Genetic Diversity of *Casuarina equisetifolia*

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Casuarina equisetifolia natural distributed in Australia, Thailand, Malaysia, Indonesia, the Philippines, Melanesia, Polynesia and Guam, etc. The EST-SSR markers were used to determine the genetic diversity and population structure among the 29 typical natural and introduced populations. Based on 13 pairs of EST-SSR primers with amplified stability, clear band and higher polymorphism were obtained and used. The 308 alleles can be identified from the 13 SSR loci, average alleles number per loci was 23.69, range of alleles number was from 11 to 48. Range of effective alleles number, Shannon's index, observed heterozygosity and effective heterozygosity were 1.533-7.029, 0.691-2.139, 0.270-0.655 and 0.393-0.858, respectively. According Shannon's index, the order of genetic diversity level from high to low of the 5 regions was: African introduced (AF)>Asia natural (AN)>Oceania natural (OP)>Central American introduced (CI)>Asia introduced (AI);the order of genetic diversity level of the 29 populations was given. The serious inbreeding between populations was occurred during the whole distribution. The 70.12% of total variance was from the individuals within populations. The order of variance was: AN (81.15%) > AI (74.58%)>CI (72.29%)>AF (68.43%)>OP (61.45%). Though variation from populations accounted for only 25.42 % to 38.49% of the total variation, given the serious inbreeding that identified in the population, population selection should also attach great importance in future. Based on UPGMA dendrogram of the 29 populations proved that introduced populations of China should be from Asia natural populations, while introduced populations of Kenya, and India and Veitnam might from Oceania natural populations.

Population structure and regeneration status of *Prunus africana* (Hook.f.) Kalkm. after selective and clear felling in Kibale National Park, Uganda

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Prunus africana is a globally threatened indigenous medicinal tree species, and food for many primates. Its population has declined in Sub-Saharan Africa due to unsustainable harvest and poor protection. In this study, we determined the population density, population structure and regeneration status of *P. africana* in the former clear felled, selectively logged, and primary forests of Kibale National Park, and assessed the effects of dense cover of *A. pubescens* on its regeneration. Trees were measured from 180 randomly established plots. The densities of *P. africana* seedlings and saplings differed significantly among the three forests while that of poles and mature trees did not. The density of seedlings was significantly higher in the selectively logged than in primary forests. The density of saplings was higher in clear felled than in selectively logged forests. Tree density was not negatively affected by *A. pubescens* cover. Clear felled areas had a more stable population structure with better regeneration, while selectively logged and primary forests had unstable population structures with poor recruitment potential. Our results show that *P. africana* regenerates more in intensively disturbed forest areas than less disturbed or primary forests, highlighting the importance of regenerating forests in the conservation of *P. africana*.

High-throughput development of SSR markers in diverse Liriodendron chinense germplasm

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Liriodendron chinense, ranges widely in subtropical China and northern Vietnam, however, inhabits several small isolated populations and is now an endangered species due to its limited seed production. The objective of this study was to develop a set of SSR markers useful for genetic studies in*L. chinense*and their characterization in diverse germplasm. We developed novel SSR markers for *L. chinense*from randomly sequenced regions of the genome using next-generation sequencing. In total, 6,147 SSR markers were isolated from 2.84 GB genomic sequences. The most common of SSR motifs were dinucleotide (70.09%), followed by trinucleotide motifs (23.10%). The motif AG/TC (33.51%) was the most abundant, followed by TC/AG (25.53%). A set of 13 SSR primer combinations were tested for amplification and their ability to detect polymorphisms in a set of 109*L. chinense*individuals, representing distinct varieties or germplasm. The number of alleles per locus ranged from 8 to 28 with an average of 21 alleles.The expected heterozygosity (HE) varied from 0.19 to 0.93 and observed heterozygosity (HO) ranged from 0.11 to 0.79. The SSR markers characterized and tested in this study provide a valuable tool to detect polymorphisms in*L. chinense*for future genetic studies and breeding programs.

Grafting selected Brazil nut (*Bertholletia excelsa*) genotypes in Acre, Brazil: sprout survival and vigor / *Enxertia de genótipos de castanheira selecionados no Estado do Acre: pegamento e vigor dos brotos*

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O manejo da castanheira-da-amazônia, atividade reconhecida como alternativa para a conservação da Amazônia, tem suas limitações quanto a produtividade, logística e acesso aos castanhais nativos. Isso justifica investimentos para seleção e disponibilização de material genético de alta qualidade. A Embrapa iniciou, em 2013, um programa de melhoramento genético com materiais do AC, RR e AP. No Acre foram selecionados 20 genótipos, nos Seringais Filipinas e Cachoeira, os quais foram caracterizados e enxertados em pomar clonal. Este trabalho apresenta o pegamento dos enxertos aos 180 dias, além do vigor das brotações aos 470 dias. Genótipos do Filipinas tiveram melhor pegamento (87,5%) que os do Cachoeira (67%). Os genótipos C204, F217 e F391 foram os melhores, com destaque para o F391 que apresentou melhor desenvolvimento dos brotos. Considerando que o enxertador e a forma de conservação das hastes foram semelhantes, as diferenças observadas podem estar associadas à época de coleta das hastes, uma vez que no Cachoeira foi final de outubro e no Filipinas início de novembro. Além disso, dos 11 brotos classificados como vigorosos, 10 foram do Filipinas. Diferenças genéticas também podem explicar as variações observadas, embora a incompatibilidade entre enxerto e porta-enxerto seja um aspecto que ainda precisa ser estudado.