

Population genomics of grey wolves and wolf-like canids in North America

North America is currently home to a number of grey wolf (*Canis lupus*) and wolf-like canid populations, including the coyote (*Canis latrans*) and the taxonomically controversial red, Eastern timber and Great Lakes wolves. We explored their population structure and regional gene flow using a dataset of 40 full genome sequences that represent the extant diversity of North American wolves and wolf-like canid populations. This included 15 new genomes (13 North American grey wolves, 1 red wolf and 1 Eastern timber/Great Lakes wolf), ranging from 0.4 to 15x coverage. In addition to providing full genome support for the previously proposed coyote-wolf admixture origin for the taxonomically controversial red, Eastern timber and Great Lakes wolves, the discriminatory power offered by our dataset suggests all North American grey wolves, including the Mexican form, are monophyletic, and thus share a common ancestor to the exclusion of all other wolves. Furthermore, we identify three distinct populations in the high arctic, one being a previously unidentified "Polar wolf" population endemic to Ellesmere Island and Greenland. Genetic diversity analyses reveal particularly high inbreeding and low heterozygosity in these Polar wolves, consistent with long-term isolation from the other North American wolves.

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Summary of available surveillance data on hepatitis C virus infection from eight Arctic countries, 2012 to 2014

We summarised available hepatitis C virus (HCV) surveillance data for 2012–14 from Arctic/sub-Arctic countries/regions. We sent a HCV data collection template by email to public health authorities in all jurisdictions. Population statistics obtained from census sources for each country were used to estimate rates of reported acute and chronic/undifferentiated HCV cases. Seven countries with Arctic regions (Canada, Denmark, Finland, Greenland, Norway, Sweden and the United States, represented by the state of Alaska), including three Canadian territories and one province, as well as 11 Russian subnational Arctic regions, completed the data collection template. Data on acute HCV infection during 2014 was available from three Arctic countries and all Russian Arctic regions (rate range 0/100,000 population in Greenland, as well as Nenets and Chukotka Autonomous Okrugs (Russian subnational Arctic regions) to 3.7/100,000 in the Russian Republic of Komi). The rate of people with chronic/undifferentiated HCV infection in 2014 ranged from 0/100,000 in Greenland to 171.2/100,000 in Alaska. In most countries/regions, the majority of HCV-infected people were male and aged 19–64 years. Differences in surveillance methods preclude direct comparisons of HCV surveillance data between Arctic countries/regions. Our data can inform future efforts to develop standardised approaches to HCV surveillance in the Arctic countries/regions by identifying similarities/differences between the surveillance data collected.

Forfatter: PP Gounder ; Anders Koch; G Provo ; A Lovlie ; JL Ederth ; M Axelsson ; CP Archibald ; B Hanley ; A Mullen ; M Matheson ; D Allison ; H Trykker ; TW Hennessy ; M Kuusi ; V Chulanov ; BJ McMahon **Type:** Article | Artikel **Årstal:** 2018 **Emner:** Viral hepatitis; Surveillance; Prevention and control; Indigenous populations; North America; Northern Europe **Titel på tidsskrift:** Euro Surveillance **Volume på tidsskrift:** 23 **Nummer på tidsskrift:** 40 **DOI nummer:** <https://dx.doi.org/10.2807%2F1560-7917.ES.2018.23.40.1700408>

