

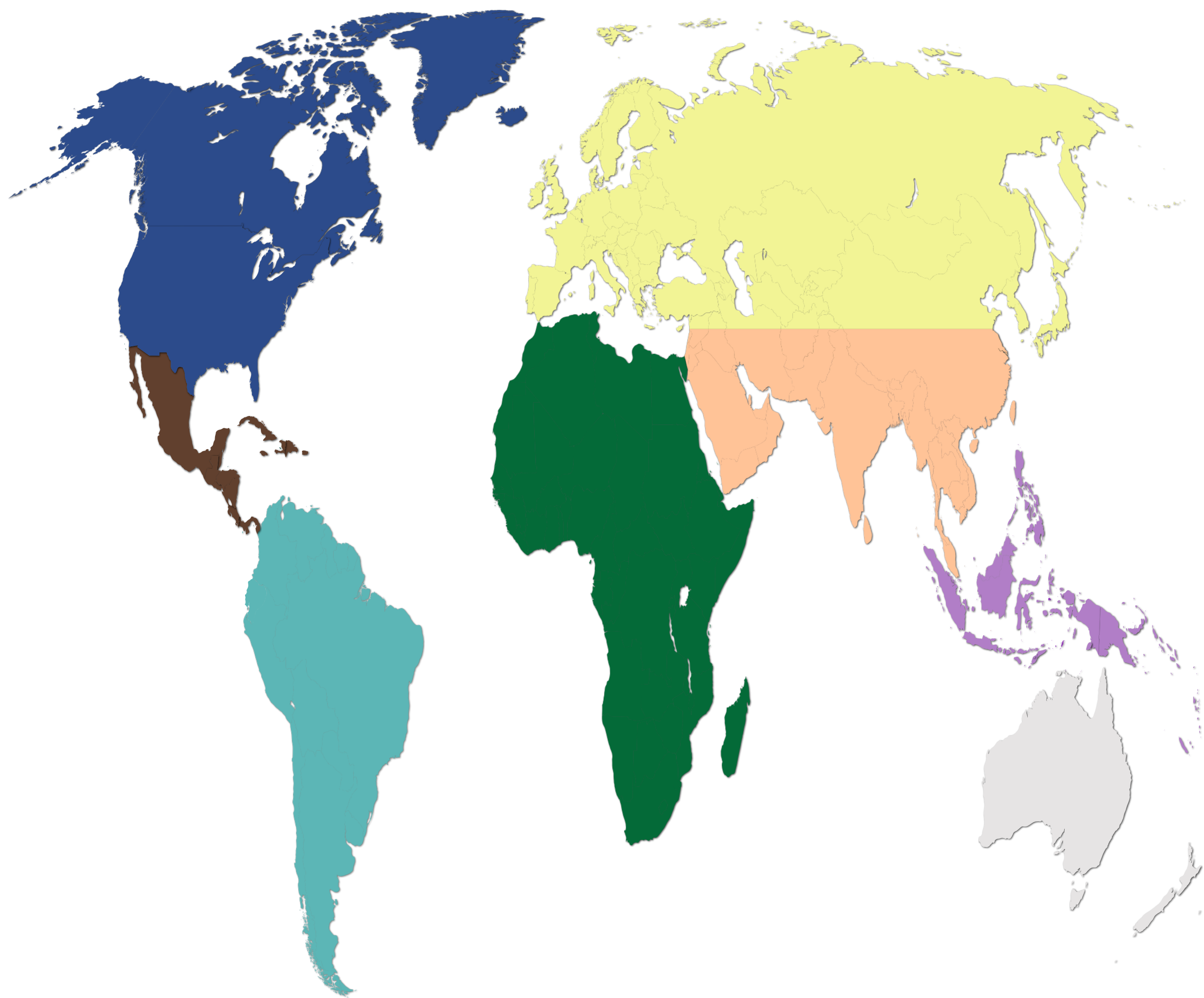
# A global blueberry phylogeny: evolution, diversification, and biogeography of tribe Vaccinieae (Ericaceae)



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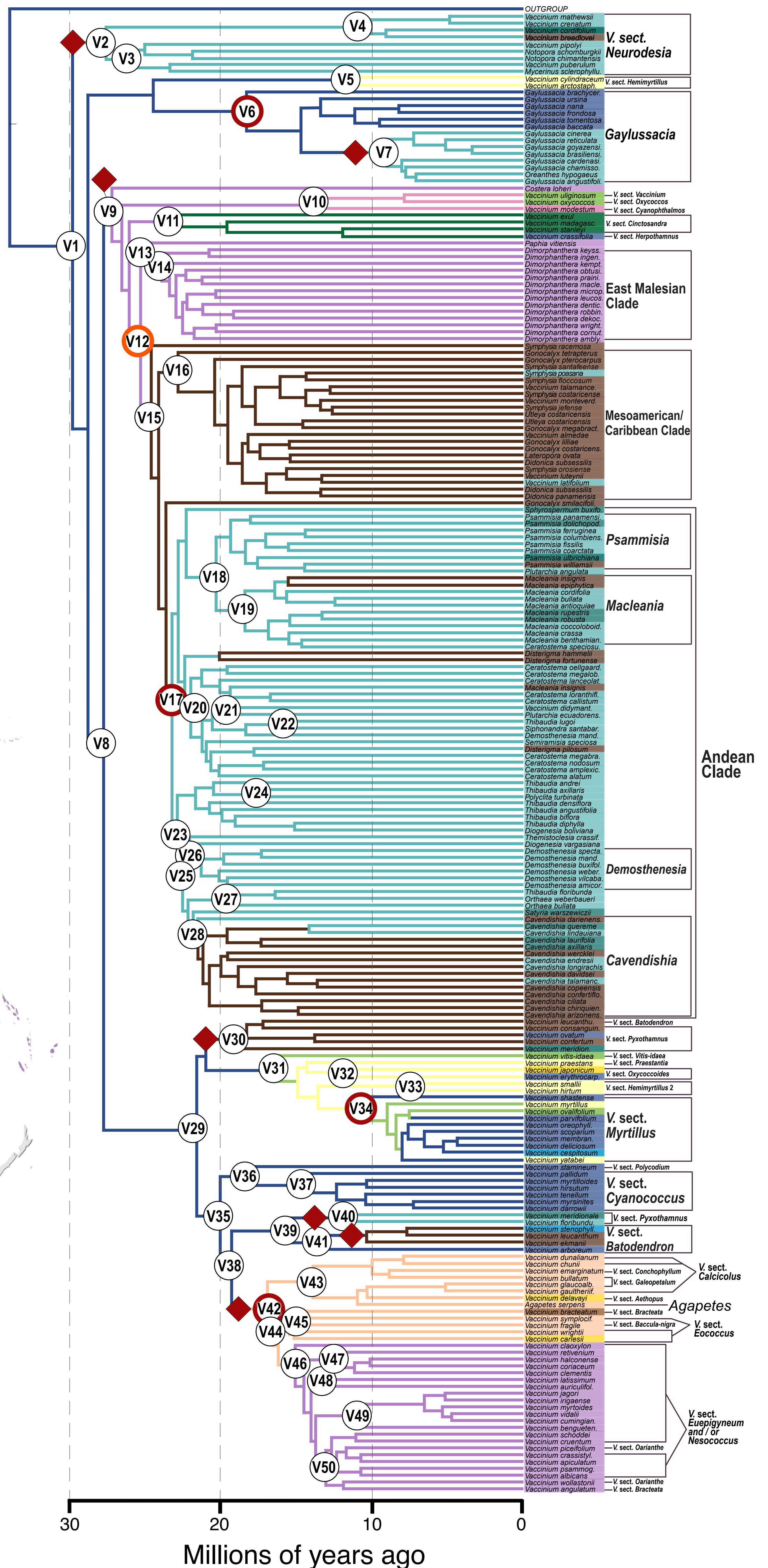
## OVERVIEW

Vaccinieae is a morphologically diverse and species-rich tribe in the Ericaceae. Although the majority of its diversity is tropical, Vaccinieae is best known for temperate crops (i.e., blueberries, cranberries, huckleberries) of the genus *Vaccinium*. *Vaccinium* itself has been previously suggested to be highly polyphyletic, and taxonomic boundaries of most other genera remain uncertain. To better understand the extent of polyphyly of *Vaccinium* in the context of closely related genera, and gain insights into the evolutionary history of Vaccinieae as a whole, we assembled a nuclear dataset (Angiosperms353) for over 200 taxa representing 30 of the 34 genera in the tribe and 25 of the 30 sections of *Vaccinium*. We additionally constructed a plastome dataset for a subset of these taxa. We conducted phylogenetic and time-calibrated biogeographic analyses to address the following questions: 1—What are the phylogenetic patterns within Vaccinieae? 2—How do the clades compare with current generic and sectional? 3—Where and when did major dispersal and diversification events take place? We recovered seven major clades corresponding to previously delimited genera and sections of *Vaccinium*, but ca. 30 more that do not correspond to previously delimited groups. Instead, groups generally align with geography. Biogeographic reconstruction suggests that tropical diversity of Vaccinieae results from multiple independent movements into tropical habitats from temperate ancestral areas, mostly North American. Dispersal events were found to align with major geographic changes such as the uplift of the Andes, some of which coincide with increased diversification rate. Morphological characters often used in infratribal classification evolved multiple times in the tree and showed little correspondence to the topology at the deeper levels of the tree, with the exception of a pseudo-10-locular ovary, which appears to have evolved from a 5-locular ovary once and was newly found to group many sections of *Vaccinium* into a single clade. Options for reclassification range from the recognition of a single species of *Vaccinium* and many more genera, to the recognition of the single genus *Vaccinium* with many more sections. We consider an infratribal reclassification premature pending more taxonomic and phylogenetic study of the many problematic generic and sectional boundaries needing resolution.



- North America
- Middle America
- South America
- Northern Eurasia
- Central Eurasia
- South Insular Asia
- Africa
- N. America + N. Eurasia
- C. Eurasia + S. Eurasia
- M. America + S. America
- N. America + M. America
- N. Eurasia + C. Eurasia + S. Eurasia
- N. Eurasia + C. Eurasia

- ◆ Movement into the tropics
- Positive diversification rate shift
- Hypothesized polyploid clade



## CONCLUDING REMARKS

The finding of rampant non-monophyly across the tribe has important implications for our understanding of the subdivisional classification of the tribe. It challenges conventional taxon limits and highlights the need for extensive future research, particularly for taxa in tropical regions. We aim to highlight in more detail the degree to which clades are misaligned with taxonomic boundaries and comment on various reclassification strategies in a follow-up publication (Becker et al., in prep.). At the extremes, options for a ranked reclassification range from narrowing *Vaccinium* to the single species *V. uliginosum* (the type of the genus) and raising the sections of *Vaccinium* to the genus level, to expanding *Vaccinium* to encompass the entirety of Vaccinieae and lowering the rank of genera to sections within *Vaccinium*. We advocate for detailed systematic studies of localized regions of the Vaccinieae phylogenetic tree that includes the search for morphological characters that can help to support clades recovered here, and to elucidate clade membership in the absence of molecular data. To this end, two areas of active research from members of our team are the focus on Hawaiian *Vaccinium* and *V. sect. Cyanococcus*. In each case, it is clear that current estimates dramatically underestimate true species diversity. This also appears to apply to South Insular Asian *Vaccinium* and Andean taxa.