

Report for *Puccinia striiformis* race analyses/molecular genotyping, GRRC, Flakkebjerg, DK- 4200 Slagelse, Denmark.

Mogens Støvring Hovmøller, Julian Rodriguez-Algaba, Tine Thach, Annemarie Fejer Justesen & Jens Grønbech Hansen, 8 February, 2019.

Email: mogens.hovmoller@agro.au.dk

Key highlights 2018

- Central Asia/East Africa: **Pst11**, first detected in Central Asia in 2012, became the most prevalent genetic group of yellow rust in East Africa in 2018, detected in Ethiopia, Kenya, Rwanda and Tanzania. The recent inter-continental spread into East Africa was confirmed by the presence of only a single race in group **PstS11** irrespective of sample origin.
- South America: **PstS13** was completely dominating in both Argentina and Chile, in 2018 severely affecting both wheat and triticale cultivars. Only one race has been detected in this group, associated with severe rust epidemics on triticale in northern Europe and durum wheat in southern Europe.
- Europe: **PstS10**, a.k.a. *Warrior(-)*, was the most prevalent group consisting of one dominating genotype. The original Warrior group (**PstS7**) was less prevalent, but spreading to new areas. Additional groups were detected in many countries.
- North Africa: A distinct race (and genotype) of the genetic group **PstS14**, first detected in 2016, made up 100% of samples from Morocco, causing severe rust epidemics in 2017. A new unique genotype was observed in Egypt - not previously detected anywhere by GRRC.
- Virulence to *Yr5* and *Yr15* was not detected.
- Summary of SSR genotyping and race phenotyping results from GRRC (2008-2018) is available online (<http://www.wheatrust.org/>), including an updated [table](#) showing the relationship between races and genetic groups.

This report presents results mainly based on Simple Sequence Repeat (SSR) genotyping of samples of *Puccinia striiformis* from wheat and triticale collected across four continents in 2018, with reference to 2017 results. The testing of additional samples from 2018 is ongoing with emphasis on additional race testing of representative isolates from existing and new genetic groups. Over the years, we have observed a strong connection between genetic group and race, which is defined by the pattern of compatible and incompatible interactions between host and pathogen. The race phenotype is considered 'virulent' in case of a compatible interaction, conferred by 'high' infection type scores on one or more host differential lines with a common *Yr*-gene, and 'avirulent' in case of incompatible interactions conferred by 'low' infection types. Race typing requires access to spore samples of alive, pure isolates and strict experimental conditions (Hovmøller et al. 2017). In contrast, SSR genotyping was based on samples of rust infected plant material without prior recovery and spore multiplication.

As opposed to virulence phenotyping, the SSR genotyping results reveals genetic diversity and relationships within and among genetic groups. Results from previous years are available as pdf files from the GRRC website, where the results are also available on [maps and charts](#).

Nomenclature of races and genetic groups

Common names based on SSR genotyping were assigned for genetic groups and races demonstrating high epidemic potential. The genetic groups have been named **Pst** followed by a digit. Race variants were 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 were maintained, e.g., *Warrior* and *Kranich*, which are named according to the wheat variety where they caused the first confirmed epidemic outbreaks. 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 new mapping tools allow the user to highlight particular countries, years and races/genotypes. The occurrence of prevalent races/genotypes are shown on maps in case geographical coordinates have been provided. Submission and preparation of samples

Submission and preparation of samples

Prior to submission of rust infected leaf samples, a request is sent by e-mail to GRRC to obtain an import permit. Information about, e.g., host variety, sampling date, location, and disease severity must be provided for interpretation of results. The details of sampling preparation are given at <http://wheatrust.org/submission-of-isolates/>. On this page you will find a video demonstrating ideal sampling procedures. Focus sampling areas in 2019 outside Europe will be selected in collaboration with staff at the international centers and NARCs in Africa and Asia, with a focus on high-risk epidemic areas. Bilateral agreement with private/public enterprises is also possible. Since 2011, GRRC has accepted samples of both yellow rust, leaf rust and stem rust.

A total of 325 samples from 10 countries in Africa and Asia were handled, each sample generally consisting of multiple rust infected leaves. Subsets were selected for genotyping without prior recovery, whereas the best looking samples were chosen for recovery using a mixture of susceptible seedlings of Cartago, Morocco and Anja (Table 1). Ninety-nine isolates were recovered and further multiplied. Recovery rates varied from case to case, emphasizing the importance of optimal handling and preservation of samples, and submission without delay. A total of 267 samples were submitted from 16 European countries (Table 2), and 65 samples from South America were handled. A total of 256 isolates were recovered in 2018.

Several cycles of multiplication were made to obtain sufficient amount of spores 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 the procedures published in 'Methods and Protocols', open-access for [downloads](#) for non-commercial and educational purposes. The genotyping of isolates based on DNA extraction from infected leaves (single lesions) was generally successful, following

Table 1. Number of samples of yellow rust handled in 2018, Africa and Asia.

Country	Dead	Recovered	Grand Total
Afghanistan	12		12
Egypt	15		15
Eritrea	8		8
Ethiopia	62	19	81
Iran	5		5
Kenya	67	20	87
Morocco	39	27	66
Rwanda	1	8	9
Tanzania	5	1	6
Uzbekistan	12	24	36
Grand Total	226	99	325

Table 2. Number of samples of yellow rust handled in 2018, Europe.

Country	Dead	Recovered	Grand Total
Austria	2	1	3
Belgium	6	7	13
Czech Republic	22	6	28
Denmark	6	45	51
Estonia	2		2
France	6	4	10
Germany	2	3	5
Italy	34	2	36
Latvia	9	8	17
Netherlands		3	3
Norway	1	6	7
Poland		4	4
Slovakia	7	6	13
Spain	12	12	24
Sweden	15	30	45
Ukraine	6		6
Grand Total	130	137	267

the procedures of [Thach et al. 2016](#). The methodology proved very useful for generating results based on 'original samples' in case of poor recovery, and for confirming genetic purity and assignment of races to specific genetic lineages.

Table 3. Number of samples of yellow rust handled in 2018, South America.

Country	Dead	Recovered	Grand Total
Argentina	38	4	42
Chile	7	16	23
Grand Total	45	20	65

2018 results

A total of 396 samples from 28 countries and four continents were successfully genotyped. In Table 4a,b,c, results are compared with results for 2017 samples, some of which were finalized in 2018.

Table 4a-c. SSR genotyping of samples of yellow rust collected in 2017 and 2018. Results are shown as number of isolates and frequency. For nomenclature of genetic groups (Pst1-14), see [GRRC updated table](#) and Ali et al., 2017. Cross references to significant races and virulences are shown in Table 5. Graphical presentation of results available on www.wheatrust.org.

a) Geographic group	Country	Genetic group	Crop season Year		Number of isolates Total	% of isolates Total	
			2017	2018			
Africa, C&W Asia	Afghanistan	Other		8	8	2.2	
	Azerbaijan	PstS7	2		2	0.5	
	Egypt	Other		2		2	0.5
		PstS1/PstS2*			9	9	2.4
	Eritrea	Other	9	5	14	3.8	
	Ethiopia	PstS11	48	28	76	20.6	
		PstS1/PstS2	9	3	12	3.3	
	Iran	PstS1/PstS2		3	3	0.8	
	Iraq	Other	3		3	0.8	
		PstS1/PstS2	6		6	1.6	
		PstS3	1		1	0.3	
		Kenya	Other	1		1	0.3
		PstS11	13	30	43	11.7	
		PstS1/PstS2	4	9	13	3.5	
	Morocco	PstS14	38	54	92	24.9	
	Russia	Other	4		4	1.1	
	Rwanda	PstS11		3	3	0.8	
		PstS1/PstS2	4	6	10	2.7	
	Tanzania	PstS11		3	3	0.8	
		PstS1/PstS2	4	3	7	1.9	
Uzbekistan	PstS11	1		1	0.3		
	PstS9	31	25	56	15.2		
Africa, C&W Asia Total			178	191	396	100	

b) Geographic group	Country	Genetic group	Crop season Year		Number of isolates Total	% of isolates Total
			2017	2018		
S. America	Argentina	PStS13	30	17	47	65.3
		PStS14	5		5	6.9
		PstS7	3		3	4.2
	Chile	PStS13		17	17	23.6
S. America Total			38	34	72	100

*PstS1/PstS2: These two aggressive strains are only distinguishable by SCAR markers (Walter et al. 2016), which have not yet been applied on 2018 samples

Table 4a-c (continued).

b) Geographic group	Country	Genetic group	Crop season Year		Number of isolates Total	% of isolates Total
			2017	2018		
Europe	Austria	PstS7	1	3	4	0.9
	Belgium	PstS10	2	10	12	2.6
		PstS7	1	1	2	0.4
	Czech Republic	PstS10		3	3	0.7
		PstS7		9	9	2.0
	Denmark	PstS10	79	34	113	24.8
		PstS13	15	2	17	3.7
		PstS14	1	4	5	1.1
		PstS7	4	2	6	1.3
		PstS8	6		6	1.3
	Estonia	PstS7		2	2	0.4
	France	PstS10		4	4	0.9
		PstS7	4	4	8	1.8
		PstS8	2		2	0.4
		Other	1		1	0.2
	Germany	PstS13	5	5	10	2.2
	Italy	PstS10	3		3	0.7
		PstS13	47	8	55	12.1
		PstS14	1	1	2	0.4
		PstS4	2	16	18	4.0
	Latvia	PstS10	5		5	1.1
		PstS13	2		2	0.4
		PstS14	6	9	15	3.3
		PstS4	1		1	0.2
		PstS7	1	2	3	0.7
		Other		1	1	0.2
	Netherlands	PstS10	11	3	14	3.1
		PstS13	1		1	0.2
		PstS7	1		1	0.2
	Norway	PstS10	17	1	18	4.0
		PstS7	2	1	3	0.7
		Other	2		2	0.4
	Poland	PstS10		1	1	0.2
		PstS13	1		1	0.2
		PstS7	2		2	0.4
	Slovakia	PstS10		1	1	0.2
		PstS14		1	1	0.2
		PstS7		2	2	0.4
	Spain	PstS10		10	10	2.2
		PstS13		4	4	0.9
		PstS14		6	6	1.3
		PstS7		4	4	0.9
Sweden	PstS10	14	23	37	8.1	
	PstS12	1		1	0.2	
	PstS13	4	3	7	1.5	
	PstS14	2		2	0.4	
	PstS4	1		1	0.2	
	PstS7	5	3	8	1.8	
Ukraine	PstS8	11	4	15	3.3	
	PstS13		4	4	0.9	
Europe Total			264	191	455	100,0

In 2018, **PstS11** was detected in two additional countries in East Africa, Rwanda and Tanzania, now being the most prevalent group in East Africa, in particular in Kenya and Ethiopia. **PstS11** was first detected in Afghanistan in 2012, later spreading to other countries in this region. Only a single race has been detected in **PstS11** (virulence phenotype: -,2,-,4,-,6,7,8,-,-,17,-,-,27,32,-,AvS,-), but often associated with new epidemics on previously resistant cultivars in affected areas.

Another genetic group, **PstS14**, containing only a single race, (virulence phenotype: -,2,3,-,-,6,7,8,9,-,-,17,-,25,-,32,Sp,AvS,-) dominated in Morocco, where it made up 100% of samples investigated. This suggests that the race *PstS14* may be adapted to many cultivars, and potentially cause large scale epidemics. *PstS14* was detected in Europe at low frequency, and in 2017 also in South America for the first time. Otherwise, the aggressive strain **PstS1/PstS2** was detected at multiple locations in CWANA, the most frequent race carrying virulence to *Yr27* (Table 5). In Uzbekistan, **PstS9** is by far the most prevalent group (most common virulence phenotype: 1,2,3,4,-,6,-,-,9,-,-,17,-,25,27,32,-,AvS,Amb), which was also the case in 2016-2017. In Eritrea, a specific group not yet assigned a group number was prevalent. We were unable to recover any of these isolates, but it may refer to a *Yr10* and *Yr27*-virulent race prevalent in Eritrea 2002-2011 (virulence phenotype: -,2,-,-,-,6,7,8,-,10,-,-,24,-,27,-,-,AvS,-).

A novel genotype was detected in Egypt, some relationship with **PstS1/PstS2**, **PstS13** and **PstS14**, but additional analyses and live samples are required to make a firm conclusion about origin and epidemic potential. None of the Egyptian 2018-samples could be recovered, possibly due to long time between sampling and lab arrival. It would be valuable to follow up, taking into account the yellow rust outbreaks observed in Egypt in 2018.

In South America, **PstS13** was widespread in Argentina and Chile (Table 4b), where unusual severe and widespread epidemics of yellow rust affected wheat crops in many areas both in 2017 and 2018. Only a single race has been detected in *PstS13* irrespective of sampling origin (virulence phenotype: -,2,-,-,-,6,7,8,9,-,-,-,-,-,AvS,-). **PstS13** has been detected in most European countries (Table 4c), including Ukraine in the east, in northern Europe giving rise to severe epidemics on multiple cultivars of Triticale and in Southern Europe affecting durum wheat severely. The race found in the **PstS13** genetic group has also proven highly epidemic on multiple wheat cultivars in Argentina and on triticale in Chile.

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,-). In terms of virulence, this race is almost similar to *Warrior* (**PstS7**), which is present in most European countries, but in lower frequencies than previously. In 2018, the *Kranich* race (**PstS8**) was not detected outside Sweden, but likely present in other countries at low frequency.

Race typing: Only few isolates of the 2018 samples have so far been race typed, giving priority to molecular genotyping of a high number of samples from countries world-wide. During winter/spring 2019, selected samples representing existing and new tentative genetic groups will enter race typing. Results will be published on www.wheatrust.org. A full updated summary of prevalent races in each genetic group since 2000 is presented in Table 5, - and also available on www.wheatrust.org

Table 5. Correspondence between genetic groups and prevalent races of *P. striiformis* sampled from epidemic sites since 2000, Global Rust Reference Center.

Common names for prevalent races and genetic groups in yellow rust - GRRC, February 2019			
Genetic group	Race	Virulence phenotype*	Prevalence in geographical region
PstS0	<i>Brigadier</i>	1,2,3,-,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	<i>Brigadier,v4</i>	1,2,3,4,-,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	<i>Madrigal_Lynx</i>	1,2,3,-,-,6,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	<i>Madrigal_Lynx,v4</i>	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,-,-,AvS,-	Europe
	<i>Robigus</i>	1,2,3,4,-,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	<i>Robigus,v7</i>	1,2,3,4,-,-,7,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	<i>Solstice_Oakley</i>	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	<i>Solstice_Oakley,v7</i>	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	<i>Tulsa</i>	-,-,3,4,-,6,-,-,-,-,-,25,-,32,-,AvS,-	Europe
	<i>other</i>	other	Europe, South America
PstS1	<i>PstS1</i>	-,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	North America, Australia
	<i>PstS1,v17</i>	-,2,-,-,-,6,7,8,9,-,-,17,-,25,-,-,-,AvS,-	North America
	<i>PstS1,v10,v24,v27</i>	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
	<i>other</i>	other	North America
PstS2	<i>PstS2</i>	-,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa, West Asia, South Asia
	<i>PstS2,v1</i>	1,2,-,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa, West Asia
	<i>PstS2,v3</i>	-,2,3,-,-,6,7,8,9,-,-,-,25,-,-,-,AvS,-	East Africa
	<i>PstS2,v27</i>	-,2,-,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia, North Africa
	<i>Pst2,v1,v27</i>	1,2,-,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa, West Asia
	<i>PstS2,v3,v27</i>	-,2,3,-,-,6,7,8,9,-,-,-,25,27,-,-,AvS,-	East Africa
	<i>PstS2,v10,v24</i>	-,2,-,-,-,6,7,8,9,10,-,-,24,25,-,-,-,AvS,-	East Africa, West Asia
	<i>PstS2,v3,v10,v24,v27</i>	-,2,3,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
	<i>PstS2,v10,v24,v27</i>	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	West Asia
	<i>Other</i>	other	East Africa & West Asia
PstS3	<i>PstS3</i>	-,-,-,-,6,7,8,-,-,-,-,-,-,AvS,-	North Africa, West Asia
	<i>PstS3,v10,v24</i>	-,-,-,-,6,7,8,-,10,-,-,24,-,-,-,-,AvS,-	West Asia
	<i>PstS3(-)</i>	-,-,-,-,6,7,8,-,-,-,-,-,-,-,-	Europe, South Asia
PstS4	<i>Triticale2006</i>	-,2,-,-,-,6,7,8,-,10,-,-,24,-,-,-,-	Europe
	<i>Other</i>	other	Europe
PstS5	<i>PstS5</i>	1,2,3,4,-,6,-,-,9,-,-,-,25,-,32,-,AvS,Amb	Central Asia
	<i>PstS5,v17</i>	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,Amb	Central Asia, South Asia
	<i>Other</i>	other	Central Asia, South Asia
PstS6	<i>PstS6</i>	1,2,-,-,-,6,7,-,9,-,-,17,-,-,27,-,-,AvS,-	East Africa, Central Asia, South Asia
PstS7	<i>Warrior</i>	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,Amb	Europe
PstS8	<i>Kranich</i>	1,2,3,-,-,6,7,8,9,-,-,17,-,25,-,32,-,AvS,Amb	Europe
PstS9	<i>PstS9</i>	1,2,3,4,-,6,-,-,9,-,-,-,25,27,32,-,AvS,Amb	Central Asia, South Asia
	<i>PstS9,v17</i>	1,2,3,4,-,6,-,-,9,-,-,17,-,25,27,32,-,AvS,Amb	Central Asia
	<i>Other</i>	other	Central Asia
PstS10	<i>Warrior(-)</i>	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe, North Africa
PstS11	<i>PstS11</i>	-,2,-,(4),-6,7,8,-,-,-,17,-,-,27,32,-,AvS,-	Central Asia, East Africa
PstS12	<i>Hereford</i>	-,2,3,-,-,6,7,8,-,-,-,17,-,25,-,32,-,AvS,-	Europe
PstS13	<i>Triticale2015</i>	-,2,-,-,-,6,7,8,9,-,-,-,-,-,-,AvS,-	Europe, South America
PstS14	<i>PstS14</i>	-,2,3,-,-,6,7,8,9,-,-,17,-,25,-,32,(Sp),AvS,-	Europe, North Africa

*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.

Literature

- Ali S, Rodriguez Algaba J, Thach T, Sørensen CK, Hansen JG, Lassen P, Nazari K, Hodson DP, Justesen, AF, Hovmøller MS, 2017. Yellow Rust Epidemics Worldwide Were Caused by Pathogen Races from Divergent Genetic Lineages. *Frontiers in Plant Science*, Vol. 8, 1057, 06.2017.
- 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.
- 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, Ali S, De Vallavieille-Pope C, Justesen AF, Hovmøller MS, 2016. Worldwide population structure of the wheat rust fungus *Puccinia striiformis* in the past. *Fungal Genetics and Biology* 87, 1-8.
- Walter, S., Ali, S., Kemen, E., Nazari, K., Bahri, B. A., Enjalbert, J., ... Justesen, A. F. (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

Acknowledgements

Submission of samples of rust infected plant material was facilitated by more than 100 collaborators from multiple organisations and countries (Table 6). Sampling in Africa and Asia was coordinated by Dave Hodson (CIMMYT), sampling in EC-VCU network trials was coordinated by Valérie Cadot (Geves), France, and sampling in South America was organised by Francisco Sautua and Marcelo A. Carmona, Universidad de Buenos Aires. 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 Department for International Development (DFID), and FAO. 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 Latvian Plant Protection Research Centre Ltd.

A summary of the results can be shared within relevant countries and organizations providing appropriate citation of this report.

Table 6. People contributing to sampling and submission of rust infected leaves in 2018.

Country	Collectors 2018	Country	Sampled by
Afghanistan	E. Mohmand, A. Bari Stanikzai, Z. Ahmazada, A. Noori, A. Raqib Lodin, G. Ghanizada, A. Latif Rasekh	Germany	Kerstin Flath
Argentina	Agustín Bilbao	Iran	Afshari, F.
	Agustín Pulido	Italy	Anna Maria Mastrangelo
	Alejandro Porfiri		Biagio Randazzo
	Ana Rodriguez		Giuseppina Goddi
	Ana Storm		Francesca Nocente
	Andrea Rosso		Virgilio Balmas
	Buck Semillas	Kenya	R. Wanyera
	Carina Cáceres	Latvia	Līga Feodorova-Fedotova
	Carlos Grosso	Morocco	Ezzahiri Brahim
	Claudio Bosco	Netherlands	Lubbert van den Brink
	Cristina Palacios	Norway	Andrea Ficke
	Diego Alvarez		Chloe Grieu
	Enrique Alberione		Morten Lillemo
	Fabricio Mock	Pakistan	Sajid Ali
	Franco Petrelli	Poland	Ewelina Piwowarczyk
	Gustavo Duarte		Pawel Czembor
	Ignacio Erreguerena	Rwanda	Dave Hodson, Innocent Habarurema
	Julián Garcia, Oro Verde	Slovakia	Svetlana Slikova
	Liliana Wehrhahne, Adelina Larsen	Spain	Dolors Villegas
	Manuela Gordo		Enrique Can
	Marcos Mitelsky		Ibal Elorza
	Margarita Sillon, Magliano F		Jesús Goñi
	Mauro Montarini		Luis Urquijo
	Norma Formento		Neus Pulg; Nieves Apa
	Victoria Gonzales, Daniel Ploper	Sweden	Alexia von Ehrenheim
Austria	Michael Oberforster		Alf Djurberg
	Thomas Massinger		Anna Berlin
Belgium	F. De Brouwer; J. Pannecoque		Anna Gerdtsen
	G. Jacquemin & R. Meza		Anna-Karin Krijger
Bhutan	Dave Hodson, Sangay Tshewang		Charlotte Norén
Chile	C. Jobet and R. Galdames		Elisabeth Bölenius
	Carola Vera; Ricardo Madariaga		Erling Christensson
	Erik Von Baer		Eva Mellqvist
Czech Republic	Alena Hanzalova		Frans Johnson
	Pavel Kraus		Gunilla Berg
Denmark	Susanne Sindberg		Johanna Holmblad
	Ghita Cordsen Nielsen		Jonas Törngren
Egypt	Atef Shahin, Wasief Youssief		Julia Dahlqvist; Anna von Heideken
Eritrea	Ashmelash Wolday		Karin Andersson
Ethiopia	Ashenafi		Kristian Jochnick
	Bekele Abeyo; Ayele Badebo		Lars Johansson
	Dave Hodson		Lina Norrlund
	Zerihun T.		Lukas Hallberg
France	Emmanuel Heurmez		Robert Dinwiddie
	Gorichon	Tanzania	Rose Mongi; Dave Hodson; Ari Uyole
	J.P. Maigniel	Ukraine	Vitaliy Paljasniy
	Laurent Pageaud	Uzbekistan	Zafar Ziyaev
	Marc Leconte		
	Mathieu Grare		
	S. Barraix; V. Cadot		