

What can we learn from population genomics studies of *Curtobacterium flaccumfaciens* pv. *flaccumfaciens*, the cause of tan spot on mungbean?

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The bacterium *Curtobacterium flaccumfaciens* pv. *flaccumfaciens* (*Cff*) is the cause of tan spot (in some regions known as ‘wilt’) on mungbean (*Vigna radiata*) and other legumes worldwide. The pathogen was first reported in mungbean paddocks in Queensland in 1984, and subsequently in New South Wales in 1986, causing yield losses of up to 25% in hot and dry seasons. No chemical control is available, and disease management relies on pathogen exclusion, through the use of clean seed, and deployment of moderately susceptible varieties. Breeding programs are currently working to incorporate better resistance into new mungbean varieties. The success of breeding programs depends on a thorough understanding of the genetic diversity and evolution of the pathogen population(s). This project was designed to elucidate the genotypic diversity of *Cff* population(s) and investigate sources of inoculum that contribute to tan spot epidemics in the northern grains region (Queensland and northern New South Wales). Whole genome re-sequencing of 100 *Cff* isolates detected moderate genotypic diversity, with a narrower genetic background compared to the global *Cff* population. One highly adapted clonal lineage was found to dominate the population with a frequency of 45%. This study showcases how population genomics studies can be used to test hypotheses relating to disease epidemiology and provide useful information for resistance breeding programs. The results provide insights on *Cff* population structure and epidemiology, and have direct application for breeding programs by providing a set of *Cff* isolates that represent the genetic diversity of the pathogen population(s) in the northern grains region.