

Pantoea stewartii stewartii DC283 Genome Project

Genome project for Pantoea stewartii stewartii DC283

Stewart's wilt and blight caused by *P. stewartii* is the most significant bacterial disease of sweet corn and maize in North America. This organism has an intriguing obligatory association with an insect vector, the corn flea beetle (*Chaetonomia pulicaris*), essential for the infection of seedlings each growing season. The genome structure of *P. stewartii* is also unusual, with a quarter of the content distributed across 10-13 plasmids. This large number of extrachromosomal elements and the unequal copy number make sequencing challenging. This task is ongoing by our collaborators, led by George Weinstock, at the Baylor College of Medicine Human Genome Sequencing Center, where assembled [draft sequences are currently available](#) for download and BLAST. Preliminary annotation and analysis by GEL personnel and collaborators is underway. For more information or access to preliminary annotations contact [Jeremy Glasner](#).