

## Population genetics of *Puccinia triticina* in Central Asia and the Caucasus

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Isolates of *Puccinia triticina* collected from common wheat in the Central Asia countries of Kazakhstan, Uzbekistan, Tajikistan, Kyrgyzstan, and the Caucasus countries of Azerbaijan, Georgia, and Armenia were tested for virulence to 20 isolines of Thatcher wheat with different leaf rust resistance genes, and for molecular genotype at 23 simple sequence repeat (SSR) loci. After clone correction within each country, 99 isolates were analyzed for measures of population diversity, variation at single SSR loci, and for genetic differentiation of virulence phenotypes and SSR genotypes. Isolates from Central Asia and the Caucasus were also compared with 16 *P. triticina* isolates collected from common wheat in North America that were representative of the virulence and molecular variation in this region, and two isolates collected from durum wheat in France and the U.S. A total of 88 virulence phenotypes and 91 SSR genotypes were characterized. Populations from the Caucasus, Uzbekistan, Tajikistan and Kyrgyzstan, were not significantly ( $p > 0.05$ ) differentiated for SSR variation with  $F_{st}$  and  $R_{st}$  statistics. Populations from the Caucasus, Uzbekistan, Tajikistan and Kyrgyzstan, were significantly ( $p < 0.05$ ) differentiated from the populations in South Kazakhstan and North Kazakhstan for SSR variation. All populations from Central Asia and the Caucasus were significantly differentiated from the North American and durum isolates for SSR variation and virulence phenotypes. There was a high correlation between virulence phenotype and SSR genotype at the population level and among individual isolates. Geographic barriers and differences in wheat cultivars may account for the differentiation of *P. triticina* populations in Central Asia and the Caucasus.