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Abstract

The baobab trees (genus *Adansonia*) have attracted tremendous attention because of their striking shape and distinctive relationships with fauna¹. These spectacular trees have also influenced human culture, inspiring innumerable arts, folklore and traditions. Here we sequenced genomes of all eight extant baobab species and argue that Madagascar should be considered the centre of origin for the extant lineages, a key issue in their evolutionary history^{2,3}. Integrated genomic and ecological analyses revealed the reticulate evolution of baobabs, which eventually led to the species diversity seen today. Past population dynamics of Malagasy baobabs may have been influenced by both interspecific competition and the geological history of the island, especially changes in local sea levels. We propose that further attention should be paid to the conservation status of Malagasy baobabs, especially of *Adansonia suarezensis* and *Adansonia grandidieri*, and that intensive monitoring of populations of *Adansonia za* is required, given its propensity for negatively impacting the critically endangered *Adansonia perrieri*.

Synopsis. Iconic baobabs comprise a single genus of plants distributed in Africa with disjunct distributions in Madagascar and in northern Australia. Multiple evolutionary hypotheses have been proposed for their origin. Genomic data including full chromosome-level assemblies coupled with biogeographic evidence and modeling suggest that Madagascar is the 'birthplace' of baobabs with subsequent colonization and spread to continental Africa and Australia. Demographic analyses imply population diminution in multiple species with at least two facing an uncertain future because of possible reduced ecological resilience.