Molecular markers for tracking the origin and worldwide distribution of invasive strains of Puccinia striiformis

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Molecular markers for tracking the origin and worldwide distribution of invasive strains of *Puccinia striiformis*


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Abstract

Investigating the origin and dispersal pathways is instrumental to mitigate threats and economic and environmental consequences of invasive crop pathogens. In the case of *Puccinia striiformis* causing yellow rust on wheat, a number of economically important invasions have been reported, e.g., the spreading of two aggressive and high temperature adapted strains to three continents since 2000. The combination of sequence-characterized amplified region (SCAR) markers, which were developed from two specific AFLP fragments, differentiated the two invasive strains, *PstS1* and *PstS2* from all other *P. striiformis* strains investigated at a worldwide level. The application of the SCAR markers on 566 isolates showed that *PstS1* was present in East Africa in the early 1980s and then detected in the Americas in 2000 and in Australia in 2002. *PstS2* which evolved from *PstS1* became widespread in the Middle East and Central Asia. In 2000, *PstS2* was detected in Europe, where it never became prevalent. Additional SSR genotyping and virulence phenotyping revealed 10 and six variants, respectively, within *PstS1* and *PstS2*, demonstrating the evolutionary potential of the pathogen. Overall, the results suggested East Africa as the most plausible origin of the two invasive strains. The SCAR markers developed in the present study provide a rapid, inexpensive, and efficient tool to track the distribution of *P. striiformis* invasive strains, *PstS1* and *PstS2*.

Introduction

Invasive species, genotypes and/or specific strains of microorganisms may pose a serious threat to the stability of ecosystems and increase the fluctuations in crop productivity (Palm 2001; Lee 2002; Hodson 2011). The increasing number of invasive crop pathogens, which has been reported in the recent past, is thereby contributing
to reduce food security in general (Parker and Gilbert 2004; Desprez-Loustau et al. 2007). The development of risk-assessment and management strategies for food production relies on knowledge about origin, migration routes and distribution of threatening strains of plant pathogens (Campbell 2001; Perrings et al. 2002), which require efficient tracking and monitoring systems. In case of crop pathogens which may spread rapidly and across long-distances, research and monitoring should address pathogen variability at continental or global scales.

The inconspicuous nature of many crop pathogens makes the application of molecular markers and population genetic analyses highly valuable (McDonald 1997; Gladiex et al. 2008; Hovmøller et al. 2008; Ali et al. 2014b). Their application in different populations and environments may provide the basis for further development of markers targeting specific strains and/or essential epidemiological features (Carvalho et al. 2001; Hodson et al. 2012; Zamor et al. 2012). Development and application of such markers have proven to be highly valuable for the efficient detection and tracking of invasive strains/species and could be applied to a wide range of microbial invasive species like fungi (Kroon et al. 2004; Hodson et al. 2012), viruses (Brown 2000), bacteria (Carvalho et al. 2001) and algae (Zamor et al. 2012). Several molecular marker techniques have been exploited to understand microbial population biology e.g., Random Amplified Polymorphic DNA (RAPD), Restriction Fragment Length Polymorphism (RFLP), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR) and Single Nucleotide Polymorphism (SNP) markers (McDonald 1997). The AFLP markers, which were widely used in the 1990s and 2000s to detect genetic variation in populations with very low genetic diversity (e.g., Justesen et al. 2002; Enjalbert et al. 2005) can be converted into sequence-characterized amplified region (SCAR) markers (Paran and Michelmore 1993). The codominant, single-locus SCAR markers allow a quick and easy PCR amplification-based detection of the defined fungal strains (Hermosa and Grondona 2001; Naeimi and Koscszubé 2011). Application of SCAR markers facilitates testing of a large number of isolates and could be useful to track the origin and spread of microbial pathogens with long distance dispersal capacity and invasion potential.

The wheat yellow/stripe rust pathogen, *Puccinia striiformis* can undergo long distance dispersal and has caused numerous invasions (Zadoks 1961; Wellings and McIntosh 1990; Markell and Milus 2008; Hovmøller et al. 2015). While the recently suggested centre of diversity of *P. striiformis* is in the Himalayan and near-Himalayan region (Ali et al. 2010, 2014a,b; Thach et al. 2016), the pathogen is distributed worldwide and is often associated with severe economic losses (Stubbs 1985; Hovmøller et al. 2002, 2011; de Vallavieille-Pope et al. 2012). Losses can be especially high when the epidemics are associated with exotic strains or populations, as these are rarely considered in breeding for disease resistance locally (Chen et al. 2002; Wellings 2007). Several cases of economically important incursions have been reported for *P. striiformis* but only very recently the origin of these were confirmed (Ali et al. 2014a; Hovmøller et al. 2015). In the early 20th century, the pathogen was reported for the first time in North and South America (Carleton 1915; Rudorf and Job 1934), most likely spreading from NW Europe (Hovmøller et al. 2011; Ali et al. 2014a). It was introduced accidentally in Australia in 1979 from NW Europe (Wellings and McIntosh 1990; Hovmøller et al. 2008) through human transmission (Wellings 2007). The strains first detected in South Africa in 1996 were later shown to be genetically related to populations in the Middle Eastern and Mediterranean regions, possibly spread by wind (Boshoff et al. 2002; Hovmøller et al. 2008; Ali et al. 2014a). Apart from these recent incursion events in previously noncolonized areas, *P. striiformis* has been important in the context of invasion and recolonization through emergence of new races and strains. For example, virulence to the resistance gene Yr9 was detected in races in East Africa (Ethiopia) in 1986, and the same virulence was in subsequent years observed in the Middle East and Indian subcontinent and thereby seriously affecting Yr9-resistant wheat varieties across large areas for more than a decade (Singh et al. 2004). Since 2000, the emergence of two high temperature-adapted aggressive strains, *PstS1* and *PstS2*, resulted in geographical expansion of *P. striiformis* epidemics into Western Australia and the Southeastern USA, where the disease had not previously been considered a problem (Chen 2005; Milus et al. 2009). Since 2011, invasive strains of the “Warrior” and “Kra- nich” races have largely replaced the pre-existing NW European populations (Hovmøller et al. 2015; Hubbard et al. 2015).

*PstS1* and *PstS2* were clearly distinct from the local pre-2000 populations of North America, Australia and Europe (Hovmøller et al. 2011) and representative isolates of these were shown to be more aggressive and adapted to high temperatures than typical isolates from Europe and North America (Markell and Milus 2008; Milus et al. 2009). *PstS1* resulted in *P. striiformis* epidemics in the south-central USA in 2000 and following years (Chen 2005; Milus et al. 2006) and in Western Australia in 2002 (Wellings et al. 2003). *PstS2* was reported in NW Europe with similar aggressiveness and strong differentiation from local *P. striiformis* populations but it did not have an adverse economic impact because most European wheat varieties were resistant to this strain (Mboup et al. 2012; Hovmøller et al. 2015). *PstS2* was also present in the

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Mediterranean region and the Middle East–Red Sea area. Although both strains were related to a genetic group prevalent in Western Asia, North Africa and the Red Sea Area (Ali et al. 2014a), the exact geographical origin and spread of the two strains remain unknown, and the monitoring of further spread of these two strains would greatly benefit from the development of efficient and easy-to-apply diagnostic tools.

PstS1 and PstS2 differed from each other by only two polymorphic AFLP fragments and from other strains by at least 14 AFLP markers (Hovmøller et al. 2008). In this study we converted two AFLP markers into SCAR mark-
ers; P19M24.225 being specific to both PstS1 and PstS2 and distinguishing these from all other strains investigated; and P12M26.150 which was present in PstS1 and other isolates and thereby distinguishing PstS2 isolates from all others considered in the study (Hovmøller et al. 2008). Conversion of these AFLP bands into strain specific SCAR markers should provide a valuable and simple monitoring and tracking tool. The present study was designed (1) to develop PCR based SCAR markers for rapid and efficient detection of the two invasive strains PstS1 and PstS2, (2) to assess the distribution of the two strains on a worldwide scale using these SCAR markers, and (3) to detect variation within the strains and to infer potential origin of these by comparing SSR genotypes and virulence phenotypes of PstS1 and PstS2 with the worldwide genetic grouping (Ali et al. 2014a) and the virulence phenotypes of historical isolates from the “Stubbs collection” (Thach et al. 2016).

Materials and Methods

Selection and virulence assessment of isolates

A set of 566 isolates of P. striiformis were selected from a worldwide set of more than 5000 isolates available at BIOGER-CPP, INRA, France and the Global Rust Reference Center (GRRRC) at Aarhus University, Denmark. Isolates were selected primarily from year 2000 and onwards (525 of 567 isolates; Table 1) when the invasive P. striiformis strains were first detected (Milus et al. 2006; Hovmøller et al. 2008). Isolates were sampled by either the authors or their international collaborators from local field trials, trap nurseries or commercial fields as single lesions on detached wheat leaves (Table 1). The virulence phenotype of P. striiformis isolates was determined using differential cultivars and additional varieties (Hovmøller and Justesen 2007; Thach et al. 2015).

Using the published virulence phenotype (Hovmøller et al. 2008; Milus et al. 2009) for invasive strains PstS1 and PstS2 as selection criteria, virulence profiles of P. striiformis isolates from the historic Stubbs collection (Thach et al. 2015), comprising 2708 unique wheat yellow rust isolates sampled on six continents in 66 countries between 1958 and 1995 were inspected in order to identify historic samples with virulence profiles similar to those of PstS1 and PstS2. A subset of these isolates from the Stubbs collection (Thach et al. 2015), was selected for genotyping with the newly developed SCAR markers (Table 1). Worldwide race groups were inspected at the database www.wheatrust.org using the “yellow rust” and “pathotype by country” and “race groups” selections.
Isolation of genomic DNA

Genomic DNA was extracted either from 5 to 10 mg of urediniospores (dikaryotic) using a modified CTAB protocol (Enjalbert et al. 2002; Hovmøller et al. 2008) or from wheat leaf segments bearing a single lesion (Ali et al. 2011). Extracted DNA was quantified on an agarose gel or with the NanoDrop 2000 spectrophotometer (Thermo Fisher Scientific Inc., Waltham, MA, USA) and stored at −20°C.

Purification and sequencing of AFLP bands

The two AFLP markers P19M24.225 and P12M26.150 (Hovmøller et al. 2008), were excised for selected positive isolates with a scalpel from AFLP gels that were blotted onto Whatman™ paper and aligned with the corresponding autoradiogram. Excised AFLP bands were dissolved in Tris-EDTA pH 8.0 by incubation at 60°C for 2 h and the resulting DNA solution was collected by centrifugation at 12000 rcf for 20 min. The respective AFLP fragments were amplified with primers PstI+O and MseI+O (Vos et al. 1995; Justesen et al. 2002) in a Thermocycler (Eppendorf, Hamburg, Germany) using PCR conditions consisting of 94°C for 2 min 30 sec and 40 cycles of 94°C for 30 sec, 56°C for 1 min, and 72°C for 1 min, and a final extension at 72°C for 5 min. Standard PCR was performed in total reaction volume of 25 μL containing the Eppendorf Taq DNA polymerase kit (Eppendorf) and 2.5 mM of dNTPs and using 15 μL DNA solution.

PCR products were either cloned into the vector pGEM-T (Promega, Fitchburg, WI, USA) according to the manufacturer’s instructions or purified from an agarose gel with the Qiagen II gel extraction kit (Qiagen, Hilden, Germany) prior to sequencing (Macrogen Europe, Amsterdam, The Netherlands) with primer pairs T7/SP6 or PstI+O/MseI+O respectively. Using Geneious® Pro 6.1.4 software (Biomatters Ltd., Auckland, New Zealand), the obtained sequences were trimmed for low quality and vector traces after BLAST search against the NCBI

Table 3. Confirmation of the P. striiformis invasive strain-specific SCAR markers through their application to previously characterized isolates assigned to invasive aggressive and endemic nonaggressive groups.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Country</th>
<th>Sampling year</th>
<th>AFLP marker grouping (Hovmoller et al., 2008)</th>
<th>Aggressiveness test (Milus et al. 2009)</th>
<th>Interpretation based on SCAR markers</th>
</tr>
</thead>
<tbody>
<tr>
<td>MT83</td>
<td>USA</td>
<td>1983</td>
<td>NW European group</td>
<td>Nonaggressive</td>
<td>SCP19M24 Nonaggressive</td>
</tr>
<tr>
<td>Mex89.009</td>
<td>Mexico</td>
<td>1989</td>
<td>NW European group</td>
<td>Nonaggressive</td>
<td>SCP19M24 Nonaggressive</td>
</tr>
<tr>
<td>AR90-01</td>
<td>USA</td>
<td>1990</td>
<td>NW European group</td>
<td>Nonaggressive</td>
<td>SCP12M26 Nonaggressive</td>
</tr>
<tr>
<td>DK16/02</td>
<td>Denmark</td>
<td>2002</td>
<td>NW European group</td>
<td>Nonaggressive</td>
<td>SCP12M26 Nonaggressive</td>
</tr>
<tr>
<td>DK26/02</td>
<td>Denmark</td>
<td>2002</td>
<td>Strain 2</td>
<td>Aggressive</td>
<td>SCP12M26 Aggressive</td>
</tr>
<tr>
<td>E02/03</td>
<td>Eritrea</td>
<td>2003</td>
<td>Strain 2</td>
<td>Aggressive</td>
<td>SCP12M26 Aggressive</td>
</tr>
<tr>
<td>AR05-4G-3</td>
<td>USA</td>
<td>2005</td>
<td>Strain 1</td>
<td>Aggressive</td>
<td>SCP12M26 Aggressive</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>SCP12M26 Aggressive</td>
</tr>
</tbody>
</table>

Figure 1. Gel electrophoresis depicting the PCR fragments generated after amplification of the SCAR markers SCP19M24 or SCP12M26 for representative isolates of P. striiformis invasive strains PstS1 and PstS2 and other isolates. Other isolates may also have lost the SCP12M26a1 fragment, however, these were not designated PstS2 unless they also have the P19M24a1 fragment. In the figure a1 refers to allele 1 and a2 to allele 2.
Development of PCR markers for invasive *P. striiformis* strains

Genomic sequences flanking the sequenced AFLP fragments were obtained by BLASTn search against (1), the sequence read archive, whole-genome shotgun contigs, and transcriptome shotgun assemblies available for *P. striiformis* at GenBank; (2), *Puccinia* Group transcripts and genomic sequences of the *Puccinia* Group Sequencing Project, Broad Institute of Harvard and MIT (http://www.broadinstitute.org/); and (3), a shotgun genome assembly for the European *P. striiformis* isolate GB75/30 generated at The Sainsbury Lab, Norwich, United Kingdom (available on request from GRRC). Primers for sequencing were designed from identified flanking genomic regions to allow amplification and subsequent sequencing from both isolates harboring and lacking the respective AFLP fragment in order to identify precisely those nucleotide changes that account for the observed AFLP polymorphisms and to design allele specific PCR primers (Table 2). Respective genomic regions were amplified with these primers from DNA of selected isolates polymorphic for the respective AFLP marker and sequenced as described. SCAR markers detecting these polymorphisms were designed for both AFLP markers P19M24.225 and P12M26.150, and termed SCP19M24 and SCP12M26 respectively (SC: abbreviation for sequence characterized).

Validation of SCAR markers

The SCAR markers developed in the study were validated against the seven representative isolates, which were originally used to define the two invasive strains (Hovmöller et al. 2008; Milus et al. 2009). The markers were further validated by comparing SCAR and AFLP results for all isolates in the study of Hovmöller et al. (2008). In case of disagreements between AFLP data for the two markers (Hovmöller et al. 2008) the polymorphic marker region was sequenced Macrogen Europe with the primers indicated in Table 2.

Screening of worldwide *P. striiformis* collection to track *PstS1* and *PstS2*

The SCAR primers were then applied to a large set of 566 worldwide representative isolates to assess the geographical distribution of strains *PstS1* and *PstS2* (Table 1). PCR was performed in a total reaction volume of 20 μL containing 1x GoTaq Flexi Buffer (5×; Promega), 1.5 mM MgCl₂, 100 μM of each dNTP, 1 μM of each primer, 0.5 U GoTaq Flexi DNA polymerase (5 U/μL; Promega) and 50 ng of genomic DNA. PCR conditions were 94°C for

---

Table 4. Relative distribution of the two invasive strains (*PstS1* and *PstS2*) in worldwide populations of *P. striiformis*.

<table>
<thead>
<tr>
<th>Geographical origin</th>
<th>Country</th>
<th>Isolates tested</th>
<th><em>PstS1</em></th>
<th><em>PstS2</em></th>
<th>Other</th>
</tr>
</thead>
<tbody>
<tr>
<td>South Asia</td>
<td>Afghanistan</td>
<td>16</td>
<td>2</td>
<td>14</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Nepal</td>
<td>19</td>
<td>-</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Pakistan</td>
<td>21</td>
<td>-</td>
<td>10 11</td>
<td></td>
</tr>
<tr>
<td>East Africa</td>
<td>Eritrea</td>
<td>18</td>
<td>-</td>
<td>7</td>
<td>11</td>
</tr>
<tr>
<td></td>
<td>Ethiopia</td>
<td>38</td>
<td>10</td>
<td>10 18</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Kenya</td>
<td>25</td>
<td>11</td>
<td>11 3</td>
<td></td>
</tr>
<tr>
<td></td>
<td>South Africa</td>
<td>1</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Central Asia</td>
<td>Kazakhstan</td>
<td>6</td>
<td>-</td>
<td>-</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>Kyrgyzstan</td>
<td>6</td>
<td>-</td>
<td>-</td>
<td>6</td>
</tr>
<tr>
<td></td>
<td>Tajikistan</td>
<td>12</td>
<td>-</td>
<td>-</td>
<td>12</td>
</tr>
<tr>
<td></td>
<td>Uzbekistan</td>
<td>8</td>
<td>-</td>
<td>2</td>
<td>6</td>
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<tr>
<td>Middle East</td>
<td>Azerbaijan</td>
<td>29</td>
<td>-</td>
<td>21 8</td>
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<tr>
<td></td>
<td>Iran</td>
<td>19</td>
<td>-</td>
<td>15 4</td>
<td></td>
</tr>
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<td>Iraq</td>
<td>8</td>
<td>-</td>
<td>-</td>
<td>7 1</td>
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<td>Israel</td>
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<td>-</td>
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<td>Lebanon</td>
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<td>7</td>
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<td>1</td>
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<td>-</td>
<td>14 3</td>
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<td>3</td>
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<td>19 1</td>
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<td>24 1</td>
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<td>4 8</td>
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</tr>
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<td></td>
<td>Portugal</td>
<td>4</td>
<td>-</td>
<td>4</td>
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<tr>
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<td>Spain</td>
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<td>-</td>
<td>4 4</td>
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<td>5</td>
<td>-</td>
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</tr>
<tr>
<td></td>
<td>Overall population</td>
<td>566</td>
<td>33 219</td>
<td>314</td>
<td></td>
</tr>
</tbody>
</table>

¹*PstS2* isolates from Europe were selected according to virulence phenotype and are not representative for the European population.

VecScreen database as well as for artificially included primer sequences of PstI+O and MseI+O and were manually corrected for sequence read errors after multiple MUSCLE alignment (integrated in Geneious® Pro 6.1.4; Biomatters Ltd.) of all homologous sequences. Identity of amplified sequences with respective AFLP markers was confirmed by alignment with the respective AFLP primers (Justesen et al. 2002).
2 min 30 sec and 35 cycles of 94°C for 30 sec, annealing at 60°C (for SCP19M24), or 63°C (for SCP12M26) for 1 min, and 72°C for 30 sec, and a final extension at 72°C for 5 min. PCR products were analyzed in 1.5% agarose gels.

**Microsatellite genotyping of P. striiformis isolates**

To study diversity within the two strains from different geographical sampling areas and to infer their likely origin, microsatellite genotyping was performed for a subset of 131 isolates representing PstS1 and PstS2 strains. Microsatellite genotyping was done with a set of 16 SSR markers (RJN3, RJN4, RJN5, RJN6, RJN8, RJN9, RJN10, RJN11, RJN12, RJN13, RJ04, RJ018, RJ020, RJ021, RJ024, WU-6), previously described (Ali et al. 2011) and used to describe the worldwide population structure (Ali et al. 2014a). These 16 SSRs were amplified in two multiplex reactions (Rodriguez-Algaba et al. 2014). The number of multilocus genotypes (MLGs) among isolates classified as PstS1 or PstS2 via SCAR markers was identified using GENCLONE (Arnaud-Haond and Belkhir 2007), and their profiles were compared with the SSR data of related multilocus genotypes (MLGs) detected in the worldwide populations by Ali et al. (2014a), particularly MLG-99, which comprised PstS1 and PstS2 representative isolates and others with related virulence profiles. Genetic differentiation between PstS1 and PstS2 isolates was investigated by calculating $F_{ST}$ values estimated with GENETIX v. 4.03 (Belkhir et al. 2004). The relationship of MLGs with the worldwide genetic groups also assessed through construction of a phylogenetic tree was based on neighbor-joining using the software POPULATION (Langella 2008).

**Results**

Two SCAR markers were developed for tracking the distribution and origin of the invasive P. striiformis strains, PstS1 and PstS2. The two markers were validated in previously characterized isolates and then applied to a set of 566 isolates to track the origin and worldwide distribution of these two invasive strains.

**Strain specific markers, SCP19M24 and SCP12M26**

Two AFLP markers (P19M24.225 and P12M26.150) were selected for cloning, resequencing, and development of SCAR markers. The marker P19M24.225 distinguished invasive strains PstS1 and PstS2 from all other
Figure 3. Prevalence of *P. striiformis* invasive strains PstS2 across Europe since first appearance in 2000. Prevalence is determined by identifying isolates with virulence phenotypes typical of PstS1 and PstS2.
Table 5. Number of resampled multilocus genotypes (MLGs) in PstS1 and PstS2 and their resampling in the worldwide P. striiformis population studied by Ali et al. (2014a).

<table>
<thead>
<tr>
<th>MLGs detected</th>
<th>Resampling in the invasive strains</th>
<th>Resampling in worldwide population</th>
<th>Assignment to worldwide genetic group</th>
<th>SSR loci differentiating from MLG-1</th>
</tr>
</thead>
<tbody>
<tr>
<td>MLG-99</td>
<td>17</td>
<td>75</td>
<td>78</td>
<td>G4</td>
</tr>
<tr>
<td>MLG-99i</td>
<td>–</td>
<td>10</td>
<td>–</td>
<td>G4</td>
</tr>
<tr>
<td>MLG-99ii</td>
<td>–</td>
<td>9</td>
<td>–</td>
<td>G4</td>
</tr>
<tr>
<td>MLG-99iii</td>
<td>–</td>
<td>6</td>
<td>–</td>
<td>G4</td>
</tr>
<tr>
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<td>2</td>
<td>–</td>
<td>G4</td>
</tr>
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<td>MLG-99v</td>
<td>–</td>
<td>3</td>
<td>–</td>
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<tr>
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<td>1</td>
<td>–</td>
<td>G4</td>
</tr>
<tr>
<td>MLG-99ix</td>
<td>–</td>
<td>1</td>
<td>–</td>
<td>G4</td>
</tr>
</tbody>
</table>

1Assignment based on phylogenetic tree and group name according to Ali et al. (2014a).

P. striiformis isolates, and marker P12M26.150 distinguished PstS2 isolates from all other isolates and hence allowed discrimination between PstS1 and PstS2 isolates.

The P19M24.225 AFLP fragment was cloned from the Danish PstS2 isolate, DK80/01, and it was present in PstS1 and PstS2 only. Resequencing of the SCP19M24 SCAR region defined the length of the genomic sequence corresponding to the AFLP fragment as 199 bp in PstS1 and PstS2 isolates and 184 bp in other isolates. The AFLP variant in PstS1 and PstS2 isolates resulted from a SNP that created a new MseI site, as well as an insertion of 15 bp within the AFLP fragment (Fig. S1). The SCAR primers detected the presence or absence of both the MseI restriction site and the 15 bp insertion and yielded a 405 bp PCR product (SCP19M24a1) in PstS1 and PstS2 isolates but not in other isolates, and a 385 bp PCR product (SCP19M24a2) in all isolates (Fig. 1). Binding specificity was increased by inclusion of an artificial mutation at the third-to-last bp (from the 3'end) of the respective reverse primers for SCP19M24a1 and SCP19M24a2 (Table 2).

The absence of the P12M26.150 AFLP marker was generally specific to PstS2 isolates, whereas PstS1 and all other isolates had this marker. The P12M26.150 AFLP fragment was cloned from the noninvasive Pakistani isolate PK09/04. Cloning and resequencing of the P12M26.150 genomic region revealed that polymorphism was due to two single base pair deletions in PstS1 and other isolates. Resequencing of the SCP12M26 SCAR region revealed two genomic sequences homologous to the AFLP fragment, one of 131 bp in all isolates (SCP12M26a2) and another (SCP12M26a1) of 129 bp in PstS1 and other isolates but not in PstS2 isolates (Fig. S2).

Owing to the high sequence similarity of the two length variants of this marker, SCAR primers were designed to detect sequence differences in the 5' and 3' flanking genomic regions (Fig. S2). The SCP12M26a1 SCAR primers (Table 2) amplified a product of 491 bp in PstS1 and other isolates but not in PstS2 isolates, and hence detected the PstS2 strain (Fig. 1). The SCP12M26a2 SCAR primers (Table 2) amplified a 262 bp product in almost all isolates. The SCP12M26a1 SCAR primers do amplify in addition to the desired 491 bp product a band of 1156 bp from the a2 sequence due to high sequence similarity in the primer binding regions; however this band was not used for diagnostic purpose (Fig. 1).

Validation of invasive strain specific markers

The results of tests of the SCAR markers SCP19M24 and SCP12M26 on the seven representative isolates that originally served to define invasive strains PstS1 and PstS2 were in agreement with the original classification (Table 3). For further validation, the SCAR markers were compared with AFLP data for another 155 isolates from a previous study. For marker SCP19M24, the two types of data were in full agreement (Table S1). Results for SCP12M26 agreed with AFLP results for another 155 isolates from the worldwide population (Table S1). Resequencing of the SCAR marker region for the remaining 12 isolates, which all were sampled in Morocco and Syria in 2009, showed that they carried a mutation in the AFLP fragment. Altogether, these results indicated that the SCAR markers were reliable diagnostic markers for tracking the invasive strains PstS1 and PstS2. While the two markers together enabled to detect the invasive strains, some isolates from Central and East Asia with a recombinant population structure had either acquired the SCP19M24a1 allele or lost the SCP12M26a1 allele.
Worldwide distribution of the two invasive strains PstS1 and PstS2

After validation of the markers, they were applied to 566 isolates representative of worldwide populations, of which 41 were sampled pre-2000 and 525 between 2000 and 2012. Either PstS1 or PstS2 were detected in all regions except South America (Table 4). In Australia, Mexico and USA only PstS1 was detected. Both PstS1 and PstS2 were found in East Africa in Eritrea, Ethiopia and Kenya, with equal frequencies in Kenya and Ethiopia (Table 4). In South Asia and Middle East, North Africa, Central and Southern Europe only PstS2 was detected at varying frequencies. Five isolates sampled in Kyrgyzstan, Afghanistan and Tajikistan, which represent areas where recombination is likely to occur, were diagnosed as PstS1 with the SCAR test. However, the AFLP genotypes of these were clearly different from PstS1.

Considering the temporal changes in the relative frequencies of the two invasive strains over years, PstS1 was detected as early as 1982 and 1986 in East Africa, much earlier than PstS2 which was first detected in 2000 in Europe (Fig. 2 and Table 4). While PstS1 was only observed sporadically after 2000 outside the Americas and Australia, PstS2 was detected in West and Central Asia in 2003 and then became prevalent in the Mediterranean.
PstS2 remained prevalent in Middle East and North Africa 
till 2012 (the latest year examined). In Europe, 
PstS1 was 
not detected while PstS2 never became prevalent in the 
native population (Fig. 3).

Within strain microsatellite and virulence polymorphism

Microsatellite genotyping of 131 isolates of PstS1 and 
PstS2 revealed the presence of 10 distinct MLGs (Table 5). The most prevalent MLG, in the present 
study, designated MLG-99 according to Ali et al. (2014a), was detected in both PstS1 and PstS2. In this 
study MLG-99 was detected in Australia, Central Asia, 
Middle East, East Africa and North Africa, and North 
America (Fig. 4). MLG-99iv was also detected in both 
PstS1 and PstS2. All the MLGs differed only at one locus 
from the MLG-99, except MLG-99vi, which differed at 
two loci. All the MLGs detected in PstS1 and PstS2 were 
assigned to the genetic group G4, the Middle East-East 
African group (Ali et al. 2014a). There was no significant 
genetic differentiation between the PstS1 and PstS2 iso-
lates as shown by the FST statistic value = 0.00083 (P-
value < 0.001). 

The majority of isolates defined by SCAR markers as 
PstS1 or PstS2 had virulence corresponding to host resis-
tance genes Yr2, Yr6, Yr7, Yr8, Yr9, and Yr25 (Table 6). Additional virulence to Yr27 was also common in the 
Middle East and Central Asia. Less frequent and often 
locally confined additional virulence was observed for 
Yr1, Yr10, and Yr24.

Origin of the two invasive strains

The origin of the two invasive strains was inferred 
from their presence in temporally spaced populations, 
their virulence phenotype and microsatellite genotype in 
comparison with worldwide reference data. The viru-
ulence phenotype of 138 isolates from the historic 
Stubbs’ collection sampled between 1958 and 1995, 
resembling the virulence phenotype of PstS1 and PstS2, 
all originated from East Africa. The SCAR test of 13 of 
these revealed the presence of PstS1 as early as 1982 in 
Kenya and in 1986 in Ethiopia (Fig. 2) but PstS2 was 
not detected among these early samples (Fig. 2). The 
phylogenetic tree based on the microsatellite genotyping 
of a total of 132 PstS1 and PstS2 isolates, which 
showed no or limited divergence from isolates collected 
in the Middle East/East Africa, further supported an 
East African origin (Fig 5). 

Virulence phenotype related to the strain PstS1/S2 in 
the pre-2000 Stubbs collection suggested that they first 
appeared in Kenya and subsequently in Ethiopia, Rwanda, 
Burundi, and Tanzania. Two variant virulence phenotypes 
were detected in the older East African isolates, compared 
to more recent invasive strains, differing from PstS1 in 
virulence to Yr3 or Yr25 (data not shown).

Discussion

The development of a simple, reliable, and easy-to-apply 
molecular diagnostic tool enabled to describe the world-
wide distribution of the invasive P. striiformis strains 
PstS1 and PstS2 along with identification of its origin in 
East Africa.

Invasive strain specific SCAR markers

The two SCAR markers were developed for rapid detec-
tion of invasive strains PstS1 and PstS2 in the P. stri-
formis population. The SCAR markers were conserved 
across samples of diverse geographical origin, as revealed 
through DNA sequencing of the SCAR fragments (data 
not shown). These SCAR markers are indicative of PstS1 
and PstS2 in clonal populations of P. striiformis and are 
thus reliable and rapid diagnostic markers for tracking and monitoring of these aggressive invasive strains. They 
can be used on a worldwide scale to detect their arrival 
and prevalence to feed into prediction and early warning
Origin and Distribution of *PstS1*/*PstS2*

*PstS1* was first reported in 2000 in the USA and in 2002 in Australia while *PstS2* was first reported in 2000 in Europe and then in Africa and Asia (Chen et al. 2002; Hovmøller and Justesen 2007; Markell and Milus 2008). However, analyses of pre-2000 isolates revealed the presence of *PstS1* as early as 1982 in Kenya, followed by the neighboring countries, Ethiopia in 1986, Rwanda and Burundi in 1988, and Tanzania in 1990. Moreover, *PstS1* was not detected outside East Africa until first appearance in North America and Australia (Hovmøller et al. 2008), and East Africa was the only region where both strains were detected. Finally, isolates which had been categorized as *PstS1*/*PstS2* by the SCAR test were all assigned the East African/Middle East genetic group based on microsatellite genotyping (Ali et al. 2014a). All these facts confirmed East Africa as the most likely origin of the two invasive strains.

With an origin in East Africa, *PstS1* would have spread further in the region and later on to North America and Australia. Mutation of *PstS1* into *PstS2* and its subsequent spread into the Middle East, North Africa and subsequently Europe resulted in their first detection in 2002 (Flath and Bartels 2002; Hovmøller and Justesen 2007; Hovmøller et al. 2008). In the post-2000 worldwide populations, either *PstS1* or *PstS2* was present in all regions investigated. During their worldwide dispersal, the two strains diversified in terms of virulence and multilocus genotypes; at least 10 distinct MLGs were detected in *PstS1*and *PstS2*, though all were closely related to the Middle Eastern-East African genetic group G4 (Ali et al. 2014a). The most prevalent multilocus genotype, identified in the present study corresponding to MLG-99 in Ali et al. (2014a) was the most common MLG worldwide. Although virulences to the resistance genes Yr2, 6, 7, 8, 9, 25 were characteristic of *PstS1* and *PstS2* (Milus et al. 2006; Hovmøller et al. 2008), further additional virulences would have been acquired by the strain during its spread and establishment.

The first appearance of *PstS1* in USA (in 2000) and Western Australia (in 2002) was followed by severe yellow rust epidemics in these areas (Chen et al. 2002; Milus et al. 2006; Wellings 2007). *PstS2* was first detected in West and Central Asia in 2003 (samples from earlier years were not available) and soon became prevalent in Middle East and North Africa, where it was found at the origin of major epidemics, see www.wheatrust.org. The high temperature adaptation of these two strains (Milus et al. 2006, 2009; Markell and Milus 2008) could have resulted in their establishment in warm climates, which were previously not considered to be conducive for *P. striiformis* (Milus et al. 2006; Markell and Milus 2008). The spread of these two invasive strains may be associated with the break-down of the widely deployed Yr9 resistance gene in the Middle East and South Asia in the 1980s and 1990s (Singh et al. 2004). The overall aggressiveness of the strains very likely contributed to their prevalence worldwide, particularly in the warmer climates of Middle East and North Africa.

In some regions, like Middle East and North Africa, these invasive strains (*PstS2* in this case) became dominant in the locally adapted *P. striiformis* populations and virulence phenotype data available at the database www.wheatrust.org suggests that these strains continue to affect wheat production. This has resulted in the shift in the population in Middle East and North Africa, where the pre-2000 populations were strongly divergent from current populations (Bahri et al. 2009; Ali et al. 2014a; Thach et al. 2016). In other regions, like South Asia, they did not dominate the native *P. striiformis* population (Ali et al. 2014b,c). Although *PstS2* was detected in Europe in 2000 (Flath and Bartels 2002; Hovmøller et al. 2008), it never increased in frequency to dominate the native population of NW Europe (Hovmøller et al. 2015). This could be due to the lack of virulences to the resistance genes in widely deployed varieties in Europe (Hovmøller 2007; de Vallavielle-Pope et al. 2012), as in the case of another Mediterranean strain, *PstS3* (Ali et al. 2014a), which never established in NW Europe due to the lack of certain virulences (Mboup et al. 2012; Hovmøller et al. 2015). This emphasizes the benefit of deploying crop varieties representing a diverse set of resistance genes to counteract the potential threat of invasive strains.

Conclusions

The SCAR markers developed in the current study provide a rapid, inexpensive, and efficient tool to track the
distribution of \textit{P. striiformis} invasive strains, \textit{PstS1} and \textit{PstS2}. The study also revealed the distribution of the two strains across the world and identified East Africa as their origin. The worldwide spread and establishment of the two invasive strains reflect the adaptive potential of crop pathogens and the homogeneity in agricultural ecosystems, where genetically uniform crop varieties often are grown across large areas. The markers will enable further tracking of these strains, while the information in the study should encourage a better management of agro-ecosystems in terms of resistance gene deployment to combat future invasion risks.

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**Conflict of Interest**

None declared.

**References**


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**Supporting Information**

Additional Supporting Information may be found online in the supporting information tab for this article:

**Fig. S1.** Sequence alignment and primer binding sites for the polymorphic genome regions of SCAR marker SCP19M24.

**Fig. S2.** Sequence alignment and primer binding sites for the polymorphic genome regions of SCAR marker SCP12M26.

**Table S1.** Comparison of the performance of SCAR markers in relation to that of AFLP markers.