

## Genome size and phylogenetics of subfamily Vanilloideae inferred from NextGen anchored phylogenomics

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Phylogenetic relationships among genera of tribe Vanilleae continue to remain elusive. One of the possible reasons is that five of the nine genera of the tribe are mycoheterotrophs. These orchids are poorly represented in earlier molecular studies that relied heavily on plastid loci. Interestingly, even the relationships among some photosynthetic genera remain unresolved (e.g., the relationship between South American *Epistephium* and the clade of New Caledonian endemic genera *Clematepistephium* + *Eriaxis*). We have inferred the phylogeny of tribe Vanilleae through the use of Anchored Phylogenomics that targets ca. 500 low copy nuclear genes via Next Generation DNA Sequencing. Furthermore, we are able to recover the plastome sequence from most of our sample, and compare the trees. Our results are different from any previous study in that they show *Epistephium* forming a clade with *Clematepistephium* + *Eriaxis*, as well as *Lecanorchis*. Challenges were met in sequencing members of tribe Pogonieae for outgroup analysis because of the enormous genome size exhibited by these orchids (the largest in the family). As such, we embarked on a study also to estimate genome size for most genera of Vanilloideae. Not only does the subfamily have the largest known orchid genome, but it also contains the largest diploid chromosome number reported for Orchidaceae: *Epistephium lucidum* ( $2n = \text{ca. } 170$ ). Our data shows that there is at least an 18-fold range of genome size in Vanilloideae, from 2.985 pg for *Eriaxis rigida* to 55.4 pg in *Pogonia ophioglossoides*.