

Biology Seminar



12:30 - 1:30 pm
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BGS 0165



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Plant virology: from metagenomics to molecular genetics

Viruses are obligate intracellular pathogens intrinsically linked to all known forms of life. While they are only active inside of cells, viruses can have outsized impacts that can change entire ecosystems. This seminar will address two areas of research in the Griffiths lab that illuminate how a single mutation can have drastic effects on fruit production, and how we can examine an entire orchard or farm and identify changes to a single molecule or nucleotide through metagenomics. Tomato brown rugose fruit virus (ToBRFV) recently emerged in 2014 in the middle east, and has rapidly spread worldwide resulting in substantial losses to growers. Key to the success of ToBRFV is escape of the longstanding resistance gene *Tm-2²*. Seed companies responded quickly to this virus, identifying new sources of resistance and rapidly breeding them into commercial elite varieties. The identity of these putative resistance genes, and how effective they are against ToBRFV, is largely unknown. We determined the genome of ToBRFV from three Canadian greenhouses through nanopore sequencing to evaluate how the virus was responding to these new resistance genes. We identified amino acid polymorphisms in two ToBRFV proteins associated with resistance escape, which expands the ongoing story of resistance and escape central to viral biology. The second part of this seminar will describe pollen-based metagenomic approaches towards plant virus monitoring in commercial fruit production systems including blueberries, apples, and cherries. Fruit production is reliant on honey bee pollination for optimal fertilization, but pollination can be a major transmission route for plant viruses. Honey bees collect small amounts of pollen from multiple flowering individuals within their foraging range, providing an enriched plant-based sample suitable for metagenomic approaches to study virus diversity and biology. RNAseq of honey bee collected pollen revealed a surprising diversity of viruses in fruit production systems, including viruses widely present in multiple species and in multiple regions. Viruses in the Ilarvirus genus are particularly associated with pollen transmission. Ilarviruses have multipartite genomes, where the complete genome of the virus is divided into three separate RNA molecules that are packaged into virions and transmitted independently. Here we employed pollen-based metagenomics in apple and cherry orchards to investigate the multipartite nature of ilarviruses.

