|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Group** | **Functional group** | **Species** | **Data**  (# individuals: length/  # markers) | **Between Volcanoes**  %  variation  % variation (p-value) | **Within volcanoes**  % variation | **Timeframe** |
| **Planthoppers** | Herbivore | *Nesosydne chambersi*1 | mtDNA: COI (187:653)  nucDNA: microsatellites  (292:13) | 0.05\*\*\*  0.04\*\*\* | 0.77\*\*\*  0.21\*\*\* | Within species divergence10: =2,600 (95% HPD: 1.2-35.1 x 103), and 20,100 (95%HPD: 7.4-135.0 x 103) years for two population pairs1 |
|  | Herbivore | *Nesosydne raillardiae*2 | mtDNA: COI (33:581) | 0.26\*\*\* | 0.49\*\*\* | na |
|  | Herbivore | *Nesosydne bridwelli*2 | mtDNA: COI (34:677) | na | 0.18\*\* | na |
| **Psyllids** | Herbivore | *Trioza HB2,3* | mtDNA: COI &  cytB (29:857) | -0.14\*\*\* | 0.92\*\*\* | na |
|  | Herbivore | *Trioza HC2,3* | mtDNA: COI &  cytB (17:857) | 0.17\*\* | 0.53\*\* | na |
| **Fly** | Fungivore | *Drosophila sproati*4 | mtDNA: COII (232:570) | 0.11\*\*\* | 0.81\*\*\* | Max age11=1.15  (95%HPD: 0.75-1.5) my.7 |
| **Cricket** | Detritivore | *Laupala cerasina*5 | nucDNA: AFLP (631) | 0.30\*\*\* | 0.58\*\*\* | na |
| **Spiders** | Predator | *Tetragnatha anuenue*6 | mtDNA: COI (162: 607) | 0.23\*\*\* | 0.041\*\*\* | na |
|  | Predator | *Tetragnatha brevignatha*6 | mtDNA: COI (54:605) | 0.16\* | 0.00 | na |
|  | Predator | *Tetragnatha quasimodo*6 | mtDNA: COI (149:439)  nucDNA: allozymes (46:9) | 0.09\*\*\*    0.34\*\*\* | 0.037\*\*\*  na | na |
|  | Predator | *Theridion grallator*6 | mtDNA: COI (209:1270)  nucDNA: allozymes (224:8) | 0.30\*\*\*  0.19\*\*\* | 0.05\*\*\*  na | na |
|  | Predator | *Ariamnes* *spp.*6 | mtDNA: COI (8:420) | 0.05 | na | na |

mtDNA=mitochondrial DNA, nucDNA=nuclear DNA: \*\*\* < 0.001, \*\* < 0.05, \*<0.10; na = no information available

1 Goodman et al. 2012

2 this paper

3 These *Trioza* species are in the process of being described; HB and HC are their provisional identifiers (Percy in

prep)

4 Eldon et al. 2013

5 Mendelson and Shaw 2005

6 Roderick et al. 2012

7 Magnacca and Price, in review

8 Supplementary information, this paper

9 Croucher et al. 2012

10 Within-species divergence, estimated using IM.

11 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.

12Node age = Age of the most recent common ancestor of the monophyletic group on Hawaii Island, estimated

using BEAST.