

Population genetics of *Puccinia triticina* in North America

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A total of 146 isolates of *Puccinia triticina* from common wheat in the U.S. and Canada and five isolates from durum wheat from Mexico were tested for virulence on 20 Thatcher near-isogenic lines and for molecular genotypes at 23 simple-sequence repeat (SSR) loci. Eighty-nine virulence phenotypes and 73 SSR genotypes were identified. Genotypic diversity, allelic variation at single SSR loci, and genetic differentiation of virulence phenotypes and SSR genotypes was calculated. Isolates either virulent or avirulent to both *Lr2a* and *Lr2c* resistance genes were significantly differentiated ($p < 0.05$), based on SSR variation with F_{ST} and R_{ST} statistics, from isolates avirulent to *Lr2a* and virulent on *Lr2c*. Isolates with virulence to *Lr1*, *Lr2a*, *Lr2c* and avirulent to *Lr3* were also significantly differentiated from other groups of isolates. Isolates virulent to *Lr17* were significantly differentiated from isolates avirulent to *Lr17*. Isolates from common wheat avirulent to *Lr1*, *Lr2a*, *Lr2c* and *Lr3* were significantly differentiated from the other leaf rust races. Isolates from durum wheat were genetically different from all isolates from common wheat. Clonal reproduction of *P. triticina* in North America maintains a general relationship between virulence phenotypes and SSR genotypes.