

Global phylogeography of *Rhizophora* species

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Abstract

To reveal the global phylogeographic pattern of mangroves, we investigated the genus *Rhizophora* that is one of the most representative mangrove plants. Phylogenetic analysis using about 4 kbp of cpDNA sequences showed that the presence of the two distinct clades. One of them was composed of three species of the Indo-West Pacific region (IWP), *R. apiculata*, *R. mucronata* and *R. stylosa*. The other one was composed of the two species of the Atlantic-East Pacific region (AEP), *R. mangle* and *R. racemosa*, and surprisingly *R. samoensis* that is one of IWP species. Analysis of geographic distribution of haplotypes clearly showed the distinctive genetic diversification between the Pacific and Atlantic populations in both *R. mangle* and *R. racemosa* in the AEP. This result suggests that the American continent is a strong geographic barrier that prevents gene flow by sea- dispersal for *Rhizophora* species. On the other hand, an identical haplotype was found among the Atlantic populations of the AEP species, and another identical one was shared among populations of the Pacific *R. mangle* and *R. samoensis* from South Pacific. These results suggest that recent transoceanic long distance seed dispersal would be responsible for maintaining the wide distribution range of *R. mangle*, and that *R. samoensis* may not be distinguished from *R. mangle*. In the analyses using microsatellite markers, genetically differentiated populations of *R. mangle* were further detected in the South Atlantic. Although there are no known land barriers, the bifurcating South Equatorial Current at the northeastern horn of Brazil might be a potential barrier to gene flow and may promote the genetic differentiation of these populations. Other recent results obtained from IWP species will also be introduced in the presentation.

Keywords

comparative phylogeography, IWP, AEP