

PHYLOGENY OF MAJOR SOUTHERN PINES (SUBSECTION *AUSTRALES*, GENUS *PINUS*, FAMILY PINACEAE)

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Southern pines are an evolutionarily young and closely related group. Their natural habitat stretches across southeastern states of the USA. Four of these species have been considered of major economic importance: shortleaf (*Pinus echinata* Mill.), slash (*P. elliottii* Engelm.), longleaf (*P. palustris* Mill.) and loblolly (*P. taeda* L.) pine. They are largely sympatric although recent glacial periods could have forced them into isolated refugia. Hybridization observed among these species in both natural and controlled environments further suggests tight links among them. The short time since speciation, sympatry, and demographic processes are likely primary causes of difficulties with systematic classification within this group in studies published to date. We investigated the phylogeny of the four southern pines using data from nuclear molecular markers. We utilized various phylogeny reconstruction techniques, including maximum likelihood and Bayesian methods. Despite a representative data sample and modern analytical approaches, our results reflected the difficulties in reaching classification consensus evident in past studies. However, we also observed a tendency for certain alternative topologies being supported by groups of genes that differed in their putative functionality.

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