71	0	1.0	0	0.45 / II
Beres / Fleks	0	0.5	0	-0.88 / PNI
Beres / Blueboy II	0	0	5.0	1.52 / PO
Beres / Rendezvous	0	0	0	0.67 / PPD
Beres / Century	0	1.0	0	0.58 / II
Beres / TAM-200	0	1.0	0.2	1.65 / PO
Matuo / Tobarzo	0	0	0	0.27 / II
Matuo / Polka	0	0.1	0	-0.20 / II
Matuo / Arthur-71	0	0	0	-0.54 / II
Matuo / Fleks	0	0	0	-0.93 / PNI
Matuo / Blueboy II	0	0	5.0	1.38 / PO
Matuo / Rendezvous	0	5.0	0	0.57 / PPD
Matuo / Century	0	1.0	0	-3.01 / D
Matuo / TAM-200	0	0	0.1	1.82 / PD
Tobarzo / Polka	0	0	0	-0.71 / PNI
Tobarzo / Arthur-71	0	1.0	0	0.38 / II
Tobarzo / Fleks	0	0.1	0	0.32 / II
Tobarzo / Blueboy II	0	0.5	1	0.63 / PPD
Tobarzo / Rendezvous	0	0	0	0.57 / PPD
Tobarzo / Century	0	0	0.1	1.0 / PPD
Tobarzo / TAM-200	0	0	0.1	5.01 / PO
Polka / Arthur-7	0.5	1.0	0	-3.12 / D
Polka / Fleks	0.5	0.5	0	-1.08 / D
Polka / Blueboy II	0.5	1.0	0	0.9 / PPD
Polka / Rendezvous	0	0	0	0.73 / PPD
Polka / Century	0.5	1.5	0	- 5.1 / D
Polka / TAM-200	0.5	1.5	0.1	- 4.0 / D

Note: PO – positive overdominance, PPD – partial positive dominance, II – intermediate inheritance, PNI – partial negative inheritance, D – depression (negative dominance), MYR – Myronivska

Source: developed by the authors of this study

In terms of resistance to *Puccinia recondita*, dominance (heterosis) was established in five (14.72%) hybrid combinations – Beres/Blueboy II, Beres/TAM-200, Matuo/TAM-200, Tobarzo/TAM-200, Matuo/Blueboy II (Table 3). Partial positive dominance was observed in nine (26.47%) hybrids, intermediate inheritance – in 11 (32.35%), partial negative inheritance – in 8.82%, and depression was observed in six (17.64%) hybrid combinations. Beres, Tobarzo, and Matuo varieties, which were involved in the crossing as a mother form, better transmitted the trait of resistance against *Puccinia recondita* pathogen.

The damage to plants by *Tilletia caries* over two years ranged within 0-70%, and the average development was 35.6%. High resistance to this pathogen was demonstrated by the accessions

protected by effective resistance genes: Sel.M 65-3157 (*Bt9*), Sel.M. 66-23 (*Bt10*, *11*) (USA), Lutescens 6028 (*Bt12*, *13*), Erythrosporum 5221 (*Bt14*) (UKR, MIW), Ferrugineum 220/85 (*Bt15*, *16*), Erythrosporum 4318/88 (*Bt17*), Erythrosporum 60-89 (*Bt18*, *19*), Ferrugineum 124-88 (*Bt20*, *21*) (UKR, SGI) (Table 4). In the study of collection accessions against *Tilletia caries*, 13 immune (0%), 17 highly resistant (1-5%), 16 resistant (10-15%), 26 slightly susceptible (20-30%), and 39 susceptible (over 40%) winter wheat samples were identified. The average development of the disease caused by *Tilletia caries* in the collection nursery was 67.3%. The varieties Rada (SVK), Famulus (DEU), SHARK/F4.105W21 (USA), Reya (UKR), Ekspromt, and lines Erythrosporum 24210, Line 46 (UKR) showed immunity to *Tilletia caries* (Table 5).

Table 4. Characteristics of *Tilletia caries* resistance donors with known resistance genes (average for 2023-2024)

Cultivar, line	Resistance gene	Origin	Damage intensity, %
			Stinking smut
Polka (vulnerable cultivar)	<i>St</i>	HUN	56.3
Turkeu CI 1558-B	<i>Bt4</i>	USA	5.2
Sel. 34-32	<i>Bt5</i>	USA	3.9
RiO Ci 10064	<i>Bt6</i>	USA	6.8
P.I. 178210	<i>Bt8</i>	USA	5.1
Sel.M. 65-3157	<i>Bt9</i>	USA	0
Sel. M. 66-23	<i>Bt10</i> , <i>11</i>	USA	0
Lutescens 6028	<i>Bt12</i> , <i>13</i>	UKR	0
Erythrosporum 5221	<i>Bt14</i>	UKR	0
Ferrugineum 220 / 85	<i>Bt15</i> , <i>16</i>	UKR	0
Erythrosporum 4318 / 88	<i>Bt17</i>	UKR	0
Erythrosporum 60-89	<i>Bt18</i> , <i>19</i>	UKR	0
Ferrugineum 124-88	<i>Bt20</i> , <i>21</i>	UKR	0

Source: developed by the authors of this study

Table 5. Intensity of damage to the best samples of winter wheat of the collection nursery by the pathogen *Tilletia caries* (average for 2023-2024)

Cultivar, line	Country of origin	Damage intensity, %
Polka (vulnerable cultivar)	HUN	45.9
Rada	SVK	0
Famulus	DEU	0
SHARK/F4105W21	USA	0
Reia	UKR	0
Warwick SRW	CAN	1.6

Table 5. Continued

Cultivar, line	Country of origin	Damage intensity, %
Erythrospermum 24210	UKR	0
Line 46	UKR	0
UN 49	TUR	5.6
Mukhran	GEO	5.9
Nyva	UKR	1.8
Eksprompt	UKR	0
Nezabudka	UKR	5.1
Fermerka	UKR	5.4

Source: developed by the authors of this study

When investigating the population of the stinking smut pathogen, the study found that the local population was avirulent or slightly virulent to resistance genes: *Bt6*, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21. To determine the genetics of the resistance trait in a series

of sources of resistance to *Tilletia caries* (Erythrospermum 24210, Eksprompt, Line 46 (UKR)), a series of crosses of donors with the vulnerable variety Polka (HUN), donors with each other and test varieties carrying effective resistance genes was conducted (Table 6).

Table 6. Degree of phenotypic dominance of resistance trait against *Tilletia caries* in F_2 , 2024

Combination	Plant damage, %			Degree of phenotypic dominance (h_p) / type of dominance
	♀	F_1	♂	
Erythrospermum 24210 / Polka	0	3.6	41.5	0.82 / PPD
Eksprompt / Polka	0	11.4	31.0	0.26 / II
Line 46 / Polka	0.1	14.0	40.0	0.3 / II
Erythrospermum 24210 / Eksprompt	0	0	0	0.1 / II
Erythrospermum 24210 / Line 46	0	0	1.6	1.0 / PPD
Eksprompt / Line 46	0	1.2	1.6	-0.5 / II
Eksprompt / Sel. M.65-3157	0	0	0	0.12 / II
Eksprompt / Sel. M 66-23	0	0	0	0.25 / II
Eksprompt / Ferrugineum 220/85	0	0	0	0.45 / II
Eksprompt / Erythrospermum 4318 / 88	0	0.5	1.5	0.33 / II
Eksprompt / Erythrospermum 60-89	0	1.4	2.2	-0.27 / PNI
Eksprompt / Ferrugineum 124-88	0	0.8	1.7	0.05 / II
Erythrospermum 24210 / Sel. M.65-3157	0	0	0	0.8 / PPD
Erythrospermum 24210 / Sel. M 66-23	0	0	0	0.71 / PPD
Erythrospermum 24210 / Ferrugineum 220 / 85	0	0	0	0.6 / PPD
Erythrospermum 24210 / Erythrospermum 4318 / 88	0	0	1.5	1.0 / PPD
Erythrospermum 24210 / Erythrospermum 60-89	0	1.4	2.4	-0.16 / PNI
Erythrospermum 24210 / Ferrugineum 124-88	0	0.5	2.1	0.52 / PPD
Line 46 / Sel. M.65-3157	0.1	0	0	1.0 / PPD
Line 46 / Sel. M. 66-23	0.1	0	0	1.0 / PPD
Line 46 / Ferrugineum 220 / 85	0.1	0	0	1.0 / PPD
Line 46 / Erythrospermum 4318 / 88	0.5	1.2	1.5	-0.2 / PNI
Line 46 / Erythrospermum 60-89	0.3	1.2	1.2	-0.04 / PNI
Line 46 / Ferrugineum 124-88	0.1	2.3	1.8	-1.42 / D

Note: PPD – partial positive dominance, II – intermediate inheritance, PNI – partial negative inheritance, D – depression (negative dominance)

Source: developed by the authors of this study

The analysis of the results obtained during the evaluation of the degree of phenotypic dominance of resistance to *Tilletia caries* in F_1 of soft winter wheat, created based on diverse parental forms, demonstrated a wide range of inheritance types. Specifically, several characteristic patterns could be identified within this sample: from partial positive dominance and intermediate inheritance to partial negative dominance and negative dominance. Such distribution of inheritance indicated a complex genetic mechanism that regulated resistance to the pathogen, as well as a major influence of both parental genotypes and the environment on the formation of dominant traits in first-generation hybrids. Based on the degree of phenotypic dominance in 2023, the study found that among F_1 hybrid combinations, 41.63% showed partial positive dominance against *Tilletia caries*. Intermediate inheritance of the trait was found in 37.5% of hybrids, partial negative inheritance was found in 16.7% of hybrid combinations, and depression was found in 36.37%.

The highest partial positive dominance was found in hybrid combinations using the resistance donor Sel. M. 65-3157 (*Bt* 9), Sel. M. 66-23 (*Bt*10, 11): ErythrospERMum 24210/Sel. M.65-3157, ErythrospERMum 24210/Sel. M.66-23, Line 46/Sel. M.65-3157, Line 46/Sel. M. 66-23. ErythrospERMum lines 24210 and Line 46, which were involved in the cross as the mother form, better transmitted the trait of resistance against *Tilletia caries* pathogen. One of the key causes of substantial yield losses, which can range from 15% to 50% depending on the level of pathogen virulence and climatic conditions in a given year, is fungal infection. These pathogens have a considerable impact, specifically, on the yield of wheat varieties, as noted by O.V. Barabolya & S.V. Borovko (2024). The findings of A. Palamarchuk et al. (2018), who assessed the extent of the affected areas, indicated that the most common diseases were septoriosiS (43.69%) and powdery mildew (44.32%). Diseases such as root rot (29.83%) and brown leaf rust (22.65%) were intermediate in terms of prevalence, while helminthosporium

(9.76%) was recorded in only a small number of regions. As for the intensity of these diseases, the average value for powdery mildew was 3.71%, for septoriosiS – 3.21%, for root rot – 2.92%, for brown leaf rust – 2.57%, and for helminthosporium the lowest value was recorded – 0.85%.

D. Datta et al. (2006; 2007) suggested that leaf rust (*Puccinia triticina* Eriks.) occurs in all regions of wheat (*Triticum aestivum* L.) cultivation in the world. The cultivation of resistant varieties is the most effective, environmentally friendly, and cost-effective method of rust control. It is vital that the genetic base of rust resistance in cultivated varieties is expanded and that lines with more than one effective resistance gene are developed. The genetic material they created with combined resistance *Lr*9 + *Lr*24 was developed by combining host-pathogen interaction and a molecular marker. D. Pal et al. (2024) confirmed that identifying and introducing wheat varieties with diverse resistance is the best way to control all types of rust. The researchers used the *Lr*9, *Lr*19, and *Lr*24 markers to authenticate the presence of specific genes in the selection for brown rust resistance. Analogous studies were conducted by A. Hanzalova et al. (2022), who for 10 years (1995-2004) studied the virulence of leaf rust in Slovakia on Linex (NIL) with genes *Lr*1, *Lr*2a, *Lr*2b, *Lr*2c, *Lr*3a, *Lr*9, *Lr*10, *Lr*11, *Lr*15, *Lr*17, *Lr*19, *Lr*21, *Lr*23, *Lr*24, *Lr*26, and *Lr*28. Based on the findings of field trials, the highly resistant to leaf rust varieties Arida (*Lr*13, *Lru*), Eva (*Lr*3, *Lru*), and Solara (*Lru*) were developed.

The high efficiency of the identified resistance genes of the *Puccinia recondita* population was evidenced by the findings of studies by many foreign scientists. According to J. Kolmer (2013), foliar rust caused by *Puccinia triticina* is the most common rust of wheat worldwide. The researchers noted that many different races of *P. triticina* are detected annually in the USA, which differ in virulence and leaf rust resistance genes in different wheat lines. Molecular markers have been used to characterise rust populations in the United States and around the world. S. Xu et al. (2024)

conducted a comparative study of twenty-three improved spring wheat (*Triticum aestivum* L.) lines from the Ottawa Research and Development Centre (ORDC) and four known varieties. The study covered agronomic performance at eight sites in Eastern Canada (Ottawa CEF-C1, Ottawa CEF-C2, St. Isidore, Harrington, Palmerston, Princeville, Kincardine, Beloeil) and Fusarium head blight (FHB) resistance. The reaction of the lines to six races of leaf rust (LR) was studied under vegetative conditions using the Morocco variety as a control to assess the development of the disease. The findings revealed that most of the tested lines did not show noticeable differences compared to the four control varieties. At the same time, ECSW05 and ECSW48 were distinguished by greater yields, moderate resistance to FHB and resistance to most of the studied LR races. They can serve as a valuable source of LR resistance for further breeding programmes in the region.

T. Bakhshi *et al.* (2024) found that varieties with combinations of race-neutral resistance genes stayed resistant for many years, even though the races of the leaf rust population were constantly changing. O.V. Babayants *et al.* (2006) confirmed the data on resistance genes, indicating that genotypes containing any or all of these four genes *Bt10*, *Bt11*, *Bt12*, and *Btp* can be used as a source of resistance to *Tilletia caries*. A.M. Mourad *et al.* (2022) found that four isolates carrying the *Bt10*, *Bt11*, *Bt12*, and *Btp* genes conferred resistance to Turkish and Nebraska species of stinking smut. Genotypes carrying any or all these four genes can be used as a source of resistance. In the study by Ž. Liaukas & V. Ruzgas (2008), among the tested genotypes with known resistance genes *Bt1-15*, Z, only two resistance genes provided full efficiency in PI 554120 and Jaila 305, which carry *Bt8*, and in Eryth-5221, which carries *Bt14*. Other single resistance genes considered effective (infection up to 10.0%) were *Bt5*, 9, 11, 12, 13M 15, Z. E.V. Alekseenko & E.I. Kirchuk (2022) found that breeding lines originating from *Lr* gene carriers derived from Western European wheat varieties

demonstrated a significant advantage over the standard variety in terms of average brown rust resistance scores. This advantage was observed regardless of the crossing schemes used. A series of crossing combinations were analysed in the study, which resulted in the identification of several promising breeding lines, such as L.17018, L.18016, L.21919 and L.16718. These lines could serve as valuable genetic sources to improve the trait of brown rust resistance in winter wheat.

T.I. Mukha & L.A. Murashko (2019) studied 170 collection accessions of winter wheat originating from different ecological and geographical regions. Among them, 13 samples with a strong level of resistance to the pathogen *Fusarium ear blight* were identified. Of particular note were two samples that showed immunity to stinking smut. The damage of the studied samples by the pathogen *Fusarium graminearum* ranged from 1.0% to 3.2%, while the comparable control variety Natula had a damage that reached 18.0%. Other winter wheat samples showed genotype-dependent resistance to 2-5 different diseases. The most noteworthy were varieties with resistance to five major diseases, including ear blight, stinking smut, root rot, powdery mildew, and brown rust. This group included the varieties Rhea, Rada, and Warwick SRW. Furthermore, the study identified accessions that showed resistance to four of these diseases, including Famulus, Zlatina 2, Catalus, and TX9801170/Sophisticated. These findings highlighted the significance of breeding to increase the immunity of winter wheat to a wide range of pathogens and improve its adaptive potential. Fermerka, MV-VERBUNKOS, and Dromos were resistant to three diseases.

Overall, the findings obtained suggested a significant variability in the resistance of winter wheat accessions to the main pathogens of brown leaf rust and smut, which was explained by both the presence of effective resistance genes and the specificity of their inheritance in hybrid combinations. The study found that among the tested sources there were both immune and highly resistant samples capable of providing

reliable plant protection under conditions of spread of pathogens of different virulence. The data obtained on the phenotypic dominance of the resistance trait in hybrid combinations allowed identifying promising combinations of parental forms for further breeding. Thus, the results of the study created a scientifically sound basis for the development of winter wheat varieties with complex resistance to dangerous fungal diseases and preparation of recommendations for breeding programmes.

Conclusions

The study found that the average development of *Puccinia recondita* in the collection nursery was 15.9%, while the average development of *Tilletia caries* was 35.6%. Twenty-four (30.8%) collection accessions were found to be immune to brown rust, and varieties protected by the known resistance genes Arthur-71 (*Lr9*), McNair 2203 (*Lr9*), Agrus (*Lr19*), Century (*Lr24 + Lr42*), TAM-200 (*Lr24 + Lr43*), V1275 (*Lr19*) (USA), VR89Bo22 (*Lr19*) (FRA), immunity to *Tilletia caries* – varieties Rada (SVK), Famulus (DEU), SHARK/F4. 105W21 (USA), Rhea, Eksprompt (UKR) and lines ErythrospERMum 24210, Line 46 (UKR). The study found that highly effective genes *Lr9*, *Lr19* retain sTable resistance, and genes contained in winter wheat varieties are also highly effective: Rendezvous (*Lr37*) (ANG), Century (*Lr42*), TAM-200 (*Lr43*), Arthur-71, Mc Nair 2203, Flex (USA), VR89Bo 22 (FRA). High resistance against the pathogen *Tilletia caries* was

observed in the cultivars protected by effective resistance genes: Sel. M 65-3157 (*Bt9*), Sel. M. 66-23 (*Bt10*, *11*) (USA), Lutescens 6028 (*Bt 12*, *13*), ErythrospERMum 5221 (*Bt14*) (UKR), Ferrugineum 220/85 (*Bt15*, *16*), ErythrospERMum 4318/88 (*Bt17*), ErythrospERMum 6089 (*Bt18*, *19*), Ferrugineum 124-88 (*Bt20*, *21*) (UKR).

The study proved that in terms of resistance to the pathogen *Puccinia recondita*, superdominance (heterosis) was established in five (14.72%) hybrid combinations: Beres/Blueboy II, Beres/TAM-200, Matuo/TAM-200, Tobarzo/TAM-200, Matuo/Blueboy II. Based on the degree of phenotypic dominance, it was found that among F_1 hybrid combinations, 41.63% showed partial positive dominance: ErythrospERMum 24210/Polka, ErythrospERMum 24210/Line 46, ErythrospERMum 24210/Sel. M.65-3157, etc., against *Tilletia caries*, no overdominance was found. The prospect of further research is to analyse the efficiency of the breeding process of creating winter soft wheat varieties immune to pathogens by using highly resistant source material.

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Conflict of Interest

None.

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Ступінь домінування ознаки стійкості проти збудників хвороб у F_1 пшениці озимої

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Анотація. Одним із найефективніших і водночас екологічно безпечних заходів інтегрованого захисту пшениці від хвороб є розробка резистентних сортів через селекцію, адаптовану до специфічних агрокліматичних умов. Мета роботи – фітопатологічна оцінка колекційних зразків озимої пшениці на штучних інфекційних фонах у польових умовах та визначення домінування стійкості гібридів F_1 до *Puccinia recondita* і *Tilletia caries*. Дослідження проведені впродовж 2023, 2024 рр. у селекційній сівоzmіні на природньому, штучному інфекційному фонах та лабораторних умовах лабораторії селекції озимої пшениці Миронівського інституту пшениці імені В. М. Ремесла Національної академії аграрних наук України за загальноприйнятими методиками. На штучних інфекційних фонах бурої іржі та твердої сажки вивчено 189 колекційних номерів пшениці озимої. Встановлено, що імуністету до збудника *Puccinia recondita* володіли сорти, захищені генами стійкості Arthur 71 (Lr9), McNair 2203 (Lr9), Agrus (Lr19) Century (Lr24+Lr42), TAM-200 (Lr24+Lr43), V1275 (Lr19), VR89Bo22 (Lr19), імуністету до *Tilletia caries* відобразили сорти пшениці озимої Rada (SVK), Famulus (DEU), SHARK/F4.105W21 (USA), Рея (UKR), Експромт, лінії Еритроспермум 24210 та Лінія 46 (UKR). При вивченні складу популяції *Puccinia recondita* встановлено, що середню ефективність проявили гени: Lr10, Lr13, Lr25 та Lr34 (ген вікової стійкості) за ступеня ураження ліній – 5-10 %. Стабільно зберігали високу стійкість і продовжували залишатися високоефективними гени Lr9, Lr19. За

стійкістю проти збудника *Puccinia recondita* наддомінування (гетерозис) встановлено у п'яти (14,72 % від загальної кількості гібридних комбінацій) гібридних комбінаціях Beres / Blueboy II, Beres / TAM-200, Matuo / TAM-200, Tobarzo / TAM-200, Matuo / Blueboy II. Зазначено, що місцева популяція збудника *Tilletia caries* авірулентна або слабко вірулентна до генів стійкості: Bt6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21. Дослідження генетики ознаки стійкості до даного захворювання засвідчило, що серед гібридних комбінацій F_1 41,63 % проявили частково позитивне домінування (ЧПД). Наддомінування до збудника твердої сажки не виявлено

Ключові слова: бура іржа; ген стійкості; сорт, лінія; тверда сажка; фон