

Genetic Differentiation and Migration in Worldwide Populations of the Wheat Leaf Rust Fungus, *Puccinia triticina*

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Collections of the wheat leaf rust fungus, *Puccinia triticina*, were obtained from North America, South America, Central Asia, the Middle East, Europe, Turkey, Russia, Ethiopia, and China from common wheat and durum wheat to examine the genetic diversity within each continental region and genetic relationships between regions. Approximately 100 single uredinial isolates from each region were tested for virulence to 20 near-isogenic Thatcher wheat lines and for molecular genotype with 23 SSR primers. There was relatively little variation in the average number of SSR alleles per locus between regions, varying from 2.2 (South America) to 3.1 (China). Populations in all regions had significantly higher than expected SSR allele heterozygosity and had very high (>3.0) index of association values, indicating clonal reproduction worldwide. All populations had significant correlation with virulence, varying from 0.43 (North America) to 0.56 (Europe). Genetic differentiation of SSR genotype groups based on principal coordinate plots and Bayesian analysis varied from eight groups in Europe to three groups in China and two groups in Russia. In all regions overall differentiation based on R_{ST} was greater than differentiation based on F_{ST} . Mutation and genetic drift likely contribute to differentiation of SSR genotype groups in *P. triticina*. Within all populations F_{ST} and R_{ST} differentiation based on SSR genotype groups was higher than differentiation based on geographical regions, indicating the migration of SSR genotypes within continental regions. Collections from tetraploid durum wheat in North America, South America, Europe, the Middle East, and Ethiopia had distinct virulence pathotypes that were avirulent to most genes in the Thatcher differential lines and had distinct SSR genotypes compared to collections from common, hexaploid wheat. There was little or no significant differentiation of SSR genotypes of isolates collected from durum wheat from the various regions, indicating a likely recent migration of *P. triticina* types from a single source. Isolates from hexaploid wheat in North America, South America, Europe, the Middle East, Pakistan, and Ethiopia that have virulence to *Lr1*, *Lr3*, *Lr3bg*, *Lr17*, *Lr26*, and are avirulent to *Lr28* were first detected in Mexico in the mid 1990s and were subsequently detected in the US and Canada (1996), Uruguay (1999) France (2000) and Israel (2000). SSR genotypes of these isolates were nearly identical indicating a rapid migration between continental regions. In Ethiopia, tetraploid landrace emmer and durum wheats have historically been grown and common hexaploid wheats have increased in cultivated area in recent years. The *P. triticina* population in Ethiopia was highly distinct for virulence and SSR genotypes, likely due to the selection pressure exerted by the diverse host population. Isolates collected from the tetraploid wheats were either avirulent to the susceptible common wheat Thatcher, and had very distinct SSR genotypes, or had virulence and SSR genotypes identical to other isolates collected from cultivated durum wheats worldwide. Isolates from common wheat were almost exclusively identical for virulence and SSR genotype to the isolates that were first detected in Mexico and spread to the US, Canada, Europe, and the Middle East. The lack of virulence and SSR diversity suggests that these isolates were recently introduced to Ethiopia.