BACKGROUND
The flora of the Society Islands is known for its high endemism. It is, however, severely threatened by anthropogenic pressures, mainly habitat destruction and plant invasions (Meyer & Salvat 2009). Revealing phylogeny of island endemics does not only enhance our understanding of species diversification but also can benefit conservation by providing insight into past population dynamics based on coalescent theory.

OPHIIHRIZA IN SOCIETY ISLANDS
South Pacific islands hold 14 species, among which nine species are restricted to the largest islands of Tahiti, Moorea, and Raiatea. These are typical examples of the endangered endemics (Fig. 1). Their similar morphology (Darwin, 1876) suggests that these species were derived from a single common ancestor; however, it has not been tested with molecular tools.

PHYLGENETIC POSITION OF THE SOCIETY ISLANDS’ SPECIES
The Society Islands’ species formed a clade with the species from Western Polynesia and Eastern Melanesia such as O. rupestris and O. lepenthina.

Fig. 2. Bayesian 50% majority rule consensus tree based on the ITS data. The strict consensus tree of the most parsimonious trees was topologically highly congruent with the Bayesian phylogeny. Bayesian posterior probabilities (left) and bootstrap percentages (right) are shown. Xanthophytmum and Neurocyaxa (the tribe Ophiihrizae) are outliers.

MOLECULAR MAKERS
Nuclear ribosomal DNA (nrDNA): ITS (aligned length = 595 bp)
Chloroplast DNA (cpDNA): psbE-trnL, psbA-trnT, trnL-trnF, trnL-trnH, trnL-trnC (3.186 bp)

Fig. 3. Assuming that there is no horizontal gene transfer or admixture between individuals from different species, multispecies coalescent analysis was conducted to estimate a species tree that is most probably given the unlinked multi-locus data (i.e., the ITS data and the combined cpDNA data), using BEAST (Heled & Drummond, 2010). Maximum clade credibility tree is shown and clade posterior probability is indicated.

HISTORICAL CHANGES IN POPULATION SIZE
For O. subumbellata, Extended Bayesian Skyline Plot (EBSP) analysis indicated that the effective population size (Ne) in Tahiti Island was much larger in the past than now (reproductive individuals < 100–500, Meyer & Frödén, 2011).

Fig. 6. EBSP is a method based on data from multiple loci to infer a shared history of changes in Ne (Heled & Drummond, 2008). Multi-locus data of a small number of individuals from a large background population can potentially recover past population size changes, which cannot be characterized by analysis of a single locus (e.g., only ITS or cpDNA). The mean, median, and 95% highest posterior density (HPD) interval of the population size (a product of generation time in years [= 1] and Ne) are plotted against time.

MAIN REFERENCES

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