

# Elevation and phylogeny shape herbaceous seed dormancy in a biodiversity hotspot of southwest China

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January 11, 2023

## Abstract

Seed dormancy contributes greatly to successful establishment and community stability and shows large variation over a continuous status scale in mountain ecosystems. Although empirical studies have shown that seed dormancy status (SDS) is shaped by elevation and phylogenetic history in mountain ecosystems, few studies have quantified their combined effects on SDS. Here, we collected mature seeds from 51 populations of 11 *Impatiens* species (Balsaminaceae) along an elevational gradient in the Gaoligong Mountains of southwest China and downloaded 19 bioclimatic variables from WorldClim v.2.1 for each *Impatiens* population. We used internal transcribed spacer (ITS), *atpB-rbcL*, and *trnL-F* molecular sequences from the GenBank nucleotide database to construct a phylogenetic tree of the 11 species of *Impatiens*. SDS was estimated using mean dormancy percentage of fresh seeds germinated at three constant temperatures (15, 20, and 25 °C). Logistic regression model analysis was performed to quantify the effects of phylogeny and environment on SDS. Results showed that there was a significant phylogenetic signal of SDS in the *Impatiens* species. Furthermore, elevation and phylogeny accounted for 63.629% of the total variation in SDS among the *Impatiens* populations. The logistic model indicated that climatic factors accounted for 20.832% of the total variation in SDS among the *Impatiens* species, and model residuals were significantly correlated with phylogeny, but not with elevation. Our results indicated that seed dormancy is phylogenetically conserved, and climate drives elevational patterns of SDS variation in mountain ecosystems. This study provides new insights into the response of seed plant diversity to climate change.

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