GRRC 2022 report of stem and yellow rust genotyping and race analyses

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Key highlights stem rust

- **Clade I (Ug99) was not observed outside East Africa, however, two new races with reduced virulence to Sr21 were detected in Kenya.**
- **Clade III-B (race TTRTF) was widespread in southern part of Europe, and recently detected in Tunisia, Switzerland and Sweden. Since its detection in Sicily in 2016, TTRTF has been confirmed in 10 countries in Europe, and in 4 countries in Africa/Asia.**
- **Clade IV-B (races TKTTF, TKRTF and TTTTF) was observed in Tanzania and Tunisia and in 9 European countries in 2021 and 2022. TKRTF was observed in a single isolate from Spain; TTTTF was observed in East Africa but not in Europe.**
- **Clade IV-F (races TKKTF, TKFTF) was detected in 4 African countries in 2021-2022, and widespread in Europe (14 countries). Previously, race TKKTF has been detected in Azerbaijan, Egypt, Iran, Iraq and Tajikistan. Race TKFTF was not detected outside of Europe.**
- **Two genetic groups were prevalent in Europe in 2021-2022, Clade IV-B, and Clade IV-F. Significant spread has been observed in recent years, particularly in France, but also in other countries in Central/West Europe and Africa.**

Key highlights yellow rust

- **PstS16 became widespread in Ethiopia in 2021-2022 after exotic incursion from Asia in 2020. An additional incursion was detected 2021-2022, but the new genotype remained at low frequency.**
- **PstS17 (new named group, provisionally termed “ME2018) was detected in East Africa (Ethiopia) for the first time. This group has been detected in the Middle East since 2018, but in 2021-2022 also detected at low frequency in the Baltic states.**
- **Genetic group PstS13, which is widespread on several continents, was detected for the first time in Northern Africa (Tunisia). A single race/genotype is prevalent in this group although local variants have been observed.**
- **PstS10 was the most prevalent genetic group in Europe. At least 4 races were detected, each adapted to local, widely grown wheat varieties.**
- **PstS11 and PstS1/2 were confirmed in multiple countries in East Africa.**
- **Additional genetic groups, including groups which have not yet been named (collectively termed ‘Other’), were either absent or detected in low frequencies.**
- **Samples from Nepal 2021-2022 were genetically different from previous named groups, revealing many genotypes of which some were dominating.**

Summary of SSR genotyping and race phenotyping results from GRRC (2008-2022) is available on the GRRC website (http://www.wheatrust.org/), including updated tables showing the relationship between races and genetic groups.

This report presents results from molecular genotyping and race typing based on samples of rust infected wheat, barley and triticale collected in 2022 across four continents, i.e., Europe, Asia, Africa and South America. The report comprises results for wheat yellow/stripe rust (*Puccinia striiformis*) and wheat stem rust, *P. graminis* f.sp. *tritici*. The testing of additional samples from 2022 and 2023 is ongoing with emphasis on alignment of results from different rust diagnostic laboratories and genotyping approaches with the aim of presenting the global landscape for yellow and stem rust infecting wheat.

In 2022, a total of 833 samples/derived isolates from 20 countries were handled (Table 1, Table 5). Each sample generally consisted of multiple rust infected leaves or stems. Incoming rust samples entered a recovery procedure in parallel to Simple Sequence Repeat (SSR) genotyping. More than 350 samples were successfully recovered. In case of detection of more than a single genotype within a sample, additional genotyping was based on purified samples. Subsets of recovered isolates were race phenotyped using bioassays consisting of differential wheat lines inoculated with live spore samples multiplied under strict experimental conditions (Hovmøller et al. 2017; Patpour et al., 2022).

Nomenclature of races and genetic groups

Genetic groups of yellow rust were named Pst followed by a digit. Race variants were indicated by the additional virulence observed compared to the virulence profile of the core genetic group. For detailed rationale of race typing and naming of significant *P. striiformis* races and genetic groups, see Ali et al. (2017), Hovmøller et al. (2017), and updated summaries on the GRRC website. A new distinct genetic group in yellow rust, first detected in the Middle East in 2018 (provisionally termed “ME2018”), was named PstS17 for future reference. The genetic grouping of stem rust was based on Szabo et al. (2022) and detailed alignment of the SSR and SNP genotyping results between the Cereal Disease Lab (USA) and GRRC; the race phenotyping was based on 20 internationally agreed wheat lines differentiating virulence in stem rust (Jin et al., 2008; Patpour et al., 2022).

A strong correlation between genetic group and race phenotype was observed for clonal populations of yellow rust, and similarly, most races of wheat stem rust were associated with specific genetic groups (‘clades’). A comprehensive documentation of the nomenclature of stem rust races and genotypes, and the underlying experimental procedures are available on the GRRC website, where new mapping tools were implemented. In sexual populations unique and diverse genotypes and races are often observed. These and other infrequent groups are termed “Other” in tables in this report and in online maps and charts (www.wheatrust.org).

2022 results – wheat stem rust

A total number of 202 samples were received in 2022 (Table 1). Genotyping results of 249 samples from 2021 and 141 samples from 2022, in total representing 20 countries, are presented in Table 2. Race typing was completed for 124 representative isolates from these two years. The prevalent races and virulences detected by GRRC within each genetic group since 2012 are shown in Table 3. Graphical presentation of results available on *www.wheatrust.org.* Detailed results for Europe 2016-2021, including genetic diversity with respect to race and genotype in local populations in proximity to the alternate host, *Berberis* spp., were published by Patpour et al. (2022).

No major changes were observed in stem rust in 2021-2022 compared with previous years (Table 2). In Clade I (Ug99 group), two new races with reduced virulence to *Sr21* were detected in East Africa (Fig. 1), and Clade III-B showed additional spread to northern Europe (Sweden).

Table 1. Number of stem rust samples and derived isolates in 2022 (D: dead, L: live/recovered)

		2022		Total
Geographic group	**Country**	**D**	**L**	
Africa, CW Asia	Ethiopia		2	2
	Kenya		23	23
	Nepal	2		2
	Tanzania	41		41
	Tunisia		18	18
Africa, CW Asia Total		**43**	**43**	**86**
Europe	Austria		4	4
	Belgium		2	2
	Czech Republic		3	3
	Denmark	4		4
	France	12	7	19
	Germany	3	11	14
	Italy	13	7	20
	Norway		6	6
	Poland		5	5
	Slovakia		3	3
	Spain	20	7	27
	Sweden	1		1
	United Kingdom		8	8
Europe Total		**53**	**63**	**116**
Grand Total		**96**	**106**	**202**

Detailed remarks (Table 2): Clade I (Ug99 group) was only observed in East Africa (Kenya and Tanzania). So far, this group has not been detected in Europe. Six different races were detected in this clade, of which race TTKTT was the most prevalent (55% of tested isolates in 2021-2022) and PTKTT (32%), the latter being avirulent to *Sr21* (Table 3; Fig. 1).

Clade III-B (TTRTF, ‘Sicily race’), was detected in two African countries in 2021-2022, Tanzania and Tunisia, and in six European countries, Austria, Czech Republic, Italy, Slovakia, Sweden (first detection), and Switzerland. Since its first detection in 2016, TTRTF has been confirmed in 10 countries in Europe, and 4 countries in Africa/Asia.

Clade IV-F (containing two closely relate races, TKKTF and TKFTF), was detected in four African countries in 2021-2022, Ethiopia, Kenya, Tanzania and Tunisia, and 14 European countries. These includes Austria, Belgium, Czech Republic, Denmark, France, Germany, Italy, Norway, Poland, Slovakia, Slovenia, Spain, Sweden and Switzerland. Previously, Clade IV-F has also been detected in Azerbaijan, Egypt, Iran, Iraq and Tajikistan in our studies. Race TKFTF was not detected in Africa.

Clade IV-B (containing closely related races, TKTTF, TKRTF and TTTTF), was observed in Tanzania and Tunisia in 2021-2022, and in nine European countries, including Belgium, Denmark, France, Germany, Norway, Slovakia, Spain, Sweden and the United Kingdom. In clade IV-B in Europe, only race TKTTF was observed, except one from Spain showing TKRTF. In East Africa, both TKTTF and TTTTF have been observed in this group.

Clade VIII (containing two closely related races, RFCNC (predominant) and HFCNC), was only observed in Eastern Europe. In contrast to prevalent races, these two races were avirulent to *Sr6*, *Sr9b*, *Sr9d, Sr9e* and *Sr38* (Table 3).

Table 2. Distribution of isolates of *P. graminis* f.sp. *tritici* from 20 countries in 2021 and 2022 in prevalent genetic groups (Other: MLGs not yet assigned a named group).

Geographic group	Country	SSR name	2021	2022	Total
Africa, CW Asia	**Ethiopia**	Clade IV-F	4	2	6
	Kenya	Clade I	57	20	77
		Clade IV-F	3		3
	Nepal	Other		1	1
	Tanzania	Clade I	7	14	21
		Clade III-B	1		1
		Clade IV-B	3	18	21
		Clade IV-F	1	7	8
	Tunisia	Clade III-B	22	1	23
		Clade IV-B	1	15	16
		Clade IV-F	2		2
Africa, CW Asia Total			**101**	**78**	**179**
Europe	**Austria**	Clade III-B	3		3
		Clade IV-A.1	1		1
		Clade IV-F	2		2
	Belgium	Clade IV-B	3	1	4
		Clade IV-F		1	1
	Czech Republic	Clade III-B	2		2
		Clade IV-F	4		4
		Clade VIII	1		1
	Denmark	Clade IV-B	3		3
		Clade IV-F	1		1
	France	Clade IV-B	21	12	33
		Clade IV-F	16	2	18
	Germany	Clade IV-B	7		7
		Clade IV-F	1	4	5
	Italy	Clade III-B	21	17	38
		Clade IV-F	10	1	11
	Norway	Clade IV-B	1		1
		Clade IV-F	1	5	6
		Other	3		3
	Poland	Clade IV-F	5		5
	Slovakia	Clade III-B	4		4
		Clade IV-B	1		1
		Clade IV-F	2		2
	Slovenia	Clade IV-F	1		1
	Spain	Clade IV-B	6	5	11
		Clade IV-F	4	15	19
	Sweden	Clade III-B	6		6
		Clade IV-B	3		3
		Clade IV-F	2		2
		Other	1		1
	Switzerland	Clade III-B	4		4
		Clade IV-F	6		6
	United Kingdom	Clade IV-B	2		2
Europe Total			**148**	**63**	**211**
Total			**249**	**141**	**390**

Table 3. Relationship between genetic groups and prevalent races detected by GRRC (cf. Table 2).

Common names of prevalent races and genetic groups in stem rust - GRRC, May 2023			
Genetic group	**Race name**	**Virulence phenotype**	**Prevalence in geographical region**
Clade I	PTKTK	*5,-,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,31,38,McN*	Africa
	PTKTT	*5,-,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,24,31,38,McN*	Africa
	TTKSF	*5,21,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,-,-,-,38,McN*	Africa
	TTKSK	*5,21,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,-,-,31,38,McN*	Africa, CW Asia
	TTKST	*5,21,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,-,24,31,38,McN*	Africa
	TTKTK	*5,21,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,31,38,McN*	Africa
	TTKTT	*5,21,9e,7b,11,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,24,31,38,McN*	Africa
Clade II	JRCQC	*-,21,9e,-,11,6,-,9g,-,-,-,17,9a,9d,-,-,-,-,-,McN*	Africa
	JRCQF	*-,21,9e,-,11,6,-,9g,-,-,-,17,9a,9d,-,-,-,-,38,McN*	CW Asia
Clade III-B	TTRTF	*5,21,9e,7b,11,6,8a,9g,36,9b,-,17,9a,9d,10,Tmp,-,-,38,McN*	Africa, CW Asia, Europe
Clade IV-A.1	TKTTF	*5,21,9e,7b,-,6,8a,9g,36,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Africa, CW Asia, Europe
Clade IV-A.2	TKTTF	*5,21,9e,7b,-,6,8a,9g,36,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Africa, Europe
Clade IV-B	TKTTF	*5,21,9e,7b,-,6,8a,9g,36,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Africa, CW Asia, Europe
	TTTTF	*5,21,9e,7b,11,6,8a,9g,36,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Africa
Clade IV-C	TKTTF	*5,21,9e,7b,-,6,8a,9g,36,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	CW Asia
Clade IV-D	TKKTF	*5,21,9e,7b,-,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Europe
Clade IV-E.1	TKKTF	*5,21,9e,7b,-,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Europe
Clade IV-E.2	TKKTF	*5,21,9e,7b,-,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	Europe
Clade IV-F	TKKTF	*5,21,9e,7b,-,6,8a,9g,-,9b,30,17,9a,9d,10,Tmp,-,-,38,McN*	East Africa, Europe
	TKFTF	*5,21,9e,7b,-,6,8a,9g,-,-,30,17,9a,9d,10,Tmp,-,-,38,McN*	Europe
Clade VIII	RFCNC	*5,21,-,7b,-,-,8a,9g,-,-,-,17,9a,-,10,-,-,-,-,McN*	Europe
	HFCNC	*-,21,-,7b,-,-,8a,9g,-,-,-,17,9a,-,10,-,-,-,-,McN*	Europe
Figures and symbols designate virulence and avirulence (-) corresponding to stem rust resistance genes: Sr5, Sr6, Sr7b, Sr8a, Sr9a, Sr9b, Sr9d, Sr9g, Sr10, Sr11, Sr17, Sr21, Sr24, Sr31, Sr30, Sr36, Sr38, SrTmp and susceptible control 'McNair701'. In many cases, the virulence phenotype was deducted based on more than a single differential line.			

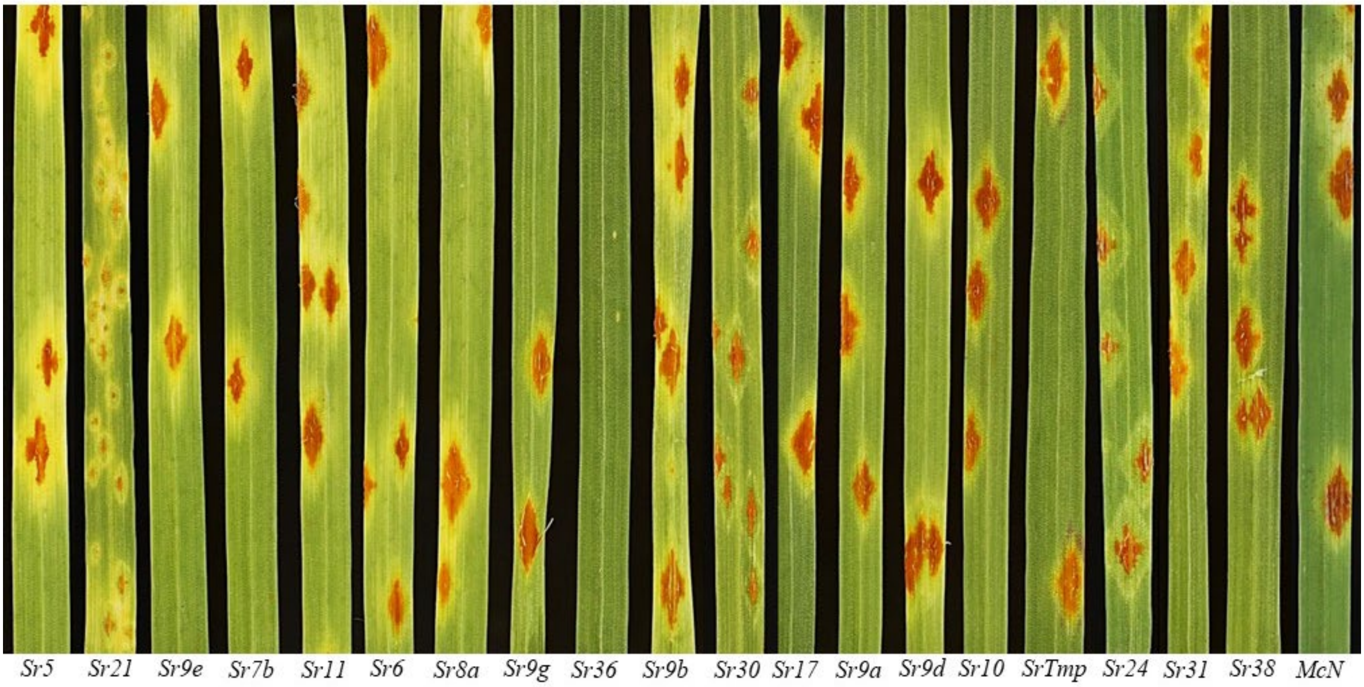

Figure 1. Infection type responses on wheat differential lines of a stem rust race (PTKTT, Clade I), which has evolved in the UG99 group in East Africa, note the low infection type for *Sr21*.

2022 results – wheat yellow rust

A total of 623 samples from 20 countries and four continents were handled in 2022, of which 249 were successfully recovered.

Table 4. Number of yellow rust (*P. striiformis*) samples and derived isolates in 2022 (D: Dead, L: live).

		2022		Grand Total
Geographic group	**Country**	**D**	**L**	
Africa, C&W Asia	Ethiopia	127	20	147
	Iraq	13		13
	Kenya	2	26	28
	Tanzania	23		23
	Tunesia		5	5
Africa, C&W Asia Total		**165**	**51**	**216**
Europe	Belgium	23	12	35
	Czech Republic	18	1	19
	Denmark	11	22	33
	Ethiopia	2		2
	France	8	31	39
	Germany		11	11
	Great Britain	1	3	4
	Italy	3		3
	Norway	22	5	27
	Poland	10	22	32
	Spain	12	9	21
	Sweden	13	13	26
	United Kingdom		22	22
Europe Total		**123**	**151**	**274**
South America	Uruguay	20	30	50
South America Total		**20**	**30**	**50**
South Asia	Nepal	76	17	93
South Asia Total		**76**	**17**	**93**
Grand Total		**384**	**249**	**633**

A total of 259 isolates from Africa, Asia, and South America, and 188 from Europe were successfully genotyped in 2022 (Table 5). Race typing was done for 34 isolates for alignment and confirmation of genetic grouping and emergence of new races within these. Common races and virulence phenotypes within groups are shown in Table 6. Graphical presentation of results available on www.wheatrust.org.

In East Africa, PstS16 was only confirmed in Ethiopia in 2022, but recent tests of 2023 samples from Uganda suggest the presence of PstS16 in farmer fields at two locations (data not shown). Onwards spread of PstS16 is expected, taking into account the broad virulence spectrum of isolates in this genetic group and the rapid spread in Ethiopia in previous years.

The new named genetic group, PstS17 (provisionally termed ME2018) was detected for the first time in East Africa in 2022; and confirmed on at least four locations. PstS17 was first detected in the Middle East, where it has been widespread since 2018. In 2021-2022, this group was also detected in the Baltic states in Europe.

PstS13 was prevalent in several countries in South America, where it was first detected in 2017, and in 2022, it was detected for the first time in Northern Africa (Tunisia). In Europe, PstS13 was mainly detected on triticale, but also durum wheat, rye, spelt and bread wheat were affected. Previous alignment experiments in collaboration with University of Sydney, Australia, confirmed PstS13 in Australia, where it is one of the most widespread races (Ding et al., 2021).

PstS10 is highly dominating in Europe, but also present in South America and since 2018 confirmed in Australia (Ding et al. 2021). At least four races have been detected in PstS10 in Europe, each adapted to local, widely grown wheat varieties, typically named after the wheat varieties where they first caused significant epidemics. These races differ by quantitative shifts in rust susceptibility of commercial varieties, e.g., from 'resistant' to 'susceptible' or from 'susceptible' to 'extreme susceptible'. It has not yet been possible to differentiate the new races within PstS10 by molecular techniques nor by standard wheat differential lines. The Warrior and Kranich groups, which represent the original incursions into Europe in 2011, have rarely been observed in recent years.

PstS14 was completely dominating in Iraq in 2021 and 2022, which represents the first detection of this group in Asia. PstS11 was still prevalent in East Africa, now confirmed in eight countries in East Africa and in the Middle East.

The aggressive races in PstS1 and PstS2, which are not distinguishable by SSR genotyping, share epidemiological features such as adaptation to warmer temperatures. Therefore, in future correspondence, these two groups will be merged in a common genetic group, termed PstS1/2, and only separated when needed in particular cases, which is possible by two SCAR markers developed for this purpose (Walter et al., 2016).

Samples from Nepal 2021-2022 were genetically different from previous named groups, revealing multiple genotypes, some of which were dominating, which is consistent with previous results from the near-Himalayan region in Asia.

Table 5. Distribution of isolates in *P. striiformis* from 20 countries in prevalent genetic groups. (Continues next page).

			Crop season		
Geographic group	**Country**	**SSR name**	**2021**	**2022**	**Total**
Africa, C&W Asia	**Afghanistan**	Other	11		11
		PstS16	72		72
	Ethiopia	PstS17		5	5
		Other		3	3
		PstS1/2		9	9
		PstS11	34	37	71
		PstS16	34	77	111
	Iraq	PstS14	32	12	44
	Kenya	PstS1/2		2	2
		PstS11	34	18	52
	Tanzania	Other		1	1
		PstS1/2		16	16
	Tunesia	PstS13		5	5
Africa, C&W Asia Total			**217**	**185**	**402**
South America	**Paraguay**	PstS13	2		2
	Uruguay	PstS10	1	4	5
		PstS13	18	34	52
		PstS7	1	6	7
South America Total			**22**	**44**	**66**
South Asia	**Nepal**	Other	**19**	**30**	**49**
Grand Total			**258**	**259**	**517**

Table 5. Distribution of isolates in *P. striiformis* from 20 countries in prevalent genetic groups. (Continued).

			Crop season		
Geographic group	**Country**	**SSR name**	**2021**	**2022**	**Total**
Europe	**Belgium**	PstS10		31	31
		PstS15		1	1
	Czech Republic	PstS10	10	19	29
		PstS13	1		1
		PstS7	1		1
	Denmark	Other		1	1
		Other PstS15	2		2
		PstS10	17	25	42
		PstS13	3	1	4
		PstS15		1	1
		PstS7	1		1
	Estonia	PstS17	3		3
	France	PstS10	6	27	33
		PstS15	1	1	2
		PstS7	1		1
	Germany	PstS10	4		4
		PstS13	2		2
	Great Britain	PstS10		4	4
	Hungary	PstS7	1		1
	Italy	PstS10	6		6
		PstS13	7	2	9
		PstS7	1		1
	Latvia	PstS17	1		1
		PstS15	1		1
	Netherlands	PstS10	4		4
	Norway	Other	1		1
		PstS10	26	19	45
		PstS13		3	3
		PstS7	1	1	2
	Poland	Other	3		3
		PstS10	1	7	8
		PstS13	4		4
		PstS7	1	3	4
	Portugal	PstS10	2		2
	Slovakia	PstS10	1		1
		PstS13	1		1
		PstS14	1		1
	Spain	PstS10	5	12	17
		PstS13	1		1
		PstS14	1	7	8
	Sweden	Other		1	1
		PstS10	25	21	46
		PstS13	6	1	7
	United Kingdom	PstS10	21		21
Europe Total			**174**	**188**	**362**
Grand Total			**432**	**447**	**879**

Table 6. Correspondence between genetic groups and prevalent races of *P. striiformis* sampled from epidemic sites since 2000, Global Rust Reference Center.

Common names of prevalent races and genetic groups in yellow rust - GRRC, May 2023			
Genetic group	**Race**	**Virulence phenotypec**	**Prevalence in geographical region**
PstS0	Brigadiera	1,2,3,-,-,-,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	Solstice_Oakley	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Tulsa	-,-,3,4,-,6,-,-,-,-,-,-,-,25,-,32,-,AvS,-	Europe
PstS1/2	PstS1/2b	-,2,-,-,-,6,7,8,9,-,-,-,-,25,-,-,-,AvS,-	North America, Australia
	PstS1/2,v1	1,2,-,-,-,6,7,8,9,-,-,-,-,25,-,-,-,AvS,-	East Africa
	PstS1/2,v3	-,2,3,-,-,6,7,8,9,-,-,-,-,25,-,-,-,AvS,-	East Africa
	PstS1/2,v27	-,2,-,-,-,6,7,8,9,-,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia, North Africa
	PstS1/2,v1,v27	1,2,-,-,-,6,7,8,9,-,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia
	PstS1/2,v3,v27	-,2,3,-,-,6,7,8,9,-,-,-,-,25,27,-,-,AvS,-	East Africa
	PstS1/2,v10	-,2,-,-,-,6,7,8,9,10,-,-,24,25,-,-,-,AvS,-	East Africa, West Asia
	PstS1/2,v10,v27	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	West Asia
	PstS1/2,v3,v10,v27	-,2,3,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
PstS3	PstS3	-,(2),-,-,-,6,7,8,-,-,-,-,-,25,-,-,-,AvS,-	Europe, Asia
	PstS3,v1	1,(2),-,-,-,6,7,8,-,-,-,-,-,25,-,-,-,AvS,-	Asia
PstS4	Triticale2006	-,2,-,-,-,6,7,8,-,10,-,-,24,-,-,-,-,-,-	Europe
PstS5	PstS5	1,2,3,4,-,6,-,-,9,-,-,-,-,25,-,32,-,AvS,Amb	Central Asia
	PstS5,v17	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,Amb	Central Asia, South Asia
PstS6	PstS6	1,2,-,-,-,6,7,-,9,-,-,17,-,-,27,-,-,AvS,-	East Africa, Central Asia, South Asia
PstS7	Warrior	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,Amb	Europe, North Africa
PstS8	Kranich	1,2,3,-,-,6,7,8,9,-,-,17,-,25,-,32,-,AvS,Amb	Europe
PstS9	PstS9	1,2,3,4,-,6,-,-,9,-,-,-,-,25,27,32,-,AvS,Amb	Central Asia, South Asia
	PstS9,v17	1,2,3,4,-,6,-,-,9,-,-,17,-,25,27,32,-,AvS,Amb	Central Asia
PstS10	Warrior(-)	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe, North Africa
	Kalmar	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe
	Benchmark	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe
	Amboise	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe
PstS11	PstS11	-,2,-,(4),-,6,7,8,-,-,-,17,-,-,27,32,-,AvS,-	Central and West Asia, East Africa
PstS12	Hereford	-,2,3,-,-,6,7,8,-,-,-,17,-,25,-,32,-,AvS,-	Europe
PstS13	Triticale2015	-,2,-,-,-,6,7,8,9,-,-,-,-,-,-,-,-,AvS,-	Europe, South America, West Asia
	Triticale2015,v10	-,2,-,-,-,6,7,8,9,10,-,-,24,-,-,-,-,AvS,-	Europe
PstS14	PstS14	-,2,3,-,-,6,7,8,9,-,-,17,-,25,-,32,(Sp),AvS,-	Europe, North Africa, West Asia
PstS15	PstS15	1,2,3,-,-,6,7,-,9,-,-,17,-,25,-,32,-,AvS,Amb	Europe
PstS16	PstS16	1,2,3,(4),-,6,7,8,9,-,-,17,-,25,27,32,-,AvS,-	South Asia, East Africa
PstS17	PstS17	-,2,-,-,-,6,7,8,-,-,-,17,-,-,-,32,(Sp),AvS,Amb	Middle East, Europe, East Africa
	PstS17,v10	-,2,-,-,-,6,7,8,-,10,-,17,24,-,-,32,(Sp),AvS,Amb	Middle East

a) Many more races in PstS0 in the past, now rarely observed. b) PstS1 and PstS2 not distinguishable by race and SSR (but SCAR). c) Figures and symbols designate virulence and avirulence (-) corresponding to yellow rust resistance genes: Yr1, Yr2, Yr3, Yr4, Yr5, Yr6, Yr7, Yr8, Yr9, Yr10, Yr15, Yr17, Yr24, Yr25, Yr27, Yr32, and the resistance specificity of Spalding Prolific (Sp), Avocet S (AvS) and Ambition (Amb), respectively. In PstS10, Kalmar, Benchmark and Amboise can only be distinguished by these varieties.

Submission and preparation of samples

Samples of rust infected wheat are submitted according to an import permit issued by GRRC valid for one country and one year in compliance with the Nagoya Protocol about control, access and utilization of genetic resources. The details of sampling preparation are available at http://wheatrust.org/submission-of-isolates/; a video demonstrates the ideal sampling procedures. Bilateral agreement with private/public enterprises is also possible. Since 2011, GRRC has accepted samples of both yellow rust, leaf rust and stem rust. Several cycles of spore multiplication were generally made to obtain sufficient spore amounts for storage and race analyses. In case of signs of multiple genotypes/races within a sample, these were generally sub-cultured for purification according to standard GRRC procedures (Hovmøller et al. 2017), open-access for downloads for non-commercial and educational purposes. The SSR genotyping of isolates based on DNA extraction from infected leaves (single lesions) was highly successful for appropriate discrimination of genetic groups, following the procedures of Thach et al. 2016, Patpour et al., 2022.

Supporting literature

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- Ding Y et al. 2021. Incursions of divergent genotypes, evolution of virulence and host jumps shape a continental clonal population of the stripe rust pathogen Puccinia striiformis. Molecular Ecology, 20.09.2021.
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- Patpour, M., Hovmøller, M. S., Rodriguez-Algaba, J., Randazzo, B., Villegas, D., Shamanin, V. P., et al. (2022) Wheat Stem Rust Back in Europe: Diversity, Prevalence and Impact on Host Resistance. Frontiers in Plant Science, 13 https://www.frontiersin.org/articles/10.3389/fpls.2022.882440/full
- Szabo, L., Olivera Firpo, P.D., Wanyera, R., Visser, B., and Jin, Y. 2022. Development of a diagnostic assay for differentiation between genetic groups in clades I, II, III and IV of *Puccinia graminis* f. sp. tritici. Plant Disease https://doi.org/10.1094/PDIS-10-21-2161-RE.

Acknowledgements

Submission of samples of rust infected plant material in 2022 was facilitated by a large number of collaborators from multiple organisations and countries (Table 7). Sampling in Africa was coordinated by Dave Hodson (CIMMYT); sampling in EC-VCU network trials was coordinated by Valérie Cadot (Geves), France. Samples for alignment of methodologies and results between European rust diagnostic laboratories were kindly privided by collaborators from NIAB (UK), INRAE (France), JKI (Germany) and IHAR (Poland). Additional sampling from several areas was based on bilateral agreements, e.g., Jordbruksverket, Sweden (Gunilla Berg), and Norwegian University of Life Sciences, Norway (Morten Lillemo). Handling and recovery of incoming samples and inoculations by Ellen Jørgensen, production of healthy plants by Jakob Sørensen, and DNA/PCR work by Janne Holm Hansen is greatly acknowledged. The activities were funded by a variety of organisations and research councils: Race typing and genotyping of international (non-European) samples were facilitated by Melinda & Bill Gates Foundation and the UK Foreign, Commonwealth & Development Office (FCDO). Analyses of European samples was supported by European Union's Horizon 2020 research and innovation programme under grant agreement No 773311 (RustWatch), Jordbruksverket, Sweden, and the Research Council of Norway (Hveterust). Final editing of this report by Charlotte Hamann Knudsen is greatly acknowledged.

Table 7. People submitting samples of rust infected leaves/stems of cereals 2022. (Continues next page).

	Country	Collector	Yellow rust	Stem rust
Africa, Asia and South America	**Ethiopia**	Almaz Weytso	x	
		Anduamlak A	x	
		Asela Kesho	x	
		Belachew Bekele	x	
		Dawit	x	
		Dereje Amare	x	
		DZ Pathology Team	x	
		Gerald	x	
		Girma Abebe	x	
		Jemal T	x	
		Kabna Asefa	x	
		Kitessa G	x	
		Luche Soboka	x	
		Mequanint Andualem	x	
		Nurhussein Seid	x	
		Solomon B	x	x
		Tamene	x	
		Tamirat N	x	x
		Tilahun Bayisa	x	
		Yitagesu Tadesse	x	
		Yoseph Alemayehu	x	
		Zerihun Eshetu	x	
	Iraq	Emad Al-Maaroof	x	
	Kenya	Zennah Kosgey	x	x
	Tanzania	Charles Msuya		x
		Christina Petro Buluba		x
		Hosea Nyato		x
		Michael Paul		x
		Moses Mbwana		x
		Salome Wilson Munissi	x	x
		Seni Maico		x
	Tunisia	Amor Yahyaoui		x
		Sarrah Ben M’Barek		x
		Wided Abdedeyam		x
	Uruguay	R. García	x	
		Venancio Riella	x	
		F. Pereira	x	
	Nepal	Basistha Acharya	x	
		Bhajuman Maharjan	x	
		Bhojradi	x	
		Dhurba Thapa	x	
		Khem Pant	x	
		M. Subedi	x	
		Prem Bahadur Magar	x	
		R. Basnet	x	
		Roshan and NWRP	x	
		Suraj Baidya	x	

	Country	Collector	Yellow rust	Stem rust
Europe	**Austria**	Michael Oberforster		x
		Monika Opalo		x
	Belgium	Pierre Hellin		x
		Rodrigo Meza	x	
		Damien Eylenbosch	x	
	Czech Republic	Alena Hanzalová	x	x
		Pawel Kraus	x	
	Denmark	Ellen Jørgensen	x	
		Finn Borum	x	
		Lise Nistrup Jørgensen	x	x
		Peter Spies		x
		Susanne Sindberg	x	x
	France	Anne-Lise Boixel		x
		Benjamin Estassy		x
		Cédric Picard		x
		Christine Despresse		x
		Emmanuel Heumez		x
		Fanny Savaete		x
		Hélène Navier		x
		Jean-Philippe Maigniel	x	x
		Mark Leconte	x	
		Tiphanine Vidal	x	
		Valerie Dufayet		x
	Germany	Adnan Sisic		x
		Bärbel Liebherr	x	
		S. Hagen	x	
		Thomas Zschaeckel	x	
		Uta Liesenberg	x	x
		Volker Heiden	x	
	Italy	Biagio Randazzo	x	x
		Virgilio Balmas	x	x
	Netherlands	L. van den Brink	x	
	Norway	Andrea Ficke	x	
		Ingvild Evju	x	
		Jafar Razaghien	x	
		Morten Lillemo	x	x
		Nils K. Aker	x	
		Rune Karlsen	x	
		Stine Vandsemb		x
		Thomas J. Brown	x	
	Poland	Ewelina Piwowarczyk	x	
		Pawel Czembor	x	x
	Slovakia	Svetlana Šliková	x	x
	Spain	Dolors Villegas	x	
		Fernando Martinez-Moreno	x	x
		Josefina Sillero	x	
	Sweden	Alf Djurberg	x	
		Elin Almén	x	
		Eva Johansson		x
		Eva Mellqvist	x	
		Gunilla Berg	x	
		Lars Johansson	x	
		Lina Norrlund	x	
		Linda Geijersstam	x	
		Lovisa Eriksson	x	
		Mahboobeh Yazdani		x
		Mahbubjon Rahmatov		x
	Great Britain	Amelia Hubbard	x	
		Clare Lewis		x