

The origin, diversification and adaptation of a major mangrove clade (Rhizophoreae) revealed by whole-genome sequencing

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Abstract	<p>Mangroves invade some very marginal habitats for woody plants-at the interface between land and sea. Since mangroves anchor tropical coastal communities globally, their origin, diversification and adaptation are of scientific significance, particularly at a time of global climate change. In this study, a combination of single-molecule long reads and the more conventional short reads are generated from <i>Rhizophora apiculata</i> for the de novo assembly of its genome to a near chromosome level. The longest scaffold, N50 and N90 for the <i>R. apiculata</i> genome, are 13.3Mb, 5.4Mb and 1.0Mb, respectively. Short reads for the genomes and transcriptomes of eight related species are also generated. We find that the ancestor of Rhizophoreae experienced a whole-genome duplication similar to 70 Myrs ago, which is followed rather quickly by colonization and species diversification. Mangroves exhibit pan-exomemodifications of amino acid (AA) usage as well as unusual AA substitutions among closely related species. The usage and substitution of AAs, unique among plants surveyed, is correlated with the rapid evolution of proteins in mangroves. A small subset of these substitutions is associated with mangroves' highly specialized traits (vivipary and red bark) thought to be adaptive in the intertidal habitats. Despite the many adaptive features, mangroves are among the least genetically diverse plants, likely the result of continual habitat turnovers caused by repeated rises and falls of sea level in the geologically recent past. Mangrove genomes thus inform about their past evolutionary success as well as portend a possibly difficult future.</p>
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