

# DNA Traces the Migration of BC's Alpine Species

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For many years, the idea that an enormous ice sheet covered all of BC during the last ice age was a widely-accepted theory. But recent advances in DNA sequencing of plants are helping change this idea. In fact, field work and DNA analyses are even challenging the pervasive idea that following the ice age, plants that returned to BC solely came from outside of BC.

Surprising new insights into the history of BC's flora are emerging from the analysis of alpine plant

DNA. The same approach traces the 'Out of Africa' migration of our own species. We are interested in plants of the widespread northern hemisphere alpine-Arctic tundra, whose history is strongly linked with the coming and going of glaciers during the Pleistocene Epoch. Via the Arctic, BC's mountains provide a pathway of migration among lower latitude mountains of Europe, Asia and North America.

We have studied five species to date. The results indicate that following

the last ice age, the ancestors of some of the plants now living here arrived from the north and south as has long been proposed. But surprisingly, there is compelling evidence that some populations survived within the limits of the ice sheet in previously unsuspected 'refugia' (areas that were not covered by ice).

It is commonly held that an ice sheet covered almost all of BC about 15,000 years ago. After the ice melted, plants and animals recolonized BC as



Figure 1, Mountain Sorrel

Geographic distribution of mountain sorrel genetic types by region, from 140 populations (~ 1 sample/population). Each circle represents a geographic region. Each colour represents a genetic type. Circles including the same colour share the same genotype. Numbers within circles are the number of genotypes found only in that geographic region. Arrows indicate the most likely direction of migration. Dashed line between eastern Russia and Siberia indicates an apparent barrier to migration as no genetic types are shared across this line.

Photo by Kendrick Marr taken in Tweedsmuir Provincial Park, on Well's Gray Peak, 2010.



suitable habitats became available. It is easy to imagine that warmth requiring lowland species migrated from the south. But where did the cold-adapted high mountain species come from? In 2001 we began collecting and preserving for DNA analysis leaves of 10 widespread north hemisphere alpine-Arctic tundra species from diverse and remote areas of northern BC, while at the same time making comprehensive plant collections of this poorly known region (See Winter 2013 edition of *What's inSight*).

If ice-free areas did exist within BC during the last ice age, then tundra species, adapted to survive cold climates, would have been present. To place BC in its proper context we needed samples from outside of the province. We enlisted the assistance of more than 40 botanists in the US,

Yukon, Asia and Europe to collect samples for us. Leaves removed from historical, dried collections (herbaria) held at the Universities of Colorado, Wyoming and Washington filled in key geographic gaps, although the success rate in retrieving DNA information was lower than with freshly collected tissue.

In 2010, a grant from the *Walton Innovation Fund* gave us the important opportunity to collect samples from the Altai Mountains of southern Siberia. In 2011 and 2012 we made collections in eastern Russia and Alaska, generously supported by the *October Hill Foundation*. The collecting locations from Russia and Alaska occur along the likely migration route of tundra species connecting the mountains of Central Asia/Himalayas and western North America.

For this study small sections of DNA are 'sequenced' from many individuals of the same species. Sequencing reveals the order of the four chemical 'bases', commonly abbreviated as 'A', 'T', 'G' and 'C', that make up the DNA molecule. When a cell divides, its DNA is copied so that its daughter cells receive the full complement of DNA, but occasionally errors ('mutations') occur: e.g. an 'A' might be replaced by a 'T', 'C' or 'G' or several bases might be inserted or deleted during replication. Descendants of an individual in whom a mutation occurs bear that same mutation. Individuals that bear the same DNA sequence belong to the same 'genotype' or lineage. The longer a population remains in one location, the greater the number of mutations that will accumulate, thus the greater the number of genotypes. When a species spreads



Figure 2, Altai fescue

Distribution of genetic variation by region in Altai fescue from 54 populations (~5 samples/population).

into new locations, such as a previously glaciated landscape, only a few individuals establish the new population, thus it is unlikely that all of the genotypes of the source population will be present in the new population. The number of genotypes decreases with each subsequent dispersal event. Generally speaking the more genotypes in a region the older the landscape is likely to be.

The first species we analyzed, 'mountain sorrel' (Figure 1), revealed that populations survived the last ice age in multiple regions including Beringia (those parts of Alaska and the Yukon that have never been glaciated), the western USA and, contrary to expectations, within the borders of BC. Survival in BC was demonstrated by two genotypes occurring only in BC, and not found north or south of our province.

Populations from eastern Russia and those from Alaska share many genotypes as would be expected, since during glacial periods sea level was lower and a broad expanse of land connected eastern Asia to

western North America. The absence of shared genotypes between Siberia and North America indicates a very long period of separation. Fewer genotypes occur in southern BC than in northern BC and for the most part, the same genotypes do not occur in both areas, suggesting different landscape histories. Surprisingly, few genotypes occur in the Arctic, an indication that the species spread there relatively recently.

The DNA sequences of the grass Altai fescue (Figure 2) hold surprises too. Most of the genetic diversity of this northern species is found in BC and the southern Yukon, not central Asia! It must have migrated from northwest North America to Russia, where almost no genetic diversity exists, and despite the species' name, the roots of this grass are North American.

The migration patterns revealed by this study could not have been predicted without our genetic studies. They raise important questions about the origin of BC's

plant and animal species and bring into question the concept of a province-smothering ice sheet at the end of the ice age. Our goal is to analyze another six species for which we already have samples, to strengthen the case for this deep time interpretation view of our alpine tundra flora. Some tundra species are adapted to a harsh landscape with little soil development and short growing seasons; others grow only in meadow habitats with more soil development and longer growing seasons (i.e. milder climatic conditions). Studies of additional species might reveal the nature of the ice-free habitats, even what kind of animal life they might have supported. Each species may have its own story and thus illuminate more widely the origin of the flora of the northern hemisphere.

This project has ramifications for international research and has the potential to reshape our understanding of British Columbia's natural history. The next step, the analysis of each one of the additional six species samples necessary to further this research, involves DNA extraction and sequencing which costs approximately \$12,000 per species.

If you are interested in furthering our growing understanding of British Columbia's natural history, and would like to donate to support this research project, please contact Jonathan Dallison, Major Gifts Manager, at 250-413-7756 or [jdallison@royalbcmuseum.bc.ca](mailto:jdallison@royalbcmuseum.bc.ca).



Photo by Kendrick Marr of Dr. Richard Hebda, in a meadow of Altai Fescue in the Altai Mountains of southern Siberia.