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The strategy should take into account both the species' patterns of genetic variation and the forestry/socio-economic context, and may combine in situ, ex situ or other conservation measures. ... Case Study 1.3 Shorea lumutensis: genetic variation and conservation: genetic variation and conservation.

Shorea lumutensis: genetic variation and conservation

The genetic diversity of four natural and four planted populations of Shorea guiso in the Philippines were investigated using microsatellite DNA markers to compare patterns of variation within and...

Genetic variation in natural and planted populations of ...

Abstract. The genetic diversity within and among populations of Shorea leprosula and Shorea parvifolia from Indonesia was investigated using amplified fragment length polymorphisms (AFLPs). The results indicated that *S. leprosula* is genetically more variable than *S. parvifolia*. At the population level, a higher level of genetic diversity was revealed for *S. leprosula* with a percentage of polymorphic loci (PPL p) of 53.32% and an expected heterozygosity (H_{ep}) of 0.16 in comparison with *S.*

Genetic diversity within and among populations of Shorea ...

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started a study of genetic variation in forest trees (*Shorea acuminata*) which is one of high quality timbers in Indonesia. *Shorea acuminata* Dyer is a member of the genus *Shorea* (section *Mutica*) in the Dipterocarpaceae family. This tree is distributed in a mixed dipterocarp forest in Malaysia, Sumatra and Lingga (Ashton 1982). In

Chloroplast DNA variation of Shorea acuminata Dyer in ...

Zulfahmi, Siregar IZ, Siregar UJ (2010) Chloroplast DNA variation of Shorea acuminata Dyer in Sumatra assessed by microsatellite markers. Biodiversitas 11: 107-111. Shorea acuminata Dyer is member of the Dipterocarpaceae family. It is ecologically and commercially important in the Indonesian region.

Chloroplast DNA variation of Shorea acuminata Dyer in ...

Very little is known about the levels and patterns of DNA polymorphism in populations of tropical trees. In this study, we investigated population genetic structure of the four following Shorea ...

(PDF) Nucleotide variation in the GapC region of four ...

Teacher's notes 1.3 Shorea lumutensis: genetic variation and conservation 3 Slide 8 - shows the need for research if conservation is to be effective. Slide 9 - shows the main topics that were researched and provide the basis for the results presented in the study. It is important to note that ecological and genetic studies are complementary and not either/or.

Shorea lumutensis: genetic variation and conservation

The patterns of morphological and genetic variability exhibited by this species also have implications in terms of biomonitoring. Low genetic variability indicates that patterns of phenotypic variability among shore crab populations are likely to reflect differences between local environments.

Patterns of morphological and genetic variability in UK ...

The analysis of genetic variation in populations of infectious agents may help us understand their epidemiology and evolution. Here we study a model for assessing the levels and patterns of genetic diversity in populations of infectious agents. The population is structured into many small subpopulations, which correspond to their hosts, that are connected according to a specific type of ...

Patterns of genetic variation in populations of infectious ...

Genome-wide Patterns of Genetic Variation Among Elite Maize Inbred Lines Jinsheng Lai et al. Nat Genet. 2010 Nov. Show details Nat Genet Actions. Search in PubMed Search in NLM Catalog Add to Search . 2010 Nov;42(11):1027-30. doi: 10.1038/ng.684. Epub 2010 Oct 24. ...

Genome-wide Patterns of Genetic Variation Among Elite ...

Genetic variation in a population is derived from a wide assortment of genes and alleles. The persistence of populations over time through changing environments depends on their capacity to adapt ...

The Genetic Variation in a Population Is Caused by ...

We performed whole-genome multi-locus sequence typing for 2554 genes in a large and heterogenous panel of 180 Listeria monocytogenes strains having diverse geographical and temporal origins. The subtyping data was used for characterizing genetic variation and evaluating patterns of linkage disequilibrium in the pan-genome of L. monocytogenes. Our analysis revealed the presence of strong ...

Whole genome genetic variation and linkage disequilibrium ...

Patterns of genetic variation in Mendelian and complex traits Annu Rev Genomics Hum Genet. 2000;1:387-407. doi: 10.1146/annurev.genom.1.1.387. Authors M E Zwick 1 , D J Cutler, A Chakravarti. Affiliation 1 Department of Genetics, and Center ...

Patterns of genetic variation in Mendelian and complex traits

The levels and distribution of standing genetic variation in a genome can provide a wealth of insights about the adaptive potential, demographic history, and genome structure of a population or species. As structural variants are increasingly associated with traits important for adaptation and speciation, investigating both sequence and structural variation is essential for wholly tapping this ...

Chromosome-level assembly of the Atlantic silverside ...

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The results of these analyses may lead to new insights into the relationships between genetic variation (DNA mutations) and disease. NorthShore, a setting for innovative research NorthShore is committed to advancing medical research through our state-of-the-art research programs, as well as providing exceptional patient care.