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Pinus taeda

Descriptor

genetic variation

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Abstract

Allozyme frequencies were studied in range-wide collections from 23 populations of longleaf pine (*Pinus palustris*) and 33 populations of loblolly pine (*P. taeda*) from the coastal plain of the southern USA. Gel electrophoresis was used to resolve 16 loci of 10 enzyme systems in both species, and an extra 6 loci of 4 enzyme systems in longleaf pine. F statistics for both species indicated very little inbreeding. In longleaf pine, there was a linear decrease in allozyme variation from west to east. It is suggested that this is a result of migration from a single refugium in the west (south Texas or northeast Mexico) after the Pleistocene, with a loss of variability due to stochastic events during migration. In loblolly pine, there was no east-west trend and there appeared to be a tendency for more variation in the central part of the natural range, and it is suggested that this species was located in two refugia during the Pleistocene, one in Texas/Mexico, and another in Florida/Caribbean.

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