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Virulence and diversity of *Puccinia striiformis* in South Russia

Galina V. VOLKOVA, Olga A. KUDINOVA*, Irina P. MATVEEVA

FSBI Federal State Budgetary Scienti!c Institution, All-Russian Scienti!c Center of Biological Plant Protection, 350039 Krasnodar, Russia
*Corresponding author. E-mail: alosa@list.ru

Summary. *Puccinia striiformis* causes wheat yield losses in all countries where wheat is cultivated. Virulence and diversity of the *P. striiformis* were assessed in 2013–2018 in South Russia, and this showed that the North Caucasian population of the pathogen was diverse. One hundred and eighty two virulence phenotypes were identified in 186 *P. striiformis* isolates. Among isolates collected in 2014, 2015, and 2018, all phenotypes were unique. In the 2013 and 2017 populations, phenotypes with few (one to eight) virulence alleles prevailed. In the 2014, 2015, and 2018 populations, most of the phenotypes contained greater numbers (nine to 19) of virulence alleles. Over the 5 years of research, the pathogen population lacked isolates virulent to the host *Yr* resistance genes *3, 5, 26,* and *Sp*. Single (from 1 to 5%) occurrences of isolates virulent to host lines with *Yr* genes *3a, 17, 24, 3b + 4a + H46,* and *3c + Min* were identified. Differences in frequencies of virulence alleles between years in the *P. striiformis* populations (Ney indices, N) were generally non-significant (N = 0.11 to 0.23), with the exception of the populations in 2013 and 2017 (N = 0.37). The minimum N values was found for the populations of 2015 and 2018 (N = 0.10). Over the five years of this study, the dynamics of the virulence of the population and jumps in the frequency of isolates with respect to many *Yr* genes were identified. This feature of the *P. striiformis* populations in South Russia, combined with high phenotypic diversity, indicates the ability for rapid race formation and morphogenesis in response to changes in biotic and abiotic factors.

Keywords. Yellow rust, virulence, effective resistance genes, pathogen population.

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INTRODUCTION

The yellow rust pathogen (*Puccinia striiformis* West. f. sp. *tritici* Erikss. et Henn.) causes wheat yield losses in all countries where this crop is grown (Singh *et al*., 2004; Bux *et al*., 2011; Hovmøller *et al*., 2017). This pathogen can also infect barley, rye and more than 50 species of herbs (Waqar *et al*., 2018). *Puccinia striiformis* has rapid coupled evolution with the formation of new virulent races that can infect previously resistant wheat varieties (Wellings and McIntosh, 1990; Hovmøller and Justesen, 2007). Recent spread of the pathogen has been limited to regions with temperate climates. Since 2010, new races of *P. striiformis* have caused serious yellow rust epidemics in India, Iran, Pakistan (Afshari, 2008; MacKenzie, 2011), the United States of

America and Canada (Wan and Chen, 2014), Australia (Wellings and Kandel, 2004), Ethiopia (Gebreslasie *et al*., 2020), Egypt (Ashmawy *et al*., 2019; Shahin *et al*., 2020) and other countries.

In Russia, until the end of the 1960s, yellow rust had no economic significance, although the disease was periodically recorded (Morozova, 1974). Since 1990, in the south of Russia, there has been a steady expansion of the area affected by this disease (Chuprina *et al*., 1999; Shumilov and Volkova, 2013). The main regions of South Russia are Krasnodar, Stavropol and Rostov. These regions are leading in the production of winter cereal crops (49% of the total Russian production), and are characterized by favourable weather conditions for the development of phytopathogens, including *P. striiformis*. Foci of infection appear in epiphytotic years due to migration of the pathogen from the Transcaucasus, where a maternal *P. striiformis* population with high variability is formed, to foothills in Dagestan, Ossetia, Ingushetia, Kabardino-Balkaria, adjacent steppe regions of the Stavropol and Krasnodar Regions (Chuprina *et al*., 1999). The infected area in 1995 to 1997 in some regions of southern Russia was 56 to 63% (Berdysh, 2002). In 1997, in Krasnodar region, the infected area varied between 30 and 90% (Dobryanskaya *et al*., 1999). In 2001, an epiphytotic of yellow rust occurred (Berdysh, 2002). In 2004 and 2008, the development of yellow rust, especially in the southern foothill zone of the region, reached 20 to 40% with wheat yield losses of 10 to 15% (Sanin and Nazarova, 2010). The proportion of *P. striiformis* in the pathocomplex during 2001 to 2008 averaged 8% and varied from 5 to 22%. In 2004, moderate yellow rust development was noted, while in 2001 to 2003 and 2005 to 2007, low level of this disease occurred. In 2009-2011, the development of yellow rust ranged from 0.3 to 6.1%. In 2012, the pathogen was not detected in the region, which is most likely due to the low temperatures that occurred in winter. In 2013 to 2017, development and spread of yellow rust remained at the level of previous years and fluctuated from 0.2 to 3.5%. In 2018, the development of the disease was less than 2% (Volkova *et al*., 2018; Matveeva, Volkova, 2019).

Traditionally, in large areas of cultivation, yellow rust is controlled by the use of effective fungicides. However, with the trend towards "greening" of agricultural production, biosafety methods for protecting wheat from yellow rust are becoming increasingly important, with method being the use of disease-resistant wheat varieties (Aktar-Uz-Zaman *et al*., 2017). To effectively use their potential, a substantiated strategy for host variety distribution in agrolandscape niches is necessary, but this cannot be achieved without knowledge of virulence of phytopathogen population (Wellings, 2011). Thus, monitoring the virulence dynamics of the *P. striiformis* population is an important tool for disease management (Chen, 2005; Ali *et al*., 2017).

The aim of the present study was to assess diversity and virulence dynamics of *P. striiformis* populations in southern Russia during 2013 to 2018.

MATERIALS AND METHODS

Route surveys and sample collection

The collection of yellow rust material was carried out in late May to early June of each year, from wheat crops and plant breeding sites in the main grain-producing regions of southern Russia, including Krasnodar, Stavropol and Rostov. Leaves with urediniopustules were wrapped in filter paper and labelled with dates and localities of collection, and were stored during the survey periods in a portable refrigerator. When storing samples in the laboratory, collected leaves were dried and then placed in a refrigerator at 2–4°C.

Weather conditions of growing seasons

In 2013, spring was prolonged with frequent rains, which favourably affected development of yellow rust. In 2014, positive deviations of air temperature prevailed in the early spring period. Heavy rains fell in the second half of March, which contributed to the development of yellow rust on crops. The spring of 2015 was early, unstable, and protracted, with intense frosts in late March to early April, and there were intense frosts (-1 to -5°C). The cold weather in April reduced growth and development of diseases, but these conditions did not affect yellow rust development. In spring of 2017, frequent rains and low temperatures favoured yellow rust development. 2018 was an unfavourable year for development of yellow rust. The combination of high temperatures and low soil moisture in spring limited development of the pathogen.

Multiplication of Puccinia striiformis *isolates*

Multiplication of infectious material for isolation of *P. striiformis* monopustule isolates was carried out on the highly susceptible wheat variety Kaw (United States of America). This was carried out in a greenhouse, using optimal temperature (15 to 18°C), humidity (60 to 80%) and lighting (12,000 to 15,000 lux) for development of

the pathogen (Anpilogova and Volkova, 2000). Wheat plants were grown in 0.5 L capacity pots, five to eight plants in each pot, until their second leaves appeared (germination phase). The wax bloom was then removed from the plants by lightly rubbing the leaves with slightly moistened fingers, and suspensions of urediniospores of the respective populations were applied at low concentration. Water was then applied to the plants with a pump sprayer and the plants were placed in a humid chamber for 18 to 20 h at 13 to 16°C, after which they were transferred to isolated boxes in a greenhouse. After 13 to 14 d, when first signs of disease appeared, only one plant with a single chlorotic spot was left in each pot. This plant was covered with an insulator 10 cm in diameter, with a double layer of gauze fixed on top.

Multiplication of *P. striiformis* isolates was carried out on the same variety using the methods described above. Urediniospores were collected into test tubes, which were identified isolate identifications and agroclimatic zones.

Virulence analysis of Puccinia striiformis *isolates*

To study the virulence of the pathogen population, standard sets of host differentials and lines, carrying 41 resistance genes (Table 1), were used. Perforated pots each containing 25 mL of sand were placed on trays, and were irrigated with Knop's nutrient solution (stock solution: 100 g calcium nitrate, 25 g potassium phosphate, 25 g of magnesium sulphate, 12.5 g potassium chloride, 0.1 g of ferric chloride, in 1 L water). For irrigation, 100 mL of the stock solution was diluted in 10 L of water and the trays were filled with the nutrient mixture (Smirnova and Alekseeva, 1988).

Sprouted seeds of differentials and near isogenic lines were sown into pots, at five seed per pot. In the 1-2 true leaf phase, When resulting plants were at the one to two leaf stage, they were inoculated with each of *P. striiformis* isolates. A tray with each set of varieties and lines was designated by the isolate number with which the plants were infected. At 14 to 18 d after inoculation, when the type of reaction was well pronounced, the reaction was assessed. The type of reaction was determined using the Gassner and Streib scale (Roelfs *et al*., 1992). Varieties and lines with reaction type i, 0, 1 and 2 were considered resistant to the isolate, and type 3.4 as susceptible. a virulence formula was then determined, where the effective resistance genes of each host plant were indicated in the numerator, and the ineffective genes were indicated in the denominator (Green, 1965).

Table 1. Sets of host plant differentials, near isogenic lines of variety Avocet and additional varieties with known resistance genes for characterizing *Puccinia striiformis* virulence.

Varieties and lines	*Yr* Gene(s)	Varieties and lines	*Yr* Gene(s)
International set		Fielder	6+20
Chinese 166*	1	Tyee	Tye
Lee*	7+22+23	Tres	Tr1+Tr2
Heines Kolben	2+6	Hyak	17
Vilmorin 23	3a+4a+V23	Express	Exp1+Exp2
Moro*	10+Mor	*Australian set on the base of*	
Strubes Dickkopf	SD+25	*variety Avocet*	
Suwon 92× Omar	SU	Yr1 / 6 Avocet S	1
Clement*	2+9+Cle	Yr5 / 6 Avocet S*	5
T. spelta album	5	Yr6 / 6 Avocet S	6
European set		Yr7 / 6 Avocet S	7
Hybrid 46	3b+4b+H46	Yr8 / 6 Avocet S*	8
Reichersberg 42	7+25	Yr9 / 6 Avocet S*	9
Heines Peko	2+6+25	Yr10 / 6 Avocet S	10
Nord Desprez	3a+4a+ND	Yr15 / 6 Avocet S	15
Compair*	8+19	Yr17 / 6 Avocet S	17
Carstens V	25+32	Yr24 / 6 Avocet S	24
Spaldings prolific	Sp+25	Yr26 / 6 Avocet S	26
Heines VII*	2+HVII	Yr27 / 6 Avocet S	27
American set		Yr32 / 6 Avocet S	32
Lemhi	21	YrSp / 6 Avocet S	Sp
Paha	Pa1+Pa2+Pa3	Avocet Resistans	A
Druchamp	3a+Dru+Dru2	Jupateco 73 R	18
Produra	Pr1+Pr2	additional varieties	
Yamhill	2+3a+Yam	Minister	3c+Min
Stephens	3a+Ste+Ste2	Vuka	4b

* Host varieties and lines also included in the American set of differentiator varieties.

Statistical analyses of results

The level of diversity of *P. striiformis* phenotypes was assessed using the Shannon index (Hw) according to the formula (Kolmer *et al*., 2003):

$$H_w = -\sum pi \ln(pi)/\ln(n)$$

where *pi* is the frequency of *i*-th phenotype in the population, and *n* is = the total number of isolates of the population.

The diversity of the *P. striiformis* population The frequencies of virulence genes was described using the Ney diversity index (H_s) (Kosman and Leonard, 2007):

$$H_s\,(P) = \Sigma[1 - q_i^2 - (1 - q_i)^2]/k,\ 1 \le i \le k,$$

where q_i is the frequency of i-th gene in this population, and k= number of genes.

The differences of frequencies of virulence genes between the *P. striiformis* populations were assessed using Ney's genetic distance (Kosman, 1996):

$$N = \Sigma \Sigma x_{ij} y_{ij} / \sqrt{\Sigma\Sigma x^2_{ij} \Sigma\Sigma y^2_{ij}},$$

where x_{ij} and y_{ij} indicate frequencies of i-th allele, in the j-th year in compared populations.

RESULTS

Virulence of the wheat yellow rust pathogen population

For the period from 2013 to 2018, virulence of 186 isolates of *P. striiformis* was described (Table 2). Of 41 host lines with resistance genes, 38 showed different responses to *P.* striiformis infection.

Over the 5 years of study, the pathogen population lacked isolates virulent to the *Yr* resistance genes *3, 5, 26,* or *Sp*. Single (from 1 to 5%) occurrences were observed of isolates virulent to lines with the *Yr* genes *3a, 17, 24, 3b + 4a + H46,* or *3c + Min*. In 2009, 1010 and 2011, isolates affecting varieties with *Yr17* occurred with a frequency of 30%, while isolates virulent to the *Yr3c + Min* gene were absent in the population (Shumilov *et al*., 2015). The frequency of *P. striiformis* isolates virulent to the lines with the *Yr* genes *4 + 12, 6, 7 + 25, 2 + HVII, 32, 2 + 9,* or *SD* remained at an average level and varying from 6 to 20%.

The frequency of isolates on host lines with the *Yr* genes *1, 2, 4b, 21, SU, 2 + 6, 7 + 22 + 23,* or *8 + 19* remained stably high (30-80%). On differentiator varieties with the *Yr* genes *39 + Alp* and *Da1 + Da2* the frequency of isolates was high in all years of study, except 2017. On varieties and lines with *Yr* genes *7, 9, 10, 15, 18, 25, 10 + Mor , 3a + 4a + V23,* or *25 + 32*, high polymorphism of the pathogen reaction types was observed. There was also a decrease in the frequency of isolates for the line with the *Yr8* gene, and an increase for the line with the *Yr3a + 4a + ND* genes.

Table 2. Frequency (%) of isolates with virulence alleles in the North Caucasian population of *Puccinia striiformis f. tritici* during 2013 to 2018.

Yr genes of virulence	*Yr* gene frequency (%) and Years of assessment				
	2013	2014	2015	2017	2018
1	30.6	87.8	78.3	40	52.7
2	50.0	69.4	65.7	30	45.1
3a	0.0	2.0	0.0	5	1.6
4+12	8.3	6.1	7.0	20	5.8
4b	25.0	81.6	71.6	55	42,4
6	0.0	6.1	8.2	0	2.8
7	11.1	8.2	10.4	40	0.0
8	19.4	10.2	11.8	5	0.0
9	0.0	67.3	12.5	45	22.2
10	16.7	79.6	18.1	10	5.1
15	11.1	81.6	37.4	30	13.9
17	0.0	4.1	1.2	0	4.8
18	8.3	51.0	10.6	40	62.7
21	58.3	79.6	44.8	30	64.3
24	0.0	4.1	0.0	0	2.8
25	19.4	85.7	20.2	30	18.6
27	11.1	2.0	2.1	0	0.0
29	30.6	69.4	56.7	15	49.1
32	0.0	12.2	10.1	5	17.2
2+9	0.0	12.2	10.8	20	10.8
SU	22.2	57.1	48.3	15	44.4
SD	5.6	8.2	5.2	5	7.2
10+Mor	5.6	46.9	10.1	20	5.6
3a+4a+V23	16.7	51.0	34.1	35	28.4
2+6	48.9	73.5	51.0	40	46.1
7+22+23	41.7	75.5	59.7	45	52.5
2+HVII	11.1	6.1	10.9	20	19.4
25+32	0.0	65.3	1.2	15	14.8
8+19	55.6	65.3	31.8	40	41.4
3a+4a+ND	19.4	10.2	16.1	20	35.6
2+6+25	8.3	30.0	24.6	35	16.7
7+25	19.4	8.2	6.1	20	10.4
3b+4a+H46	0.0	2.0	0.0	5	3.6
A	19.4	63.3	54.4	35	72.2
Da1+Da2	13.9	32.7	27.5	0.0	18.4
39+Alp	41.7	57.1	49.8	0.0	51.3
3, 5, 26, Sp	0.0	0.0	0.0	0.0	0.0
3c+Min	2.8	0.0	0.0	0.0	1.6
Number of isolates	36	49	45	20	36

Diversity of Puccinia striiformis *populations by virulence phenotypes*

The study of the phenotype composition of the North Caucasian population of the wheat yellow rust pathogen revealed significant diversity; 182 virulence phenotypes were identified from 186 *P. striiformis* isolates. Among the isolates from the populations of 2014, 2015, and 2018, all the phenotypes were unique. In the 2013 pathogen population, four phenotypes occurred twice. Diversity of the populations (frequencies of virulence alleles) remained at a moderate average level (Table 3).

Table 3. Ney and Shannon indices for *Puccinia striiformis* populations in South Russia, during 2013 to 2018.

Year	Number of *P. striiformis* isolates	Number of phenotypes	Ney index (Hs)	Shannon index (Sh)
2013	36	32	0.21	0.96
2014	49	49	0.27	1.0
2015	45	45	0.26	1.0
2017	20	20	0.27	1.0
2018	36	36	0.27	1.0

Table 4. Ney indices for *Puccinia striiformis* populations in South Russia during 2013 to 2018, as indicated by the frequencies of virulence alleles.

Compared pairs	Year of assessments of *Puccinia striiformis* populations			
	2013	2014	2017	2018
2013		0.23	0.37	0.17
2014			0.15	0.14
2015	0.18	0.11	0.21	0.10
2017				0.20

Differences between Puccinia striiformis *populations in 2013 to 2018 by frequencies of virulence alleles*

The populations of *P. striiformis* in 2013 to 2018 was compared for the number of virulent alleles (Figure 1). The population of the pathogen in 2013 was characterized by reduced virulence, and phenotypes with small numbers (1-8) of virulence alleles. In contrast, the 2014 population was characterized by a predominance of highly virulent isolates with medium and high levels of virulence alleles.

The 2015 *P. striiformis* population was also dominated by isolates with medium numbers of virulence alleles. In the 2017 population of the pathogen, isolates with short virulence formulae prevailed, although isolates with a medium and high content of virulent alleles totalled 50%. The 2018 population was characterized by an approximately equal ratio of isolates containing medium and large numbers of virulence alleles. Thus, from year to year, the virulence of the populations varies greatly, which indicated the pathogen ability for rapid race formation in response to changes in biotic and abiotic factors.

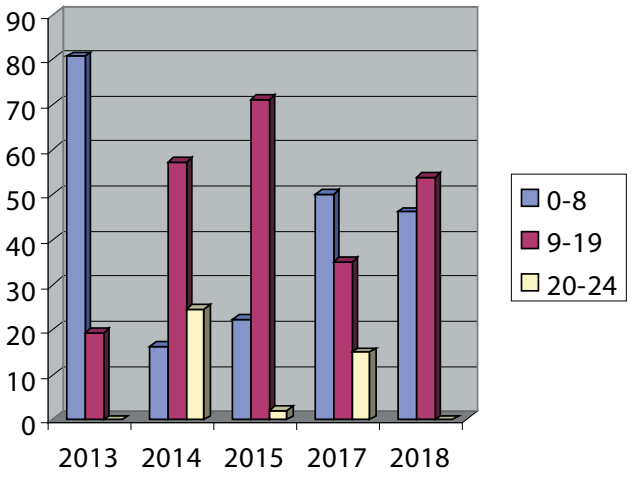

Figure 1. Frequency of *Puccinia striiformis* phenotypes with different numbers of virulence alleles in South Russia during 2013 to 2018.

The differences in frequencies of virulence alleles in the *P. striiformis* populations between years, as shown by Ney indices were generally insignificant (Table 4), with the exception of populations in 2013 and 2017 (N = 0.37).

The minimum Ney index value was found between *Puccinia striiformis* populations in 2015 and 2018 (N = 0.10).

DISCUSSION

The established diversity of the *P. striiformis* population in southern Russia in terms of virulence phenotypes, noted earlier in previous studies (Shumilov *et al.*, 2015; Volkova, 2020), has been primarily associated with the large number of cultivated winter wheat varieties. In the Krasnodar region, about 98 varieties are grown, in the Rostov region, 125 varieties, and in the Stavropol region, 140 winter wheat varieties are used.

The effective *Yr* genes *3, 5, 26,* and *Sp* partially retained their efficiency shown in previous years. For host lines with resistance genes *Yr5* and *YrSp*, this tendency has continued since 2009 (Shumilov, 2013), although the moderate frequency of isolates virulent to *Yr26* in 2009 to 2011 was about 6%. In populations of the *P. striiformis* in other continents, the effectiveness of a number of resistance genes has been similar. For example, in western Canada for many years (1984 to 2013) the host lines with *Yr* genes *1, 5, 15,* and *SP* were not affected by the pathogen, and starting in 2010, isolates virulent to *Yr* genes 24 and *26* started to occur (Brar *et al.*, 2016; 2018). In the United States of America, *Yr* genes *5,* and *15* have been effective since 1960 (Liu *et al.*, 2017). In contrast, in Kazakhstan, *Yr5, Yr9, Yr26,* and *Yr27* are considered to be effective genes (Rsaliev, 2008), while in South Russia *Yr9* has lost its effectiveness and the frequency of *P. striiformis* isolates infecting

Yr27 was from 2 to 11% (Table 2). Isolates from Pakistan and the United States of America were avirulent to lines with genes *Yr5*, *Yr15*, and *YrSP* (Bux *et al*., 2012). The *Yr26* gene, which was effective in South Russia, is gradually losing effectiveness in regions of China, which are especially prone to yellow rust. This is probably due to active use of this gene in wheat breeding in these regions (Han *et al*., 2015). In 2015, *P. striiformis* isolates virulent to *Yr26* were also found in Mexico (Huerta-Espino and Singh, 2017). In Europe, western and central Asia and Africa, this gene has retained effectiveness (Howmoller *et al*., 2020). The appearance and spread of new races in Europe and North Africa, which are annually recorded in new territories, causes concern. For example, the race "Warrior" (*PstS7*), discovered in 2011 in the United Kingdom (virulence profile *Yr1, 2, 3, 4, 6, 7, 9, 17, 25, 32, Sp, AvS,* and *Amb),* and introduced into the European population of the pathogen, caused increased yield losses in many varieties (Rahmatov, 2016). In 2016, a virulent race was found in Ukraine and Azerbaijan (Hovmøller *et al*., 2018). In Russia, *Yr3* and *YrSp* still retain their effectiveness, but the appearance of virulent races in neighbouring regions dictates the need for careful monitoring of the virulence of *P. striiformis* populations.

Thus, the *Yr5, Yr15*, and *Yr26* genes have remained effective in different regions of the world for many years. This is probably due to their origins. The *Yr5* gene was obtained from the wild species *Triticum spelta album*, the *Yr 15* gene from *Triticum dicoccoides*, (Gerechter-Amitai *et al*. 1989), and the *Yr26* gene was transferred from durum wheat to soft wheat via amphiploid with *Aegilops tauschii* (McIntosh and Lagudah, 2000). These three genes belong to the group of so-called *ASR* genes, which are distinguished by their efficacy at all stages of plant growth (Wang and Chen, 2017). For the *P. striiformis* population in southern Russia, the frequency of isolates virulent to lines with *Yr15* genes varied from 11 to 82%.

Dynamics of the frequency of *P. striiformis* isolates to some differential varieties and lines with *Yr* genes can be traced, starting from 2009 (Figure 2 and Figure 3) (*Shumilov*, 2013).In 2014, there was a sharp increase in the frequency of pathogen isolates virulent to varieties and lines with genes *Yr25 + 32* and *Yr10 + Mor.* In subsequent years, the frequencies decrease. A similar surge was observed for most of the other *Yr* genes, including *1, 2, 4b, 9, 10, 15, 21, 25, 29, SU, 3a + 4a + V23, 2 + 6,* and *7 + 22 + 23.* In general, however, there were no significant differences between the 2014 population and other populations. This indicates that the pathogen populations were clonal, and the variability was probably due to weather conditions or rotation of varieties, and not from pathogen introductions from outside the region.

Comparing the frequencies of virulence alleles with similar results in previous years indicates that the resistance of some effective genes has gradually been lost (see Figures 2, and 3). For example, the frequency of isolates virulent to testers with the genes *Yr3a + 4a + ND* and *Yr2 + 9* in 2009 to 2011 did not exceed 5%, while from 2013 to 2015 this was greater ranging from 6 to 19%.

A specific feature of the North Caucasian *P. striiformis* populations has been the low or moderate frequency of occurrence of isolates virulent to a number of differential lines based on the wheat variety Avocet, as compared to pathogen populations in Canada and the United States of America. For example, in the pathogen population in Canada in 2012, there was high frequency of pathogen isolates (70 to 100%) with virulence to *YrA, Yr2, Yr6, Yr7, Yr8, Yr9, Yr17, Yr26, Yr27, Yr31* and *Yr32* (Kumar *et al*., 2012). In the South Russian population, the frequency of isolates virulent to most of these lines ranged from 6 to 17%. Therefore, for a complete

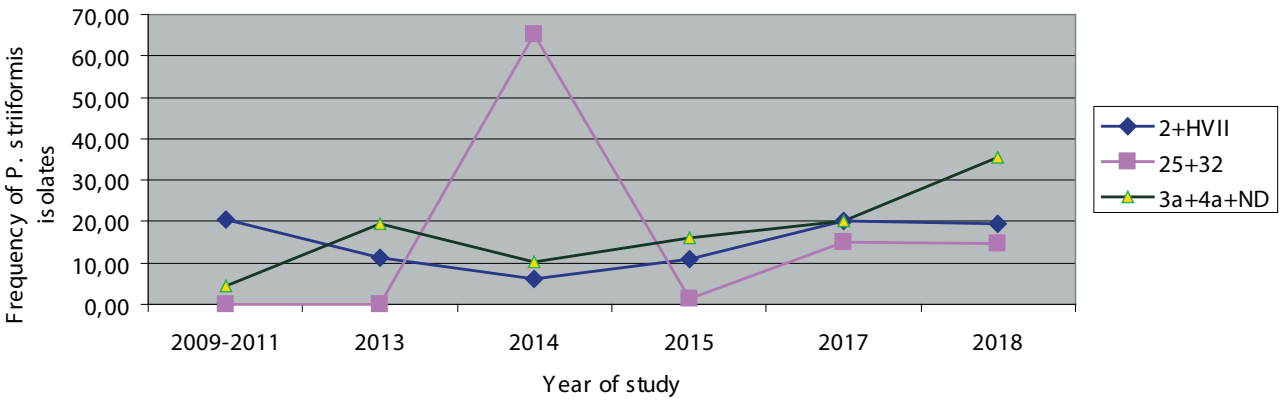

Figure 2. Frequencies of *Puccinia striiformis* isolates in South Russia from 2009 to 2018 with virulence to the European set of differential wheat varieties.

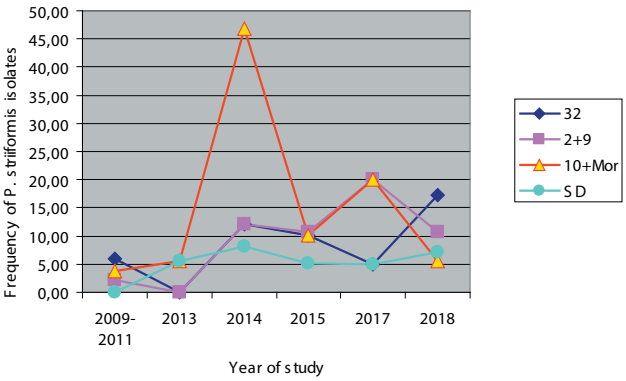

Figure 3. Frequencies of *Puccinia striiformis* isolates in South Russia during 2009 to 2018, with virulence to the host varieties and lines of the International and Australian differential sets.

and objective analysis of the virulence of the *P. striiformis* population, differentiation in the southern region of Russia was carried out using the international, American, European and Australian host differential sets.

CONCLUSIONS

These studies of the *P. striiformis* populations in South Russia have shown that even in conditions unfavourable for the pathogen, yellow rust of wheat occurred in the region every year, and in some areas there were foci of the disease with of up to 50% severity. Effective host genes for resistance to *P. striiformis* were the *Yr* genes *3, 5, 26,* and *Sp*. At the same time, host lines with genes *Yr5* and *Yr Sp* have continued to be resistant since 2009. Single (from 1 to 5%) occurrences of isolates virulent to host lines with several *Yr* genes were observed, including gene *3a, 17, 24, 3b + 4a + H46,* and *3c + Min*. According to the Shannon diversity indices, phenotypic composition of the *P. striiformis* population in South Russia has been established. This confirms is a characteristic feature of the population, as described in previous studies (Shumilov *et al*., 2015; Volkova *et al*., 2020). The differences in *P. striiformis* populations in the frequency of virulence genes between years are insignificant. During the five years of the present study, there were intensive virulence dynamics and changes in the frequency of virulence to host *Yr* genes in the pathogen population. This feature in South Russia, combined with high phenotypic diversity, indicates the ability of *P. striiformis* for rapid race formation and morphogenesis in response to changes in biotic and abiotic environmental factors. This dictates the need for continued monitoring of an important pathogen in this region. The obtained long-term data on the dynamics of virulence of *P. striiformis* are important for understanding the interaction mechanisms of this host-pathogen system, and provide a necessary link in breeding for resistance to yellow rust in South Russia.

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