

Identification of *Phytophthora infestans* lineages through genetic markers

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Phytophthora infestans is an oomycete that causes late blight in potatoes and economic loss of potato crops worldwide. Validation that infected fields are caused by *P. infestans*, as well as to determine which lineage may be involved, could greatly improve our abilities to mitigate these infestations. Using bioinformatics and lab tools, such as polymerase chain reaction and pyrosequencing (PyroMark, Qiagen), we are examining known mitochondrial and nuclear DNA data to locate potential single nucleotide polymorphisms and insertion/deletion polymorphisms. With these polymorphisms, we hope to build diagnostic tests to determine different lineages of *P. infestans* (US-1_1, US-8, US-22, US-23, and US-24). Eventually, these tools may be implemented in a field setting, providing a rapid and precise tool for real-time pathogen diagnostics.