**Phylogenomics of the recalcitrant Annonaceae Subfamily Malmeoideae**

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Annonaceae (ca. 2400 species of trees, shrubs and lianas) are species-rich and ecologically important in tropical lowland forests of both the Neotropics and the Old World. The backbone phylogeny of the family has come into focus in recent years, but there are notable exceptions. Intertribal relationships in subfamily Malmeoideae (7 tribes, 49 genera, >770 species) and intergeneric relationships in its largest tribe, Miliuseae (26 genera, ca. 540 species, center of diversity in continental Southeast Asia and western Malesia), remain very poorly understood. This has impeded downstream analyses such as investigations of the historical biogeography and character evolution in the family.

We used a phylogenomic approach to resolve the relationships in subfamily Malmeoideae. Data from sequencing of total genomic DNA on the Illumina HiSeq2000 platform was used to assemble near-complete plastome and partial nuclear-ribosomal DNA sequences. The dataset comprised 55 newly sequenced accessions including samples of all seven tribes and representatives of ca. 90% of the genera in the subfamily. This data was analysed separately and by integrating a supermatrix of previously published DNA data using likelihood and Bayesian phylogenetic reconstruction methods.

We present the first near-complete plastome sequences for Annonaceae, and highlight observed structural mutations including a major inversion (ca. 7.3 kb) in the large single-copy unit of Miliuseae taxa. The resulting phylogenetic reconstructions provide various new insights into intertribal and intergeneric relationships in Annonaceae subfamily Malmeoideae. These new insights and their implications for the historical biogeography of Annonaceae and character evolution in subfamily Malmeoideae are discussed.