

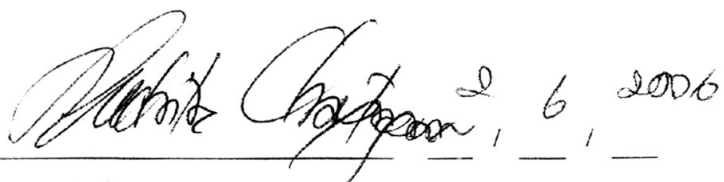
Rungsun Laphom 2006: Evaluation of Genetic Diversity of Some Bamboos in Thailand
Using AFLP (Amplified Fragment Length Polymorphism) and Microsatellite Markers.
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The genetic diversity, relationship and DNA fingerprinting of 25 species of bamboos were investigated using AFLP (Amplified Fragment Length Polymorphism) markers. After preliminary screening of 64 primer pairs, 14 primer pairs were selected as the suitable primer pairs for successful DNA amplification. In total 642 putative loci were scored. The percentage of polymorphic loci was 98.13, which indicates a high level of genetic diversity among the investigated species. The average number of DNA bands per primer pair was 45.86. The following primer combinations: E-AAC/M-CAA, E-ACC/M-CTT and E-AGG/ M-CTC produced the highest number of unique DNA banding patterns. The similarity index and cluster analysis (UPGMA) of the investigated bamboo species were carried out using NTSYS-pc version 2.01e program. The results showed that investigated species were clustered into five groups. The four unknown species, which were named as Paipongyoo, Paimanmoo, Paileangman and Paikrasan were closely associated with Pairuak (*Thyrsostachys siamensis*), Paishangnuan (*Dendrocalamus membranaceus*), Paileang (*Bambusa multiplex*) and Paikhaolam (*Cephalostachyum pergracile*), respectively. Eighteen species displayed some unique banding patterns. Pairai (*Gigantochloa albociliata*) had the highest number of unique DNA bands. These results indicate that AFLP markers may be a useful for identification of the bamboo species in the future.

Genetic diversity of nine natural populations of Paipa (*Bambusa bambos*) in Thailand was estimated using nine microsatellite loci. High level of polymorphism was observed across all populations. The average number of alleles per locus, observed heterozygosity and expected heterozygosity at all loci were 6.11, 0.294 and 0.369, respectively. Sa Kaeo province population had the highest observed and expected heterozygosity (0.333 and 0.440). Population differentiation estimate (F_{st}) was rather high (0.2432). Based on the obtained results, the criteria for *in situ* and *ex situ* gene conservation of *B. bambos* were suggested.

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Student's signature

 26, 2006

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