We collected Rhododendron species for morphological and molecular studies from the eastern Himalayan region of North Sikkim, India (between 2000 and 5000 m elevation); R. arboreum alone was collected from Himachal Pradesh, India.We used existing sequence information with the dual purpose of understanding the phylogenetic positions of the Indian species in a larger context, and to use our only source of field observations, the newly included Indian species Our choice of outgroup, Empetrum L., was based on previous studies showing it to be the closest sister group of Rhodo- dendron (Kron 1997; Goetsch et al. 2005).analyses.ML analyses (1000 bootstrap replicates) were conducted on an exon-intron partitioned dataset applying the GTR + gamma model (HKY not implemented) using RAxML-HPC2 Work- flow on XSEDE (8.2.6) on the CIPRES Science Gateway (Miller et al. 2010).Reconstruction of ancestral states We used maximum parsimony (MP: Mesquite 3.04, Maddi- son and Maddison 2015), maximum likelihood and Bayesian (ML: BayesTraits V2, Meade and Pagel 2014) methods to reconstruct ancestral states.For MP analyses we obtained a strict consensus of the 99% most credible trees, randomly resolved this tree to get 100 resolved trees and estimated branch-lengths using ML (PAUP* 4.0a147: Swofford 2002).The log BF (Bayes Factor) was used to determine whether the difference in the marginal likelihood of the two models was significant [log BF2 was taken to favour the dependent model (Pagel and Meade 2014, Bayes- Traits V2)].Two criteria were used to determine conver- gence of chains: average standard deviation of less than 0.01 for split frequencies and a Potential Scale Reduction Factor (PSRF) value of 1.We performed phylogenetic tests of correlation using ML and Bayesian methods as implemented in BayesTraits V2 (Meade and Pagel 2014).For ML analy- ses, we used the likelihood ratio test (LRT) to determine whether the difference in the likelihood scores between the independent and dependent model was significant; the model showing a significantly higher likelihood was accepted.We used the Steppingstone sampler to calculate the log marginal likelihood for both the independent and dependent models--to test the hypothesis of a correlation between monosymmetry and pigment pattern.We explored the use of different methods in order to uncover the range of possible directions of evolution because MP and statistical methods are known to differ in their estimates (Cunningham et al. 1998).Ancestral state reconstructions were performed on both binary- and three-state codings for three characters (i.e. flexion of stamens, arrangement of sta- mens and flexion of style).Four Markov Chain Monte Carlo (MCMC) chains were run for 8.6 x 106 generations, with a sampling fre- quency of 1000.The first option models the null hypothesis of no correlation between the two traits being tested and the second models our proposed hypoth- esis of a correlation between the two traits; the model with a higher likelihood is better supported.Amplified products were sequenced at external sequenc- ing facilities (using an AB1 Sequencer, Applied Biosys- tems) sequences retrieved from TreeBASE: M2277 (Goetsch et al. 2005).We partitioned the data into regions of introns and exons (Online Resource 3).We removed uninformative apomorphic insertions/ deletions longer than 50 bases.