

PHYLOGENETIC ANALYSIS OF GENUS *SALIX*

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Salicaceae is a large family with 2 to 4 genera. The family was originally divided into genus *Salix* and genus *Populus*. Subsequently genus *Chosenia* and genus *Toisusu* were separated from genus *Salix*. Later, other author again included these genera into genus *Salix*. The phylogenetic relationships within genus *Salix* are also unclear. The fundamental differences in taxonomic systems of Salicaceae and within genus *Salix* are mostly caused by scarceness of informative morphological characters that can be used for phylogenetic analyses (Azuma et al. 2000). An important contribution to taxonomic confusions in Salicaceae is also caused by extremely high variation of morphologic characters within particular genera. Some morphological characters with high polymorphs may vary convergently in independent lineages. The usage of such traits often leads to taxonomy that does not reflect phylogenetic relationships (Brunsfeld et al. 1992).

In our research we applied new molecular-genetic approaches. The phylogenetic analyses are based on DNA sequences of nuclear and also chloroplast regions. The sequences which we used are more evolutionary divergent than sequences so far used in genus *Salix*, therefore dendrograms will have higher resolution and probably can answer the fundamental questions about evolutionary relationships in Salicaceae and within genus *Salix*.