



Understanding successful host switches of honeybee Varroa mites using whole genome sequencing and population genomics

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Varroa mites are ectoparasites infesting honeybee colonies and originally found only in Asia. One century ago, the Western honeybee *Apis mellifera* was introduced into the native range of the Asian honeybee *A. cerana*. This new, sudden contact between the two species gave the opportunity for parasite spill over. *V. destructor* successfully switched hosts on *A. mellifera*, at least in three independent events. The invasive K strain has subsequently spread worldwide and is considered as the main driver of honeybee global decline. Recently, *V. jacobsoni* has emerged as a new threat by jumping twice in Papua New Guinea. In light of these reports, additional host switch could occur but the genetic mechanisms behind the quick adaptation and success of Varroa are poorly understood. More broadly, the repeated host switches provide an opportunity to examine to what extent parallel evolutionary event occur using similar vs. different mechanisms. Using NGS technology, we aim to i) study the population structure between native and invasive Varroa, ii) identify and compare signatures of selection after each host switch, iii) detect whether gene flow has occurred or is still occurring among host populations. Whole genome sequencing of 24 *V. destructor* and 20 *V. jacobsoni* mites collected in their native area on *A. cerana* and *A. mellifera* show a population divergence with host specificity in *V. destructor*, while the pattern in *V. jacobsoni* suggests ongoing differentiation. In both species, host switches were associated with massive genetic differentiation across hosts, though the actual regions involved were different. Our results reveal cryptic diversity in the Varroa species complex with a new subgroup on *A. cerana*. To assess the contribution of native populations after jumps, we are estimating population size and migration rates under IM model for four host-parasite populations. Disentangling genetic and demographic factors for Varroa success could help to predict future invasion.