

Blast from the past: Jack pine genetics support a coastal glacial refugium

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Can a road-trip across eastern North America, ancient ice sheets, and DNA samples unlock the ancestral history of jack pine trees? Julie Godbout and colleagues from the Université Laval, Quebec, Canada, certainly hoped that driving across northeastern U.S. and Canada to collect samples from jack pine trees would shed some light on how glaciers may have impacted present-day pine genetics.

About 20,000 years ago, ice sheets covered most of the northern terrestrial surface of the continent of North America. For some boreal species this Last Glacial Maximum period may have profoundly influenced their present-day distribution and genetic diversity. Glaciers may have separated populations into isolated pockets and/or created barriers to dispersal and therefore gene flow.

In the November issue of the *American Journal of Botany*, Godbout and colleagues examined the genetic structure of jack pine (*Pinus banksiana*), one of the dominant tree species in the North American boreal forest, to see if they could determine its geographic history since the Last Glacial Maximum. In previous studies they had discovered that populations of jack pine from central and western Canada were genetically distinct from eastern populations. Moreover, the eastern populations were genetically quite diverse and heterogeneous, much more so than the central and western groups. Why was this?

"This study follows up a first rangewide phylogeographical work on jack pine that set us thinking that populations from the Maritimes region

[New Brunswick, Nova Scotia, and Prince Edward Island] were genetically distinct from the rest," Godbout stated.

On their road trip across New England and the Maritimes provinces the authors completed their sampling of 1240 jack [pine trees](#) in 83 populations, collecting pine needles and young seedlings. Pine seeds generally are more restricted geographically in their dispersal than pollen, which can be dispersed for hundreds of kilometers by the wind, so the authors extracted both mitochondrial DNA (inherited only via seeds) and chloroplast DNA (passed down via both seeds and pollen) to help piece together the geographic structure of the species.

The authors found interesting differences between how the mitochondrial DNA (mtDNA) and the chloroplast DNA (cpDNA) were distributed geographically. Based on the mtDNA, the eastern populations were genetically distinct from the central and western Canada populations—supporting their earlier findings. Within the eastern populations one of the 15 distinct mitotypes (mitochondrial haplotypes) was almost exclusively found in the Maritimes region and there were some genetically diverse populations in New York, Vermont, and Maine. These data indicate that perhaps these populations descended from a unique ancient population that may have been isolated from others during the last maritime ice age.

The cpDNA structure was much more uniform across the entire region, although three of the 16 most abundant chlorotypes were found primarily in the same maritime region as the one distinct mitotype. The more uniform cpDNA data probably reflect the fact that pollen is much more widely dispersed than seeds—thus dispersal via pollen since the last ice age may obscure ancient population structures. Genomes dispersed only in the seeds (such as mtDNA) may have much lower levels of gene flow and thus may better reflect past genetic patterns compared to genome dispersed in pollen.

"We believe that this genetic structure is directly related to the species particular glacial history in a region supposedly affected by fluctuations of the Atlantic Ocean sea-level during glaciations," Godbout said.

"Indeed, since a large amount of water was sequestered in the ice sheets, some emerged parts of the continental shelf suitable for the survival of jack pine possibly sheltered small glacial populations geographically isolated from populations located southward on the Atlantic plain."

This would point to a three-prong ancestry for jack pines—one from populations located on the southern edge of the glaciers in central and western parts of Canada west of the Appalachian Mountains, a second one in the east from an Atlantic coastal population, and a third in the Maritimes area potentially from an isolated population on the fringe of the ice cap.

"The aim of this work was to verify whether populations of jack pine, a typical tree of the North American boreal forests, presented a distinctive genetic signature in the Maritimes region, which proved to be true," Godbout concludes. Moreover, "If jack pine survived the ice age in a cryptic refugium along the Atlantic coast, other species may have also experienced a similar event."

"It may be interesting to compare our results with other phylogeographical works targeting the Atlantic and/or eastern boreal region species," Godbout notes. "This may allow the detection of genetic trends consolidating (or not) the hypothesis of a coastal refugium in the northern Atlantic region, as was previously done in the Pacific Northwest region. Unfortunately, at this time, few phylogeographical studies investigating this area are available."

And Godbout's take-home from the road trip? She jokes, "An alternative conclusion of this work would be that the entire state of Maine is really beautiful."

More information: Julie Godbout, Jean Beaulieu, and Jean Bousquet (2010). Phylogeographic structure of jack pine (*Pinus banksiana*; Pinaceae) supports the existence of a coastal glacial refugium in northeastern North America. *American Journal of Botany* 97(12): 1903-1912. [DOI:10.3732/ajb.1000148](https://doi.org/10.3732/ajb.1000148)

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