

Population genetic analyses of *Taxodium distichum*, a wetland coniferous tree in North America, based on amplicon sequencing

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論 文 名 : Population genetic analyses of *Taxodium distichum*, a wetland coniferous tree in North America, based on amplicon sequencing
(北米産湿地性針葉樹ヌマスギのアンプリコンシークエンス解析に基づく集団遺伝学的解析)

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論 文 内 容 の 要 旨

Studies of natural genetic variation can elucidate the genetic basis of phenotypic variation and the past population structure of species. The study species, *Taxodium distichum*, is a unique conifer that inhabits the flood plains and swamps of North America. Morphological and ecological differences in two varieties, *T. distichum* var. *distichum* (baldcypress) and *T. distichum* var. *imbricarium* (pondecypress), are well known, but little is known about the level of genetic differentiation between the varieties and the demographic history of *T. distichum*.

First, I analyzed nucleotide polymorphisms at 47 nuclear loci from 96 individuals collected from the Mississippi River Alluvial Valley (MRAV), and Gulf Coastal populations in Texas, Louisiana and Florida using high-throughput DNA sequencing. Standard population genetic statistics were calculated and demographic parameters were estimated using a composite-likelihood approach. *Taxodium distichum* in North America can be divided into at least three genetic groups, baldcypress in the MRAV and Texas, baldcypress in Florida, and pondecypress in Florida. The levels of genetic differentiation among the groups were low but significant. Several loci showed the signatures of positive selection, which might be responsible for local adaptation or varietal differentiation. Baldcypress was genetically differentiated into two geographical groups, and the boundary was located between the MRAV and Florida. This differentiation could be explained by population expansion from east to west. Despite the overlap of the two varieties' ranges, they were genetically differentiated in Florida. The

estimated demographic parameters suggested that pondcypress split from baldcypress during the late Miocene.

In addition, I conducted an association study between genetic differences and drought tolerance. In 2012, a serious drought hit the western part of the USA and baldcypress trees in Texas were affected. Interestingly, some trees were seriously damaged but others were in fairly good conditions even though they grew in close proximity. To infer the relationship between genetic variation and tolerance to the severe drought, I determined sequences at 141 nuclear loci of 95 trees sampled from two river tributaries in Texas showing different health conditions after the drought. No significant correlation between genetic variation and the tree condition after the drought was found. However, one locus showed a significant difference in genotype frequencies between groups categorized by the tree height. It is not clear whether this locus is actually involved in drought tolerance or not because I failed to find a relationship between the height and tolerance to the draught, but the locus may be under selection if there is a positive relationship between the two traits.