**Abstract**

Populations of clonal or partially clonal organisms typically violate assumptions Hardy-Weinberg equilibrium, which is a common assumption in many population genetic analyses. Due to complete linkage of the genome, it is important to test for linkage between all unique multilocus genotypes before proceeding to perform population genetic analyses for these populations, given the violation described above. It has been previously demonstrated that a measure of multilocus linkage disequilibrium, the index of association, is sensitive to very high amounts of clonal reproduction or population structure within a population. Due to limitations in resources these experiments were performed using simulations of ideal populations with identical numbers of microsatellite loci and individuals. It is not clear, however if these indices have the ability to detect other population demographics such as admixture or migration. Moreover, the effect of population size, sample size, and marker type have not been thoroughly explored, which is critical when analyzing phytopathogenic microbial populations, from which samples of fewer than 20 isolates is not uncommon.

With current availability of mass computing clusters, we have the ability to fully explore the sensitivity of measures of multilocus linkage disequilibrium to partially clonal populations, subdivided populations, admixed, and populations with migration. We will utilize time-forward simulators to construct sets of populations that differ in not only the above characteristics, but also differing in the type of loci, number of loci, and number of individuals sampled. These will tests the hypotheses that 1) admixture and migration negatively affect the sensitivity of the index of association, 2) higher sample sizes of individuals or loci will result in less variance, and 3) a higher number of microsatellite markers will be needed to overcome the amount of homoplasy present in biallelic markers.