Formation of a research network for conservation of genetic diversity of mangroves: knowledge gaps, studies, and future directions

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Abstract

There is a general consensus that major mangrove species are widely distributed in the tropical and subtropical regions. However, the status of genetic diversity of mangroves is still relatively unknown. In the last 25 years, mangroves have been devastated at an alarming rate (1-2% yr^{-1} in Asia in 1990s) prompting several rehabilitation programs. Both mangrove degradation and planting activities can disrupt and alter natural gene flow, thus, threatening genetic diversity even before it is studied. In an attempt to shed knowledge on genetic diversity of mangroves, the Chiba University in collaboration with its international partners, initiated mangrove sampling primarily in SE Asia as well as in some parts of the Atlantic-East Pacific (AEP) since the early 2000s. An international network for conservation genetics of mangroves was launched in February 2010 supported by Japan-East Asia Network of Exchange for Students and Youths (JENESYS) Programme promoted by the Japan Society for the Promotion of Science (JSPS). The network aims to provide a global scale understanding of the genetic diversity of major mangrove species. To date, samples totaling about 30 populations for 6 groups of major mangroves were collected. Our collection is composed of 30 individuals from one population representing one population per 1,000 km^2. We used molecular methods such as cpDNA and nucDNA sequencing in analyzing the phylogeography, speciation, genetic structure and distribution patterns of some major mangroves (e.g. *Rhizophora, Bruguiera, Xylocarpus* and *Sonneratia* spp.). We have also developed SSR markers using genomic data obtained by Next Generation Sequencing techniques, and started studies to investigate gene flow between populations and population differentiation in finer scale. In the future, we aim to strengthen the network through biannual workshops, collaborative international research, and co-publications.

Keywords
population structure, comparative phylogeography