
New genomic tools to explore the evolutionary history of African rainforest trees

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Abstract

Long-term stability has been considered for long as a prime cause of the remarkable biodiversity of tropical rainforests. However, palaeoecological evidence of substantial change in the tropical vegetation resulting from global climate fluctuation call for a reassessment of the temporal dynamics of biodiversity. Through the AFRIFORD program we aim to understand how past environmental changes have shaped the current distribution and composition of African rainforests and the genetic diversity of their constituent tree species through integrative phylogeography. The development of next generation sequencing and bioinformatic tools support new challenges to reconstruct whole genomes, and to infer the history of forest vegetation, including species belonging to distinct functional groups. First, the capture and sequencing of chloroplast genomes at deep multiplexing levels have been undertaken on the polyploid species of the genera *Azelia* and *Guibourtia* (Fabaceae) to better understand the association between diversification, polyploidy and ecological niches. Secondly, we will focus on the phylogeography of both the rainforest tree *Greenwayodendron suaveolens* (Annonaceae), characteristic of Central African mature forests, and the pioneer and short-living tree *Musanga cecropioides* (Urticaceae). These new phylogeographical patterns, including up to 140 individuals per species, revealed distinct cpDNA phylogroups, in Upper and Lower Guinean forests. Populations could have been fragmented into a restricted number of refugia in the past that seems display diverse demographic signatures. But ongoing molecular dating should provide a more precise temporal framework for comparing the diversification of each phylogroups, and the role of their life history traits in terms of resilience during glacial/interglacial oscillations.

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