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# Poster Presentations

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## Inferring movement of potato psyllids among host plants using NextRAD sequencing

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Herbivores often move among spatially interspersed host plants, tracking high-quality resources through space and time. This dispersal is of particular interest for vectors of plant pathogens. Existing molecular tools to track such movement have yielded important insights, but often provide insufficient genetic resolution to infer spread at finer spatiotemporal scales. Here, we explore the use of Nextera-tagmented reductively-amplified DNA (NextRAD) sequencing to infer movement of a highly-mobile winged insect, the potato psyllid (*Bactericera cockerelli*), among host plants. The psyllid vectors the pathogen that causes zebra chip disease in potato (*Solanum tuberosum*), but understanding and managing the spread of this pathogen is limited by uncertainty about the insect's host plant(s) outside of the growing season. We identified 1,978 polymorphic loci among psyllids separated spatiotemporally on potato or in patches of bittersweet nightshade (*S. dulcumara*), a weedy plant proposed to be the source of potato-colonizing psyllids. A subset of the psyllids on potato exhibited genetic similarity to insects on nightshade, consistent with regular movement between these two host plants. However, a second subset of potato-collected psyllids was genetically distinct from those collected on bittersweet nightshade; this suggests that a currently unrecognized source, i.e., other nightshade patches or a third host-plant species, could be contributing to psyllid populations in potato. Oftentimes, dispersal of vectors of pathogens must be tracked at a fine scale in order to understand, predict, and manage disease spread. We demonstrate that emerging sequencing technologies that detect genome-wide SNPs of a vector can be used to infer such localized movement.

### Audience Take Away:

- Next generation sequencing approach was used in this case to explain the movement of very small insects, what could be very difficult to be explained in other way.
- This research opens the opportunity to explore the origin and migration of other guilds moving from sites.
- This molecular tool shows versatile applicability in research.

### Biography

Ph.D. and M.Sc. in Entomology (WSU, USA and WUR, Netherlands, respectively). I had internships and work and laboratory practices in Japan, Spain and New Zealand. My research runs about developing integrated pest management of agricultural pests, including vector-pathogen relationships and biological control. I'm focused on molecular characterization and identification of pathogens and insect vectors of emerging plant diseases. I develop research projects to help low-income farmers and to improve agriculture in the Ecuadorian Highlands. I have been working in the National Institute of Agricultural Research of Ecuador for two decades.