

Genomics of plant toxin resistance in entomopathogenic nematodes

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Some specialist insect herbivores have evolved the ability to sequester specialized metabolites from their host plant. The sequestered compounds can be deterrent or toxic for the herbivore natural enemies. The western corn rootworm (WCR), *Diabrotica virgifera*, stabilizes and sequesters a maize benzoxazinoid, which can be reactivated upon attack. Additionally, the WCR constantly exude a benzoxazinoid detoxification product. Both compounds can considerably limit for the success of entomopathogenic nematodes (EPNs) in infecting a WCR larva. EPN strains that have co-evolved with the WCR in their natural range (North America) are able to tolerate the presence of benzoxazinoids in their hosts but strains that originate from areas where WCR has been present for less than 50 years do not have this ability and suffer from the chemicals. In this study, we de novo assembled and annotated a chromosome-scale assembly of the EPN *H. bacteriophora* and conducted whole genome sequencing of 35 strains within this and other closely related *Heterorhabditis* species from different locations across the globe. These data not only increased the resolution of nematode phylogeny, but further provided indirect evidence linking the evolutionary history of the EPN strains to benzoxazinoid tolerance. We discuss the relevance of these findings for the development of efficient and sustainable pest-management strategies.