NC STATE UNIVERSITY

Summer Research Symposium

Eighth Annual North Carolina State University Undergraduate Summer Research Symposium

Jane S. McKimmon Center
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Session I, D-11

Increased Resolution of Wheat Powdery Mildew (Blumeria graminis f. sp. tritici) Population Structure Using SSR Markers

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Blumeria graminis f. sp. tritici, a biotrophic ascomycete, is the causal agent of powdery mildew on wheat. Prevalent in humid wheat-growing regions, powdery mildew can lead to yield losses of up to 34% on susceptible cultivars. Native to the Persian Gulf region, wheat was imported into Virginia by English colonists and into Texas by Spanish colonists roughly 500 years ago. Biotrophic organisms cannot survive without living hosts, therefore it is hypothesized that wheat mildew was introduced to the U.S. concurrently with its host. Previous work using single nucleotide polymorphisms (SNPs) for population inferences demonstrated a common ancestor between U.K. and Israeli (Old World) powdery mildew and U.S. (New World) mildew. In addition, SNP markers indicated mildew populations were subdivided into 3 distinct regions: Mid-Atlantic U.S., Southern U.S., and Old World. However, SNP markers were not significantly polymorphic for in depth analysis of population structure and migration. Due to a higher mutation rate, Simple Sequence Repeats (SSRs) should be more polymorphic than SNPs and provide increased resolution of population subdivision. In order to obtain SSR loci, a SSR enriched DNA library was created and screened, yielding ten unique, polymorphic microsatellite loci. Of these, three have been optimized and used to genotype 203 powdery mildew isolates collected from the U.S., U. K., and Israel. These three markers provided confirmation of the population structure previously demonstrated using SNPs. Furthermore, combining SNP and SSR markers increased the power of the analysis to infer an additional population subdivision between isolates from Israel and the U.K. not evident using SNPs alone. Development of further SSR loci should allow for analysis of migration rates and directions between varying spatial scales.