

Dissecting the oat crown rust pathosystem: identifying virulence factors and developing sources of adult plant resistance

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My PhD work looks into both worlds of the crown rust pathosystem: the pathogen, *Puccinia coronata* f. sp. *avenae*, and the host, oat (*Avena sativa* L.). Oat is one of the most important cereals in the world, but its production is persistently constrained by crown rust. For decades, numerous studies have been conducted to understand the pathosystem but crown rust remains an important disease that devastate oat production. The quest to understand the molecular basis of the disease might be far from over, but resources to make it a possibility are starting to become available. Chapter 1 and the review paper in Appendix 1 provide a general background about oat and crown rust. The chapter outlines the recent advances in oat and crown rust research that were not covered in the review paper. The review paper, on the other hand, presents details on the life cycle of the pathogen, economic importance, and disease management measures currently implemented for crown rust. Rusts are known to be “shifty” and the genetic variability of crown rust, in particular, has undermined efforts to control the disease. To help understand this variability, Chapter 2 presents a study on the evolution of virulence of crown rust populations in a 25-year period, with the use of the recently released crown rust genomes. In this chapter, I conducted a genome-wide association study (GWAS) to detect putative candidate avirulence (*Avr*) genes using genotype data called against 12SD80 and 12NC29 reference genomes. Several candidate *Avr* genes have been identified through phenotyping with the oat differential lines, which also gave insights on the similarity of some of the *Pc* genes. This study may have meaningful impacts for diagnostics and tracking of pathogen movement using molecular markers and possibly race-typing based on genetic profiles in the future. Chapters 3 to 5 focus on the opposite side of the pathosystem and look into finding and developing sources of oat adult plant resistance (APR). The apparent constant gain of pathogen virulence without fitness cost creates a shortage of resistance genes for crown rust breeding and compels us to deploy genes with broad-spectrum effects, in combination with race-specific genes. Chapter 3 describes a linkage mapping study of five recombinant inbred line (RIL) populations that identified two major quantitative trait loci (QTL) for APR on oat chromosome 4D and a minor QTL on chromosome 6C. Further, four more RIL populations were mapped in Chapter 4, where an additional four unique QTL were discovered on chromosomes 5D, 7C, 4D, and 7A. These are the first mapping studies that employed markers that are anchored to the OT3098 v1 oat reference genome. Moreover, qPCR markers linked to the QTL were developed for marker-assisted selection. Chapter 5 presents a pyramiding approach with the use of three sets of diallel crosses that attempt to generate different combinations of all available QTL for APR. These include the seven QTL mapped in Chapters 3 and 4 and a QTL on chromosome 4A from the MNBT lines. In the first set of crosses, up to three QTL were pyramided and lines with eight different combinations of at least two QTL were developed. These lines will be further tested in different years and locations and will be released as breeding germplasm to oat breeders. The different QTL combinations can potentially extend the durability of crown rust resistance in the field. This is all for managing a “shifty” fungus, because after all, a variable pathogen calls for variable disease measures.