Green Student Lab

Deep sequencing of small RNA for detection of viruses in plants

Viral crop damage is one of the major problems in the field of agriculture leading to costly losses (Anderson *et al.*, 2004). To prevent the loss of crops detecting the viral infection early on it is key to prevent it from spreading. Current viral detection methods include electron microscopy techniques, assays based on polymerase chain reaction (PCR), enzyme linked immunosorbent assays (ELISA) or microarrays. However, these methods all require specific knowledge of the target, like viral proteins that could serve as antigens or part of the viral genome for specific amplification.

Small interfering RNA (siRNA) studies have shown that virus infected cells in animals produce virus derived small RNAs resulting in specific antiviral immunity. A previous study has used deep sequencing of small RNAs to detect viruses. This study simultaneously identified previously undetected dormant viruses. In addition, they performed a *de novo* assembly of a complete viral genome out of the siRNA data.

The students on this project will acquire small RNA next-generation sequencing (NGS) data (Ion Proton platform) of a plant X. These small RNA sequences are analyzed with bioinformatics approaches, such as comparison with siRNA from other species to identify siRNAs from viruses. Finally, we will try to identify potential target virus siRNAs by bioinformatics and wet lab techniques.

Involved company:

- Syngenta

Research questions:

- Can we set up a quantitative diagnostic tool for viruses for other plants using small RNA deep sequencing?
- How does the virus migrate through the plant after infection (localization of the virus)?
- What virus is present in a wild-type plant compared with the breeding material?

Techniques:

- RNA isolation
- NGS (Ion Torrent platform)
- Sequence alignment