**SPECIES DELIMITATIONS WITHIN THE *Picea abies/obovata* COMPLEX**

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Species delimitations have long been controversial within the Norway-Siberian (*Picea abies* – *P. obovata*) spruce complex, and indeed, whether they represent two distinct species at all. To address this standing question, we are sequencing the whole-chloroplast genomes of 30 individuals from across the range ofNorway and Siberian spruce and analyzing their relationships within a complete *Picea* phylogenetic framework. Our first results support the hypothesis that Norway spruce actually comprises at least two species separated by millions of years of evolution: one in Fennoscandia and another in continental Europe. However, we found more equivocal support for the status of Siberian spruce, as chlorotypes from this putative species were intercalated within both Fennoscandian and continental European spruce clades. A similar lack of reciprocal monophyly was also observed at 42 mitochondrial gene loci analyzed in a subset of individuals. As some combination of hybridization and incomplete lineage sorting could explain this pattern, we are additionally analyzing genome-wide variation at > 40,000 SNPs in exemplar accessions from the Fennoscandian, continental European, and Siberian clades. This strategy will help clarify the relationships among the Norway/Siberian spruce and also enable identification of introgressed loci using recently-developed statistical methods. Understanding the species boundaries and extent of hybridization between Norway and Siberian spruce will provide a sound foundation for future work on the genetic basis of adaptation of these economically and ecologically important species.