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THE DONOR PROPERTIES OF RESOURCES RESISTANCE AGAINST THE EXCITER OF WHEAT RUST WHEAT

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ABSTRACT

A collection of soft winter wheat specimens investigated on the artificial infectious background of the leaf rust pathogen and selected resistance among them. The genetics of resistance sign in varieties and specimens were determined by hybridological analysis of F_2: Lovrin 32, KM 1485-6-8, VR 89 Bo 22, Beres, Tobarzo, 0-74-8-2, MIKM 1851-80, 4347-4, NS 326-99, 5517 A-5-5 Yr, Florida 302, VR 87 Bo 15, Matyo, NS 1308, 200-830, Polka, NS 2630/1, NS 18-30, HBE 0140-119, HBE 208-120, HBE 0303 156, HBE 0425-156, Tx91v4511, Tx92v4511, Plyska, Zernogradskaya 31, Volshebnitsa, Myronivska 40, Myronivska ostysta, Myronivska 28, Estet, Volynska napivintensivna, Kyivska 8, Expromt, Mironivska 29, Remeslivna, Garant, Selyanka, Erythrospermum 15761, Erythrospermum 12557, Erythrospermum 12735, Vympel odeskyiy during 1990–2018. The gene non-identity of the investigated donors was determined. In a variety of VR 89 Bo 22, 2 resistance genes, one of them *Lr19*, was investigated. The results of investigations of the composition of the leaf rust pathogen population by a series of isogenic lines and varieties of carriers of known effective resistance genes are presented. The high resistance against the leaf rust pathogen in the forest-steppe of Ukraine provide the genes *Lr9*, *Lr19*, *Lr37*, *Lr42* + *Lr24*, *Lr43* (*Lr21* + *Lr39*) + *Lr24*, *Lr9* + *Lr26*, *Lr10* + *Lr24*.

Keywords: wheat; gene pool; donor; infectious background; resistance genes

INTRODUCTION

Soft wheat is the leading grain crop by value in the world **(El-Khoury, 2009)**. The yield potential of this crop is not fully realized due to the damage to crops by phytopathogens. The diseases significantly reduce the yield and quality of the grain winter wheat. The gross collection losses are up to 20% annually, and in the epiphytotic years – 50% **(Novohatka, 1979)**. Breeding disease-resistant varieties are the most effective method in the struggle against wheat diseases **(Palamarchuk et al., 2019)**.

The creation of resistant varieties largely depends on the correct selection of initial material, determination of genetic factors of resistant control. However, the sources of resistance, the genetic nature sign of resistance to disease, is known identified not enough **(Dinh et al., 2020)** Therefore, the search and investigation of the immunological features of effective donors of resistance is the main problem in the creation of new competitive winter wheat varieties. Breeders need characteristic the varieties, not only by their phenotypic expression but also by their genetic characteristics recommended for hybridization **(Vyerchenko et al., 2019)**.

The leaf rust, the exciter of which is the fungus *Puccinia recondita* f. sp. *tritici*, is one of the most common diseases of wheat in Ukraine and the world. Breeding efficiency for leaf rust resistance can be improved by using different *Lr* resistance genes. More than 90 *Lr* genes are registered in the International Catalog Gene Symbol Directory, half of which are alien to date **(McIntosh, et al., 2003; McIntosh, et al., 2007; McIntosh, et al., 2008; McIntosh, et al., 2009; McIntosh, et al., 2010; McIntosh, et al., 2011; McIntosh, et al., 2012; McIntosh, et al., 2014; McIntosh, et al., 2016; McIntosh, et al., 2017; McIntosh, et al., 2018; McIntosh, et al., 2019)**. It is a great interest to investigate the resistance of wild relatives and endemic wheat species, identifying among them new immune forms and new effective resistance genes.

The immunity of *Triticum durum* and *T. dicoccum* must be widely used in the breeding of soft wheat for resistance to leaf rust **(Leonova et al., 2013)**. There are no reliable sources of resistance against this pathogen in the culture. But breeders are most interested in resistant varieties found among soft and durum wheat. World collections provide the possibility to use the achievements of breeding in different countries **(Kovalyshyna and Dmytrenko, 2017)**.

The investigation resistance against the disease of the gene pool of wheat is an important task, which can best be a solution from the attitude of the theory of co-evolution of the plant and pathogen **(Mushtruk et al., 2020)**. Only based on such testimony can the right approach be made to the choice of sources of stability and the most effective method of breeding.

Scientific hypothesis

The scientific hypothesis is founded on identifying nature inheritance and manifest resistance genes to exciter of leaf rust. It is attaining by investigation of composition population exciter of disease and identifies resistance genes at collectible samples soft wheat. It is making it possible to increase the resistance gene pool and creating new heterogeneous varieties of soft wheat.

MATERIAL AND METHODOLOGY

The research material was winter wheat the collection specimens received from the World Collection Federal Center for Plant Genetic Resources, All-Russian Institute of Plant Genetic Resources, The Plant Production Institute named after V. Ya. Yuryev of NAAS and varieties of winter wheat from research institutions in Ukraine were materials for investigation.

The investigations were conducted under the conditions of artificial inoculation by the agent of leaf rust in the field infectious nursery of the Mironivka wheat institute named after V.M. Remeslo. A local and synthetic population of the pathogen obtained from the Institute of Plant Protection of the National Academy of Sciences of Ukraine was used for creating an artificial infectious background. The wheat plants contaminated with leaf rust spores in the field in the phase of plant exit into the tube according to the method of **(Bober et al., 2020)**. The variety of Mironivska 10 susceptible to this pathogen is used as an accumulator of infection in experiments. The resistance of plants against the disease was determined on a scale resistance of plants against the disease was determined on a scale **(Strahov, 1951)**, according to which the affection is expressed in relative percentages of leaf area covered with pustules of the pathogen **(Geshele, 1971)**.

Experiments on the evaluation of varieties and collections samples of wheat for disease resistance using artificial inoculation were laid out according to the schemes used in the system of state variety testing of crops **(Tkachyk, 2014)**, using the method developed by us to evaluate the resistance of wheat varieties against pathogens of major diseases **(Trybel et al., 2010)**.

The method of intraspecific hybridization, which was carried out by the "twell method" following the method used for creating the hybrid material of winter wheat **(Merezhko et al., 1973)**.

To identify resistance genes and the nature of the inheritance of the trait of resistance to the agent of leaf rust, using the method of hybridological analysis **(Radchenko and Odintsova, 2008)**. All samples were crossed with tester lines - carriers of known effective resistance genes MC Nair 2203 (*Lr9*), Flex (*Lr19*), Osage (*Lr24*) to identify effective resistance genes. Samples were crossed with each other according to an incomplete diallel scheme to determine the allelic ratio of genes.

Statistical analysis

To obtain information on the number and interaction of resistance genes, the obtained ratios of classes of resistant and susceptible plants (actual) were compared with one of the theoretically expected cleavages using the chi-square (χ^2) correspondence criterion.

The assumption that the difference between the actually obtained and theoretically expected splits is random was rejected if $\chi^2_{fact.}$ exceeded the critical χ^2_{st}. ($\chi^2_{0.05} = 3.84$). The error of results in statistical analysis $p = 0.05$. Statistical processing was performed in Microsoft Excel 2016 in combination with XLSTAT. Values were estimated using mean and standard deviations.

RESULTS AND DISCUSSION

The greatest immunological diversity of forms can be detected in the centers of co-origin of the host plant and the pathogen according to the coevolution theory of the host plant and the pathogen **(Leary et al., 2018)**. The center of origin of wheat is located in the Trans-Asian Center, which includes the Caucasus, which plays a leading role in it **(Dorofee, 1972)**. There is also a center for leaf rust formation **(Leppik, 1970)**.

In the work of scientists discovered the pattern in the distribution of immune forms among wheat species for the first time. He considered where there is a species or racial specialization of the pathogen, immune forms and varieties can be found. The Caucasus is the center of origin of many endemic, rust-resistant forms, and should occupy the first place in the globe in terms of the abundance of genetic and physiological types of wheat pointed **(Khaneghah et al., 2018)**. The *Triticum timopheevii* with complex resistance against all types of rust, powdery mildew, and soot was found in the Caucasus.

10 highly resistant endemic species of wheat and its relatives with the highest immunity to rust, in particular: *Triticum monococcum, T. timopheevii, T. militinae, T. Zhykovski, T. fungicidum, Haynatriticum, Aegilops umbellulata* are distinguished **(Varella et al., 2017)**.

In the work **(Casey et al., 2016)** found forms immune to rust, powdery mildew, and soot among *Triticum dicoccum*.

The principles of researching gene pool of wheat resistance against leaf rust, based on **(Flor, 1971)** theory of "gene-for-gene", developed **(Lodgering, Johnston and Hendricks, 1974; Berlyand-Kozhevnikov et al., 1985)**.

The majority number of leaf rust resistance genes identified in cultivated wheat varieties are derived from its wild relatives and endemic wheat species. The almost half of the known *Lr* genes are alien and transferred to *Triticum aestivum* from different types of wheat, egilops, couch grass, elimus according to the information given in the gene symbol catalogs **(McIntosh et al., 2003; McIntosh et al., 2007; McIntosh et al., 2008; McIntosh et al., 2009; McIntosh et al., 2010; McIntosh et al., 2011; McIntosh et al., 2012; McIntosh et al., 2014; McIntosh et al., 2016; McIntosh et al., 2017; McIntosh et al., 2018; McIntosh et al., 2019)**. The effective sources of resistance genes against the causative agent of leaf rust are *aegilops speltoides* – genes *Lr28, Lr35, Lr36, Lr47, Lr51, Lr66; Aegilops tauschii – Lr4, Lr21, Lr22a, Lr32, Lr39, Lr42; Aegilops umbellulata – Lr9, Lr76; Aegilops triuncialis – Lr58, LrTr; Aegilops ventricosa – Lr37; Aegilops kotschyi – Lr54; Aegilops sharonensis – Lr 56;*

Aegilops peregrine – Lr59; Aegilops neglecta – Lr62; Aegilops geniculate – Lr57; Elymus trachycaulis – Lr55; Secale cereale – Lr25, Lr26, Lr45; Thinopyrum elongatum – Lr19, Lr29, Lr24; Triticum timopheevii – Lr18, Lr50; Triticum spelta – Lr44, Lr65, Lr71; Triticum dicoccoides – Lr53, Lr64; Triticum timopheevii spp. *viticulosum – LrTt1; Triticum turgidum – Lr61;Triticum monococcum – Lr63.* All found effective resistance genes except *Lr10* and *Lr23* are alien.

The new highly efficient resistance genes against the local leaf rust population: *LrAc1*, *LrAc2* – from *Aegilops cylindrical*, *LrTe1*, *LrTe2* – from *Triticum erebuni* and *LrAd1*, *LrAd2* – from amphidiploid Ad4 (*Triticum dicoccoides* x *Triticum tauschii*) are identified by **Babaiants (2011)**. The collection samples obtained from the National Center for Plant Genetic Resources of Ukraine, varieties of different breeding establishments of Ukraine, and Mironivka Institute of Wheat named after V. M. Remeslo were investigated to select sources of resistance to leaf rust under conditions infectious background of the pathogen on a specially assigned phytoplot.

The effective resistance genes for the Forest Steppe zone of Ukraine leaves: *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr37*, *Lr42* + *Lr24*, *Lr43* (*Lr21* + *Lr39*) + *Lr24*. It was installed as result investigations of the composition population leaf rust on a series of isogenic lines of Thatcher variety and varieties of carriers of known effective resistance genes (Table 1-2).

There was a slight lesion of *Lr19* gene carrier, indicating that clones were virulent against it. In some years, there was a slight lesion of the pathogen and on varieties protected by the *Lr9* gene. The varieties protected by the *Lr24* gene lose their stability. The *Lr37*, *Lr42* + *Lr24*, *Lr43* (*Lr21* + *Lr39*) + *Lr24*, *Lr9* + *Lr26*, *Lr10* + *Lr24*, *Lr19* + *Lr25* genes have shown high efficiency in recent years.

Genes show the high efficiency against the local population of the brown rust pathogen in the Forest-steppe of Ukraine: *Lr9*, *Lr19*, *Lr37*, *Lr42* + *Lr24*, *Lr43* (*Lr21* + *Lr39*) + *Lr24*, *Lr9* + *Lr26*, *Lr10* + *Lr24* **(Kovalyshyna, 2013)**, *Lr24*, *Lr25*, *Lr28*, *Lr34*, *Lr36*, *Lr41*, *Lr42* are determined by results of investigations domestic researchers **(Lisova, 2012)**. The virulence genes against *Lr9*, *Lr19*, *LrAc1*, *LrAc2*, *LrTe1*, *LrTe2*, *LrAd1*, *LrAd2* are rarely found in the Steppe of Ukraine **(Babaiants, 2011)**.

The genetics of the trait resistance of these samples was able to determine by hybrid analysis of F_2 (Table 3). The resistance of variety the Lovrin 32, KM 1485-6-8, VR 89 Bo 22, Beres, Tobarzo, Mironivska 40, Mironivska ostysta, Estet, Mironivskay 28, Volynska napivintensivna, Kyivska 8 is controlled by two dominant genes (15 : 1) (confidence probability p = 0.95). The resistance to the agent of leaf rust is controlled by two genes, one of which is dominant and one is recessive (13 : 3) in varieties 0-74-8-2, MIKM 1851-80, 4347-4, NS 326-99, Pliska, 5517 A-5-5 Yr, Florida 302, VR 87 Bo 15, Matyo, HBE 0140-119, HBE 208-120, Expromt, Mironivska 29, Remeslivna, Garant, Selyanka (confidence probability p = 0.95). Two complementary genes (9 : 7) control resistance in samples NS 1308, 200-830, Polka, Zernogradskaya 31, Volshebnitsa, Vympel odeskyiy, Erythrospermum 15761 (confidence probability p = 0.95). Two duplicate recessive resistance genes (7 : 9) identified in samples NS 2630/1,

Table 1 Affection exciter leaf rust *Lr*-line Thatcher series of soft spring wheat (Mironivskyiy Institute of Wheat named after V. M. Remeslo, NAAS, 2006 – 2018).

The name of the line	Pedigree	Gene of resistance	Origin	The intensity of the affection, %			
				2006 – 2010	2011 – 2015	2016	2018
TcLr1	Thatcher*6/Centenario	*Lr1*	CAN	34.0	27.5	3.0	20.0
TcLr2a	Thatcher*6/Webster	*Lr2a*	CAN	38.0	18.5	5.0	15.0
TcLr2c	Thatcher*6/Brevit	*Lr2c*	CAN	42.0	26.5	5.0	10.0
TcLr3	Thatcher*6/Democrat	*Lr3*	CAN	42.0	27.5	7.0	15.0
TcLr3bg	Thatcher*6/Bage	*Lr3bg*	CAN	40.0	22.5	5.0	10.0
TcLr3ka	Thatcher*6/ Klein Aniversario	*Lr3ka*	CAN	40.0	32.5	7.0	5.0
TcLr9	Thatcher*6/*Ae.umbellu*	*Lr9*	CAN	0.4	0	0	0
TcLr10	Thatcher*6/Lee	*Lr10*	CAN	29.0	20.0	7.0	10.0
TcLr11	Thatcher*6/Hussar	*Lr11*	CAN	21.5	20.0	6.0	10.0
TcLr12	Thatcher*6/Exchange	*Lr12*	CAN	14.0	7.5	7.0	7.0
TcLr13	Thatcher*6/Frontana	*Lr13*	CAN	12.0	6.5	3.0	3.0
TcLr14a	Thatcher*6/Hope	*Lr14a*	CAN	21.5	25.0	10.0	15.0
TcLr14b	Thatcher*6/Bowie	*Lr14b*	CAN	37.0	22.5	10.0	15.0
TcLr19	Thatcher*6/*Agropiron elongatum*	*Lr19*	CAN	0.4	0	0	0
TcLr23	Thatcher*6/Gabo	*Lr23*	CAN	28.0	11.5	3.0	5.0
TcLr24	Thatcher*6/ *Agropiron elongatum*	*Lr24*	CAN	5.0	10.0	1.0	1.0
TcLr25	Thatcher*6/Rosen (*Secalecereale*)	*Lr25*	CAN	2.5	1.5	0	0
TcLr26	Thatcher*6/Imperial (*Secalecereale*)	*Lr26*	CAN	21.0	27.5	10.0	15.0
TcLr29	Thatcher*6/ *Agropiron elongatum*	*Lr29*	CAN	34.0	15.0	5.0	10.0
TcLr30	Thatcher*6/Terenzio	*Lr30*	CAN	36.0	25.0	3.0	15.0
TcLr32	Thatcher*6/*Aegilops taushii*	*Lr32*	CAN	33.0	36.0	5.0	10.0
TcLr34	Thatcher*6/Terenzio	*Lr34*	CAN	33.0	15.0	3.0	5.0
Leaf Rust Monogene Line ECH		*LrEch*	CAN	26.0	25.0	1.0	1.0
Myronivska 10 (standart susceptibility)		–	UKR	45.0	58.7	30.0	60.0

Note: *In 2017, no research was conducted.

Table 2 Characteristics of soft winter wheat collection samples with known *Lr* genes for resistance to leaf rust (Mironivskyiy Institute of Wheat named after V. M. Remeslo, NAAS, 2006 – 2018).

No	The name of the line	Gene of resistance	Origin	The intensity of the affection, %			
				2006 – 2010	2011 – 2015	2016	2018
1	Arthur 71	*Lr9*	USA	0	0.02	3.0	0
2	Mc Nair 2203	*Lr9*	USA	0	0	1.0	0
3	Agrus	Lr19	USA	0	0.1	1.0	1.0
4	Flex	*Lr19*	USA	1.8	0.2	1.0	0
5	V1275	*Lr19*	FRA	0.1	0.2	0	1.0
6	VR 89 Bo 22	*Lr19*	FRA	0.2	0.2	0	1.0
7	Frederik	*Lr23*	CAN	3.0	7.0	5.0	5.0
8	Osage	*Lr24*	USA	3.9	3.0	1.0	2.0
9	Blueboy II	*Lr10+ Lr24*	USA	0.8	2.8	1.0	2.0
10	Transfer	*Lr19+ Lr25*	USA	0.8	0.6	0	0
11	Rendezvous	*Lr37*	GBR	0	0	3.0	1.0
12	203-238	*Lr9+ Lr26*	BGR	0	0.5	0	1.0
13	Century	*Lr24+ Lr42*	USA	0	0	0	0
14	TAM-200	*Lr24+ Lr21 + Lr39*	USA	0	0	0	0
15	Myronivska 10 (standard susceptibility)	–	UKR	45.0	45.0	30.0	60.0

Note: *In 2017, no research was conducted.

Table 3 Genetic characteristics of leaf rust resistance donors (Mironivskyiy Institute of Wheat named after V. M. Remeslo, NAAS, 1990 – 2018).

Resistance donors	Cleavege by phetype (resistant: susceptible)	The nature of interaction genes
Lovrin 32, Myronivska 40, Myronivska ostysta, KM 1485-6-8, VR 89 Bo 22, Myronivska 28, Estet, Volynska napivintensyvna, Kyiivska 8, Beres, Tobarzo 0-74-8-2, MIKM 1851-80, 4347-4, Plyska, NS 326-99, 5517 A-5-5 Yp, Florida 302, VR 87 Bo 15, Expromt, Myronivska 29, Remeslivna, Garant, Selyanka, Matyo, HBE 0140-119, HBE 208-120	15: 1 9 *A-B-* : 3 *A-bb* :3 *aaB-* : 1 *aabb*	Genes *A* and *B* are manifesting equally. Resistance dominates in both cases (two duplicates dominance genes)
	13: 3 9 *A-B-* : 3 *A-bb* : 3 *aaB-*: 1 *aabb*	Genes *A* and *B* are manifesting equally. Resistance dominates in case *AA* and recessive *bb* (two duplicates genes, one dominance and one recessive)
NS 1308, Erytrospermum 15761, 200-830, Vympel odeskyii, Zernogradskaya 31, Volshebnitsa, Polka	9: 7 9 *A-B-* :3 *A-bb* : 3 *aaB-* : 1 *aabb*	Genes *A* and *B* are interacting complementary. The presence of *A* or *B* alone is not sufficient to demonstrate the resistance of the phenotype (complementation of two dominant genes)
Erytrospermum 12557, Erytrospermum 12735, NS 2630/1, NS 18-30, Tx 91 v 4511	7: 9 9 *A-B-* : 3 *A-bb* : 3 *aaB-* : 1 *aabb*	Genes *a* and *b* are manifested equally. Recessive resistance in both cases (two duplicate recessive genes)
HBE 0303 156, HBE 0425-156	3: 1 1 *A* : 2 *Aa* : 1 *aa*	One dominant gene
Tx 92 v 4511	1 : 3 1 AA : 2 Aa : 1 aa	One recessive gene

NS 18-30, Tx 91v4511, Erythrospermum 12557, Erythrospermum 12735 (confidence probability $p = 0.95$). One dominant resistance gene (3 : 1) contains samples HBE 0303 156, HBE 0425-156, and the collection sample Tx 92v4511 contains one recessive resistance gene against leaf rust (1 : 3) (confidence probability $p = 0.95$).

The splitting observed, by crossing sources of resistance among themselves in all combinations of F_2, which confirms the non-identity of genes in these donors. The crossing of resistance donors with testers of known efficient genes *Lr9*, *Lr19*, *Lr24* observed splitting into resistance and unresistance except for the combination of VR 89 Bo 22 x Flex (*Lr19*). In ones, splitting into resistance and unresistance phenotypes was not detected. This indicates that VR 89 Bo 22 contains the *Lr19* genes (confidence probability $p = 0.95$).

The genetic control of the resistance sign in 42 donors was investigated. The variety VR 89 Bo 22 contains the

Lr19 genes. Other donors of this sign have resistance genes independent of the known effective ones, which makes it possible to replenish the leaf rust resistance gene bank and create new heterogeneous winter wheat varieties on this basis.

Successful breeding requires a clear understanding of the evolution of the pathogen and host-pathogen interactions, of the types of resistance, methods of material evaluation, resistance genes, and the nature of inheritance of this trait and its relationship to other economic and biological traits. It is only based on such testimony that the right approach to the choice of sources of resistance and the most effective method of breeding work can be worked out.

CONCLUSION

The more than 200 collections samples and varieties of winter wheat of different ecological and geographical origins were evaluated for resistance to leaf rust on the artificial infectious background of its pathogen during 1990 – 2018. 42 samples were identified that examined the genetics of resistance to the disease among them. The samples: Lovrin 32, KM 1485-6-8, VR 89 Bo 22, Beres, Tobarzo, 0-74-8-2, MIKM 1851-80, 4347-4, NS 326-99, 5517 A-5-5Yr, Florida 302, VR87Bo15, Matyo, NS 1308, 200-830, Polka, NS 2630/1, NS 18-30, HBE 0140-119, HBE 208-120, HBE 0303 156, HBE 0425-156, Tx91v4511, Tx92v4511, Plyska, Zernogradskaya 31, Volshebnitsa, Myronivska 40, Myronivska ostysta, Myronivska 28, Estet, Volynska napivintensivna, Kyivska 8, Expromt, Myronivska 29, Remrslivna, Garant, Selyaynka, Erythrospermum 15761, Erythrospermum 12557, Erythrospermum 12735, Vympel odeskyiy contain resistance genes are independent of each other and known to be effective (confidence probability p = 0.95). In the variety VR 89 Bo 22 one of the genes *Lr19*. This makes it possible to replenish the leaf rust resistance gene bank and create new heterogeneous varieties of winter wheat.

As a result of studying the composition of the leaf rust population on a series of isogenic lines of Thatcher variety and varieties of carriers of known effective resistance genes, we determined that the resistance genes of the forest-steppe zone of Ukraine remain: *Lr9*, *Lr19*, *Lr24*, *Lr25*, *Lr37*, *Lr42*+*Lr24*, *Lr43* (*Lr21* + *Lr39*) + *Lr24*.

As a result of research, it was found that the wheat variety Myronivska Ukrainian selection is quite productive in comparison with other varieties and resistant to pathogens of various diseases, especially to the pathogen (brown rust).

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