

Correction

Following the publication of “A statistical approach for distinguishing hybridization and incomplete lineage sorting” by Simon Joly, Patricia A. McLenachan, and Peter J. Lockhart (*American Naturalist* 174:E54–E70), we noticed an inversion in one of the sequence data sets analyzed. The inversion occurs in the *psbA-trnH* spacer between positions 91 and 116 (TreeBase accession S2284, matrix 4341). Overlooking this inversion resulted in inferring 18 nucleotide substitutions between sequences that differ by this inversion. In this correction, we reanalyze the data on New Zealand alpine *Ranunculus* when treating this inversion as a single evolutionary event.

The new concatenated chloroplast data set (with the inversion removed) resulted in a different gene tree (fig. 1). Although the inversion is present in all taxa from breeding group 1 and in the two individuals that were inferred to contain an introgressed chloroplast in the original study (*Ranunculus crithmifolius* from Mount Lyndon and *Ranunculus insignis* from Mount Hutt), these two individuals are now nested within sequences of breeding group 2. The presence of the inversion in *R. crithmifolius* and *R. insignis* thus probably represents an independent evolutionary event. A species tree search by gene tree parsimony using this modified chloroplast phylogeny resulted in two most parsimonious

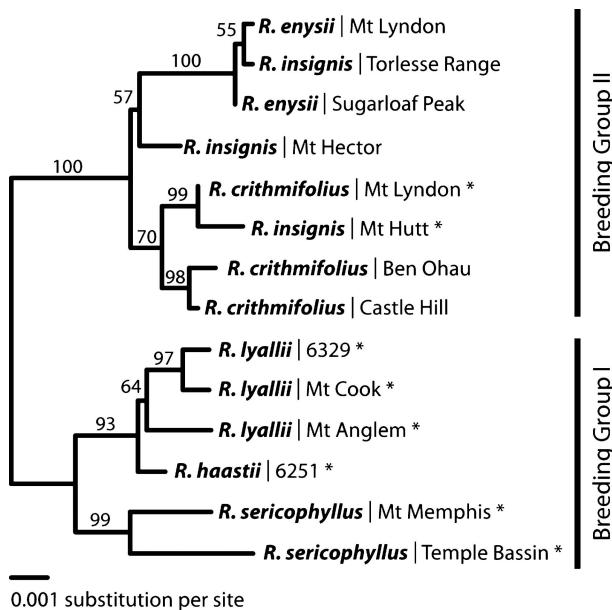


Figure 1: Maximum likelihood phylogeny (TVM + I) obtained by heuristic search in PAUP*. The asterisks indicate individuals in which the *psbA-trnH* inversion is present. Bootstrap proportions were obtained from 1,000 replicates.

unrooted trees that differ from each other only by the relative positioning of species of breeding group 2: one tree was identical to that of the original publication, with *Ranunculus enysii* and *R. insignis* being sister species, whereas in the other, *R. crithmifolius* and *R. insignis* grouped together. We ran MCMCcoal on both species trees and tested for the presence of hybridization using both species tree topologies following the exact same procedures as in Joly et al. (2009), with one exception. We used a heredity scalar of 0.5 for chloroplast markers for estimating population sizes and divergence times, which is the correct heredity scalar for plastid DNA in hermaphrodites (we thank M. Lascoux for pointing out this problem). This reanalysis could not reject the hypothesis that the observed distances were the result of lineage sorting alone ($P > .05$). The presence of hybridization in the New Zealand alpine *Ranunculus* thus remains inconclusive.

The fact that hybridization could not be detected in this *Ranuculus* data set does not undermine the ability of our method to identify hybridization events, as simulation studies have shown that it is efficient. It also does not rule out the presence of hybridization in this group because some species are still nonmonophyletic in the chloroplast tree and it is possible that sequencing more nucleotides would reveal instances of hybridization.

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Submitted February 18, 2010
