XII GRRC report: *Puccinia striiformis* race analyses/ molecular genotyping 2018

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

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, 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 **PstS11** irrespective of sample origin.
- South America: **PstS13** was completely dominant in both Argentina and Chile, 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 dominant 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) in 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 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 a reference to the results from 2017. 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 live, pure isolates and strict experimental conditions (Hovmøller et al., 2017; Sørensen et al., 2016). 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 reveal 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 to genetic groups and races demonstrating high epidemic potential. The genetic groups were 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 cultivar 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 tools allow the user to highlight particular countries, years and races/genotypes. The occurrence of prevalent races/genotypes is shown on maps in case geographical coordinates have been provided.

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 cultivar, 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 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, emphasising 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 a sufficient amount of spores for storage and race analyses. In case of signs of multiple genotypes/races within a sample, these were generally subcultured 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 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 1. Number of samples of yellow rust handled in 2018, Africa and Asia.

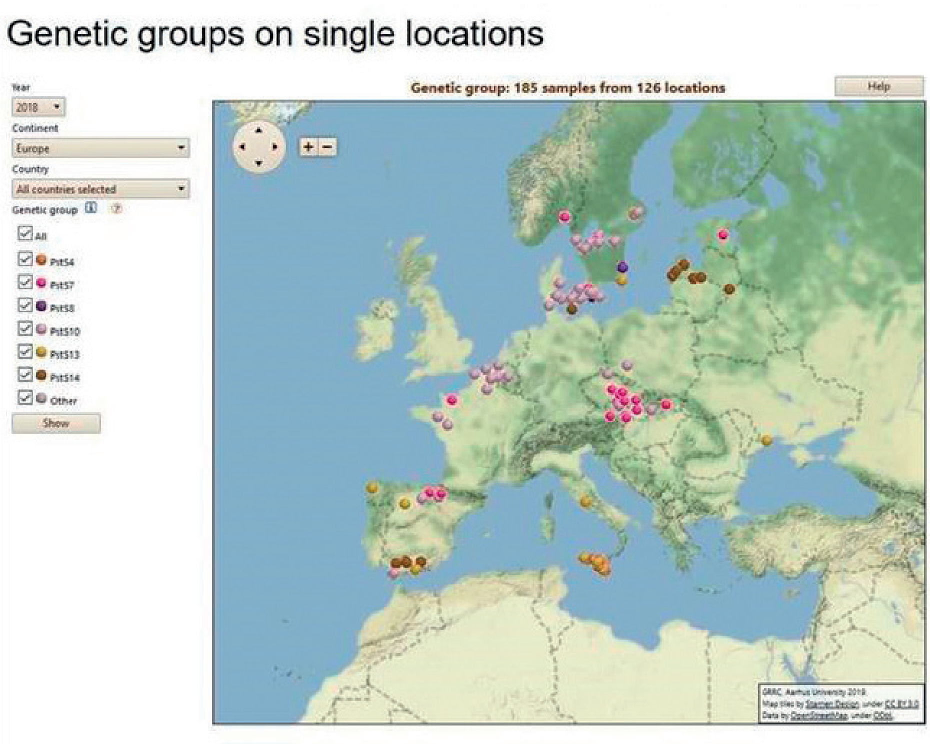
Country	Dead	Recovered	Grand total
Afghanistan	12		12
Egypt	15		15
Eritrea	8		8
Ethiopia	62	19	81
Iran	5		5
Kenya	67	20	87
Morocco	39	27	66
Rwanda	1	8	9
Tanzania	5	1	6
Uzbekistan	12	24	36
Grand total	**226**	**99**	**325**

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**

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**



Example of screen shot from the 'wheatrust.org' showing geographical locations of genetic groups of wheat yellow rust.

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 the samples from 2017, some of which were finalised 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. (Continues on the next page).

a) Geographic group	Country	Genetic group	Crop season		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	11
	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**	**369**	**100**

b) Geographic group	Country	Genetic group	Crop season		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).

c) Geographic group	Country	Genetic group	Crop season		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
		PstS8	11	4	15	3.3
	Ukraine	**PstS13**		4	4	0.9
Europe, total			**264**	**191**	**455**	**100**

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 proved 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 most 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 worldwide. During spring 2019, selected samples representing existing and new tentative genetic groups will enter race typing. Results will be published on www.wheatrust.org. A fully updated summary of prevalent races in each genetic group since 2000 is presented in Table 5 and is 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	*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
	Robigus,v7	1,2,3,4,-,-,7,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Solstice_Oakley	1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Solstice_Oakley,v7	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,-,AvS,-	Europe
	Tulsa	-,-,3,4,-,6,-,-,-,-,-,-,-,25,-,32,-,AvS,-	Europe
	Other	Other	Europe, South America
PstS1	*PstS1*	-,2,-,-,-,6,7,8,9,-,-,-,-,25,-,-,-,AvS,-	North America, Australia
	PstS1,v17	-,2,-,-,-,6,7,8,9,-,-,17,-,25,-,-,-,AvS,-	North America
	PstS1,v10,v24,v27	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
	Other	Other	North America
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, West Asia
	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,v3,v10,v24,v27	-,2,3,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	East Africa
	PstS2,v10,v24,v27	-,2,-,-,-,6,7,8,9,10,-,-,24,25,27,-,-,AvS,-	West Asia
	Other	Other	East Africa, West Asia
PstS3	*PstS3* *PstS3,v10,v24* *PstS3(-)*	-,-,-,-,-,6,7,8,-,-,-,-,-,-,-,-,-,AvS,- -,-,-,-,-,6,7,8,-,10,-,-,24,-,-,-,-,AvS,- -,-,-,-,-,6,7,8,-,-,-,-,-,-,-,-,-,-,-	North Africa, West Asia West Asia Europe, South Asia
PstS4	*Triticale2006* *Other*	-,2,-,-,-,6,7,8,-,10,-,-,24,-,-,-,-,-,- Other	Europe Europe
PstS5	*PstS5* *PstS5,v17* *Other*	1,2,3,4,-,6,-,-,9,-,-,-,-,25,-,32,-,AvS,Amb 1,2,3,4,-,6,-,-,9,-,-,17,-,25,-,32,-,AvS,Amb Other	Central Asia Central Asia, South Asia 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* *PstS9,v17* *Other*	1,2,3,4,-,6,-,-,9,-,-,-,-,25,27,32,-,AvS,Amb 1,2,3,4,-,6,-,-,9,-,-,17,-,25,27,32,-,AvS,Amb Other	Central Asia, South Asia Central Asia Central Asia
PstS10	*Warrior(-)*	1,2,3,4,-,6,7,-,9,-,-,17,-,25,-,32,Sp,AvS,-	Europe, North Africa
PstS11	*PstS11*	-,2,-,(4),-,6,7,8,-,-,-,17,-,-,27,32,-,AvS,-	Central 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
PstS14	*PstS14*	-,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.

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

Country	Collectors 2018
Afghanistan	E. Mohmand, A. Bari Stanikzai, Z. Ahmazada, A. Noori, A. Raqib Lodin, G. Ghanizada, A. Latif Rasekh
Argentina	Agustin Bilbao
	Agustín Pulido
	Alejandro Porfiri
	Ana Rodriguez
	Ana Storm
	Andrea Rosso
	Buck Semillas
	Carina Cáceres
	Carlos Grosso
	Claudio Bosco
	Cristina Palacios
	Diego Alvarez
	Enrique Alberione
	Fabricio Mock
	Franco Petrelli
	Gustavo Duarte
	Ignacio Erreguerena
	Julián Garcia, Oro Verde
	Liliana Wehrhahne, Adelina Larsen
	Manuela Gordo
	Marcos Mitelsky
	Margarita Sillon, Magliano F
	Mauro Montarini
	Norma Formento
	Victoria Gonzales, Daniel Ploper
Austria	Michael Oberforster
	Thomas Massinger
Belgium	F. De Brouwer; J. Pannecoucque
	G. Jacquemin & R. Meza
Bhutan	Dave Hodson, Sangay Tshewang
Chile	C. Jobet and R. Galdames
	Carola Vera; Ricardo Madariaga
	Erik Von Baer
Czech Republic	Alena Hanzalova
	Pavel Kraus
Denmark	Susanne Sindberg
	Ghita Cordsen Nielsen
Egypt	Atef Shahin, Wasief Youssief
Eritrea	Ashmelash Wolday
Ethiopia	Ashenafi
	Bekele Abeyo; Ayele Badebo
	Dave Hodson
	Zerihun T.
France	Emmanuel Heurmez
	Gorichon
	J.P. Maigniel
	Laurent Pageaud
	Marc Leconte
	Mathieu Grare
	S. Barrais; V. Cadot

Country	Sampled by
Germany	Kerstin Flath
Iran	Afshari, F.
Italy	Anna Maria Mastrangelo
	Biagio Randazzo
	Giuseppina Goddi
	Francesca Nocente
	Virgilio Balmas
Kenya	R. Wanyera
Latvia	Līga Feodorova-Fedotova
Morocco	Ezzahiri Brahim
Netherlands	Lubbert van den Brink
Norway	Andrea Ficke
	Chloe Grieu
	Morten Lillemo
Pakistan	Sajid Ali
Poland	Ewelina Piwowarczyk
	Pawel Czembor
Rwanda	Dave Hodson, Innocent Habarurema
Slovakia	Svetlana Slikova
Spain	Dolors Villegas
	Enrique Can
	Ibal Elorza
	Jesús Goñi
	Luis Urquijo
	Neus Pulg; Nieves Apa
Sweden	Alexia von Ehrenheim
	Alf Djurberg
	Anna Berlin
	Anna Gerdtsson
	Anna-Karin Krijger
	Charlotte Norén
	Elisabeth Bölenius
	Erling Christensson
	Eva Mellqvist
	Frans Johnson
	Gunilla Berg
	Johanna Holmblad
	Jonas Törngren
	Julia Dahlqvist; Anna von Heideken
	Karin Andersson
	Kristian Jochnick
	Lars Johansson
	Lina Norrlund
	Lukas Hallberg
	Robert Dinwiddie
Tanzania	Rose Mongi; Dave Hodson; Ari Uyole
Ukraine	Vitaliy Paljasniy
Uzbekistan	Zafar Ziyaev

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