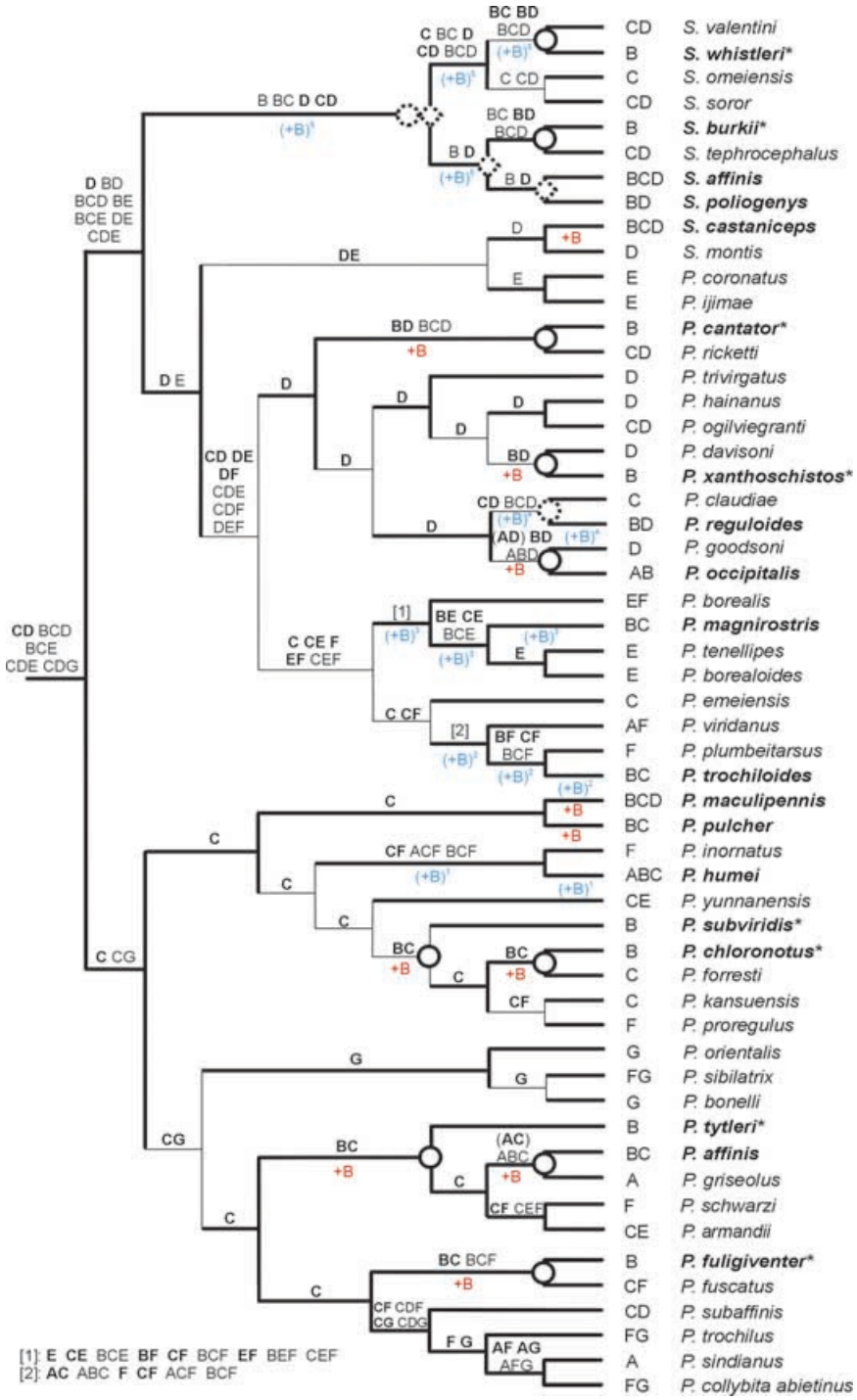

Figure 2. Reconstruction of the biogeographic history of the *Phylloscopus/Seicercus* clade using a constrained (maxarea = 3) DIVA (Ronquist 1997). The topology is from Bayesian analysis of a combined data set of mitochondrial cytochrome *b* and 12S and nuclear myoglobin intron 2 sequences. Thick branches indicate nodes with posterior probabilities $\geq$0.95. Letters at nodes refer to the geographical regions shown in Figure 1 and indicate the ancestral areas inferred for that node. Areas indicated in bold also arise in the "maxarea = 2" optimization. Symbols: "+B" indicates a dispersal event into the Himalayas; "(+$B^{1\text{-}5}$)" indicates dispersal into the Himalayas, but that the point in the phylogeny is uncertain given uncertainties in the reconstruction of the ancestral areas. Symbols denoted with an identical superscript (numbers 1–5), refer to the same bifurcation event and denote alternative inferences for that event; *circle*: vicariance; *diamond*: speciation within the Himalayas; *stippled symbol*: inferred mode of speciation only under certain optimizations of the ancestral area(s). Names in bold indicate species found in the Himalayas; those marked with $*$ are endemic to the Himalayas.