Rhododendron species from the eastern Himalayan region of North Sikkim, India, with R. arboreum also collected from Himachal Pradesh.Reconstruction of ancestral states We used maximum parsimony (MP: Mesquite 3.04, Maddison 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).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).These nodes belong to the two major clades A and B (Goe-tsch et al. 2005) and include the two major subgenera Hyme-nanthes and Rhododendron.In ML analyses on BayesTraits, we used the entire set of most credible trees to generate likelihood values for character states at particular nodes and calculated the mean likelihood value.We used 1.01 x 10.Trees obtained from Bayesi and ML estimates were scrutinised using FigTree 1.4.2 (Rambaut 2014) Tests of correlation The morphological data were tested for statistical correlation between pigment patterns and other floral traits.Correlations among the four symmetry traits were also tested (in BayesTraits V2) similar to the above ML method described.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)].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.The number of ML attempts per tree was 10.The PCR protocol (modified after Goetsch et al. 2005) used was: Initial denaturation at 94 ?C for 4 min, then a 35 cycle step with denaturation at 94 ?C for 45 s, annealing temperature gradient from 54 to 59 ?C for 45 s, and extension at 72 ?C for 1 min 15 s followed by a final extension of 7 min at 72 ?C; for some species, a Hot Start activation (Sambrook and Russell 2001) of 5 .(min was used to minimize non-specific amplification.2013) (see data matrix: Online Resource 4

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