Development of SSR markers for five mangrove species using next-generation sequencing with preliminary results of analyses of genetic diversity

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Abstract

SSR (Short Sequence Repeat, equivalent to "Microsatellite") marker is one of the most powerful and popular markers in conservation genetics to analyze genetic diversity, mating system and population structure. However, obtaining enough numbers of good SSR markers for wild plants are sometimes difficult because of complicated process of experiments. Since the development of so-called "Lian method" (Lian et al. 2006), compound SSR can be obtained relatively easier by more simple way, but it is still sometimes difficult to get enough numbers of markers as the markers are obtained "by chance". We sometimes repeated numbers of experiments in vain, yet still finally find it difficult to get markers using this method. Here, we report the results of SSR marker development by using Next Generation Sequencer (NGS), which have become popular in the past few years. We developed SSR markers for 5 mangrove species (*Bruguiera sexangula*, *Rhizophora mucronata*, *Xylocarpus granatum*, *Sonneratia alba*, *Acrostichum aureum*) using Roche 454 GS Junior which can produce data with relatively long mean read length (ca. 350bp). The massive number of sequences obtained from each species was separated into nrDNA and cpDNA then subsequently searched for candidate SSR regions through a software (QDD ver.2.1.). For the five species, more than 50 candidate SSR markers were obtained for one species. We compare the time and cost necessary for SSR marker development, and show that NGS is more effective than other methods. Results of brief population analyses for 5 major mangrove species also will be reported.

Keywords
Roche 454, QDD