Phylogenomics of the early-divergent angiosperm family Annonaceae: resolving intergeneric relationships in the recalcitrant Miliuseae tribe

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Evolutionary relationships among main lineages of the Annonaceae have become much clear in recent years. The still poorly resolved phylogeny of tribe Miliuseae (subfamily Malmeoideae), however, represents the largest impediment to understanding broad-scale evolutionary patterns within the family. The Miliuseae comprises 25 genera and ≈ 510 species of trees and shrubs with a centre of diversity in South East Asia, although the presence of small Central American and African clades raise questions about its origin. The most recent molecular phylogeny of the Miliuseae distinguished 20 well-supported clades based on chloroplast DNA regions. Relationships among the major clades were not supported, and the backbone of the phylogeny remains unresolved. Next-generation sequencing was used to sequence entire chloroplast genomes for 18 Miliuseae species, representing major clades recovered in previous phylogenies to improve the phylogenetic resolution within the tribe and to test biogeographical hypotheses. The complete chloroplast sequence is reported for first time in the Annonaceae. A large inversion in the large single copy (LSC) region of the chloroplast was detected for all members of the Miliuseae. Preliminary data suggest that the use of full chloroplast genome alignments increases the number of informative sites and phylogenetic support in deeper nodes of the phylogeny.