

GRRC report of yellow and stem rust genotyping and race analyses 2020, Flakkebjerg, DK-4200 Slagelse, Denmark.

Mogens Støvring Hovmøller, Mehran Patpour, Julian Rodriguez-Algaba, Tine Thach, Annemarie Fejer Justesen & Jens Grønbech Hansen, 26 March, 2021.

Corresponding author: mogens.hovmoller@agro.au.dk

Key highlights yellow rust 2020

- Genetic group PstS11 dominating in East Africa and confirmed in eight countries in East Africa and the Middle East.
- First detection in Africa of a unique genotype previously observed in Pakistan and Afghanistan (2017-2018).
- A new group provisionally termed ME2018, detected in Egypt in 2018 and Turkey in 2019, was observed in Latvia in 2020.
- PstS10 is the most prevalent genetic group in Europe. Four races were detected in PstS10, each adapted to local, widely grown wheat varieties.
- Genetic group PstS13 variant carrying *Yr10*-virulence detected in Germany, first detected in Poland (2018). PstS13 has severely affected triticale and durum wheat (Europe) and bread wheat (South America and Australia).
- Genetic group PstS7 (Warrior race) and PstS8 (Kranich race) were less prevalent than in previous years. Up to now, PstS7 detected in Europe, northern Africa and South America, and PstS8 in Europe.
- Additional genetic groups were detected in low frequencies, including PstS15 (single genotype and race), present in France since 2017 and Scandinavia since 2019.
- Alignment experiments confirmed the presence of PstS10 and PstS13 in Australia

Key highlights stem rust 2020

- Additional spread of stem rust in Europe, including France, Austria, Ireland and Norway.
- Clade III-B (race TTRTF), widespread in Sicily since 2016, has now been detected in seven countries in Europe and four countries in Africa/Asia. In 2020, first detection in Austria, Czech Republic, Slovakia, and Slovenia.
- Clade IV-F (race TKKTF) has been detected in 10 European countries (2019-2020), and previously in Egypt, Iran and Tunisia.
- Clade IV-B, (race TKTTF and TTTTF) has been detected in five countries in Europe and six countries in Africa. In 2020, TKTTF was detected in France, Ireland and Spain.
- Unusual races were observed in Czech Republic (RFCNC) and Denmark (QCHNC), the latter first detected in Sweden (2019).
- Clade I (Ug99) was detected in southern Iran (2019), but otherwise we did not observe this group outside East Africa.

Summary of SSR genotyping and race phenotyping results from GRRC (2008-2020) is available online (<http://www.wheatrust.org/>), including an updated table showing the [relationship between races and genetic groups](#).

This report presents molecular genotyping and race typing results based on samples of rust infected wheat, barley and triticale collected in 2019 and 2020 across four continents, i.e., Europe, Asia, Africa and Australia. The report comprises results for the wheat yellow/stripe rust (*Puccinia striiformis*) as well as the wheat stem rust, *P. graminis* f.sp. *tritici*. The testing of additional samples from 2020 and beginning of 2021 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 2020, a total of 469 samples and derived isolates from 22 countries were handled. Each sample generally consisted of multiple rust infected leaves or stems. Representative leaves/stems were selected for alive spore recovery in parallel to genotyping of incoming samples (Table 1, Table 2). More than 300 alive isolates of yellow and stem rust were recovered based on submissions in 2020. We observed a decreasing number of samples from Africa and Asia in 2020, which may reflect restrictions due to the covid-19 pandemic and decreasing resources for global rust surveillance activities.

The genotyping based on Simple Sequence Repeat (SSR) markers was applied on incoming samples of rust infected plant material without prior recovery, whereas the race phenotyping was based on bioassays using differential wheat lines inoculated with spore samples of alive, pure isolates grown under strict experimental conditions (Hovmøller et al. 2017).

Nomenclature of races and genetic groups

Genetic groups of yellow rust are named Pst followed by a digit. Race variants are designated by the additional virulence observed or (-) in case a new variant had fewer virulences than the first defined race within the considered lineage. For details, see the rationale for the naming of significant *P. striiformis* races and genetic groups (Ali et al. 2017) and an updated [summary](#) of genetic groups and races on the GRRC website. The genetic grouping of stem rust is based on Olivera Firpo et al. (2017), [Olivera et al. \(2019\)](#), and detailed alignment of the SSR and SNP genotyping results between the Cereal Disease Lab (USA) and GRRC; the race grouping is based on 20 internationally agreed wheat lines differentiating virulence in stem rust (Jin et al., 2008).

In yellow rust, we have generally observed a strong correlation between genetic groups and race phenotypes in clonal populations, similarly, most races of wheat stem rust were associated with specific genetic groups ('clades'). A more 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 recently. However, in sexual populations we observed unique and diverse genotypes and races. These and other infrequent groups are termed "other" in tables and online maps (www.wheatrust.org).

2020 results – wheat stem rust

Geographic area	Country	2020		Total
		Dead	Recovered	
Africa, CW Asia	Kenya	9	68	77
Africa, CW Asia Total		1	24	25
Europe	Austria		3	3
	Czech Republic		4	4
	Denmark	1	3	4
	France		4	4
	Hungary	1	1	2
	Ireland	1	1	2
	Italy	8	18	26
	Norway		2	2
	Poland	1		1
	Slovakia	4	5	9
	Slovenia	4	9	13
Spain	1	14	15	
Europe Total		21	64	85
C & N America	Mexico		11	11
C & N America Total			11	11
Grand Total		22	99	121

Table 1. Number of stem rust samples and derived isolates (*P. graminis* f.sp. *tritici*) in 2020.

In 2019-2020, we received fewer samples from countries outside Europe compared to previous years. Interestingly, we had samples from three European countries, where wheat stem rust is rarely observed, France, Ireland and Norway. Genotyping results of 308 samples from 20 countries representing four continents are presented in Table 2; 146 recovered isolates were race typed using a standard set of 20 wheat lines used to differentiate races of stem rust. The races and virulences detected within genetic groups are shown in Table 3 and Table 4. Graphical presentation of results available on www.wheatrust.org.

Geographic area	Country	Genetic group	2019	2020	Total	
Africa, CW Asia	Iran	Clade I	2		2	
		Clade III-B	3		3	
	Kenya	Clade I	51	25	76	
		Clade IV-B	2		2	
	Morocco	Clade IV-B	2		2	
	Tunisia	Clade III-B	4		4	
		Clade IV-F	5		5	
	Uganda	Clade I	24		24	
		Clade IV-B	9		9	
		Clade IV-F	1		1	
Africa, CW Asia Total			103	25	128	
Europe	Austria	Clade III-B		2	2	
		Clade IV-F		1	1	
	Czech Republic	Clade III-B		1	1	
		Other		2	2	
	Denmark	Clade IV-F	6		6	
		Other		2	2	
	France	Clade IV-B		4	4	
		Clade IV-F	1		1	
	Germany	Clade IV-F	2		2	
	Hungary	Other	1		1	
	Ireland	Clade IV-B		2	2	
	Italy	Clade III-B	22	12	34	
		Clade IV-F	22	11	33	
	Norway	Clade IV-F		1	1	
	Poland	- (race: TKTF)		1	1	
	Slovakia	Clade III-B		6	6	
		Clade IV-F		1	1	
	Slovenia	Clade III-B		14	14	
		Clade IV-F		2	2	
	Spain	Clade III-B	3		3	
		Clade IV-B	1	14	15	
		Clade IV-F	5		5	
		Other	33		33	
	Sweden	Clade IV-F	1		1	
		Other	1		1	
	Europe Total			98	76	174
	C & N America	Mexico	Other		6	6
C & N America Total				6	6	
Total			201	107	308	

Table 2. Distribution of isolates of *P. graminis* f.sp. *tritici* from 19 countries in prevalent genetic groups.

SSR_name	Race_name	Number of observations
Clade I	TTKSK	4
	TTKST	2
	TTKTK	3
	TTKTT	21
	-	65
Clade I Total		101
Clade III-B	TTRTF	25
	-	42
Clade III-B Total		67
Clade IV-B	TKTTF	21
	TTTTF	5
	-	8
Clade IV-B Total		34
Clade IV-F	TKKTF	24
	-	35
Clade IV-F Total		59
Other	35 races	41
	(blank)	4
Other Total		45
Grand Total		308

Table 3. Relationship between genetic groups and prevalent races detected within these in 2019 and 2020 (cf. Table 2)

Table 4. Correspondence between race name and virulence on common stem rust differential lines

Race_name	Virulence corresponding to NA differentials 1-20 (main R-gene indicated)																			
	Sr5	Sr21	Sr9e	Sr7b	Sr11	Sr6	Sr8a	Sr9g	Sr36	Sr9b	Sr30	Sr17	Sr9a	Sr9d	Sr10	SrTmp	Sr24	Sr31	Sr38	SrMcN
LKMNC	5	-	-	-	-	6	8a	9g	36	-	-	17	9a	-	10	-	-	-	-	McN
RFCNC	5	21	-	7b	-	-	8a	9g	-	-	-	17	9a	-	10	-	-	-	-	McN
RFCPC	5	21	-	7b	-	-	8a	9g	-	-	-	17	9a	-	10	Tmp	-	-	-	McN
TKKTF	5	21	9e	7b	-	6	8a	9g	-	9b	30	17	9a	9d	10	Tmp	-	-	38	McN
TKTTF	5	21	9e	7b	-	6	8a	9g	36	9b	30	17	9a	9d	10	Tmp	-	-	38	McN
TTKSK	5	21	9e	7b	11	6	8a	9g	-	9b	30	17	9a	9d	10	-	-	31	38	McN
TTKST	5	21	9e	7b	11	6	8a	9g	-	9b	30	17	9a	9d	10	-	24	31	38	McN
TTKTK	5	21	9e	7b	11	6	8a	9g	-	9b	30	17	9a	9d	10	Tmp	-	31	38	McN
TTKTT	5	21	9e	7b	11	6	8a	9g	-	9b	30	17	9a	9d	10	Tmp	24	31	38	McN
TTRTF	5	21	9e	7b	11	6	8a	9g	36	9b	-	17	9a	9d	10	Tmp	-	-	38	McN
TTTTF	5	21	9e	7b	11	6	8a	9g	36	9b	30	17	9a	9d	10	Tmp	-	-	38	McN

Clade III-B (TTRTF), present in the epidemics in Sicily in 2016, has been detected in seven countries in Europe and four countries in Africa/Asia. In 2019, first detected in Spain, Tunisia and Iran, and in 2020 first detected in Austria, Czech Republic, Slovakia, and Slovenia.

Clade IV-F, containing race TKKTF, was detected in 11 European countries in 2019-2020, and previously also in Egypt, Iran and Tunisia.

Clade IV-B contained two closely related races, TKTTF and TTTTTF. In this study, TKTTF was detected in France, Ireland and Spain in 2020, whereas TTTTTF was not detected in Europe.

Clade I (Ug99) and associated races have not been detected in Europe. However, multiple Sr31-virulent races, which were not related to clade I, were detected in a recombining population in Spain in 2019.

Additional unusual races were observed in local areas in Czech Republic (RFCNC) and Denmark (QCHNC), the latter previously detected in Sweden in 2018.

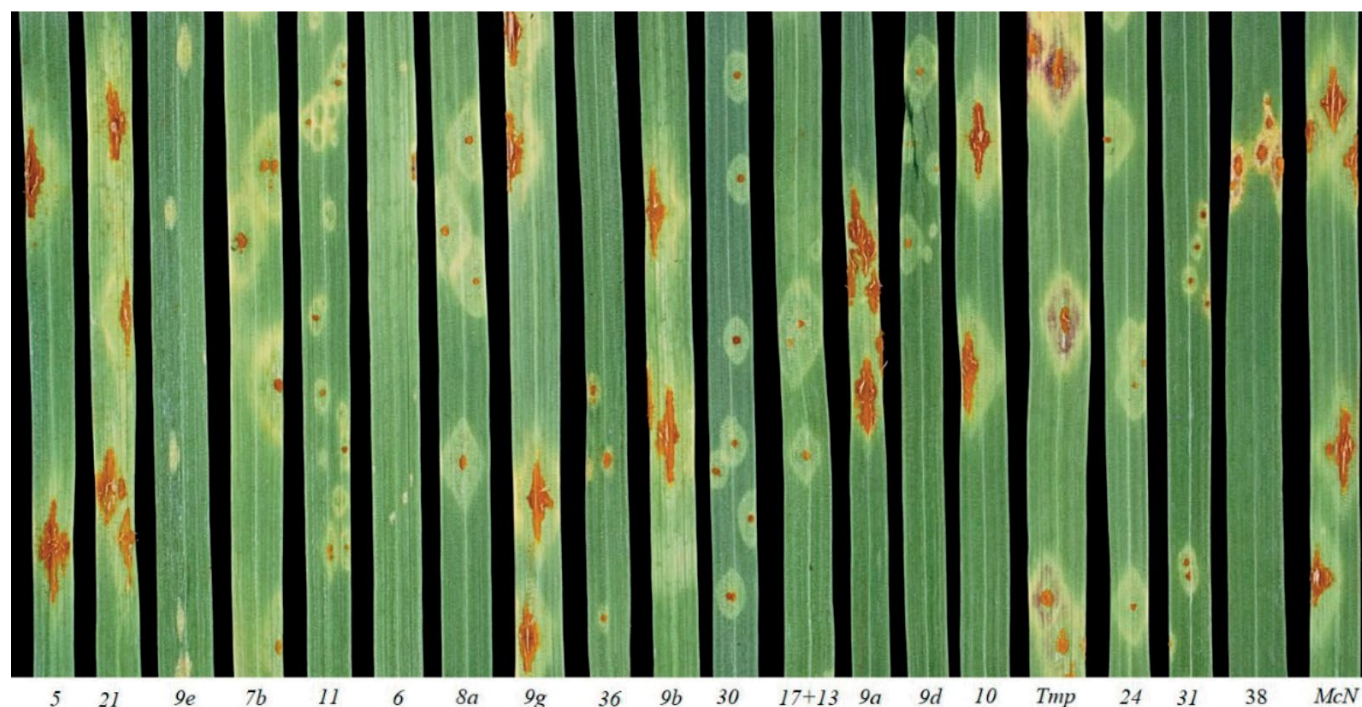


Fig. 1. Infection type responses on wheat differential lines of a stem rust race (QCHNC) with unusual virulence spectrum.

2020 results – wheat yellow rust

Despite the number of yellow rust samples from countries outside Europe was lower in 2020 than in previous years, the geographical area was expanded by including reference DNA samples from Australia representing key races detected since 1978 (Park et al., 2020).

Geographic area	Country	2020		
		Dead	Recovered	Total
Africa, C&W Asia	Ethiopia	17	9	26
	Kenya	11	4	15
Africa, C&W Asia Total		28	13	41
C&N America	Mexico	15	1	16
Australasia	Australia	30		30
Europe	Belgium		13	13
	Czech Republic	1	2	3
	Denmark	12	81	93
	France	4	13	17
	Germany		3	3
	Great Britain		7	7
	Hungary	2	4	6
	Italy	4	8	12
	Latvia		2	2
	Netherlands	1	7	8
	Norway	8	8	16
	Poland	2	5	7
	Slovakia		3	3
	Spain	10	19	29
Sweden	15	20	35	
Switzerland	6	1	7	
Europe Total		65	196	261
Grand Total		138	210	348
* Alignment experiments				

Table 5. Number of yellow rust samples and derived isolates (*P. striiformis*) in 2020.

A total of 216 samples from 18 countries and three continents were successfully genotyped (Table 6). Race typing was done for 65 isolates for alignment and confirmation of genetic grouping and new emergence of new races within genetic groups.

PstS11 is by far the most prevalent genetic group in east Africa, and in 2019 also detected in the Middle East, i.e., confirmed in Ethiopia, Kenya, Rwanda, Tanzania, Uganda and Turkey (Table 6). PstS11 was first detected in Afghanistan (2012) after which it spread to neighboring countries. A single race is prevalent in PstS11 (virulence phenotype: -,2,-,4,-,6,7,8,-,-,17,-,-,27,32,-,AvS,-). The rapid spread across wide areas, and associated rust epidemics, including previously resistant varieties in affected areas, demonstrate the potential epidemic risks associated with this race/genotype.

Table 6 (continues next page). Distribution of isolates in *P. striiformis* from 18 countries in prevalent genetic groups. Common races and virulence phenotypes within groups are shown in Table 7. Graphical presentation of results available

Geographic group	Country	SSR_name	2019	2020	Total
Africa, C&W Asia	Ethiopia	Other	1	2	3
		PstS11	25	8	33
	Iran	Other	4		4
		PstS6	1		1
	Kenya	PstS1	1		1
		PstS11	17	12	29
		PstS2	2	4	6
	Turkey	ME2018 ^{a)}	6		6
		PstS11	7		7
		PstS13	3		3
		PstS14	9		9
	Uganda	PstS1	1		1
		PstS11	3		3
		PstS2	3		3
		PstS6	6		6
	Africa, C&W Asia Total			89	26
C&N America	Mexico	Other		1	1
C & N America total				1	1

In 2020, a unique genotype was detected in Africa (Ethiopia) for the first time (shown as 'Other'). We have previously detected isolates of an identical genotype in Pakistan and Afghanistan (2017-2018) based on samples that we were unable to recover. Spore multiplication of Ethiopian samples is in progress to allow rigorous race phenotyping.

A new genotype in the Middle East (provisionally termed ME2018), first detected in dead samples from Egypt (2018), and at several locations in Turkey (2019), was detected for the first time in Europe, Latvia (2020). This observation was confirmed by independent assays of incoming infected leaves, race typing of recovered isolates, and re-submission of additional samples from the sampling area. Two races differentiated by *Yr10*-virulence were detected within ME2018.

PstS13 has been detected in multiple countries and continents in recent years. In 2019, a new *Yr10*-virulent variant was detected in Poland, and in 2020 also in Germany. PstS13 isolates are highly aggressive on several crop types, e.g., multiple triticale varieties (northern Europe and South America), durum wheat (southern Europe) and multiple spring wheat varieties (South America) resulting in significant yield losses (Carmona et al., 2019). Alignment experiments based on DNA samples supplied by the University of Sydney, Australia, confirmed PstS13 in Australia, where it was first detected in 2018 (Park et al., 2020). At present, PstS13 is widespread across three continents, Europe, South America and Australia.

Table 6 (continued).

Geographic group	Country	SSR_name	2019	2020	Total	
Europe	Belgium	PstS10	15	10	25	
		PstS13	1	1	2	
		PstS7		1	1	
	Czech Republic	PstS0			1	1
		PstS10	3	1	4	
	Denmark	PstS10	32	59	91	
		PstS13	12	9	21	
		PstS15	5	4	9	
	France	PstS10	12	10	22	
		PstS15	1	1	2	
		PstS7	3	1	4	
	Germany	PstS10	6		6	
		PstS13	4		4	
		PstS7	1		1	
		PstS8	1		1	
	Great Britain	PstS10		4	4	
	Hungary	PstS13			1	1
		PstS7	4	3	7	
	Italy	PstS10	3	8	11	
		PstS13	24	2	26	
		PstS13	1		1	
		PstS14	1		1	
		PstS2	1		1	
		PstS7	2		2	
	Latvia	ME2018 ^{a)}			1	1
		PstS10	1		1	
PstS14		18		18		
PstS7		1		1		
Netherlands	PstS10	3	7	10		
	PstS7	1		1		
Norway	PstS10	5	7	12		
	PstS13		2	2		
	PstS7		1	1		
Poland	PstS13	3		3		
	PstS7	2		2		
Slovakia	PstS10	2		2		
	PstS14	1	1	2		
	PstS7	1	2	3		
Spain	PstS10	9	17	26		
	PstS13	11	6	17		
	PstS14	7		7		
	PstS7		3	3		
Sweden	PstS10	16	15	31		
	PstS13	5	9	14		
	PstS7		1	1		
	PstS8		1	1		
Switzerland	PstS14		1	1		
Europe Total		218	190	408		
Grand Total		307	217	524		

^{a)} Temporary designation for the unique genotype first detected in Egypt 2018

PstS10 was the most prevalent group on bread wheat in Europe, so far dominated by a single race (virulence phenotype: 1,2,3,4,-,6,7,-,9,-,17,-,25,-,32,Sp,AvS,-) (Table 6). However, in recent years, new races adapted to local wheat varieties have emerged within PstS10, resulting in quantitative shifts in rust susceptibility of such varieties, e.g., from 'resistant' to 'susceptible' or from 'susceptible' to 'extreme susceptible'. So far, it has not been possible to diagnose the new races within PstS10 by molecular techniques nor by standard wheat differential lines. By 2020, four races have been detected in PstS10, typically named after the wheat varieties where they first caused significant epidemics. Alignment experiments with University of Sydney confirmed the presence of PstS10 in Australia since 2017 (Park et al., 2020).

In terms of virulence, the races within PstS10 are similar to the Warrior race (PstS7), except for the resistance specificity in the varieties Warrior (UK) and Ambition (DK). The "Warrior" race is still present in Europe, but often in low frequency and mainly in Eastern Europe. Likewise, the PstS8 group (containing the "Kranich" race) has become less frequent in Europe. A new race in a new unique genetic group, termed PstS15, was detected in France in 2017-2019, and in Denmark and Sweden in 2019-2020. The significance of this race in terms of potential shifts in rust susceptibility is subject to investigation in the EU-RustWatch project.



Fig. 2. Particular races of yellow rust produce huge amounts of dark colored telia under field conditions.

Table 7. 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 - GRRR, March 2021			
Genetic group	Race	Virulence phenotype*	Prevalence in geographical region
PstS0	Brigadier	1,2,3,-,-,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	Brigadier,v4	1,2,3,4,-,-,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	Madrigal_Lynx	1,2,3,-,-,6,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	Madrigal_Lynx,v4	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	Robigus	1,2,3,4,-,-,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Solstice_Oakley	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Tulsa	-,-,3,4,-,6,-,-,-,-,-,25,-,32,-,AvS,-	Europe
PstS1	PstS1	-,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	North America, Australia
	PstS1,v1	1,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa
	PstS1,v1,v27	1,2,-,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa
PstS2	PstS2	-,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa, West Asia, South Asia
	PstS2,v1	1,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa
	PstS2,v3	-,2,3,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa
	PstS2,v27	-,2,-,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia, North Africa
	Pst2,v1,v27	1,2,-,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia
	PstS2,v3,v27	-,2,3,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa
	PstS2,v10	-,2,-,-,-,6,7,8,9,10,-,-,24,25,-,-,-,AvS,-	East Africa, West Asia
	PstS2,v10,v27	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	West Asia
	PstS2,v3,v10,v27	-,2,3,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
PstS3	PstS3	-(2),-,-,-,6,7,8,-,-,-,-,-,-,AvS,-	Europe, North Africa, West Asia
	PstS3,v25	-(2),-,-,-,6,7,8,-,-,-,-,25,-,-,-,AvS,-	Europe, East Africa
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
PstS15	PstS15	1,2,3,-,-,6,7,-,9,-,-,17,-,25,-,32,-,AvS,Amb	Europe

* 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. Kalmar, Benchmark and Amboise are new races in PstS10, which can only be distinguished by these varieties.

Submission and preparation of samples

Samples of rust infected wheat are submitted based on an import permit issued by GRRC valid for one country and one year, among others confirming 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/>, where a video demonstrating ideal sampling procedures is also available. 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 multiplication were made to obtain sufficient amount of spores for storage and potential 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 generally successful, following the procedures of [Thach et al. 2016](#). The above procedure for sample recovery and genotyping proved very useful for generating results from all sample submissions irrespectively of recovery results reflecting the quality of incoming samples.

Litterature

- Ali et al., 2017. Yellow Rust Epidemics Worldwide Were Caused by Pathogen Races from Divergent Genetic Lineages. *Frontiers in Plant Science*, Vol. 8, 1057, 06.2017.
- Carmona, M.A., Sautua, F.J., Pérez-Hernández, O. et al., 2019. Rapid emergency response to yellow rust epidemics caused by newly introduced lineages of *Puccinia striiformis* f.sp. *tritici* in Argentina. *Trop. Plant Pathol.* 44, 385–39. <https://doi.org/10.1007/s40858-019-00295-y>
- Hovmøller et al. 2017: Race Typing of *Puccinia striiformis* on Wheat. In: *Wheat Rust Diseases: Methods and Protocols*, ed. S. Periyannan. Springer, p. 29-40. [Downloading](#) accepted for non-commercial and educational purposes.
- Park et al., 2020. Confirmation of the exotic origins of two pathotypes of the wheat stripe rust pathogen detected in 2017 and 2018, and their impact. *Cereal Rust Report 2020*, vol. 17, 4. Plant Breeding Institute, University of Sydney.
- Patpour et al., 2020. First Report of Race TTRTF of Wheat Stem Rust (*Puccinia graminis* f. sp. *tritici*) in Eritrea. *Plant Disease* 2020 104:3, 973 <https://apsjournals.apsnet.org/doi/10.1094/PDIS-10-19-2133-PDN>
- Olivera Firpo et al., 2017, Characterization of *Puccinia graminis* f. sp. *tritici* isolates derived from an unusual wheat stem rust outbreak in Germany in 2013. *Plant Pathol.* 66: 1258-1266. doi:[10.1111/ppa.12674](https://doi.org/10.1111/ppa.12674)
- Olivera et al., 2019. Presence of a Sexual Population of *Puccinia graminis* f. sp. *tritici* in Georgia Provides a Hotspot for Genotypic and Phenotypic Diversity. *Phytopathology*™ 109:12, 2152-2160 <https://apsjournals.apsnet.org/doi/10.1094/PHYTO-06-19-0186-R>
- Sørensen, CK, Thach T, and Hovmøller MS. 2016. Evaluation of spray and point inoculation methods for the phenotyping of *Puccinia striiformis* on wheat. *Plant Disease* 100:1064-1070. <http://apsjournals.apsnet.org/doi/pdfplus/10.1094/PDIS-12-15-1477-RE>
- Thach T et al., 2016. Worldwide population structure of the wheat rust fungus *Puccinia striiformis* in the past. *Fungal Genetics and Biology* 87, 1-8. doi.org/[10.1016/j.fgb.2015.12.014](https://doi.org/10.1016/j.fgb.2015.12.014)
- Walter, S. et al., 2016. Molecular markers for tracking the origin and worldwide distribution of invasive strains of *Puccinia striiformis*. *Ecology and Evolution*, 6(9), 2790-2804. DOI: [10.1002/ece3.2069](https://doi.org/10.1002/ece3.2069)

Acknowledgements

Submission of samples of rust infected plant material in 2020 was facilitated by a large number of collaborators from multiple organisations and countries (Table 8). Sampling in Africa was coordinated by Dave Hodson (CIMMYT) and sampling in EC-VCU network trials was coordinated by Valérie Cadot (Geves), France. 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). DNA samples for alignment of yellow rust in Australia were kindly provided by University of Sydney (Robert Park). Les Szabo provided reference DNA samples of previously defined stem rust genetic groups based on SNP analyses. Handling and recovery of incoming samples and inoculations by Ellen Jørgensen, production of healthy plants by Jakob Sørensen, DNA/PCR work by Janne Holm Hansen, and final editing of this report by Charlotte Hamann Knudsen is greatly acknowledged. The activities were funded by a variety of organisations and research councils: Race typing and genotyping of African rust samples in 2020 were facilitated by “Accelerating Genetic Gains in Maize and Wheat for Improved Livelihoods” (AGG project) funded by the Melinda & Bill Gates Foundation and the UK Department for International Development (DFID). 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).

Table 8. People submitting wheat rust/DNA samples in 2020.

Name	Country
Robert Park	Australia
Michael Oberforster	Austria
Nick Gemoets	Belgium
G.Jacquemin	Belgium
Hanzalova Alena	Czech Republic
Alena Hanzalová	Czech Republic
Kirsten Sæ Pedersen	Denmark
Thomas Wohlleben	Denmark
Susanne Sindberg	Denmark
Finn Borum	Denmark
Jeppe Reitan	Denmark
Lise Nistrup Jørgensen	Denmark
Yoseph Alemayehu	Ethiopia
V. Cadot	France
F. Arnoult	France
G. Bauchet	France
Laurent Paeaud	France
Emmanuel Heumez	France
C. Debiton	France
G. Bevoin	France
Marc Leconte	France
Tiphaine Vidal	France
Kerstin Flath	Germany
Philipp Schulz	Germany
Sommerfeldt	Germany
Hoffmann	Germany
Sandra Schült	Germany
Strube	Germany
Uta Liesenberg	Germany
Horn	Germany
Rose	Germany
Bernat Poos	Hungary
Steven Kildea	Ireland

Name	Country
Virgilio Balmas	Italy
Giuseppina Goddi	Italy
Biagio Randazzo	Italy
Anna Giulini	Italy
Francesca Margheri	Italy
Daniela Marone	Italy
Anna Maria Mastrangelo	Italy
Paolo De Franceschi	Italy
Giovanni Laido	Italy
Marco Nocentini,	Italy
Zannah Kosgey	Kenya
Eric, Simon, Beatrice, Joel, Festus, Zannah, Hannington	Kenya
Līga Feodorova-Fedotova	Latvia
Sridhar Bhavani	Mexico
Brink, Lubbert van den	Nederlands
Andrea Ficke	Norway
Morten Lillemo	Norway
Pawel Czembor	Poland
Alena Hanzalová	Slovak Republic
Svetlana Šliková	Slovakia
Ales Kolmanic	Slovenia
Arias Fariñas	Spain
Dolors Villegas	Spain
Amaia Caballero Iturri	Spain
Fernando Martinez-Moreno	Spain
Rebecka Östlund	Sweden
Gunilla Berg	Sweden
Sofie Pålsson	Sweden
Eva Mellqvist	Sweden
Lovisa Eriksson	Sweden
Agnes Radovic	Sweden
Linda af Geijersstam	Sweden
Lina Norrlund	Sweden
Susanna Waara	Sweden
Jessica Joaquim	Switzerland
Amelia Hubbard	United Kingdom
Sarah Wilderspin	United Kingdom