

## GRRC annual report 2019: Stem- and yellow rust genotyping and race analyses

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### Key highlights yellow rust

- Genetic group PstS11 was detected in Turkey and Uganda, so it is now prevalent in at least six countries in East Africa and the Middle East.
- A new genotype (and a unique race), first detected in Egypt (2018) and provisionally termed ME2018, was observed on both bread wheat and durum wheat in Turkey.
- At least two new races were detected in PstS10, the most prevalent genetic group in Europe. The new races were adapted to local, widely grown wheat varieties, and only detectable by including these varieties in the race testing.
- A new race with *Yr10*-virulence was detected in PstS13. Isolates of this genetic group has severely affected triticale (northern Europe), durum wheat (southern Europe) and bread wheat (South America).
- Genetic group PstS7 with the original Warrior race was less prevalent, but spreading to new areas, whereas PstS8 (with the Kranich race) was observed in few cases only.
- Additional groups were detected in several countries, e.g. PstS15 consisting of a single genotype and race, which was first observed in France and this year also in Denmark.

### Key highlights stem rust

- Clade III-B (TTRTF, the “Sicily race”), widespread in Italy since 2016, was detected in Spain, Tunisia and Iran.
- Clade IV-F, containing race TKKTF, was widespread in Europe, Africa and the Middle East, in total 9 countries in this study.
- Clade I (Ug99) and associated races were not detected outside Africa except in Iran.
- Clade IV-B, containing the races TKTTF and TTTTF, was detected in Africa and southern Europe.
- Multiple races with unusual virulence combinations were observed on cereals in local areas in Sweden and Spain, where the alternate host, *Berberis vulgaris*, is present. High genetic diversity was confirmed by genotyping.
- Genotyping provided high-resolution results for genetic grouping of isolates, which to a large extent corresponded with race groups based on virulence phenotyping.

Summary of SSR genotyping and race phenotyping results from the GRRC (2008-2019) is available on-line (<http://www.wheatrust.org/>), including an updated table showing the [relationship between races and genetic groups in yellow rust](#). Table 4 presents the same relationship for stem rust based on samples presented in this report.

This report presents molecular genotyping and race typing results from the GRRC based on samples of rust infected wheat and triticale collected in 2018 and 2019 across four continents, i.e., Europe, Asia, Africa and South America. For the first time, the report comprises results for wheat stem rust *P. graminis*

f.sp. *tritici* as well as yellow/stripe rust (*Puccinia striiformis*). The testing of additional samples from 2019 is ongoing with emphasis on additional race testing of representative isolates from existing and new genetic groups.

In 2019, a total of 672 samples and derived isolates from 21 countries were handled. Each sample generally consisted of multiple rust infected leaves or stems. Representative leaves/stems were selected for alive spore recovery, and in parallel genotyping based on the incoming sample (Table 1, Table 2). More than 500 alive isolates of yellow and stem rust were recovered based on submissions in 2019.

The genotyping was generally based on Simple Sequence Repeat (SSR) analyses of incoming samples of rust infected plant material without prior recovery, whereas the race phenotyping was based on bioassays of differential wheat lines using spore samples of recovered, pure isolates grown under strict experimental conditions (Hovmøller et al. 2017). In case that multiple genotypes were detected in an incoming sample and results were inconclusive, additional tests were based on purified samples.

### 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. Race names already adopted by the farming community in Europe are maintained, e.g., “Warrior” and “Kranich”, which are named according to the wheat variety where they caused the first confirmed epidemic outbreak. A comprehensive justification and rationale for the naming of significant *P. striiformis* races and genetic groups has been published (Ali et al. 2017) and an updated [summary](#) is available on the GRRC website. The genotypic grouping of stem rust is according to Olivera Firpo et al. (2017) and [Olivera et al. \(2019\)](#), and is based on detailed alignment of the present SSR genotyping results and SNP results from the Cereal Disease Lab, Minnesota, USA; the race grouping is based on 20 internationally agreed wheat lines differentiating virulence for the wheat stem rust fungus (Jin et al., 2008).

In yellow rust, we observed a strong correlation between genetic groups and race phenotypes for most sampling areas, similarly, most races of wheat stem rust were associated with specific genetic groups (‘clades’). In few cases, the same race phenotype of stem rust was present in several genetic groups, reflecting that additional wheat lines are needed to differentiate races of stem rust in more detail.

**Table 1.** Number of stem rust samples and derived isolates (*P. graminis* f.sp. *tritici*) handled in 2018-2019.

Geographic area	Country	2018			2019			Grand Total
		Dead	Recovered	Total	Dead	Recovered	Total	
Africa, CW Asia	Egypt	21	2	23				23
	Eritrea	7	12	19				19
	Ethiopia		4	4				4
	Iran	25	22	47		12	12	59
	Kenya	9	68	77	1	61	62	139
	Morocco					2	2	2
	Rwanda		13	13				13
	Tanzania	1	27	28				28
	Tunisia					8	8	8
	Uganda				8	37	45	45
<b>Africa, CW Asia Total</b>		<b>63</b>	<b>148</b>	<b>211</b>	<b>9</b>	<b>120</b>	<b>129</b>	<b>340</b>
Europe	Czech Republic		5	5				5
	Denmark	1		1		9	9	10
	France					1	1	1
	Germany					2	2	2
	Hungary					1	1	1
	Italy	4	60	64	1	55	56	120
	Poland		14	14				14
	Slovakia		14	14				14
	Spain				2	74	76	76
	Sweden	8	29	37	2	5	7	44
<b>Europe Total</b>		<b>13</b>	<b>122</b>	<b>135</b>	<b>5</b>	<b>145</b>	<b>150</b>	<b>285</b>
<b>Grand Total</b>		<b>76</b>	<b>270</b>	<b>346</b>	<b>14</b>	<b>265</b>	<b>279</b>	<b>625</b>

**Table 2.** Number of yellow rust samples and derived isolates (*P. striiformis*) handled in 2019.

Geographic area	Country	2019		
		Dead	Recovered	Grand Total
Africa, C&W Asia	Ethiopia	13	14	27
	Iran	2	3	5
	Kenya	1	27	28
	Turkey	9	13	22
	Uganda	12	4	16
Africa, C&W Asia Total		37	61	98
Europe	Belgium		16	16
	Czech Republic	3		3
	Denmark	8	49	57
	France	2	16	18
	Germany	6	16	22
	Hungary	2	6	8
	Italy	7	53	60
	Latvia	19	2	21
	Netherlands		4	4
	Norway		5	5
	Poland		5	5
	Slovakia	3	3	6
	Spain	6	38	44
	Sweden	11	15	26
Europe Total		67	228	295
Grand Total		104	289	393

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. Geographical location of races/genotypes is shown on maps in case such information has been provided.



Yellow rust was severe on wheat in many areas in northern Europe in 2019, in particular in the absence of effective host resistance and/or fungicide sprays. Photo: Ghita Nielsen, SEGES, Denmark.

## 2018-2019 results – wheat stem rust

A total of 348 samples from 19 countries and four continents were successfully genotyped (Table 3), and 164 of these were also race typed.

**Table 3.** SSR genotyping of samples of *P. graminis* f.sp. *tritici* collected in 2018 and 2019. Results are shown as number of isolates within a genetic group. Significant races within clades are shown in Table 4 and virulences in Table 5. Graphical presentation of results available on [www.wheatrust.org](http://www.wheatrust.org).

Geographic group	Country	Genetic group	2018	2019	Total
Africa, CW Asia	Egypt	Clade IV-E.2	8		8
		Clade IV-F	2		2
	Egypt Total		10		10
	Eritrea	Clade III-B	6		6
	Eritrea Total		6		6
	Ethiopia	Clade IV-B	2		2
	Ethiopia Total		2		2
	Iran	Clade I		1	1
		Clade III-B		6	6
		Clade IV-F	12		12
	Iran Total		12	7	19
	Kenya	Clade I	39	54	93
		Clade IV-B	2	2	4
	Kenya Total		41	56	97
	Morocco	Clade IV-B		2	2
	Morocco Total			2	2
	Rwanda	Clade I	5		5
	Rwanda Total		5		5
	Tanzania	Clade I	9		9
		Clade IV-B	7		7
	Tanzania Total		16		16
	Tunisia	Clade III-B		3	3
		Clade IV-F		5	5
	Tunisia Total			8	8
	Uganda	Clade I		21	21
		Clade IV-B		5	5
		Clade IV-F		1	1
	Uganda Total			27	27
<b>Africa, CW Asia Total</b>			<b>92</b>	<b>100</b>	<b>192</b>
Europe	Czech Republic	Other	4		4
	Czech Republic Total		4		4
	Denmark	Clade IV-F		6	6
	Denmark Total			6	6
	France	Clade IV-F		1	1
	France Total			1	1
	Hungary	Other		1	1
	Hungary Total			1	1
	Italy	Clade III-B	20	16	36
		Clade IV-B	6		6
		Clade IV-F	12	23	35
	Italy Total		38	39	77
	Poland	Clade IV-E.2	3		3
		Clade IV-F	2		2
	Poland Total		5		5
	Slovakia	Other	8		8
	Slovakia Total		8		8
	Spain	Clade III-B		4	4
		Clade IV-B		2	2
		Clade IV-F		4	4
		Other		32	32
	Spain Total			42	42
	Sweden	Other	12		12
	Sweden Total		12		12
<b>Europe Total</b>			<b>67</b>	<b>89</b>	<b>156</b>
<b>Grand Total</b>			<b>159</b>	<b>189</b>	<b>348</b>



SSR_name	Race_name	Number of observations
Clade I (Ug99)	TTKSK	4
	TTKST	11
	TTKTK	6
	TTKTT	39
	-	69
Clade I Total		128
Clade III-B	TTRTF	31
	-	24
Clade III-B Total		55
Clade IV-B	TKTTF	9
	TTTTF	13
	-	6
Clade IV-B Total		28
Clade IV-E.2	TKKTF	2
	-	9
Clade IV-E.2 Total		11
Clade IV-F	TKKTF	32
	-	37
Clade IV-F Total		69
Other	LKMNC	2
	RFCNC	8
	RFCPC	1
	Other	6
	-	39
Other Total		57
Grand Total		348

- not tested

**Table 4.** Relationship between genetic groups and prevalent races detected within these in 2018-2019 (cf. Table 2)

**Table 5.** Correspondence between race name and virulence on common stem rust differential lines.

Virulence corresponding to NA differentials 1-20 (main R-gene indicated )																				
Race_name	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, consisting of a single race, a.k.a. the “Sicily race”, was detected for the first time in three additional countries, i.e., Spain, Tunisia and Iran. In addition to the virulences shown in Table 5, this race is virulent on several durum wheat varieties (*Sr13b*) and possesses additional virulence to *Sr50* shown by higher than usual infection type for this gene (Patpour et al., 2019).

Clade IV-F, containing a single race (TKKTF) in this study, was detected in nine countries in Europe, Africa and West Asia, i.e., Egypt, Iran, Tunisia, Uganda, Denmark, France, Italy, Poland, and Spain. This widespread occurrence was quite surprising since isolates of this genetic group have only been reported and defined recently (Olivera Firpo et al., 2017, 2019). In fact, the same race phenotype, TKKTF, was also observed in clade IV-E.2 in Poland, and elsewhere in the past.

Clade IV-B was detected in Africa and southern Europe. It contained two closely related races, TKTTF and TTTTTF, which only differ by virulence to *Sr11*. In this study, TTTTTF was not detected outside Africa.

Clade I (Ug99) contained as expected several closely related races, which are difficult to separate by standard genotyping techniques. All samples, except one, were collected in East Africa, the exception originating from Iran, where Ug99 was detected several years ago.

Multiple races were derived from wheat, barley and rye in Sweden and Spain, in both cases sampled in local areas in proximity to the alternate host, *Berberis vulgaris*. Many of the races were characterized by avirulence on multiple differential lines, and many of the isolates were generally poorly adapted to wheat. The unusual virulence patterns of selected isolates are currently being investigated in more detail, in combination with rust susceptibility profiles of commercially important wheat varieties in Europe and elsewhere. The high genetic diversity was confirmed by a high number of unique and diverse genotypes.

### **2019 results – wheat yellow rust**

A total of 285 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 emergence of new races within genetic groups. The number of samples from Africa, Asia and South America was significantly lower than in 2018, reflecting a decrease in incoming samples from these areas in 2019.

PstS11 is now confirmed in six countries in Africa and the Middle East, i.e., Ethiopia, Kenya, Rwanda, Tanzania, Uganda and Turkey (Table 6). PstS11 was first detected in Afghanistan (2012) after which it spread to neighboring countries. So far, only a single race has been confirmed in PstS11 (virulence phenotype: -,2,-,4,-,6,7,8,-,-,17,-,-,27,32,-,AvS,-). The virulence of a representative set of recent PstS11 isolates from Turkey and East Africa is being investigated at present time. The rapid spread across wide areas, and associated rust epidemics, including previously resistant varieties in affected areas, demonstrate the potential risks associated with this race/genotype, and evolution of additional virulence can be expected.

A new genotype in the Middle East (provisionally termed ME2018), first detected in dead samples from Egypt (2018), was observed in 2019 at several locations in Turkey. The Turkish samples were collected from durum wheat as well as bread wheat. Confirmation of the race phenotype is ongoing.

PstS13 and PstS14 were also detected in Turkey in 2019. Both groups have been detected in multiple countries and continents in recent years, and in 2019 a new *Yr10*-virulent variant in PstS13 was detected in Europe. 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). PstS14 is highly dominant in Morocco, and otherwise present in multiple European countries, but often in low frequencies.

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, widely grown 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'. It has not been possible to diagnose such new races within PstS10 by SSR genotyping nor by standard wheat differential lines, so far only by including the varieties in question into the differential set, e.g., varieties Kalmar and/or Benchmark. However, correct diagnosis of races based on such quantitative differences requires strict and well-defined experimental conditions. In terms of virulence, the races within PstS10 are similar to the only race detected so far in PstS7 (Warrior), except for the resistance specificity in the varieties Warrior (UK) and Ambition (DK).

The Warrior race was detected in Europe but often in low frequency, in Europe. Likewise, the PstS8 group (containing the Kranich race) has become less frequent in most areas of Europe. A new race in a new unique genetic group, termed PstS15, was detected in France in 2017, 2018 and 2019 and in 2019 also in Denmark. The significance of this race in terms of potential shifts in rust susceptibility is being investigated via ongoing research activities.

**Table 6.** SSR genotyping of samples of *P. striiformis* in 2018 and 2019. Results shown as number of isolates within genetic groups, see Table 7 showing significant races and virulences within each group.

Geographic group	Country	SSR name	2018	2019	Grand Total
Africa, C&W Asia	Afghanistan	Other	8		8
	Egypt	PstS1/PstS2 <sup>a)</sup>	9		9
		ME2018 <sup>b)</sup>	2		2
	Eritrea	Other	5		5
	Ethiopia	PstS11	28	24	52
		PstS1/PstS2 <sup>a)</sup>	3		3
		Other		1	1
	Iran	PstS1/PstS2 <sup>a)</sup>	3		3
		Other		4	4
	Kenya	PstS11	30	14	44
		PstS1/PstS2 <sup>a)</sup>	9	3	12
	Morocco	PstS14	54		54
	Rwanda	PstS11	3		3
		PstS1/PstS2 <sup>a)</sup>	6		6
	Tanzania	PstS11	3		3
		PstS1/PstS2 <sup>a)</sup>	3		3
	Turkey	PstS11		5	5
		PstS13		2	2
		PstS14		5	5
		ME2018 <sup>b)</sup>		4	4
	Uganda	PstS11		3	3
		PstS1/PstS2 <sup>a)</sup>		4	4
		PstS6		6	6
	Uzbekistan	PstS9	30		30
<b>Africa, C&amp;W Asia Total</b>			<b>196</b>	<b>75</b>	<b>271</b>
Europe	Austria	PstS7	2		2
	Belgium	PstS10	10	15	25
		PstS13		1	1
		PstS7	1		1
	Czech Republic	PstS10	2	3	5
		PstS7	8		8
		PstS7	1		1
	Denmark	PstS10	34	32	66
		PstS13	2	12	14
		PstS14	4		4
		PstS15		4	4
		PstS7	2		2
		PstS8		1	1
	Estonia	PstS7	2		2
	France	PstS10	4	12	16
		PstS13	1		1
		PstS15	1	1	2
		PstS7	4	3	7
	Germany	PstS10	2	4	6
		PstS13	6	3	9
		PstS8		1	1
	Hungary	PstS7		4	4
	Italy	PstS10		3	3
		PstS13	8	24	32
		PstS13		1	1
		PstS14	1	1	2
		PstS2		1	1
		PstS4	16		16
		PstS7		2	2
	Latvia	Other	1		1
		PstS10		1	1
		PstS14	9	18	27
		PstS7	3	1	4
	Netherlands	PstS10	3	3	6
		PstS7		1	1
	Norway	PstS10	1	5	6
		PstS7	1		1
	Poland	Other	1		1
		PstS10	2		2
		PstS13	4		4
	Slovakia	PstS10	1	2	3
		PstS14	1	1	2
		PstS7	2	1	3
	Spain	PstS10	10	10	20
		PstS13	4	11	15
		PstS14	6	6	12
		PstS14		1	1
		PstS7	4		4
	Sweden	PstS10	23	16	39
		PstS13	4	5	9
		PstS7	3		3
		PstS8	4		4
	Ukraine	PstS13	4		4
<b>Europe Total</b>			<b>202</b>	<b>210</b>	<b>412</b>
S. America	Argentina	PstS13	28		28
		PstS7	3		3
	Chile	PstS13	18		18
<b>S. America Total</b>			<b>49</b>		<b>49</b>
S. Asia	Bhutan	Other	6		6
	Pakistan	Other	23		23
<b>S. Asia Total</b>			<b>29</b>		<b>29</b>
<b>Grand Total</b>			<b>476</b>	<b>285</b>	<b>761</b>

<sup>a)</sup> These two aggressive strains are only distinguishable by SCAR markers (Walter et al. 2016), which have not yet been applied on 2018-2019 samples

<sup>b)</sup> Temporary designation for a unique genotype first detected in Egypt 2018

**Table 7.** Correspondence between genetic groups and prevalent races of *P. striiformis* sampled from epidemic sites since 2000, Global Rust Reference Center, January 2020.

Common names of prevalent races and genetic groups in yellow rust - GRRC, January 2020			
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,v24	-,-,2,-,-,6,7,8,9,10,-,-,24,25,-,-,-,AvS,-	East Africa, West Asia
	PstS2,v10,v24,v27	-,-,2,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	West Asia
	PstS2,v3,v10,v24,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
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
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
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 and Benchmark 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.

The 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 incoming samples.

Race phenotyping of representative isolates was generally based on several cycles of spore multiplication. 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.



## Litterature

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**Table 8.** People submitting samples of rust infected leaves/stems of cereals 2018-2019.

Country	Collectors 2018-2019	Country	Collectors 2018-2019
<b>Afghanistan</b>	E Mohmand, A Bari Stanikzai, Z Ahmazada	<b>Iran</b>	Farzad Afshari
	A Noori, A Raqib Lodin; G Ghanizada, Latif Rasekh		Mahboobeh Yazdani
<b>Argentina</b>	Agustin Bilbao		Mansour KarimiJashni, Mohammad Razavi
	Agustín Pulido	<b>Italy</b>	Mohsen Yassaie
	Alejandro Porfiri		Angela Iori, Fabrizio Quaranta, Andreina Belocchi, Mauro Fornara
	Ana Rodriguez		Anna Maria Mastrangelo
	Ana Storm		Antonia Salerno
	Andrea Rosso		Biagio Randazzo
	Buck Semillas		Daniela Marone
	Carina Cáceres		Emilia Romagna
	Carlos Grosso		Francesca Nocente
	Claudio Bosco		Giovanni Laidò, Rossano Contato
	Cristina Palacios		Giuseppina Goddi
	Diego Alvarez		Luca Fiorilla
	Enrique Alberione		Lucio Salafia
	Fabricio Mock		Oriana Porfiri
	Franco Petrelli		Stefania Stefanelli, Marco Maccaferri
	Gustavo Duarte		Virgilio Balmas
	Ignacio Erreguerena	<b>Kenya</b>	Ruth Wanyera
	Julián García, Oro Verde	<b>Latvia</b>	Līga Feodorova-Fedotova
	Liliana Wehrhahne, Adelina Larsen	<b>Morocco</b>	Ezzahiri Brahim
	Manuela Gordo	<b>Netherlands</b>	Lubbert van den brink
	Marcos Mitelsky		Andrea Ficke
<b>Austria</b>	Michael Oberforster	<b>Norway</b>	Chloe Griefu
	Thomas Massinger		Morten Lillemo
<b>Belgium</b>	F. De Brouwer; J. Pannecoque	<b>Pakistan</b>	Sajid Ali
	G. Jacquemin & R. Meza	<b>Poland</b>	Ewelina Piwowarczyk
<b>Bhutan</b>	Dave Hodson, Sangay Tshewang		Paweł Czembor
<b>Chile</b>	C. Jobet and R. Galdames	<b>Rwanda</b>	Dave Hodson, Innocent Habarurema
	Carola Vera; Ricardo Madariaga	<b>Slovakia</b>	Svetlana Slikova
<b>Czech Republic</b>	Erik Von Baer		Alena Hanzlova
	Alena Hanzalova	<b>Spain</b>	Carlos Cantero
<b>Denmark</b>	Pavel Kraus		Dolors Villegas
	Ghita Cordsen Nielsen		Enrique Can
	Jeppe R. Andersen		Ibal Elorza
	Lise Nistrup Jørgensen		Jesús Goñi
	Susanne Sindberg		Joan Serra
<b>Egypt</b>	Thomas Olsen		Luis Urquijo
	Atef Shahin, Wasief Youssief		Manuel Calvo
<b>Eritrea</b>	Atef Shahin, Hend, Mohamed, Reda		Neus Pulg; Nieves Apa
	Asmelash Wolday	<b>Sweden</b>	Alexia von Ehrenheim
<b>Ethiopia</b>	Ashenafi		Alf Djurberg
	Bekele Abeyo; Ayele Badebo		Anders Arvidsson
	Dave Hodson		Anders Lindgren
	Zerihun Tadesse		Anna Berlin
	Clément Debiton		Anna Gerdtsen
<b>France</b>	Emmanuel Heumez		Anna-Karin Krijger
	Gorichon		Charlotte Norén
	J.P. Maigniel		Elisabeth Bölenius
	Jérôme Auzanneau		Elisabeth Lövestad
	Laurent Pageaud		Erling Christensson
	Marc Leconte		Eva Mellqvist
	Mathieu Grare		Frans Johnson
	Pascal Giraudeau		Gunilla Berg
	S. Barraix; Vallerie Cadot		Gunnel Andersson, Linda af Geijersstam
			Johanna Holmblad
<b>Country</b>	<b>Collectors 2018-2019</b>		Jonas Törngren
<b>Germany</b>	Anja Giebel		Julia Dahlqvist, Anna von Heideken
	Anne-Kristin Schmitt		Karin Andersson
	Catherine Cuendet, Getreidezuchtung Peter Kunz		Kristian Barck
	Cornelia Miersch, SMUL		Kristian Jochnick
	E. Kazman		Lars Johansson
	Friederike Schiermann		Lina Norrlund
	Henning Hartwig, PZO		Louise Aldén
	Josef Holzapfel		Lovisa Eriksson
	Kerstin Flath		Lukas Hallberg
	Matthias Haas		Robert Dinwiddie
	Paul Gruner	<b>Tanzania</b>	Rose Mongi, Dave Hodson, Ari Uyole
	Sommerfeldt, Hoffmann		Salome Munissi, Nafet, Charles, Ramdhani
	Thomas Grafe	<b>Tunisia</b>	Marcel Thierry
	Thomas Zschaackel	<b>Turkey</b>	Amor Yahyaoui
	Uta Liesenberg		Alex Morgounov
	Uwe Preiss	<b>Uganda</b>	Bosco Chemayek
		<b>Ukraine</b>	Owere, Wasukira, Wobibi, Woniala
			Vitaliy Paljasniy
		<b>Uzbekistan</b>	Zafar Ziyaev