In search of hybridity: the case of Karelian spruces

Ranelle Ivens[†], Polina Borisova², Polina Volkova², Alexey Shipunov*¹

¹Minot State University, ²Moscow South-West High School,

Norwegian spruce (*Picea abies* (L.) Karst.) and Siberian spruce (*Picea obovata* Ledeb.) are conspicuous ornamental trees growing well in North Dakota. These two species are suitable for cultivation and may be used in restoration of our tree flora suffered from 2011 catastrophic flood. The native area of these spruces is the whole Northern Eurasia: Norwegian spruce occurs mostly in the West (Europe), and Siberian spruce to the East of Ural mountains. These species meet only in narrow zone in Finnish and Russian Arctic where putative hybrid, *Picea x fennica* (Regel) Kom. (Finnish spruce) has been described. Despite of sufficient morphological research, there were no investigations employed contemporary methods of hybridization study, e.g., geometric morphometry and molecular analysis of polymorphic markers.

For morphological analysis, we employed both classical and geometric morphometry approaches. Linear measurements of cones and seed scales unequivocally show that Karelian spruces should be treated as Siberian Picea obovata. However, geometric morphometry (studies of form) of seed scales showed that Karelian trees hold the intermediate position between two species. Therefore, morphology did not return a clear answer.

For molecular analysis, we are using three polymorphic fragments which are already known as producing good results in the studies of spruces phylogeny: non-coding regions of chloroplast DNA (trnT-trnL intergenic spacer and trnL (UAA) intron) and polymorphic fragment of the second intron of mitochondrial nad1 gene. DNA of 59 samples from eight populations was extracted, and after some tuning, we now have good results of trnT-trnL fragment amplification. Since this fragment should contain a G-insert characterising Siberian spruces, results of sequencing will probably shed a light to the origin of our Karelian samples. We are planning to sequence also two other fragments.