

Population genetics of Rangifer: a circumpolar approach





Glenn Yannic, Steeve D. Côté, Joaquin Ortego and Louis Bernatchez and many other collaborators

CONTEXT

- Global climate change is predicted to impact a myriad of ecosystems, for example by altering species distributions, community composition, and ecosystem structure. Arctic ecosystems are especially vulnerable to global warming as Polar Regions are expected to exhibit the greatest degree of change.
- Rangifer is the socioecological cornerstone of circumpolar indigenous cultures, from subsistence hunting of caribou by Aboriginal people in Canada, Greenland and Alaska, to reindeer husbandry by Sami in Scandinavia and numerous herding cultures across Siberia.
- Caribou and reindeer herds are declining across their circumpolar range, coincident with increasing arctic temperatures and precipitation, and anthropogenic landscape change.
- The management of populations, however, is complicated by the uncertainty over taxonomic status and distribution, and population delineation, all of which are the central premises of conservation strategies.
- Information on genetic population structure of Rangifer is essential for both science and management, particularly between the threatened sedentary ecotype, mountain and migratory populations.





Migratory Toundra Caribou (0.1)

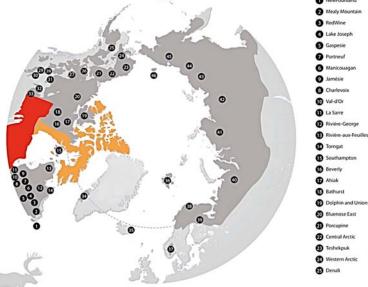




OBJECTIVE

Our study is a worldwide collaborative project, which brings together researchers and wildlife managers across the range of caribou-reindeer. This project aims at studying connectivity of caribou-reindeer populations at the circumpolar scale, particularly between the threatened sedentary ecotype, mountain and migratory populations in North America.

SAMPLING





Our sampling includes several subspecies /ecotypes:

- Migratory Tundra Caribou (e.g. Bluenose East, NWT)
- · Migratory Mountain Caribou (e.g. Narraway, AB)
- Sedentary Boreal Caribou (e.g. Saguenay, QC)
- · Eurasian Tundra Reindeer (e.g. Taymir, Russia)
- Eurasian Forest Reindeer (e.g. Kuhmo, Finland)
- We use 20 samples / herd and various DNA sources (Hairs, ear punch, blood, muscle)

Genotyping

- All samples are analyzed for:
- a) 16 microsatellites (Nvhrt-16 and Nvhrt-30, Rt-1, Rt-5, Rt-6, Rt-7, Rt-9, Rt-24, Rt-27, BL42, BM4513, BM6506, BMS745, BMS1788, FCB193 and
- b) 470-bp of the control region (L15394 and H15947 primers pairs)

Interested in participating and collaborating in the project? Contact Glenn Yannic or Steeve Côté

Glenn Yannic - Post-Doc - glenn.yannic@gmail.com - tel.: (418) 656-2131, # 12004 Steeve Côté - Professor of Ecology - steeve.cote@bio.ulaval.ca - tel.: (418) 656-2131, # 3490 Département de biologie & Centre for Northern Studies, Université Laval, Québec, Québec, G1V 0A6, Canada



























