| Group | Functional group | Species | Data (no. of individuals: length/no. of markers) | Between volcanoes[1] % variation (P-value) | Within volcanoes[1] % variation (P-value) | Timeframe |
|---|---|---|---|---|---|---|
| Planthoppers | Herbivore | *Nesosydne chambersi*[2] | mtDNA: COI (187:653) | 0.05*** | 0.77*** | Within-species divergence[11] = 2600 [95% HPD (1.2–35.1) $\times 10^3$], and 20,100 [95% HPD (7.4–135.0) $\times 10^3$] years for two population pairs[2] |
| | | | nucDNA: microsatellites (292:13) | 0.04*** | 0.21*** | |
| | Herbivore | *Nesosydne raillardiae*[3] | mtDNA: COI (33:581) | 0.26*** | 0.49*** | na |
| | Herbivore | *Nesosydne bridwelli*[3] | mtDNA: COI (34:677) | na | 0.18** | na |
| Psyllids | Herbivore | *Trioza* HB[3,4] | mtDNA: COI and cytB (29:857) | −0.14*** | 0.92*** | na |
| | Herbivore | *Trioza* HC[3,4] | mtDNA: COI and cytB (17:857) | 0.17** | 0.53** | na |
| Fly | Fungivore | *Drosophila sproati*[5] | mtDNA: COII (232:570) | 0.11*** | 0.81*** | Max age[12] = 1.15 (95% HPD 0.75–1.5) Ma[8] |
| Cricket | Detritivore | *Laupala cerasina*[6] | nucDNA: AFLP (631) | 0.30*** | 0.58*** | na |
| Spiders | Predator | *Tetragnatha anuenue*[7] | mtDNA: COI (162:607) | 0.23*** | 0.041*** | Max age[12] = 3.0 (95% HPD 2.5–4.5) Ma[10] |
| | Predator | *Tetragnatha brevignatha* (Hawaii Island)[7] | mtDNA: COI (54:605) | 0.16* | 0.00 | Max age[12] = 4.0 (95% HPD 3.0–4.75) Ma[10] |
| | Predator | *Tetragnatha quasimodo*[7] | mtDNA: COI (149:439) | 0.09*** | 0.037*** | Max age[12] = 2.5 Ma[10] |
| | | | nucDNA: allozymes (46:9) | 0.34*** | na | |
| | Predator | *Theridion grallator*[7] | mtDNA: COI (209:1270) | 0.30*** | 0.05*** | Node age[13] = 0.56 (95% HPD 0.37–0.75) Ma[9] |
| | | | nucDNA: allozymes (224:8) | 0.19*** | na | |
| | Predator | *Ariamnes* spp.[7] | mtDNA: COI (8:420) | 0.05 | na | na |

mtDNA, mitochondrial DNA; nucDNA, nuclear DNA; HPD, highest posterior density; na, no information available.

***$P < 0.001$, **$P < 0.05$, *$P < 0.10$.

[1]mtDNA and microsatellites are calculated as Phi-st; AFLPs and allozymes are calculated as $F_{ST}$.

[2]Goodman *et al.* (2012).

[3]This paper.

[4]These *Trioza* species are in the process of being described; HB and HC are their provisional identifiers (D.M.P., in prep).

[5]Eldon *et al.* (2013).

[6]Mendelson and Shaw (2005).

[7]Roderick *et al.* (2012).

[8]Magnacca and Price (in press).

[9]Croucher *et al.* (2012).

[10]Casquet *et al.* (2015).

[11]Within-species divergence, estimated using Isolation with Migration (IM: see Goodman *et al.* 2012)

[12]Max age = the node age of the phylogenetic split between this species and its sister species, calculated using divergence dating analyses performed in BEAST. In most cases, this will be an overestimate of the node age of the species itself, but is the best information we have at present.

[13]Node age = age of the most recent common ancestor of the monophyletic group on the island of Hawaii, estimated using BEAST.