Conservation units for anadromous Arctic Char (*Salvelinus alpinus*) in the Canadian Arctic informed by genetic structure, population connectivity and adaptive genomic variation

Abstract

Intraspecific genetic diversity is a crucial aspect of biodiversity conservation as it preserves evolutionary potential and enhances resilience to environmental change. Genomic-informed delineation of Conservation Units (CUs) offers ways of subdividing species into groups based on historical isolation and adaptive differentiation, to develop biologically relevant conservation and management policies. CUs have been defined in many species of harvested anadromous salmonids, but broad scale data remains lacking in the Canadian Arctic, where anadromous Arctic Char (*Salvelinus alpinus*) dominates catches in Indigenous-led subsistence and commercial fisheries. In this study, we use low-coverage whole-genome data from 30 Canadian populations of Arctic Char to define CUs based on population structure and connectivity, as well as adaptive genetic variation. We highlight two main genetic groups, each of which comprises three subgroups, or candidate CUs: the North (above the 67th parallel), including the North Baffin Island, Kitikmeot, and Inuvialuit Settlement Region CUs; and the South (below the 67th parallel), including the South Baffin Island, Ungava Bay, and Hudson Bay CUs. This delimitation is supported by areas of low effective migration between candidate CUs, as well as isolation-by-environment, which suggests adaptive differentiation. Finally, we discuss opportunities and caveats relating to linkage when identifying adaptive genetic variation from whole genome sequencing data through genome scans and Gene-Environment Associations.

Introduction

Given the numerous threats to global biodiversity, there has been a call for conservation at the levels of ecosystems, species, and within-species genetic

diversity (Laikre et al., 2020). Of these three levels, species conservation has gathered much of the attention, suggesting a simple categorization of nature and offering a common metric of biodiversity. In practice, the delimitation and definition of species is rarely straightforward (Mace, 2004; Frankham et al., 2012; Garnett & Christidis, 2017), and speciation proceeds via gradual genomic divergence among isolated populations driven by the combined effects of genetic drift and natural selection in contrasted habitats (Roux et al., 2016). Both these evolutionary forces are subject to fluctuations over long timescales, as populations reconnect in secondary contact zones, or changes in the environment shift selective pressures (Seehausen et al., 2008; Rosenblum et al., 2012). The resulting intraspecific genetic diversity is a key component of biodiversity that warrants protection, as it underpins evolutionary potential and enhances resilience to environmental change and anthropogenic pressures (Forest et al., 2007; Schindler et al., 2010).

Biological systems are inherently complex, and speciation is best understood as a continuous process. Nevertheless, discrete intraspecific classifications remain necessary to inform conservation priorities within limited budgets and to guide the management of harvested species. There exists a vast body of literature on the delineation of conservation units (CU), which generally relies on the identification of historical isolation (leading to genomic divergence) and adaptive differentiation (Waples, 1991; Moritz, 2002; Coates et al., 2018). Among the numerous CU models developed over the years, the Evolutionary Significant Unit (ESU; first proposed in Ryder, 1986) aims to provide a framework for the definition of subspecific groups that represent both unique genetic variation and the historical or ongoing connectivity among populations within a species. Depending on its definition, it can either be based exclusively on genetic characters or incorporate ecological data (Fraser & Bernatchez, 2001). As an additional concept, the Management Unit (MU) can be defined within ESUs as are demographically independent populations identified based on contemporary gene flow and population dynamics rather than deep evolutionary history. This subdivision allows managers to implement local actions, such as

supplementation, restoration, or monitoring, that maintain genetic diversity, reduce inbreeding, buffer against environmental fluctuations, and support the long-term viability of the broader ESU (Moritz, 2002).

The concept of the ESU has been translated into legislation in multiple countries (e.g., the USA 'Endangered Species Act' and the Australian 'Endangered Species Protection Act'). In Canada, the 'Species at Risk Act' applies a similar concept of Designatable Units (DU, Green, 2005), which are considered discrete if there is evidence of limited transmission of heritable traits or markers between them, or if they are separated by a natural disjunction in their distribution. A discrete unit is then considered significant if its evolutionary trajectory dates back long enough to create an evolutionary history not found elsewhere in Canada (e.g. units originating from distinct glacial refugia) or if it possesses unique and verifiable adaptive traits.

Genetic data has been central to work related to CUs, as their delineation often revolves around a two-step process: 1) describing the structure of populations, which is often hierarchical within species, and 2) choosing the level of distinctiveness appropriate for defining units, which implies some degree of subjectivity (Waples, 1995). Cytoplasmic (both mitochondrial and chloroplastic) DNA has long been used to characterize intraspecific lineages (Avise et al., 1987), while microsatellites have contributed to investigating population structure and connectivity (Ellegren, 2004). However, genomic data, i.e. genome-wide datasets produced by genotyping-by-sequencing (GBS, thousands of SNPs) or whole-genome sequencing (WGS, millions of SNPs), have the potential to improve delineation of CUs by quantifying adaptive variation in addition to neutral variation (Funk et al., 2012). This can be done by scanning the genome for loci displaying higher differentiation than expected under neutral evolution, suggesting the imprint of natural selection, or assessing correlations between allele frequencies and biologically relevant environmental variables (hereafter gene-environment associations, GEA, Rellstab et al., 2015; Dauphin et al., 2023).

Anadromous salmonids (i.e., those migrating from marine to freshwater habitats to spawn) represent a diverse group of fishes with significant economic and cultural importance worldwide. Their strong homing behavior (i.e., returning to natal sites for spawning, thus limiting gene flow among populations) plays a crucial role in shaping their population structure and is a factor long recognized as key for their conservation and management (Moulton 1939; Thompson 1959). Many salmonid populations are facing strong harvesting pressures and are actively managed within CUs to ensure sustainability and long-term population persistence. For instance, Atlantic Salmon (*Salmo salar*) along Canada's eastern coast are currently managed within 15 extant DUs (COSEWIC, 2010; Moore et al., 2014). However, further subdivisions into 19 DUs was recently suggested based on genomic data (Lehnert et al., 2023). On the western coast, Pacific Salmons (*Oncorhynchus spp.*) are divided into dozens of CUs per species, with larger watersheds, such as the Fraser River in British Columbia, supporting multiple units (Xuereb et al., 2022; DFO, 2024). Overall, CUs have proven essential for guiding effective management and sustaining salmonid populations across diverse systems.

Northern Canada is home to populations of Arctic Char (*Salvelinus alpinus*), a salmonid whose anadromous form has long been the most harvested fish across Inuit Nunangat (i.e. the homeland of Inuit; Friesen, 2004; Priest & Usher, 2004). Arctic Char fisheries are predominantly small-scale and harvested for subsistence purposes (Roux et al., 2019; Tallman et al., 2019), but collectively amount to a high replacement value, i.e., the estimated cost of substituting the harvested fish with equivalent grocery-bought protein (Brubacher, 2004). While subsistence stocks are locally managed, some regions harbour commercial fisheries that are co-managed between the Indigenous land claim body and federal government (Fisheries and Oceans Canada). Continent-wide genetic variation in Arctic Char has been investigated using mtDNA and microsatellites. These studies suggest that most North American Arctic populations derive from a single High Arctic glacial refugium, the Arctic lineage (Moore et al., 2015), with the exception of Labrador (Salisbury et al., 2019) and

Greenland (Jacobsen et al., 2022), where an additional Atlantic lineage is also present. However, recent whole-genome data revealed that admixture between the Arctic and Atlantic lineage was a prominent feature of Arctic Char genomes in all Canadian populations south of the 67th parallel, redefining the extent of the second contact between lineages (Dallaire et al., 2025). Other recent genomic datasets for the species were focused on spatial scales from local to regional and have been used to investigate questions relating to population structure and connectivity (Moore et al., 2017; Li et al., 2021), morphotype differentiation (Kess et al., 2021), and local adaptation (Madsen et al., 2019; Dallaire et al., 2021; Layton et al., 2021).

In this study, we revisit the whole-genome resequencing dataset introduced in Dallaire et al. (2025), including more than 1,000 anadromous Arctic Char whole-genomes in 30 sampling sites across the Canadian Arctic, to define candidate CUs at a national scale. To inform these units, we 1) characterize in depth the hierarchical genetic structure of populations in relation to administrative regions in the Inuvialuit Settlement Region (ISR, Northwest Territories), Nunavut, and Nunavik (Québec), and 2) identify areas of lower gene flow. Then, we aim to 3) disentangle patterns of i) isolation-by-distance, ii) isolation-by-environment, and iii) isolation-by-colonization (related to post-glacial recolonization) that characterize this structure. Finally, we 4) detect signals of natural selection and explore patterns of population structure driven by putatively adaptive genetic variation using genome scans and Gene-Environment Associations. We discuss those results through the lens of the Designatable Unit framework and explore and discuss the added value of whole-genome data to conservation genomics.

Methodology

Sequencing and SNP calling

We reanalysed sequencing data from 1016 Arctic Char from 30 Canadian populations, published in Dallaire et al. (2025). Briefly, whole-genome sequences were obtained following Therkildsen & Palumbi (2017) on DNA extracted from fin

clips from fish harvested at the mouth of rivers in the Inuvialuit Settlement Region (Northwest Territories), Nunavut, and Nunavik (Québec) between 2007 and 2023 (Fig.1a). As in Dallaire et al. (2025), data were processed following the pipeline described at https://github.com/enormandeau/wgs_sample_preparation: sequences were trimmed and aligned on the ASM291031v2 reference genome (likely from *Salvelinus malma* or a *S. alpinus* x *S. malma* hybrid; Christensen et al., 2021), duplicate reads were removed, indels were realigned and overlapping ends of paired reads were clipped.

Mapped and cleaned reads yielded an individual depth of coverage around 2X, and we estimated Genotype Likelihoods (GL) at polymorphic positions identified in Dallaire et al. (2025). Those positions were distributed on all assembled linkage groups, but SNPs in sex-linked regions identified in Beemelmanns et al. (2024) were removed from all analyses. The SNP list was filtered for paralogs and other deviations from expected patterns due to transposable elements and ancestral autoploidization in salmonids, using *ngsparalog* (Linderoth, 2018) following Dallaire et al. (2023). We kept SNPs with global minor allele frequency above 1% and with a minimal depth of coverage of 1X in at least 75% of individuals. We used *ngsLD* (Fox et al., 2019) to estimate linkage between SNPs within 500 kb using a random subset of half the samples to create a LD-pruned dataset by iteratively removing SNPs with the graph method until no SNP pairs within 200kb had an r^2 above 0.1.

Extraction of environmental data

We used the ArcGIS software v10.4 (ESRI, 2011) to extract environmental data. Marine variables represent sea-surface values for factors of potential biological importance for Arctic Char available in the BIO-Oracle v3.0 dataset (Assis et al., 2024) and were averaged in a 20 km radius around each sampled river mouth and within 5 km from the coast. This standardized approach was used to characterize the local coastal environment in accordance with current knowledge of Arctic Char marine habitat use in Arctic Canada (Spares et al., 2015; Moore et al., 2016; Harris et al., 2020). We selected annual coastal averages for five

marine variables (temperature, salinity, primary productivity, dissolved O_2, and ice cover) as they represented good predictors for values in summer, when Arctic Char occupies coastal habitats.

Freshwater variables were extracted from the RiverATLAS dataset by selecting the linear segment closest to the mouth of each sampled river, as these segments include values averaged over the entire upstream watershed. We initially considered seven variables: % of the watershed covered by lake or tree, average slope, sand fraction in the soil, and annual averages of discharge, air temperature, and precipitation. These variables are linked to both migratory challenges (e.g., slope, discharge, temperature) and spawning habitats (e.g., lake cover, sand in soil), two factors that may play an important role in local adaptation of Arctic Char (Moore et al., 2017; Dubos et al., 2023). Precipitation was later excluded because it was highly correlated with air temperature (Pearson r = 0.84), resulting in a final set of 11 environmental predictors (Table S1, Table S2, Fig. S1).

Population structure

When describing population structure in the dataset, we used a priori administrative regions to categorize sampling sites across the study area, namely the Inuvialuit Settlement Region (Northwest Territories); Kitikmeot, Kivalliq and Baffin (Nunavut); and Nunavik (Québec). We used the term Baffin instead of Qikiqtaaluk, as this administrative region also includes the High Arctic Archipelago, which was not sampled as part of this study. Note that anadromous populations of Arctic Char are less common at those latitudes where resident and landlocked Arctic Char dominate (Reist et al., 2013). North and South Baffin were further split around the 67th parallel. Note that the Pamiurluk Lake sampling site (PAM) was grouped within the Kivalliq region, despite technically being in Qikiqtaaluk, as this fish population is traditionally harvested by the people of Naujaat, a community in the Kivalliq region.

The overall distribution of genetic variation and population structure was initially evaluated through a principal component analysis (PCA) conducted on the LD-pruned dataset using PCAngsd 1.10 (Meisner & Albrechtsen, 2018). Subsequently, we examined the hierarchical population structure by applying NGSadmix (Skotte et al., 2013), estimating individual admixture proportions while varying the number of ancestral populations (*K*) from 1 to 30 (i.e. the number of sampling sites). For each value of *K*, we repeated the analysis over 50 independent runs, then used the CLUMPAK algorithm (Kopelman et al., 2015) to cluster runs with a similarity score over a fixed threshold of 0.85. We interpreted the cluster with the most runs (hereafter the major mode) for each value of K. Ancestry proportions were averaged over runs in the major mode and visualized using a stacked bar plot. To compare the fit of the model at different values of K, we 1) compared the proportion of runs in the major mode and 2) computed the ΔK (Evanno et al., 2005) by dividing the absolute value of the second order rate of change in the mean likelihood by the standard deviation of likelihoods for all runs of a given *K*.

Next, we used ngsDist (Vieira et al., 2016) on the unpruned dataset to compute genetic distances between every individual pair. We chose the uncorrected p-distance, i.e. the proportion of nucleotide sites (polymorphic in the dataset) at which they differ. SNPs with missing data in either individual of the pair were ignored. To express p-distances as the proportion of genome-wide differences between two individuals, we multiplied them by the ratio of the number of SNPs (4,044,588) to the total number of sites in the reference genome (1,516,033,356). We then built an unrooted neighbour-joining tree on the distance matrix using the BIONJ algorithm (Gascuel, 1997) in the ape v5.7 R package (Paradis & Schliep, 2019). We visualized the tree with the R packages *ggtree* (Yu et al., 2017) and *ggtreeExtra* (Xu et al., 2021), while collapsing monophyletic groups of individuals from a single sampling site, then aligned individual ancestry proportions estimated with ngsAdmix for K = 2, 7, and 30 genetic clusters with the corresponding tree tips. These values of K were chosen as they represented Arctic vs Atlantic ancestry as detailed in Dallaire et al. (2025)

(K = 2), roughly corresponded to *a priori* geographic regions (K = 7), or matched the number of sampling sites (K =30).

Connectivity, Isolation-by-distance, Isolation-by-environment

Dallaire et al. (2025) revealed strong patterns of isolation-by-distance that were distinct in groups of populations above (hereafter northern) and below (southern) the 67th parallel, with southern population pairs being more genetically distant at equal marine distances. Here, we revisited the relationship between genetic distance, as measured by the pairwise fixation index (F_{ST}) and allele frequency difference (AFD), and either marine, environmental, and ancestry distance to investigate the interplay between i) isolation-by-distance (IBD), ii) isolation-by-environment (IBE), and iii) isolation-by-colonisation (IBC; defined as the proportion of genetic distance explained by the difference in genetic background contributions from two glacial lineages that recolonized the Canadian Arctic), respectively.

F_{ST}, AFD, and marine distances were estimated as in Dallaire et al. (2025). Environmental distance between sites was calculated by performing a PCA on all environmental variables and measuring the Euclidian distance between population coordinates on the first seven axes, which encompassed 92.2% of the variation. Ancestry distance was measured as the difference in the average ancestry proportion for a sampling site in the NGSadmix analysis for K = 2, to represent a proxy of the proportion of ancestry from the Arctic and Atlantic lineages.

The correlations between each measure of genetic distance and either marine, environmental, or ancestry distances was evaluated separately using simple Mantel tests as implemented in the R package *vegan* (Oksanen et al., 2022). We then used partial Mantel tests to test whether each correlation was robust to controlling for either other type of distance (e.g. AFD ~ marine distance while controlling for ancestry distance, then for environmental distance, etc.). To control for the effect of two distance matrices conjointly, we first built a linear

model between the genetic distance and the admixture model while accounting for the category of the population pair (i.e. two northern populations, two southern populations, or one northern and one southern population), and used the residuals as a substitute for genetic distance in a partial Mantel test with marine or environmental distance. To further investigate which component of the environment could contribute to isolation-by-environment, we repeated partial Mantel tests using the difference in the value for each environmental variable as environmental distance. We compared Mantel r statistics and their associated p-values estimated from 999 permutations for tests including all populations pairs, then only northern or southern pairs. We excluded GEO from all Mantel tests due to its high genetic distance from other sites. These diverged from all patterns of isolation, likely due to heavy introgression from the Atlantic lineage in genomes from this population (Dallaire et al., 2025).

To characterize geographic areas of limited connectivity, we conducted an Estimated Effective Migration Surfaces (EEMS) analysis (Petkova et al., 2016) using FEEMS (Marcus et al., 2021). Briefly, the effective migration rate is comparable to the concept of effective population size (N_e), in that it represents the rate of migration at which an idealized stepping stone model at equilibrium would produce genetic dissimilarities equivalent to values observed in the data. In FEEMS, we modified the python scripts *spatial_graph* and *run_cv* to skip the allele frequency estimation from genotypes and used the population MAF estimated in ANGSD as input since we did not call individual genotypes. We used the R package *dggridR* (Barnes & Sahr, 2024) to create a triangular grid at resolution 7 (~ 55km between cells) over the study area. To select the value for the smoothing parameter λ, we followed the leave-one-out cross-validation method suggested in Marcus et al. (2021): we repeated the EEMS analysis after removing one population at a time with 20 values of λ varying from 0.1 to 10,000 and compared the migration surfaces for λ displaying local minima in cross-validation errors.

Loci under putative selection and gene-environment association

SNPs with a global minor allele frequency over 0.05 were investigated for signatures of selection using *pcadapt* (Luu et al., 2017) and the XtX statistic in *Baypass v2.1* (Gautier, 2015), and for Gene-Environment Associations (GEA) using the Bayes Factor statistic in *Baypass* and redundancy analyses (RDA).

We applied the *pcadapt* procedure in PCAngsd, which allows for individual genotype likelihoods as input. Briefly, *pcadapt* scans the genome using significant components of a PCA, here the first 15 PCs, as selected by PCAngsd. The multi-dimensional z-scores in output were converted to Mahalanobis distances using the orthogonalized Gnanadesikan–Kettenring method, corrected for genomic inflation following recommendations (Luu et al., 2017), then converted into p-values via a χ^2 test with 14 degrees of freedom. To build the input for *Baypass*, we converted population allele frequencies estimated in ANGSD (-domaf 1) to allele counts by multiplying (then rounding) the frequencies by the SNP-specific number of individuals to account for missing data. We first sampled 10,000 random SNPs to compute a covariance matrix with the core model in *Baypass*, then used this matrix in the standard covariate model with every SNP (maf > 0.05) and all 11 environmental variables. We ran five replicate analyses and used the median XtX as an index of selection and the median Bayes Factor (BF) as a measure of the association between the allele frequency of a SNP and each environmental variable.

As a second method to detect Gene-Environment Associations, we used redundancy analyses, which are constrained ordinations that assess the relationship between a multivariate response variable (here allele frequencies in sampling sites) and explanatory variables (the environmental factors). To account for collinearity between variables, we ran a first RDA with all variables in the R package *vegan*, then iteratively removed the variable with the highest Variance Inflation Factor (VIF) until all VIF were under 10 (we only removed Dissolved O_2 this way). We then ran a backward selection of model with the function *ordistep*, and iteratively pruned variables from the model until all

variables contribute to the model according to an ANOVA-like permutation test ($p < 0.1$). Finally, we assessed the significance of RDA axes through an ANOVA-like permutation test on the selected model and kept axes with $p < 0.05$.

Since the ancestry proportion from the Arctic and Atlantic lineages (as estimated by the NGSadmix analysis for K = 2; see also Dallaire et al. 2025) was a major determinant of the genetic variation in our study area and strongly correlated with some of the environmental variables, we also conducted a partial RDA (pRDA) using the average ancestry proportion as a covariate. We followed the same variable and axes selection steps as described above. We use the *varpart* function in the R package *vegan* to estimate the portions of the genetic variation that was explained conjunctly and distinctively by environment and lineage ancestry in the final pRDA.

Every selection scan and GEA methods described above produced summary statistics by SNP that were aggregated by gene using a windowed Z analysis (WZA; Booker et al., 2024). WZA combines the information of multiple SNPs linked in a genomic region to assess if this region is in GEA or displays signs of selection. Since linkage varies across the genome, and in the absence of a robust recombination map, we opted to use genes annotated on the reference genome instead of windows of an arbitrarily defined length. We ran separate WZAs by using as summary statistics i) the *p*-values from pcadapt, ii) the XtX and iii) BF (for each environmental variable) from Baypass, and iv) the squared loading on each significant axis of the RDA and pRDA. Briefly, those statistics were ranked, ordered and converted to empirical p-values, then to z-scores that were combined for SNPs inside each gene (i.e. between the start and end position based on the annotated reference genome) to compute a *p*-value corrected for the number of SNPs in the gene (Booker et al., 2024).

For each WZA, we listed top candidate genes (i.e. the genes with p-values < 0.001), thus showing the strongest signal of selection or association with the environment. To explore the relationship between our top candidate genes and

regions of low recombination as inferred by local PCA in Dallaire et al. (2025), we conducted a series of χ^2 tests to check if top candidates identified by each analysis were more likely than by chance to be found in long putative local ancestry tracts, then in other local PCA outlier regions not correlated with the admixture gradient between the Arctic and Atlantic (as listed in Table S3).

For each selection scan or GEA analysis, we performed a gene ontology (GO) enrichment test with goatools 1.2.3 (Klopfenstein et al., 2018) on all top candidate genes, and then on genes identified as top candidates by more than one method. We used a custom annotation table, obtained by mapping Arctic Char transcripts (accession GCF_002910315.2; ASM291031v2) against the Swissprot 1.2 database (UniProt Consortium, 2024) with blast 2.12.0 (Camacho et al., 2009), according to the pipeline GAWN v0.3.5 (https://github.com/enormandeau/gawn). As we lacked power to detect selection in WZA for genes with few SNPs, only genes on which we considered at least 5 SNPs were kept as the background set. Terms for biological processes (BP) with corrected p-values (Benjamini & Hochberg, 1995) under 0.05 were considered significantly enriched.

Results

Genetic population structure

Out of the 5.98 million polymorphic SNPs in Canadian and Greenlandic Arctic Char populations identified in Dallaire et al. (2025), 4.04 million passed the coverage filters and displayed MAF above 0.01 in Canadian populations alone. Subsequent LD-pruning reduced this number to 277,570 SNPs. To facilitate knowledge transfer to local policy makers, populations were first categorized *a priori* according to administrative regions of Inuit Nunangat: the Inuvialuit Settlement Region (ISR, Northwest Territories); Nunavik (Québec); and Kitikmeot, Kivalliq, and Baffin (Nunavut) (Fig. 1a, circles and labels).

A principal component analysis revealed a population structure consistent with geography on the first two axes (comprising 32.9% of the variation; Fig. 1b).

However, most sites in ISR and Kitikmeot were densely clustered on these axes and while HRN and KJA were distinct on the fourth axis (3.6%), the rest of north-western sites remained indistinguishable near the middle of the plot for the first 10 axes (totaling 55.8% of the variation; Fig. S2). A neighbour-joining tree based on p-distances displayed a similar geographic pattern, with north-western individuals on shorter branches than south-eastern individuals (Fig. 1c). Many sampling sites clustered into exclusive groups, with the notable exception of closely located pairs of sites: EKA and HAL (Kitikmeot; 39 km, F_{ST} = 0.010, Table S4), AKL and CRB (Kivalliq; 64 km, F_{ST} = 0.011), and SAT and KUL (North Baffin; 65 km, F_{ST} = 0.014). Interestingly, PAY and CHR were only marginally further apart (69 km), but exhibited much stronger structure (F_{ST} = 0.078). Finally, some sampling sites displayed considerable substructure, as their clade was split into subgroups (e.g., SVG, KUL-SAT) or had a few individuals grouping into smaller distant clades (e.g., NTS, KGJ).

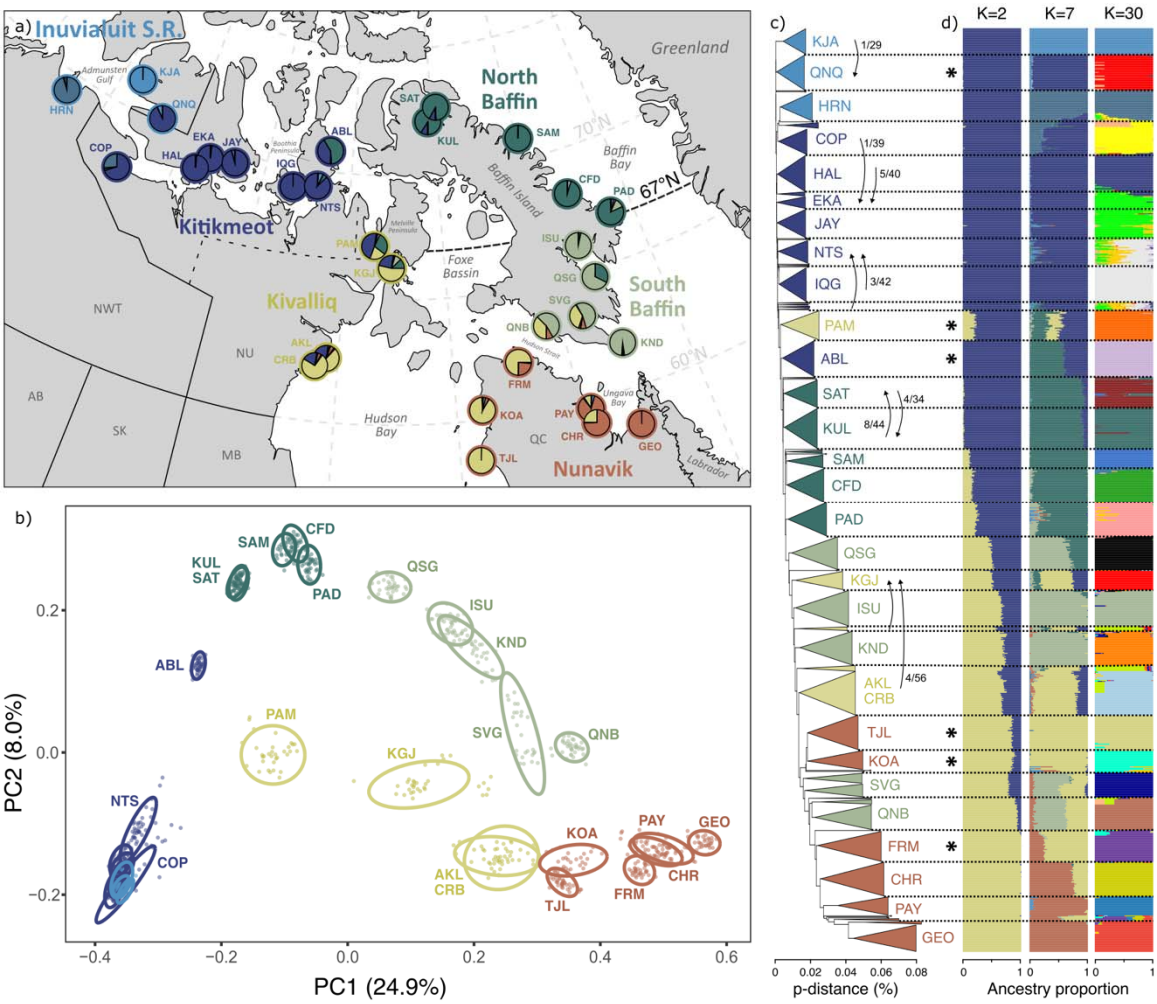

Figure 1: a) Arctic Char sampling sites with colored labels showing their administrative region of origin. Pie charts show the site average in ancestry proportion for K = 7 genetic clusters, as detailed in panel d). b) The first two axes of a principal component analysis for 277,570 independent SNPs. *95% confidence interval ellipses are drawn around each site and the percentage of variance explained by each axis is noted in parentheses. c) Unrooted neighbor-joining tree built on genome-wide uncorrected p-distances between Arctic Char samples. Monophyletic clades where at least 80% of samples originate from a single site (or a pair of neighbouring sites) are collapsed as triangles and truncated at the minimal length. Sampling sites are delimited by dashed lines and arrows note the origin of samples in smaller clades. Arrows accompanied by fractions denote clades where a portion of individuals were captured at a different site. d) Individual proportion of ancestry for K = 2, 7, and 30 genetics clusters, CLUMPAK-averaged over replicate runs in the major mode (out of 50 runs). Individuals are aligned to their position in the tree in c). Note that this figure reuses the same color palette for two codes: administrative regions in panel a) (labels, circles), b), and c); and their most concordant genetic cluster (K = 7) in panel a) (pie charts) and d). Discordance between administration regions and genetic clusters are noted by an asterisk. Additional colors for the K = 30 plot were assigned randomly.*

The *NGSadmix* analysis of ancestry proportions with *K* ranging from 2 to 30 ancestral populations revealed a highly hierarchical structure (Fig.1d, Fig. S3, Fig. S4). At K = 2, eastern Nunavik and northern sites displayed pure ancestry for different groups, and sites in between followed a cline in admixture closely matching the pattern attributed to Arctic vs. Atlantic lineage ancestry in Dallaire et al. (2025). At K = 30, the analysis discriminated most sampling sites, in line with clades identified in the neighbour-joining tree. Interestingly, K = 7 groups produced a structure parallel to geographic regions defined *a priori* (Fig. 1a, pie charts), with a few key discordances. For example, PAM clustered more closely with Kitikmeot than Kivalliq populations, and ABL aligned with North Baffin rather than Kitikmeot. Most notably, at this level of structure, populations along Hudson Bay and Ungava Bay clustered into different genetic groups, rather than aligning with the Kivalliq and Nunavik regions defined *a priori*. We hereafter refer to groups of sampling sites sharing a dominant genetic cluster at K = 7 as our proposed CUs, with the exception of HRN and KJA who were grouped into the Inuvialuit Settlement Region CUs, as discussed later.

Connectivity and isolation

Pairwise F_{ST} ranged from 0.011 (HAL-EKA) to 0.407 (IQG-GEO), while average allele frequency difference (AFD) in SNPs with MAF > 0.01 ranged from 0.033 (HAL-EKA) to 0.231 (HRN-GEO) (Table S4). The strongest predictor of genetic distance was lineage ancestry difference, with Mantel correlations (r) of 0.92 for F_{ST} and 0.90 for AFD (Fig.2a, Table S5). In comparison, marine geographical distance showed lower correlations (r = 0.65 for F_{ST}, 0.58 for AFD), and environmental distance (summarized by PCA of 13 factors) had even weaker, but still significant ($p < 0.01$), correlations (r = 0.49 for F_{ST}, 0.51 for AFD) (Table S5. At equal ancestry, marine, or environmental distances, pairs of populations from the southern group were more genetically distant than northern pairs, and the George River (GEO) was strikingly more distant from all other populations than other southern sites.

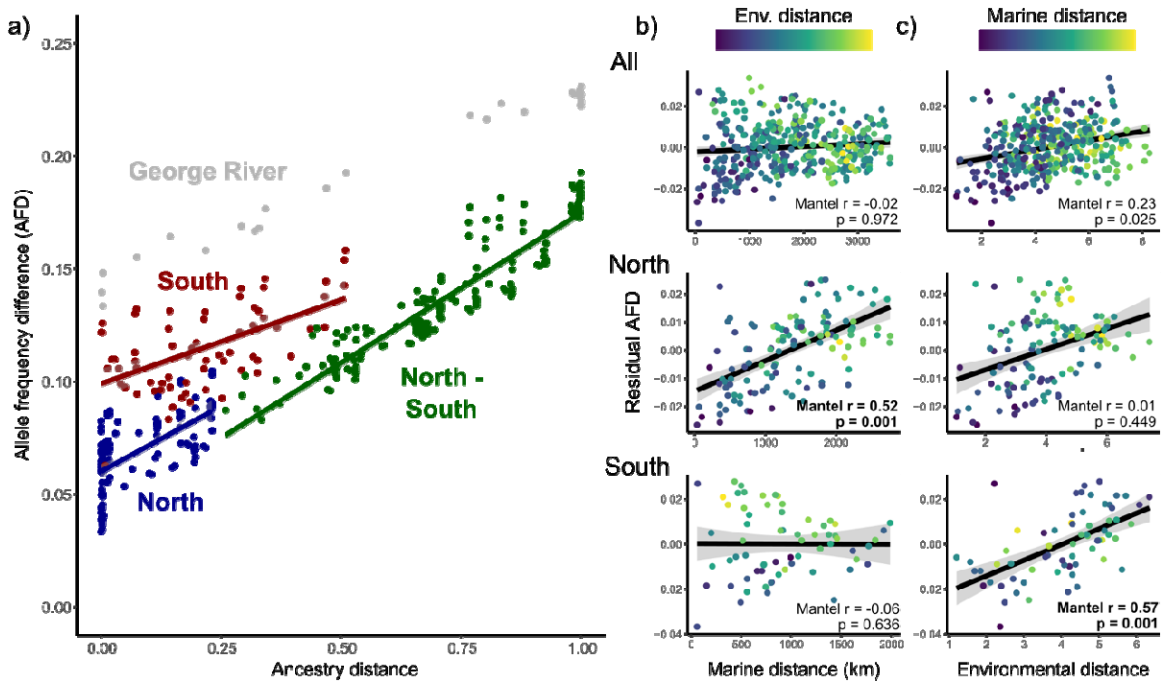

Figure 2: *a) Linear regression of allele frequency differences (AFD) between a pair of populations and their ancestry distance (i.e. the difference in their average ancestry proportion, NGSadmix, K=2). Pairs were categorized depending on if they include two northern (blue), two southern (red), or one northern and one southern population (green). Pairs including the George River (GEO) are displayed in grey and excluded from panel b-c. Partial Mantel tests were conducted between the residuals of the model from panel a and either b) marine or c) environmental distance for all populations (top), or either northern (middle) or southern ones (below). The remaining distance, i.e. b) environmental or c) marine, was used as covariable and is displayed in color (yellow to blue). Mantel r statistics are noted in bold when the associated p-value was under 0.01.*

Partial Mantel tests indicated no signs of isolation-by-distance in the global dataset when correcting for both ancestry and environmental distance (Fig.2b, r = -0.02, p = 0.972), but signs of weak isolation-by-environment when correcting for ancestry and marine distance (Fig. 2c, r = 0.23, p = 0.025). When repeating these analyses exclusively for northern or southern pairs, we revealed apparent isolation-by-distance in the North (Fig. 2b, r = 0.52, p < 0.001), and isolation-by-environment in the South (Fig. 2c, r = 0.57, p < 0.001). Partial Mantel tests with specific environmental variables indicated that difference in discharge (r = 0.33) and primary productivity (r = 0.46) explained a significant portion (p < 0.01) of the variation in study-wide AFD, while differences in primary productivity (r = 0.47)

and salinity (r = 0.42) explained a significant portion of the variation in AFD in southern pairs of sites (Table S5, Fig. S5).

We estimated effective migration rates across the study area from allele frequencies. The resulting migration map at different values of the smoothing parameter lambda mainly highlights an area of low effective migration between the previously described northern and southern regions (Fig. 3, Fig. S6). Smaller areas of low effective migration are observed over the Boothia Peninsula (between NTS and ABL), Amundsen Gulf (between HRN, KJA), Hudson Strait (between QNB and FRM), and inland Nunavik (between Hudson Bay and Ungava Bay). Sampling sites within CUs were generally connected by areas of effective migration rates higher than 1.

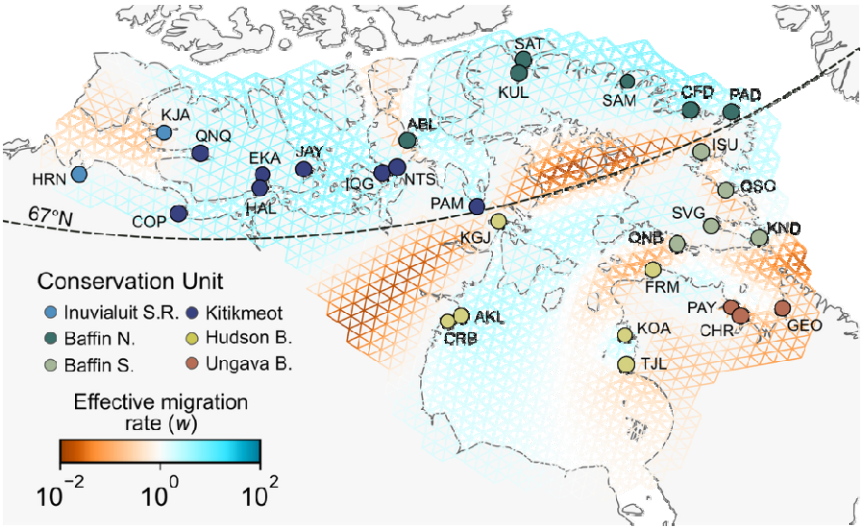

Figure 3: *Edge-specific effective migration rates (w) estimated from sampling allele frequencies in FEEMS with a smoothing parameter λ = 21.5. Sampling sites were repositioned to the nearest node on a triangular grid (cell spacing ≈ 55 km) and colored with the proposed conservation unit, following the most dominant genetic cluster in an NGSadmix analysis (K = 7), except for Inuvialuit S. R. (see Discussion for details).*

Selection scan and Gene-environment association

We investigated 2.6 million SNPs with MAF over 0.05 for signatures of selection, via pcadapt and the XtX statistic in Baypass (details below); or their association with environmental variables, with redundancy analyses without (RDA) and with

(pRDA) correction for lineage ancestry, and the Bayes Factor statistic in Baypass.

A global RDA with all 11 selected environmental factors and Arctic-Atlantic lineage ancestry (as estimated by the average ancestry proportion inferred with NGSadmix at K=2) explained 62.4% of the variation in MAF between sampling sites (Fig. 4a). Environmental factors explained 53.3% of the variation, but a large part (38.4%) was conjointly explained by lineage ancestry, as further explored by the following RDA and pRDA.

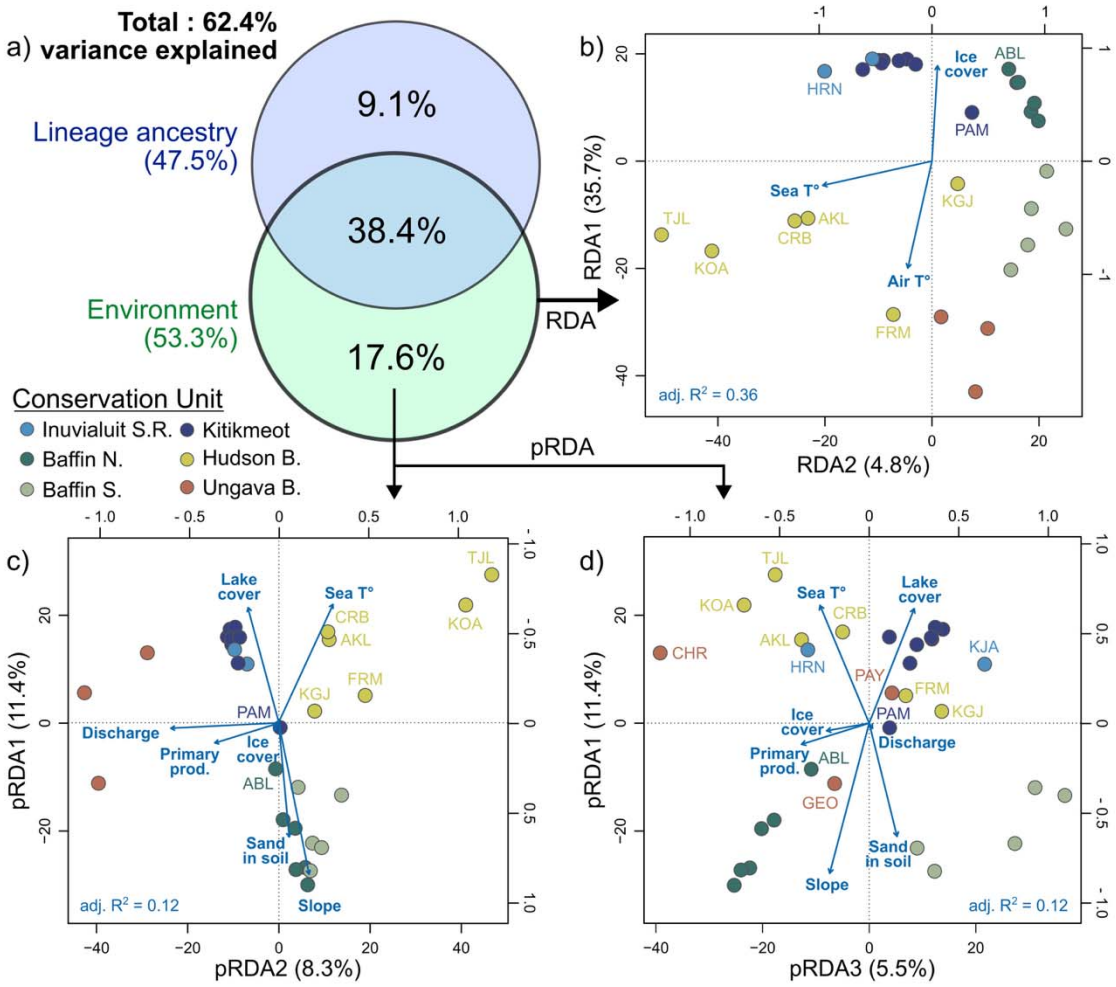

Figure 4: *a) Proportion of the variation in allele frequency explained independently and conjointly by a set of 11 environmental variables and glacial lineage ancestry, as estimated by NGSadmix (K = 2). Biplots of b) a redundancy analysis (RDA, 2 significant axes) and c-d) a partial RDA accounting for the variation in ancestry (pRDA, 3 significant*

axes). Sampling sites are represented by points color-coded by their proposed conservation unit, and vectors represent contributing environmental predictors (retained after model selection) according to the scales on top and right axes.

After backward variable selection with ordistep, the first two axes of the RDA (adjusted R^2 = 0.36) were significant ($p < 0.05$) and were largely correlated with 1) air temperature and ice cover; and 2) sea surface temperature (Fig. 4b). The first three axes of the pRDA (adjusted R^2 = 0.12) were significant and were correlated with 1) sea-surface temperature, lake cover, fraction of sand in soil, and slope; 2) discharge and primary productivity; and 3) primary productivity and ice cover (Fig 4c-d). RDA1 was highly correlated with latitude and lineage ancestry, while RDA2 and pRDA1 discriminated Baffin Island sites from the rest of the study area. Both RDA2 and pRDA2 also highlighted the genetic and environmental distinction between western (Hudson Bay: TJL, KOA) and eastern (Ungava Bay: PAY, CHR, GEO) Nunavik.

With a windowed Z analysis (WZA), we combined SNP-specific statistics from the 5 methods (a total of 18 tests: pcadapt, XtX, 2 RDA axes, 3 pRDA axes, and 11 univariate tests for the BF statistics in Baypass) for 21,379 genes (with at least 5 SNPs) to provide rank-ordered support for selection or GEA, in the form of empirical p-values (Fig. 5a). The genome scan methods (pcadapt and XtX) identified respectively 151 and 188 top candidate genes ($p < 0.001$), with significant overlap (81, or 31.2% of genes in common, Fig. 5b). The GEA methods (BF, RDA, and pRDA) identified 2,079, 381, and 544 top genes. BF had notable overlap with the other methods: 164 (7.1%) of top genes were in common with the RDA and 250 (10.5%) with the pRDA (Fig. 5b). The RDA and pRDA had a similar level of overlap, with 57 top genes in common (6.6%). Top candidate genes from the XtX, pcadapt method or associated to pRDA1 or slope had more chance to be found in putative local ancestry tracts identified in Dallaire et al. (2025), while other local PCA outlier regions were enriched in pcadapt, RDA2, pRDA1, Lake cover, and Sea T° top candidate genes (χ^2 test, adjusted $p < 0.05$; Table S6).

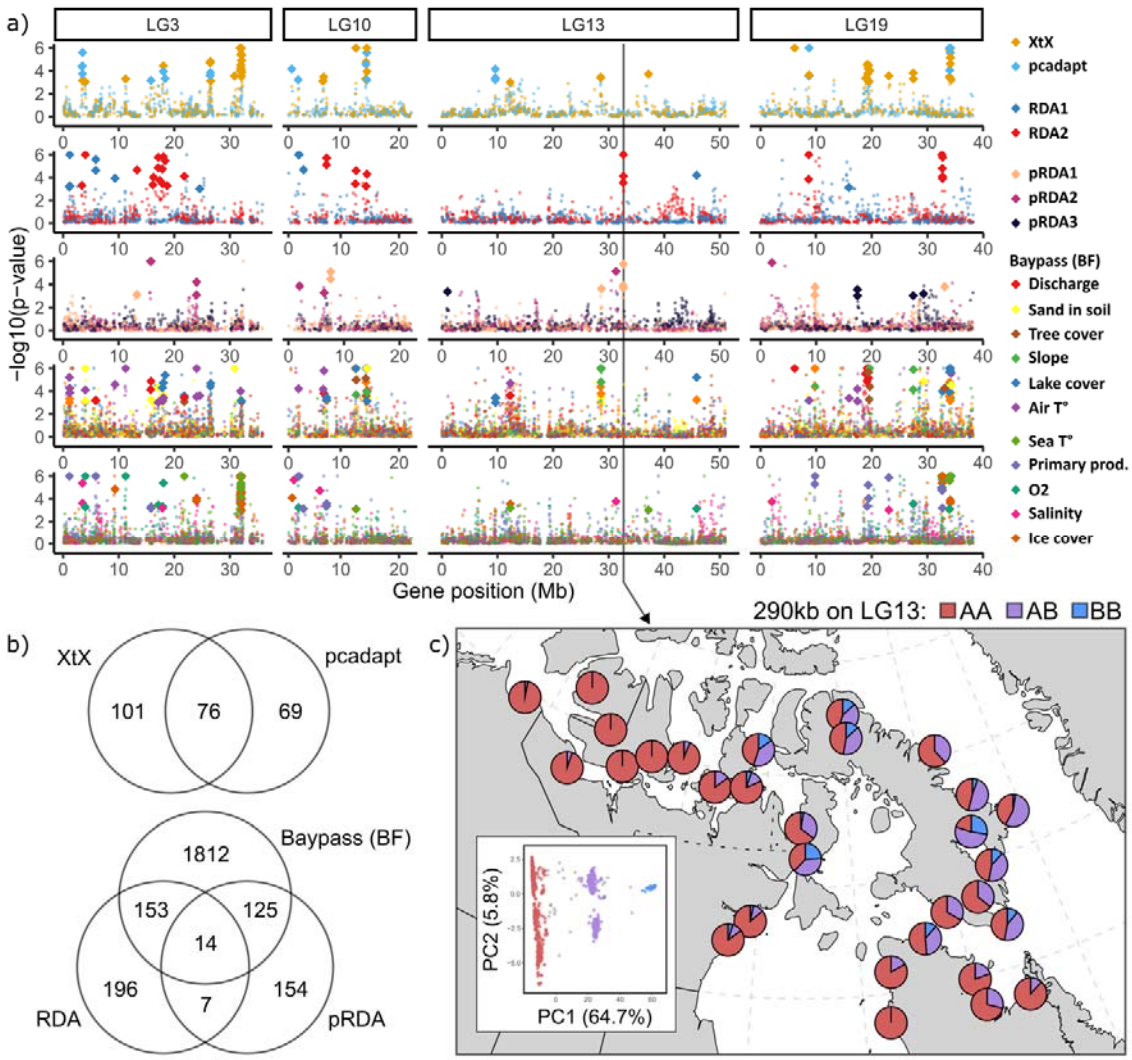

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Figure 5: *a) Support for selection scans or gene-environment associations on genes with at least 10 SNPs on 4 linkage groups, in 5 panels regrouping methods: 1) XtX (Baypass) or pcadapt; 2) redundancy analysis axes (RDA); 3) partial RDA axes; and Bayes Factors (BF, Baypass) for 4) freshwater and 5) marine variables. Support at the gene level (empirical p-values) was derived from combined per-SNP summary statistics in a windowed Z analysis (WZA). Top candidate genes (p < 0.001) for more than one type of test were highlighted with bigger diamonds than the other genes (small dots). b) Venn diagrams presenting the number of top candidate genes (p < 0.001) for selection (top) or gene environment association (bottom) and the overlap in genes between methods. c) Karyotype frequencies per sampling site for a 290kb-long putative inversion on LG13, as inferred by local PCA in Dallaire et al. (2025). The genomic position of the putative inversion is noted by an arrow in panel a.*

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The higher number of top genes identified by the BF method is linked to the univariate nature of the method, as top-ranking candidate genes were separately identified based on their correlation with each of the 11 environmental variables. Individual variables had on average 262.1 (sd = 14.7) associated top genes (empirical $p < 0.001$ in the WZA). Out of 2,079 unique BF top genes, 571 (27.4%) were associated with more than one variable (404 with two variables, 120 with three, 47 with four or more). Salinity and dissolved O_2 (55 top genes in common), followed by lake cover and slope (19 genes), were the most frequent pairs.

Across all genome scans and GEA methods, 549 out of 2,634 unique top candidate genes (20.8 %) were identified by more than one method (Table S7, Fig. S7). We tested for enrichment in gene ontology (GO) terms in lists of outlier genes from each individual test, as well as the list of genes that were outliers according to at least two methods and identified 89 unique GO terms with a p-value for enrichment under 0.001 and associated with at least three top candidate genes (Table S8). However, after correction for multiple testing, no GO terms presented corrected p-values under 0.1.

Discussion

In this study, we aimed to define conservation units for anadromous populations of Arctic Char across its continuous distribution in the Inuvialuit Settlement Region, Nunavut, and Nunavik in Arctic Canada. Through analysis of population structure and connectivity, we highlight two major population groupings, respectively above and below the 67th parallel, which we interpret as having distinct evolutionary trajectories and reduced gene flow. These northern and southern groups were further subdivided in six candidate CUs (see Fig. 3) based on genetic similarity and connectivity. While we observed interconnected patterns of isolation-by-distance and isolation-by-environment across the landscape, glacial lineage ancestry was the strongest predictor of genetic distance among populations. Using genome scans and GEA, we detected a polygenic and

complex signal of selection in the face of multiple selective pressures, highlighting putatively adaptive variation between the six candidate CUs.

Hierarchical population structure informs conservation units

As a first step toward delimiting conservation units for anadromous Arctic Char, we used a combination of common methods to assess the genetic population structure of our 30 sampling sites. This approach revealed a complex but geographically coherent and hierarchical picture of genetic structure.

At the broadest level, visible in the PCA (PC1) and NGSadmix (K = 2) results, the system is defined by an admixture cline from the Arctic lineage in the northwest to the Atlantic lineage in the southeast, as explored in detail in Dallaire et al. (2025). According to mitochondrial data, the divergence time between those lineages could reach up to 400,000 years, predating many glacial cycles (Jacobsen et al., 2022). Regardless of whether admixture occurred during previous interglacial periods, a prolonged phase of allopatry allowed these lineages to diverge significantly, which explains why much of the genetic variation observed in our current dataset reflects this secondary contact. This pattern provides an initial framework for delineating conservation units, as it reveals two distinct evolutionary trajectories: Northern sites are dominated by the Arctic lineage, while Southern sites exhibit varying degrees of admixture between the Arctic and Atlantic lineages. The distinctiveness between these two population segments is also supported by a low effective migration surface between the Kitikmeot and Kivalliq region, as well as Northern and Southern Baffin Island. Although the Northern and Southern populations do not represent entirely pure lineages, we argue that they should be managed as separate broad-scale conservation units. The persistence of this historical signal in contemporary patterns of variation suggests that secondary contact has not erased the imprint of prolonged allopatry. This dominance of ancient divergence over more recent demographic processes is particularly striking in the Arctic, where deglaciation occurred only a few thousand years ago (Dalton et al., 2020), and resembles findings in other post-glacial populations of fishes such as

salmonids (Lehnert et al., 2019) and sticklebacks (Kirch et al., 2021), where deep lineage histories continue to structure modern diversity.

However, our analysis of structure revealed additional hierarchical levels of population structure within the North and South groups, where most individuals showed pure ancestry to a genetic cluster specific to its sampling site. While the ΔK summary statistic suggested 2 groups, studies have shown that this statistic is strongly biased toward K = 2 (Janes et al., 2017). In our study, this is not surprising given the overwhelming signal of lineage ancestry that this level of structure represents. Considering that ΔK was stable from K = 4 to 30 and that significant structure between rivers is expected according to the philopatric nature of Arctic Char reproductive migrations (Gyselman, 1994; Moore et al., 2013; Dallaire et al., 2021), we argue that all 30 clusters identified by NGSadmix could represent populations with some degree of demographic independence. These results highlight the strong hierarchical nature of genetic structure in Arctic Char, as observed in other anadromous salmonids (e.g. Beacham et al., 2004; Habicht et al., 2007; Dionne et al., 2008; Gilbert-Horvath et al., 2016; Östergren et al., 2021). Importantly, this fine-scale, river-specific structure aligns with current fisheries management practices, which often implement river-specific quotas and management measures to reflect the biological reality of Arctic Char populations.

Our sampling strategy focused on broad coverage across the Canadian range of anadromous Arctic Char rather than fine-scale resolution. As such, the six candidate CUs proposed here each cover coastal areas ranging for hundreds to thousands of km, which is much larger than current CUs in other salmonids in southern Canada (e.g., Xuereb et al., 2022; Lehnert et al., 2023). However, our analyses still uncovered patterns that may hold significance for local management. For example, we identified evidence of straying between most pairs of rivers inside 100 km from each other, and in one instance, up to 400 km (one fish sampled at EKA was genetically closer to fish in COP). Despite their philopatric behavior, Arctic Chars are known to show less fidelity to their natal

site during the upstream migration in non-reproductive years (Gyselman, 1994; Klemetsen et al., 2003; Moore et al., 2013). When migrating strictly for overwintering purposes, fish might select watersheds with easily accessible winter habitats, for example the Ekalluk system in the Kitikmeot Region (EKA; Moore et al., 2017). In the case of AKL and CRB (Kivalliq), fish from either site were indistinguishable using whole-genome data, which suggests either panmixia between the two systems or that sampling at these sites is not targeting individuals during the upstream reproductive migration, but rather a mixed-stock of poorly differentiated source populations. Proper delimitation of MUs in Arctic Char would warrant additional local studies of genetic structure and migration, as was implemented in areas sustaining commercial and subsistence fisheries, such as in Cambridge Bay (Harris, Moore, et al., 2016; Moore et al., 2017), Cumberland Sound (Harris et al., 2014), Paulatuk (Harris, Boguski, et al., 2016), and Ulukhaktok (Lea et al., 2023). Going forward, whole-genome sequencing is likely not the most cost-effective method to tackle such local-scale questions. Alternatively, SNP panels can be developed to assign fish caught in mixed-stock fisheries to their population of origin, which holds promise for the accurate monitoring of fish stocks and the conciliation of commercial and subsistence fishing (Beemelmanns et al., 2025).

We chose K = 7 as an intermediate level of structure that could be used to delimit candidate CUs in Canadian anadromous Arctic Char. This level of structure subdivides our top-level Northern and Southern CUs, described earlier, and creates genetic groupings that conveniently, but somewhat unexpectedly, closely match the administrative regions of the Canadian Arctic (Fig. 1). A notable exception, however, is the union of both the Kivalliq (western) and Nunavik (eastern) coasts of the Hudson Bay in a single cluster (both coasts display signs of common ancestry until K = 17), while the rest of the Nunavik populations, around Ungava Bay, appeared as a distinct unit. Considering that K = 6 and K = 7 discriminated HRN and KJA (Fig. S4), our two westernmost sites, we suggest that these two could be paired to form a sixth CU, until additional sampling is performed in the Inuvialuit Settlement Region.

The choice of a level of genetic structure to define CUs implies subjectivity to some degree (Waples, 1995), as genetic differentiation typically occurs along a continuum rather than in clear-cut divisions. In the case of Arctic Char, many populations at the edge of candidate CUs display admixed ancestry to multiple clusters. However, the borders of the proposed CUs were supported by shifts in the dominant cluster that were concordant with areas of low effective migration in our EEMS analyses, as was for example observed in multiple marine species in Atlantic Canada (Wilcox et al., 2023). In the present study, candidate boundaries included the Boothia Peninsula between the Kitikmeot and the North Baffin CUs, and the Foxe Basin and Hudson Strait between the South Baffin and Hudson Bay/Ungava Bay CUs. While EEMS areas of low effective migration do not necessarily imply physical barriers to gene flow (Petkova et al., 2016), they should coincide with shifts in allele frequency that are relevant for informing conservation actions.

Detecting local adaptation using whole-genome data

We further used our genomic dataset to detect signals of local adaptation in Arctic Char populations to support the delineation of CUs that also reflect patterns of local adaptation to divergent environments (sensu Funk et al., 2012). By using multiple analyses on millions of genetic markers, we obtained an overwhelmingly polygenic signal at the SNP-level, with numerous peaks of differentiation or associations with the environment across all linkage groups. To summarise this amount of noise and account for the high rate of false positives in the detection of adaptation, we 1) opted for a Windowed Z Analysis (WZA) to identify top candidate genes while accounting for linkage, and 2) focused on genes that were top candidates in multiple analyses.

As such, we were interested in the relationship between signals of local adaptation and known genomic regions of low recombination, as these might either be the result of hard selective sweeps or genomic features such as inversions or centromeres (Lotterhos, 2019). Our previous work inferred the position of many long haplotype blocks (i.e. sequences containing many

polymorphisms inherited as a unit), suggesting a very low recombination rate within those segments (Dallaire et al. 2025). The haplotype frequencies of many of those putative haploblocks were heavily correlated with the admixture gradient between the Arctic and Atlantic glacial lineages. This implies that they act as local ancestry tracts and are much more constrained by post-glacial demography than spatial variation in selection, though the two are not mutually exclusive. In the partial RDA, we included each population's average ancestry proportion as a covariate in the model, so that the analysis only tests for associations between genotypes and environment once the effect of lineage admixture has been factored out. Surprisingly, both putative local ancestry tracts and other local PCA outliers (identified in Dallaire et al. 2025) were enriched in top candidates from pRDA1, despite the partial RDA specifically controlling for the effect of Arctic-Atlantic ancestry.

However, RDA2 and pRDA1 identified common top candidates in a region of the LG13 identified as a potential inversion in Dallaire et al. (2025) (Fig 5a,c). This 290 kb region overlaps seven genes, including the insulin-like 5a and a protein regulating mitochondrial genes, hinting at their importance in metabolism or energy production. The alternative karyotype for this putative inversion is present in higher frequencies in both North and South Baffin, which present contrasted habitats compared to the rest of the Canadian Arctic, with fjord-like topography (watersheds with a higher slope and lower lake cover) and colder sea-surface temperatures. It is thus possible that this putative inversion could play a role in adaptation to these environments. Chromosomal inversions suppress recombination and are known to promote co-adaptation of neighbouring genes in the face of gene flow (Dobzhansky & Sturtevant, 1938; Kirkpatrick & Barton, 2006; Wellenreuther et al., 2019). This has previously been documented in rainbow trout (*Onchorhyncus mykiss*, Pearse et al., 2019), Atlantic Cod (*Gadus morhua*, Matschiner et al., 2022), Atlantic Herring (*Clupea harengus*, Jamsandekar et al., 2024), and Atlantic Silverside (*Menidia menidia*, Tigano et al., 2021). Another larger (1.2 Mb) candidate inversion on LG12 was found to be polymorphic in Arctic Char populations from Kitikmeot (Hale et al.,

2021), but we did not find well-supported top candidate genes in this genomic region.

When using multiple genome scans and GEA methods with their respective biases, giving greater weight to markers identified by more than one method can help to reduce false positives (Forester et al., 2018). By doing so, we reduced our list of top candidates from 2,635 to 541 genes widely distributed across the genome. Despite low statistical support for GO enrichment after correction for multiple testing, we identified key gene functions related to lipid homeostasis and catabolic processes, which ranked among the best-supported GO categories across multiple sets of candidate genes. Lipid metabolism plays a critical role in the adaptation to Arctic climates, supporting membrane fluidity in cold-water ectotherms such as fishes (Ernst et al., 2016; Wang et al., 2021) and energy reserves during extreme dietary challenges such as prolonged fasting and hibernation (Olsen et al., 2021). The importance of fatty acid homeostasis in local adaptation was also observed in subarctic Atlantic Salmon populations, where genes regulating lipid metabolism were identified as drivers of adaptation (Lehnert et al., 2023).

In summary, identifying the biological processes and molecular functions involved in polygenic adaptation to multiple selective pressures remains challenging (Pritchard and Di Rienzo 2010; Le Corre and Kremer 2012; Rees et al. 2020). This is particularly true when using indirect inference of selection in the absence of phenotypic data on species with complex life cycles. Here, genome-wide, high-density SNP data provided unmatched resolution in the detection of signals of selection but required considerable data aggregation (e.g., through the WZA, as recently used in plants, Battlay et al., 2023; and *Drosophila*, Nunez et al., 2024) to make the results interpretable. This supported the importance of considering the relation between selection and recombination in our data, as highly linked regions of the genome could either be a consequence of selective sweeps or could have biased the detection of adaptation.

Putatively adaptive variation reinforces candidate CUs

Despite challenges in detecting specific targets for selection, we used the overall putatively adaptive genomic variation to highlight groups of populations that could show local adaptation to similar habitats, thus supporting the candidate Conservation Units described earlier. For example, the distribution of allele frequencies in relation to environmental variation, as described by the pRDA (Fig. 4c-d), emphasizes one of our main findings—that a distinction based on water bodies in the Ungava and Hudson Bay groups was more significant than one based on landmasses (i.e., Nunavik vs. Kivalliq). These waterbodies mainly differed in coastal sea-surface temperature and salinity, and watersheds flowing in them are topographically distinct: Nunavik watersheds are generally less steep and have higher lake cover compared with those in South Baffin, our third recommended Conservation Unit in the South Arctic region.

In the North, environmental and geographical distances between populations were too confounded to support isolation-by-environment, but putatively adaptive genetic variation supported the distinction between the Kivalliq and North Baffin CUs, as well as the inclusion of the Abernathy Lake (ABL) population, east of the Boothia Peninsula, in the North Baffin CU. Similar to our results on genome-wide variation, we observed a weaker shift in allele frequencies associated with the environment between Kitikmeot and Inuvialuit Settlement Region populations, putting into question the distinction between those two candidate CUs. However, following a precautionary approach, we recommend maintaining these population segments as separate CUs, with boundaries that could be refined through additional sampling at the western limit of our study area.

Across our study area, conclusions based on genome-wide, neutral, and putatively adaptive genetic variation were largely consistent, with the adaptive data reinforcing the neutral patterns rather than providing novel insights. While one of the promises of population genomics was to reveal previously undetected adaptive groups that could be considered for conservation (Funk et al., 2012),

there is growing evidence that genome-wide variation effectively predicts adaptive variation in many systems (Chhina et al., 2024). This was observed in other anadromous salmonids like Atlantic Salmon (Moore et al., 2014; Lehnert et al., 2023) and Coho Salmon (Xuereb et al., 2022), and this observation could be influenced by a few key factors. First, polygenic traits are expected to create weak selection signals (as identified in this study) that do not necessarily differ from neutral population structure (Pritchard et al., 2010). In contrast, large-effect loci such as GREB1L in steelhead (anadromous *O. mykiss*) and Chinook Salmon (*O. tshawytscha*), linked to migration timing, and vgll3 in Atlantic Salmon (*Salmo salar*), associated with age at maturity, underlie key phenotypes that are now explicitly considered in conservation and management (Waples et al., 2022).

Second, isolation-by-distance patterns suggest limited dispersal over large geographic scales (Aguillon et al., 2017) and straying is likely more frequent among watersheds sharing environmental characteristics. This could be either because of migratory cues such as water chemistry that differ among regional river systems (Dittman et al., 1996) or because of selection against maladapted migrants (Peterson et al., 2014) at local scales. There is in fact a long-standing hypothesis that homing evolved in anadromous salmonids as it promotes advantageous local adaptations (Quinn, 1993; McDowall, 2001; Keefer & Caudill, 2014). In contrast to the long marine migrations of other anadromous salmonids to offshore feeding areas, Arctic Char feed in coastal waters close to their natal rivers in summer (Dempson & Kristofferson, 1987; Spares et al., 2015; Moore et al., 2016), extending the potential for local adaptation to marine habitats in the species (Dallaire et al., 2021). As both freshwater and marine environments tend to be spatially autocorrelated (Legendre, 1993), it is not surprising that a significant part of the putatively adaptive genetic variation would be concordant with the neutral structure.

In this study, we reanalyzed genomic data from Arctic Char across the Canadian Arctic and provided a detailed assessment of population structure and connectivity. From this analysis, we identified six candidate Conservation Units

(CUs) within two major groups displaying distinct evolutionary trajectories. This framework offers an important baseline for understanding intraspecific diversity at a national level, which can be further refined as additional data become available. Incorporating environmental, ecological, and life-history information alongside genomic insights will be essential for improving the resolution of these units and ensuring their alignment with meaningful biological boundaries. In that regard, Inuit ecological traditional knowledge will be invaluable as it includes detailed and fine-scale observations on distinct traits between population, e.g. size, taste and color, migratory behavior, and phenology.

Ultimately, this refined understanding of Arctic Char population structure can guide resource management strategies, ensuring the protection of locally adapted populations and their associated roles in the ecology of northern freshwater ecosystems, their importance for food security, and their contribution to the development of a sustainable economy in the Canadian Arctic. Future analyses that integrate genomic baselines with monitoring programs, harvest data, and indigenous traditional knowledge could improve the practical implementation of CUs. Such an approach would allow managers to better anticipate shifts in population dynamics, adjust harvest regulations proactively, and strengthen co-management frameworks with northern communities.

Data Archiving Statement

All *Salvelinus alpinus* raw sequencing data analysed in this manuscript is available on Short Read Archive as part of project PRJNA1031558. A bioinformatical pipeline presenting the main lcWGS analyses is available at: https://github.com/xav9536/angsd_pipeline.

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