

Haplotype-phased genome assembly and population genomics of *Puccinia coronata* f. sp. *avenae*, the causal agent of oat crown rust

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Crown rust caused by *Puccinia coronata* f. sp. *avenae* (*Pca*) is one of the most destructive foliar pathogens of cultivated oat, *Avena sativa*. *Pca* displays very high genetic variability as demonstrated by the numerous virulence profiles observed in national and international rust surveys. Such levels of polymorphism may aid in the rapid evolution of virulence to resistance genes in oat varieties. Indeed, resistance genes deployed in the field are often overcome in just a few years. This fact, coupled with few releases of new resistance genes in recent years, likely explains why modern *Pca* populations are highly virulent. To better understand the molecular mechanisms of virulence, we sequenced the genomes of two *Pca* isolates using long-read single-molecule PacBio sequencing. FALCON and FALCON-Unzip genome assembly algorithms were used to generate haplotype-phased references. Capitalizing on the recent release of these genome references, a comparative population genomics study of two *Pca* populations collected from across the U.S. in 1990 and 2015, respectively, was launched. Our goal is to determine the population structure and dynamics of *Pca*, and how these contribute to virulence, as well as the occurrence of sexual reproduction. This project provides genomic resources to develop molecular markers associated with rust virulence, and ultimately to uncover the evolution of pathogenicity mechanisms in *Pca*.