

Predictability of DNA markers for population-level study based on species-level variation

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Credit: NIH

Biologists who use molecular data to study evolutionary dynamics between closely related organisms, such as populations, are constantly searching for regions of the genome with high amounts of variability.

In an attempt to answer the question of whether genes that show high levels of variability across different species could also be useful in population-level evolutionary studies, scientists in Brazil, Singapore, and

the United Kingdom teamed up to test the utility of numerous genes previously found to be useful in inferring relationships of cactus species. This study was published in the January issue of *Applications in Plant Sciences*.

"The question was whether we could use previous knowledge to predict if certain markers are useful for phylogeographic studies. In other words, could regions that are variable among closely allied species be useful in intraspecific studies?" explains Fernando Franco, professor of Department of Biology at the Universidade Federal de São Carlos in Sorocaba, Brazil, and corresponding author of the study. "To test this, we used species and populations of *Cereus* - a genus in the cactus family. We were further interested in developing this group as a biological model for evolutionary studies. Cacti are generally associated with low moisture habitats and may be useful as a model to study the impact of Pleistocene climatic change, for example."

As it turns out, the answer to the question of whether it's possible to predict the usefulness of [molecular markers](#) for phylogeographic studies is: it's not always this simple. "Our data agree with the notion of high evolutionary rate-heterogeneity of molecular markers in plants. Further, we supply a case study where this heterogeneity appears to increase in early stages of population differentiation."

Differences in DNA sequences may accumulate at different rates in different lineages. "In general, rates of molecular evolution are somewhat constant through time in animals. However, in plants, and especially in chloroplast DNA, the evolutionary rates are extremely variable across both time and lineages," explains Franco. This means that the same DNA region may evolve rapidly in one species and very slowly in the other.

Rate-heterogeneity poses a practical challenge for researchers interested

in population-level questions in the plant tree-of-life. Because the rate of evolution - and, thus, the amount of variation - is not constant, a screening step is necessary to discover regions of the genome with sufficient variability between individuals of the target species. This can make phylogeographic projects labor- and cost-intensive.

Franco concludes, "Most researchers assume that molecular markers that show variability across species, such as in a phylogenetic study, are potential candidates to perform population-level studies. While this may often be the case, this prediction is not always true. For this reason, we recommend that when designing an experiment, the initial screening step should consider the biological units (i.e., [species](#), subspecies, populations) that are as close as possible to the target units to be studied."

More information: Monique Romeiro-Brito et al. Lineage-Specific Evolutionary Rate in Plants: Contributions of a Screening for (Cactaceae) , *Applications in Plant Sciences* (2016). [DOI: 10.3732/apps.1500074](#)

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