

Saha

AgriVectors: a portal for plant diseases transmitted by insect vectors

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Plant-feeding hemipteran pests are global threats to food security and production. Agricultural disease vector systems are an under-served area of research despite being one of the fundamental challenges for increasing food consumption. We propose to build an open and comprehensive resource for plant disease systems where the pathogen is transmitted by an insect vector. The portal will connect to established public repositories such as NCBI and EMBL together with pathosystem-specific repositories like citrusgreening.org. Furthermore, topical resources such as RNAi, CRISPR, insect feeding assays like EPG, etc. will also be included and leveraged to create a knowledgebase for plant diseases and vector biology. This system will also support privileged access for databases with private and unpublished data. We have created the citrusgreening.org portal as a model for a tritrophic disease system with genomics and bioinformatics resources for the vector Asian citrus psyllid (ACP, *Diaphorina citri*), the host citrus (*C. clementina* and *C. sinensis*) and multiple pathogens including *Ca. Liberibacter asiaticus* (CLas) for the citrus greening disease. We have used Biocyc Pathway Tools databases to model biochemical pathways within each organism that can be used to explore the entire disease complex. Psyllid Expression Network (PEN) is an expression atlas with proteomics and RNAseq data for ACP from adult and nymph life stages, various conditions and multiple hosts. The citrusgreening.org model will be extended beyond gene-centric omics data to pathosystem-wide data including integrated pest management data, behavioral and climate data in addition to phenotyping information from disease trials to create the AgriVectors portal.