Puccinia striiformis causes stripe rust on cereal crops and related wild grasses. The disease is especially important in wheat and barley production around the world\(^1,2\). The fungal pathogen produces new virulent races readily that overcome cultivar resistance, causing severe damage. However, it is still not clear how \(P.\ striiformis\) evolves so fast to overcome host resistance and adapt to different production environments. Therefore, this research project was conducted to characterize the stripe rust collections from the USA and eight other countries using molecular markers to determine the pathogen population structure and understand evolutionary mechanisms of race development. In the first study, 2,247 isolates of \(P.\ striiformis\ f.\ sp.\ tritici\) (\(Pst\)), the wheat stripe rust pathogen, collected from regions of stripe rust outbreaks in the USA from 2010–2017, were genotyped using 14 simple sequencing repeat markers (SSR) to study spatial and temporal population diversity, dynamics and differentiation\(^3\). From the spatial populations identified, multilocus genotypes (MLGs) and greater genotypic diversity were identified in western than eastern regions of production in the USA. The western populations had greater differentiation and less frequent gene flow than the eastern populations. Temporal populations identified from 2010–2017 were compared with data for previously published populations from 1968–2009\(^4\), which showed long-term dynamics and fast evolution of \(Pst\) populations in the USA. In the second study, using a similar approach, 567 \(Pst\) isolates from nine countries collected from 2010–2018, including select USA isolates, were genotyped using the same 14 SSR markers to understand the worldwide distribution of molecular groups (MGs), as well as the diversity, differentiation, and migration of \(Pst\) populations\(^1,5,6\). All isolates tested clustered into 10 MGs, with some of the MGs present in all countries, indicating there have been \(Pst\) migrations among countries. MGs identified only in single countries may become new threats to other countries. High rates of gene flow were detected among countries, especially those close geographically, further suggesting frequent \(Pst\) migrations on a global scale. In the third study, 447 isolates of \(P.\ striiformis\ f.\ sp.\ hordei\) (\(Psh\)), the barley stripe rust pathogen, collected from 1993–2017 in the USA, were genotyped with the same SSR markers to study long-term dynamics, diversity, and differentiation of \(Psh\) populations\(^7,8\). The isolates clustered into six MGs which had significant differences in frequency among the 25 years. The \(Psh\) populations changed rapidly from year to year, with the most significant changes in 2000 and 2010, possibly associated with the release of resistant cultivars and a significant reduction in barley acreage. Moreover, increased heterozygosity and genotypic diversities of \(Psh\) populations were detected in 2014–2017. In the fourth study, we developed >200 secreted protein gene-based single nucleotide polymorphism (SP-SNP) markers\(^9,10\) to recharacterize USA and international isolates of \(Pst\) from the first two studies based on geographic origin, race, and genotype, and to identify SP-genes associated with avirulence genes through association analysis. In total, 19 SP-SNP markers were associated significantly with 12 avirulence genes: \(AvYr1\), \(AvYr6\), \(AvYr7\), \(AvYr9\), \(AvYr10\), \(AvYr24\), \(AvYr27\), \(AvYr32\), \(AvYr43\), \(AvYr44\), \(AvYrSP\) and \(AvYr76\).

These studies have established a molecular marker system for \(P.\ striiformis\) and provided genetic resources for monitoring changes in the pathogen population, determining genetic relationships of pathogen populations in the USA and other countries, identifying candidate avirulence genes for functional characterization, and improving our understanding of pathogen evolutionary mechanisms. The knowledge and resources should lead to better control of potentially devastating stripe rust diseases.
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