

# DNA Barcoding of Meso-American orchids for biodiversity research and conservation

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This project aims at surveying orchid diversity, establishing long-term monitoring sites and undertaking a pilot study on DNA barcoding for conservation and trade surveillance in Costa Rica. Most projects on DNA barcoding of plants have focused on taxa (e.g. several taxonomic groups from around the world), whereas our work concentrates on a defined geographical area, Costa Rica, for one taxonomic group: the hyper-diverse family Orchidaceae (orchids). Hence, among other activities of this project, we are currently working on the development of a DNA barcode for Mesoamerican orchids, in particular Costa Rican species. The project is funded by the Darwin Initiative for the Survival of Species (14-001)



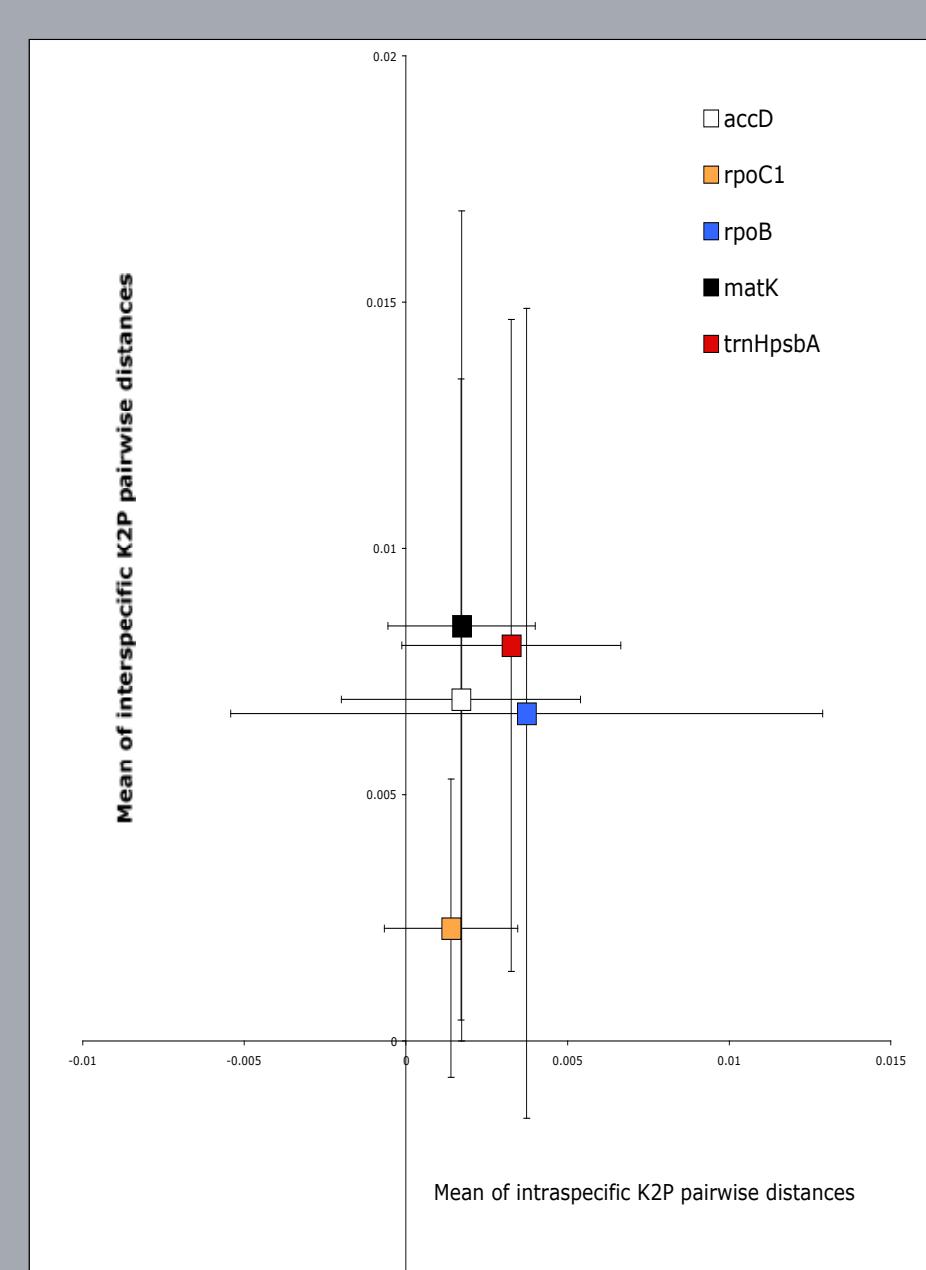
Cocos Island, one of the monitoring sites of the project, where five orchid species are found and three of them are endemics.

Costa Rica has one of the richest orchid floras in the world, with over 1300 species of orchids on a relatively small territory of 51,000 km<sup>2</sup>. In spite of the fact that this country has a well-developed network of protected areas, the orchid flora remain under constant threat from factors such as deforestation and illegal trade. Furthermore, orchids are well known to be difficult to identify, particularly when they are sterile.

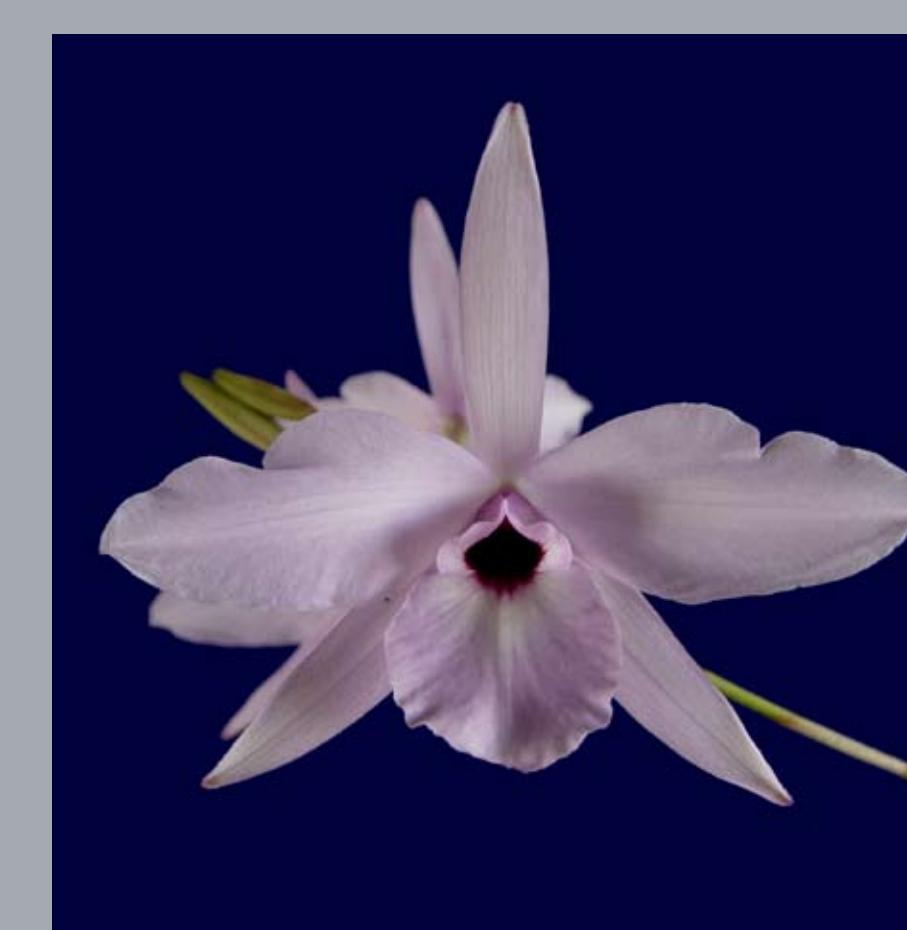
Our geographical approach on DNA barcoding, dedicated to a Mesoamerican hotspot and a hyper-diverse family, will contribute to the international initiative laid by the Plant Working of the CBOL. The use of a standardized identification tool provide many potential uses and applications, such as: identification of different life stages, identification of fragments of plant material, forensics, verification of herbal medicines/food-stuffs, biosecurity and trade in controlled species, inventories and ecological surveys.



Identifying orchids in Tapantí National Park, where over 400 species of orchids are protected.



With the highest inter-specific variation and the lowest intra-specific variation, *matK* appears to provide the greatest resolution. It is clear that no single region will be sufficient as an efficient and universal barcode for orchids. So far we recommend combining *matK* with a non-coding region like the *trnH-psbA* spacer. This would provide the most effective DNA barcode for orchids and probably most other angiosperms.



For this project, over 600 orchid specimens (about 400 species) have been collected so far, and over 700 putative DNA barcodes have been produced.

