**S4 Table. Results of the analysis of molecular variance (AMOVA) assessing the proportions of genetic variations explained by the effects of geographical subpopulations, families of host trees, and collection years/time periods.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Whole population | | | |  | Taipei subpopulation |
|  | Geographical subpopulations | Host families | Collection years | Collection time periods a |  | Genetic clusters |
| Percentage of variation among groups | 1.05% | 3.95% | 2.38% | 0.29% |  | 17.62% |
| Percentage of variation  within groups | 98.95% | 96.05% | 97.62% | 99.71% |  | 82.38% |
| Fixation index (*F*ST) | 0.0105 | 0.0395 | 0.0238 | 0.0028 |  | 0.1762 |

a The collection years were divided into three time periods, 1989-1999, 2001-2009, and 2010-2012.