EXAMINATION OF SAFFRON COD (*ELEGINUS GRACILIS*) POPULATION GENETIC STRUCTURE

By

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Abstract

The Saffron Cod (*Eleginus gracilis*) is an abundant forage fish that inhabits the coastlines of the north Pacific and Arctic oceans. We examined Saffron Cod population genetic structure to provide a reference baseline in anticipation of human and climate-change alterations of the Arctic environment. Nine microsatellites were designed to describe the genetic compositions of and variation among 40 collections of Saffron Cod from four regions (northwestern Alaska, Gulf of Alaska, Sea of Okhotsk, and Gulf of Anadyr). The northwestern Alaska collections (Bering Sea, Norton Sound, and Chukchi Sea) exhibited little genetic divergence. The Gulf of Anadyr collection differed from other regions but was most similar to those of the northwestern Alaska region. The two collections within the Sea of Okhotsk (Sakhalin Island and Hokkaido Island) differed genetically, but not to the extent they did from other regions. The collections from the Gulf of Alaska (Kodiak Island and Prince William Sound) comprised a lineage that was distinct from all of the other collections, including the geographically adjacent northwestern Alaska collections. The absence of genetic structure among northwestern Alaska collections probably reflects their recent expansion into previously unavailable habitat that became available after the Last Glacial Maximum (~16,000 years ago). The divergence of the Gulf of Alaska lineage may have resulted from recurrent episodes of isolation from previous glaciations.

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Introduction

The Saffron Cod (*Eleginus gracilis*, Tilesius 1810) is an abundant yet little studied gadid that is distributed along the coastlines of the north Pacific Ocean as far south as the Yellow Sea in the west and Sitka, Alaska in the east. They also extend through the Bering Strait northward into the Chukchi and Beaufort seas as far as Dease Strait off Nunavut in the northeast and as far as the East Siberian Sea in the west (Craig and Haldorson 1981; Cohen et al. 1990).

Saffron Cod inhabit cold, brackish to marine waters at depths down to 75 m (Wolotira 1985; Allen and Smith 1988). Juveniles and adults are associated with eelgrass or kelp (Laurel et al. 2007) and are often found in areas of tidal influence at the mouths of coastal rivers (Wolotira 1985). According to the Fishery Management Plan for Fishery Resources of the Arctic (Arctic Fishery Management Plan, NPFMC 2009), there is insufficient information to identify the essential fish habitat (EFH) for Saffron Cod eggs, larvae, and early juveniles. The EFHs for late juveniles and adults are the epipelagic and pelagic coastal waters within bays and under ice cover up to 50 m of depth along the inner shelf in areas of sand and gravel substrate (Arctic Fishery Management Plan, NPFMC 2009).

The average lifespan of Saffron Cod varies spatially and declines southward—boreal Pacific individuals live about 8-9 years and Arctic individuals up to 11-12 years (Wolotira 1985). Saffron Cod are subject to high natural morality—60-80% annually; less than 1% of the age-0 cohort survives beyond 5 years (Cohen et al. 1990). On average, the Saffron Cod grow to 35 cm but can reach a maximum total length of 60 cm (Cohen et al. 1990).

Adult Saffron Cod form small, local aggregations and undergo short seasonal migrations inshore and offshore, which are associated with spawning, feeding, and temperature changes (Wolotira 1985; Johnson et al. 2009). They reach maturity at 2-3 years (Wolotira 1985; Cohen et al. 1990). Adults spawn an average of 5-7 times in a lifetime but individuals older than 10 years may spawn up to 9-10 times (Wolotira 1985).

During summer, Saffron Cod feed intensively before moving inshore in early winter when food availability is reduced. They spawn off the ice-covered coastline at depths of 2-10 m from January to February; females release as many as 210,000 eggs that incubate over winter and hatch in the spring (Wolotira 1985). The eggs are demersal and slightly adhesive (Chen et al. 2008). They can develop in sub-zero temperatures but cannot survive at salinities below 23.2 ppt (Wolotira 1985). Larvae hatch in the early spring months of April and May before drifting for a 2-3 month planktonic larval stage after which, they descend to the bottom (Wolotira 1985). The geographic extent to which they drift is currently unknown. Larval and juvenile Saffron Cod have been collected in high abundance during trawl surveys in August and September in the northern Pacific and Arctic oceans, specifically along the Alaskan coastline of the South Chukchi Sea (De Robertis et al. 2017). Juveniles can tolerate higher salinity variability and remain in coastal waters throughout the year (Wolotira 1985; Cohen et al. 1990).

Saffron Cod are the 11th largest species group of fish and invertebrates in terms of biomass and are the second most abundant demersal fish in the Chukchi and Beaufort seas (Barber et al. 1997; Arctic Fishery Management Plan, NPFMC 2009). However, juvenile saffron cod can dominate the pelagic fish community in parts of the Chukchi Sea (Eisner et al. 2013; de Robertis et al. 2017). In the Chukchi Sea, Saffron Cod are an important food source for sea birds and marine mammals (Springer et al. 1987; Kelly 1988; USDOI Mineral Management Service 2006; Bluhm and Gradinger 2008).

For more than a century, a Russian commercial fishery has been harvesting Saffron Cod for human consumption (Wolotira 1985). Saffron Cod are fished in late fall, prior to the winter spawning season (Wolotira 1985). Several major fishing grounds in the northern Pacific include: the Chukchi Sea, Peter the Great Bay in the Sakhalin area of the Sea of Okhotsk, and the waters off the Kamchatka Peninsula (Cohen et al. 1990; Pauly and Swartz 2007). Saffron Cod do not form dense aggregations, and are better suited towards small, local "cottage industry" operations. They are caught with hook and line, trawls, seines, gill nets, hoop nets, fyke nets, and other stationary gear suited for shallow water fishing prior to winter ice formation (Wolotira 1985). A congener, Nawaga (*Eleginus nawaga*), is commonly taken in Russia for fresh or frozen human consumption in commercial fishing grounds in the Kara and Laptev seas (Cohen et al. 1990; Pauly and Swartz 2007). The demand for Saffron Cod in Canada was reduced with the widespread advent of snowmobiles in the 1960s, which replaced transportation by dog sled and the need for fish-based dog feed (Zeller et al. 2011).

Saffron Cod are caught in Alaska for subsistence (Georgette and Loon 1993; Smith et al. 1997; Sigler 2011). A 2007 Alaska Department of Fish and Game survey reported that Saffron Cod were used in 81% of households in Kivalina and in 54% of Noatak households (Magdanz et al. 2010). Commercial fishing is currently prohibited in the U.S. Federal Arctic Management Area until adequate information is available to sustainably manage a commercial fishery (Arctic Fishery Management Plan, NPFMC 2009).

Earlier contemporary ice retreat and a longer ice-free season also make the Arctic area available to offshore oil drilling. The shallow, ice-covered shelf in the seas off the coast of Alaska is believed to have large untapped oil and gas reserves. Some other areas of high oil and gas potential include the Beaufort Sea, Canada's Arctic island chains, northern Russia, the Kara Sea, and the Barents Sea (Weeks and Weller 1984)—all areas within the distributions of Saffron Cod and Nawaga. Consequently, it is important to consider the effects of contamination (Olsgard and Gray 1995) that oil development could have on Saffron Cod, which cannot be done without quality baseline information on the physical and biological components of the Arctic ecosystem.

Population genetics can contribute to conservation and management of fisheries. Management strategies are usually based on defined fish stocks, which often deviate from distinct genetic populations. A study by Reiss et al. (2009) described the population structures of 32 fish species managed in the Atlantic Ocean in relation to their current management structure. Their results indicated disparities between the current management practices and genetic population structure in six commercially important species (*Gadus morhua, Melanogrammus aeglefinus, Merlangius merlangus, Micromesistius poutassou, Merluccius merluccius,* and *Clupea harengus*). The observed management mismatch stresses the value of including genetic population structure in conservation and management plans.

Determination of the presence and nature of population structure by genetic analyses can inform management strategies and conservation efforts. For instance, if the genetic variation within a species is known, conservation measures can be taken to maintain the gene pool diversity, which may buffer it against environmental changes. The reevaluation of systematic classification with molecular analyses can also lead to new conservation strategies based on species distinction, particularly in the case of subspecies. An understanding of population structure can also highlight particular geographic regions of conservation priority in populations as well as maintaining species richness (Avise 1992; Petit et al. 1998).

Recently, genetic analyses have been combined with modeling, behavioral, and oceanographic data to bolster inferences as well as examine the spatial structure of marine populations (Selkoe et al. 2008). For example, microsatellite markers have been used to describe Chum Salmon population structure along the Pacific Rim (Beacham et al. 2009). Microsatellites have also been used to identify strong genetic discontinuity between northeastern and northwestern Pacific Cod (*Gadus macrocephalus*) populations (Canino et al. 2010). Genetic structure has been reported in other north Pacific and Atlantic Ocean gadids (Bentzen et al. 1996; Pampouile et al. 2006; Cunningham et al. 2009; and Yanagimoto et al. 2012).

To date, no population genetic study has been conducted to assemble baseline information on the Saffron Cod in the north Pacific and Arctic oceans. Because baseline knowledge of the population structure of a species is necessary to inform strategies for fisheries management and the conservation of genetic diversity, obtaining this information grows more critical as northern Pacific and Arctic environments rapidly change as a result of climate change and increasing human influence. An exploratory examination of Saffron Cod population structure would provide a reference point for future research and an early observation of the changing north Pacific and Arctic ecosystems. The purpose of this study is to address three main questions: 1) Is genetic diversity present within Saffron Cod? 2) If so, is there genetic divergence across the study regions? 3) Could physical and oceanographic features be involved in defining Saffron Cod population genetic structure?

Methods

Sample collection

The majority of adult Saffron Cod were collected during two Arctic Ecosystem Integrated Surveys (Arctic Eis) (Mueter et al. 2016) that sampled the Alaskan portions of the northern Bering Sea and Chukchi Sea in August and September of 2012 and 2013. Saffron Cod samples from other locations (south central Alaska, northwestern Alaska, Russia, and Japan) that were provided by colleagues improved sample coverage across the known species range. Samples were collected by surface, mid-water, and bottom trawls and by jigging (Table 1; Figure 1).

Cardiac and skeletal muscle tissue samples were placed in DNA preservative (Seutin et al. 1991) and stored at -20°C. Several Saffron Cod samples from Russia were provided as DNA suspended in ethanol. Most samples were from adult saffron cod, except for three collections < 150 mm, used for comparison in some analyses (G02, D02, and T05) (Table 1).

Microsatellite analysis

Nine polymorphic tetranucleotide Saffron Cod-specific microsatellite markers were designed by Savannah River Ecology Laboratory (Aiken, SC): *Elgr07*; *Elgr11*; *Elgr13*; *Elgr14*; *Elgr23*; *Elgr31*; *Elgr38*; *Elgr44*; and *Elgr45* (Smé et al. 2017). The Puregene DNA™ isolation protocol (Gentra Systems, Minneapolis, MN) was used to isolate total genomic DNA. The DNA was rehydrated with Tris-EDTA (TE) buffer (0.01 M Tris-HCl, 0.001 M EDTA, pH 8.0) and stored at -20°C. The polymerase chain reaction (PCR) amplification used to amplify the target sequences included a touchdown strategy to reduce non-target bands in the product spectrum (Don et al. 1991). All PCR reactions had ~1 unit Taq polymerase, PCR buffer (50 mM KCl_2, 10 mM Tris-HCl pH 9.0, 0.1% Triton x 100; Promega™, Madison, WI), 0.5 µM deoxyribonucleotide triphosphates, and 0.025 to 0.1 µM DNA template. Fluorescent primers labeled with an IRDye® infrared dye (10 µg/ml; LI-COR, Lincoln, NE) were also included in the reactions. The amplification profiles at each locus were: denaturation at 95°C for 5 min; 20 touchdown cycles at 95°C for 30 s followed by annealing temperatures ranging from 62-52°C (touchdown) for 30 s (decreased 0.5°C per cycle), and 72°C for 30 s; 15 cycles of 95°C for 30 s, the lowest annealing temperature (55°C) for 30 s, and 72°C for 30 s; and a final extension at 72°C for 5 min.

Approximately 1 μl of amplified PCR product and 9 μl of stop buffer (95% formamide, 0.1% bromophenol blue) was loaded onto a 0.25 mm 6% acrylamide gel (PAGE-PLUS™, Amresco, Solon, OH) in 5X TBE (TBE is 0.09 M Tris-Borate, 2 mM EDTA, pH 8) and fragments were separated electrophoretically in TBE buffer at 1500 V with a LI-COR 4300 DNA Analyzer™ (LI-COR, Lincoln, NE). Electrophoresis times varied from 2 to 3 hours depending on sizes of the PCR products. The sizes of the products were estimated with SAGA™ v.3.1 (LI-COR, Lincoln, NE) software.

Data analysis

Hardy-Weinberg expectations, fixation indices, and tests of homogeneity.—The program GENEPOP v.4.5.1 (Rousset 2008) was used to estimate allele frequencies and to identify departures from Hardy-Weinberg expectations and linkage equilibrium. Departures from Hardy-Weinberg expectations can be an indication of null alleles, which result from failed PCR amplification if mutations in the template target sequences prevent annealing of primers. Alternatively, departures can indicate mixtures of genetically distinct populations or inbreeding. Pseudo-exact tests for combinations of loci and regional groups of collections were performed. In all GENEPOP v.4.5.1 analyses, we used 10,000 dememorization steps, 5,000 batches, and 5,000 iterations per batch. False discovery rate (FDR; Benjamini and Hochberg 1995) adjustments were used to correct the significance of multiple comparisons.

Of the pseudo-exact homogeneity tests conducted between all pairs of collections, three geographic areas were defined for the northwestern Alaska collections: North Chukchi Sea (collections J06B-G03A), South Chukchi Sea (E03A-A02A), and Norton Sound (R04-CH1B).

Pairwise tests involved multiple testing, for which corrections were made by assuming that tests between collections from within a geographic region (Sea of Okhotsk, Gulf of Anadyr) or area (North Chukchi Sea, South Chukchi Sea, Norton Sound, Kodiak Island, and Prince William Sound) would be repeated tests. Corrections for multiple testing within the region or area were based on the number of tests within each area or region. Also, each set of tests between geographic regions or areas were considered as repeated tests and corrected for the number of tests.

Divergence among allele frequency distributions of Saffron Cod collections was tested in GENEPOP v.4.5.1 (Rousset 2008). The fixation index, F_{ST} (θ; Weir and Cockerham 1984) was estimated to quantify genetic divergence among populations. Hierarchical analyses were conducted to partition genetic variation within and among groups of populations with AMOVA in Arlequin v.3.5.1 (Excoffier and Lischer 2010) to evaluate population structures.

Principal components analyses and maximum-likelihood tree construction.—Principal components analysis (PCA) was used to detect individuals that were genetic outliers and to describe genetic structure. A PCA is a multivariate method that resolves linear combinations of variables that maximize the variance among samples. Plots of first and second correlation-based principal components were used to reveal outliers, for example individuals of other species that had been misidentified (Smé et al. 2017). We obtained the first two principal components from allelic counts for each individual with SYSTAT vers.13 (SYSTAT Software Inc., Richmond, CA) and plotted them. Outliers were identified by low probabilities, after correction for multiple testing of Hotelling's (1931) T squared statistic estimated from principal components.

In the second application of PCA, arcsine-squareroot transformations of allele frequencies were used in covariance matrix-based analyses to contrast genetic differences among the collections, or aggregates of collections, of Saffron Cod. Groupings of genetically similar Saffron Cod collections were visually identified as clusters in close association with one another.

Maximum-likelihood trees were used to visualize patterns of genetic structure of Saffron Cod from different geographic areas. The trees were estimated from allele frequency data to identify patterns of genetic variation among Saffron Cod collections. The CONTML procedure in the PHYLIP v.3.695 program (Felsenstein 2005) uses a restricted maximum likelihood method to construct chord distance-based trees (Cavalli-Sforza and Edwards 1967) that were plotted with TreeView v.1.6.6 (Page 1996).

Geographic structure analyses.—An isolation-by-distance (IBD) analysis was conducted to examine the relationship between genetic and geographic distances of individuals sampled off the coast of northwestern Alaska. Distances between collections were measured with ArcView 10.1 (ESRI 2011) graphic analyses. A line that connected the northwestern Alaska collections was constructed along the 10 and 20 m bathymetric contours (Supporting Figure 1). Pairwise F_{ST} values between individuals were calculated in GENEPOP v.4 (Rousset 2008) and correlations between genetic distances, quantified as $F_{ST}/(1-F_{ST})$, and the corresponding geographic distances (km) were tested for significance using a Mantel test with 1,000,000 permutations. Two estimators were used in the IBD analysis: $\hat{a}$ statistic (Loiselle et al. 1995) and $\hat{e}$ statistic (Watts et al. 2007). Loiselle et al. first described $\hat{a}$ statistic to examine the geographic dispersal of alleles in populations of the Costa Rican shrub, *Psychotria officinalis*. From $\hat{a}$, Watts et al. (2007) derived the estimator $\hat{e}$, to quantify genetic dispersion in the two-dimensional habitat of the damselfly (*Coenagrion mercuriale*) and found that $\hat{e}$ is a superior estimator under most conditions while $\hat{a}$ is suitable for more localized dispersal.

The program Spatial Analysis of Shared Alleles (SAShA; Kelly et al. 2010) was used to examine genetic structure in collections off the coast of northwestern Alaska. This method detects subtle structure by analyzing the spatial patterns of alleles that occur among collections under an assumption of panmixia.

Effective population size and bottleneck analysis.—The effective population size (N_e) is the size of an ideal population (a population in Hardy-Weinberg equilibrium) that would decrease in heterozygosity at the same rate as observed populations. Effective population size was estimated for collections and regions based on linkage disequilibrium, heterozygosity excess, and molecular coancestry with NeEstimator v.2.0 (Do et al. 2014).

A population bottleneck is an event that reduces the size of a population and often results in the loss of rare alleles. Because of their small contribution, rare alleles would be expected to have little effect on heterozygosity within a population; consequently, the heterozygosity would not be expected to change substantially in a population that passes through a bottleneck. Mutation-drift equilibrium heterozygosity can be estimated for the number of observed alleles in a sample from a population in mutation-random drift equilibrium, in which new alleles are produced by mutation, and alleles are lost at random (Luikart and Cornuet 1998). The appropriate mutational model for microsatellites is a two-phase model (TPM; 95% stepwise mutation model (SMM), 12% variance; Piry et al. 1999). Three significance tests (sign test, standardized differences test, and Wilcoxon test) were conducted with the program BOTTLENECK (Luikart and Cornuet 1998). If bottlenecks occurred more recently than 0.2-4.0

N_e generations in a population, the observed heterozygosity should be significantly larger than the simulated heterozygosity at all loci. Significantly small values suggest an expanding population resulting in heterozygosity deficiency—the opposite of the heterozygosity excess that is observed when a recent population bottleneck has occurred (Cornuet and Luikart 1996).

Relatedness within collections.—The extent of relatedness between individuals within each collection was estimated with the software package IDENTIX v1.1 (Belkhir et al. 2002), which calculated two different method of moments and maximum likelihood estimators (Lynch and Ritland [1999] and IDENTITY [Belkhir et al. 2002], respectively) to evaluate the average pairwise relatedness and its variance. A collection of related individuals would be expected to have a higher degree of relatedness than a collection of individuals that is simulated by randomizing alleles from the sample. A variance that exceeds the estimate derived from the permutated data is significant and consistent with a population mixture. For each estimate, 1,000 permutations were conducted to estimate significance. Several collections were pooled based on geographic proximity and their relatedness estimates and variances were also estimated.

Results

Data

Samples of saffron cod were collected from 40 sites along the coastlines of Japan, Russia, and Alaska (Table 1; Figure 1). Two collection sites were in the Sea of Okhotsk and one was in the Gulf of Anadyr. Two collections were made near Kodiak Island and eight collections came from Prince William Sound. The remaining 27 collections were from the northern coast of Alaska: five from the North Chukchi Sea; 11 from the South Chukchi Sea; and 11 from Norton Sound. Collection sizes ranged from one individual (J06A and J06B from the North Chukchi Sea, R04 from the Norton Sound, and PWSF and PWSH from Prince William Sound) to 115 (JLA from the Sea of Okhotsk), with a total of 1,228 fish.

The Saffron Cod were analyzed at nine microsatellite loci: *Elgr07*; *Elgr11*; *Elgr13*; *Elgr14*; *Elgr23*; *Elgr31*; *Elgr38*; *Elgr44*; and *Elgr45* (Smé et al. 2017). Correlaton-based PCA identified 10 individuals that had aberrant genotypes based on Hotelling's T squared after correction for multiple testing. Saffron Cod individuals demonstrate strong clusters in correlation-based PCA with other north Pacific gadids (Smé et al. 2017), so it is possible that the aberrant individuals were misidentified as Saffron Cod. As a result, the individuals were removed from the analysis: four from Sea of Okhotsk; five from the South Chukchi Sea; and one from the Gulf of Anadyr. The number of individuals analyzed subsequently was 1,218.

The numbers of alleles at the loci varied between 11 and 26 alleles, and allele sizes ranged from 40 (*Elgr31*) to 216 (*Elgr07*) base pairs (bp) (Supporting Table 1). Expected heterozygosities ranged from 0.735 to 0.876 in *Elgr31* and *Elgr14*, respectively (Supporting Table 2).

The analyses of 312 locus-by-population combinations revealed 17 tests that differed significantly from Hardy-Weinberg expectations (HWE), only one of which was significant after adjustment for multiple testing based on total number of tests performed (*Elgr44* in KODA, $P < 10^{-6}$ after correction) (Supporting Table 1).

Linkage equilibrium was examined in 36 overall tests of locus pairs for all collections that included at least 15 individuals. No significant tests were observed in any collections after adjustment for multiple testing ($P < 0.05$; FDR).

Genetic Structure

Pairwise homogeneity tests.—A table was constructed for all collections in which ordering of the northwestern Alaska collections was based on spatial proximity under the assumption that adjacent collections are likely to be more genetically similar and started from the far northeast in the North Chukchi Sea (Supporting Table 3). After corrections for multiple testing, the collections within each of the northwestern areas (North Chukchi Sea, South Chukchi Sea, and Norton Sound) revealed no divergence. In the Gulf of Alaska region, neither the Prince William Sound nor the Kodiak Island areas exhibited divergence among collections. However, significant divergence exists between the Prince William Sound and Kodiak Island areas, and between them and all of the other areas and regions. The two Sea of Okhotsk collections differed from each other and from every other area and region. The Gulf of Anadyr collection differed from every other area and region (Supporting Table 3). For subsequent analyses, the collections were combined into four regional groupings: two in Asian waters (the Sea of Okhotsk and Anadyr Bay) and two in North American waters (northwestern Alaska and the Gulf of Alaska). Within those regions, three geographical areas within northwestern Alaska (North Chukchi Sea, South Chukchi Sea, and Norton Sound), two within the Gulf of Alaska (Kodiak Island and Prince William Sound), and two within the Sea of Okhotsk (Hokkaido Island and Sakhalin Island) were examined.

Hierarchical tests of homogeneity and estimates of divergence (fixation coefficients θ) revealed a single weakly significant test within the Norton Sound area ($P = 0.015$; $\theta = 0.003$), which was attributable mostly to *Elgr13* ($P = 0.0055$). Nevertheless, there was no significant divergence among areas within northwestern Alaska ($P > 0.05$; $\theta < 0.001$). In contrast, there were significant differences between the two areas within the Gulf of Alaska (Kodiak Island and

Prince William Sound) ($P < 0.0001$; $\theta = 0.025$) and the two areas in the Sea of Okhotsk (Sakhalin Island and Hokkaido Island) ($P < 0.0001$; $\theta = 0.006$) and strong divergence among regions ($P < 0.0001$; $\theta = 0.053$) (Table 2).

A maximum-likelihood tree for the eight areas revealed distinct clusters for the northwestern Alaskan areas (North Chukchi Sea, South Chukchi, and Norton Sound) and the Gulf of Alaska areas (Kodiak Island and Prince William Sound). The northwestern Alaskan areas are similar, but distinct from the areas within the Sea of Okhotsk and Gulf of Anadyr. In the tree, the Gulf of Alaska areas were farthest from the northwestern Alaska areas and the Gulf of Anadyr closest (Figure 2). The clusters produced by PCA analysis were concordant (data not shown).

Geographic structure.—The homogeneity tests and the maximum likelihood tree showed little divergence among the northwestern Alaska areas. To further explore the nature of genetic structure for those collections, an IBD analysis was performed to examine the relationship between genetic divergence ($F_{ST}/(1-F_{ST})$) and geographic distances (km) between individuals collected along the coastline of northwestern Alaska. The analysis revealed no significant IBD relationship ($\widehat{a}$ statistic: b =$1.597*10^{-6}$; $P = 0.146$ and $\widehat{e}$ statistic: b = $-6.57*10^{-8}$; $P = 0.100$).

A SAShA analysis detected no significant deviation from panmixia of the geographic structure of alleles within the northwestern Alaska region. The observed and expected mean distances between shared haplotypes were 661.55 km and 659.14 km, respectively ($P = 0.351$).

Effective population size.—The effective population sizes (N_e) estimated for all areas and regions were large, suggesting little genetic drift. The majority of areas and regions had infinite point estimates for N_e as calculated from linkage disequilibrium, heterozygosity excess, and molecular coancestry. Nevertheless, wide ranges between lower and upper confidence intervals were observed (Supporting Table 4).

Bottleneck analysis.—In the bottleneck analysis, the two Gulf of Alaska areas (Kodiak and Prince William Sound) and one northwestern Alaska area (South Chukchi Sea) were significantly negative under the two-phase model (TPM; 95% stepwise-mutation model, 12% variance) suggesting population expansion. The five tests of the remaining areas from the North Pacific region (North Chukchi Sea, Norton Sound, Gulf of Anadyr, Hokkaido Island, and Sakhalin Island) were not significant. All pooled collections exhibited L-shaped modes, as expected under mutation-drift equilibrium (Supporting Table 5).

Relatedness analysis.—Few of the Lynch-Ritland and IDENTITY estimators were significant and there was little correlation between the two different estimators for any significant collection. Of the 11 pooled collections, individuals within two collections were more related than expected for IDENTITY (Prince William Sound and D02, a collection of small—less than 150 mm—individuals from the South Chukchi Sea). Sampling variances were small but significant at two Lynch-Ritland estimates (South Chukchi Sea and Kodiak Island) and one IDENTITY estimate (Hokkaido Island) (Supporting Table 6).

Discussion

The Saffron Cod collections included eight distinct geographical areas that form four regional groups: (1) northwestern Alaska (North Chukchi Sea, South Chukchi Sea, and Norton Sound), (2) the Gulf of Alaska (Kodiak Island and Prince William Sound), (3) the Sea of Okhotsk (Sakhalin Island and Hokkaido Island), and (4) the Gulf of Anadyr. Little to no divergence was observed among the northwestern Alaskan collections, but that region differs genetically from the other three. The Gulf of Alaska lineage is genetically distinct from all other regions (Smé et al. 2017); moreover, the collections from Prince William Sound and Kodiak Island differed from each other in genetic composition. The Sea of Okhotsk collections differed from one another, but not to the degree that they differed from the other regions. The Gulf of Anadyr collection is distinct from the other collections, but most similar to the northwestern collections.

The regional differences likely result from population contractions and isolation at the last glacial maximum (LGM), followed by postglacial expansions. During the LGM, the Chukchi and Bering seas were separated by a land bridge for a period of 10,000 – 15,000 years (Elias et al. 1996) and both seas were covered with ice much of the year (Caissie et al. 2010) (Figure 3). Analysis of diatom assemblages at the LGM suggests that the sea ice cover was perennial over much of the Bering Sea (Caissie et al. 2010). The presence of the land bridge and extensive sea ice cover across the continental shelf altered the flow of currents in the Aleutian Basin (Figure 3). In addition to its influence on current patterns, the pervasive ice cover and exposed land at the LGM restricted the availability of marine habitat. Many of the collection sites were not available to Saffron Cod during the LGM, and have only become gradually available during the 16,000 years since the LGM as the sea level rose. In addition, the mouths of the Yukon and Kuskokwim rivers resided at the Zhemchug and Pribilof canyons, respectively (Miller et al. 2012; Garvin et al. 2013). The freshwater inflow likely provided a suitable habitat to the estuarine, shallow water associated Saffron Cod during this period.

The end of the LGM ushered in the current Holocene epoch. In the early Holocene, a warming event in the Bering Sea caused a reduction in sea ice cover and the Bering and Chukchi shelves were flooded by about 10,000 years BP (Mann et al. 1995; Katsuki et al. 2009).

Alternating warm periods and ice ages have occurred about every 100,000 years due to a combination of fluctuating insolation cycles and the reciprocal effects of climate and continental ice sheets (e.g. Abe-Ouchi et al. 2013).

The recession of the glaciers and sea level rise after the LGM exposed previously unavailable habitat along the northern Pacific coastline, Chukchi and Bering sea shelves. During the LGM, the amount of nearshore habitat was limited due to the steep drop off to greater depths (Figure 3). The contemporary Bering Sea circulation is characterized by cyclonic currents that form part of the subarctic gyre of the North Pacific; the majority of its water flow derives from the Alaskan Stream (Stabeno et al. 1999) (Figure 1).

It is tempting to explain the genetic homogeneity among the northwestern Alaska Saffron Cod collections by the current that runs eastward along the Aleutian Islands and through passes from the Gulf of Alaska and turns northward through the Bering Sea, Norton Sound, and Chukchi Sea into the Arctic Ocean. This current is strongest around the 50 m contour; whereas adult Saffron Cod generally occur at less than 50 m and deposit eggs under ice cover at shallow depths of 2-10 m (Wolotira 1985). Moreover, the eggs are demersal and somewhat adhesive (Chen et al. 2008). Only after they hatch in early spring (around April and May) are they subject to the currents until the larvae descend to the bottom in late summer (Wolotira 1985; De Robertis et al. 2017). Note that the average contribution of a female during her lifetime is about 1 million eggs (5 reproductive years, producing 210,000 eggs each year), but only two must survive to maintain the population size. Clearly, the vast majority of larvae perish and suggests that there may be strong interannual differences in numbers of recruits. However, there was no indication of sweepstakes effects in either the estimates of N_e or relatedness within collections, which suggests that many families contributed in multiple years.

Historically during the winter, the northern Bering Sea, Norton Sound, and Chukchi Sea are ice bound (Frey et al. 2015) and reach maximum ice coverage in March (Parkinson and Cavalieri 2002). A study of mooring data in the Bering Strait from 1990 to 2015 has revealed strong seasonality in flow through the strait, with the strongest flow in the summer months (Woodgate 2018). The Alaska Coastal Current along western Alaska flows at an average of 5-15 cm/s, or 0.18-0.54 km/hr (Danielson et al. 2014). If advected into the current, a passive larva may be expected to move 650 km from the time they hatch until it settles into a demersal, nearshore life. A study using a satellite-tracked drifter released in the Kotzebue Sound in June 2015 remained in the Sound despite the oceanographic connection to the Bering and Chukchi seas (Danielson and Whiting 2016). Models that simulate movement patterns consider larvae as passive particles. However, studies of rockfish larvae suggest that they remain close to their natal sites (Buonaccorsi et al. 2004; Taylor et al. 2004). Although pelagic, many Saffron Cod may remain near shore and close to the bottom and their distribution may not be strongly influenced by currents higher in the water column.

During the LGM, the collection sites in northwestern Alaska and the Gulf of Alaska were unavailable to Saffron Cod, and have only been colonized recently. The northwestern Alaska sites may have been colonized from southwestern Bering Sea, while the Gulf of Alaska collections could have resulted from post-glacial expansion as new nearshore habitat became available in the Gulf of Alaska. The observed genetic structure is an outcome of the subsequent inundation and sea level rise from -120 m in the region (Mann et al. 1995). The flooding along the Alaskan coastline allowed Saffron Cod to expand into new habitats. The bottleneck analyses indicated population expansion signatures in both the Gulf of Alaska and South Chukchi Sea, which are consistent with recent expansions into those areas. In northwestern Alaska, little or no divergence was observed among the collections; however, the sample sizes were too small to expect a signal. The collections are spread over a relatively broad area, and no oceanographic features or great distances isolate them from one another. The low divergence among northwestern Alaska collections is not surprising because there has been little divergence time and the populations are large. Consequently, it is unlikely that migration-drift equilibrium has occurred. The nearshore waters of Norton Sound and the South Chukchi Sea have only existed in the last 10,000 years (Mann et al. 1995), and it is likely that there was a lag between that time and when the habitat became suitable for colonization, and an additional time period prior to the completion of colonization. The half-time for migration-drift equilibrium is: $t_{1/2} \approx \frac{\ln 2}{2m+\frac{1}{2N_e}}$ (Crow and Aoki 1984) where m is migration rate. Even for effective population sizes as small as 1,000 individuals, the half-time is nearly 1,000 years for gene flow rates of 0.3%. Less than 10% exchange rates are necessary to generate a disruption in the population dynamics to form two autonomously behaving populations (Hastings 1993).

The Gulf of Alaska lineage is genetically distinct from all other regions (Smé et al. 2017). The Aleutian Island chain serves as a geographic barrier between the Gulf of Alaska lineage and all other regions. Multiple glaciation cycles may have isolated the Gulf of Alaska lineage multiple times and provided the opportunity for its genetic compositions to diverge independently from the other regions, in particular, the geographically nearby northwestern Alaska region. In addition, the two collections that form the lineage—Kodiak Island and Prince William Sound—are genetically distinct from one another. The large genetic divergence of the Gulf of Alaska lineage could be explained by several glacial periods of isolation from the other regions. The genetic differentiation may also be a result of the consistent coastlines of the Gulf of Alaska region, which have not changed greatly since the LGM. The small change in geography may have allowed the Prince William Sound and Kodiak Island collections to persist in the same location and to diverge from other regions as well as from one another. The divergence is supported by the significantly different nodes on the maximum-likelihood tree (Figure 2). The distinction is also evident in the microsatellite *Elgr38*, which amplified consistently for Prince William Sound collections but not for Kodiak Island collections (Smé et al. 2017).

The Gulf of Anadyr collection differs genetically from all other collections and regions. Of all the regions, the Gulf of Anadyr collection is most similar to the northwestern Alaska collections. It is possible that the modern Gulf of Anadyr region was colonized from the northwestern Alaska region as the Bering land bridge disappeared, as recently as 11,000 years ago (Elias et al. 1996), another argument for postglacial colonization from the southwestern Bering Sea. The Gulf of Anadyr collection may have diverged after the LGM with the formation of the Anadyr current, which flows northward through the Anadyr Strait in the summer but may at times reverse in the winter (Wang et al. 2009) (Figure 1).

The Sea of Okhotsk collections are genetically distinct from all other regions, and collections from Sakhalin Island and Hokkaido Island also differ from each other, but not to the degree that they differ from other regions. The collections may be different from the other regions because the contemporary oceanographic current patterns have changed and reduced the oceanographic connection between the eastern and northwestern reaches of the Pacific Ocean. The limited oceanographic connection between the two collections (Sakhalin Island and Hokkaido Island) at the LGM may have also contributed to the genetic divergence within the region. In addition, the coastlines in these areas have remained relatively constant, suggesting that unlike western Alaska, they may not be newly colonized. The contemporary collection sites also experience different oceanographic influences. The Sakhalin Island site is located along an inlet along the sheltered Sea of Okhotsk, while the Hokkaido Island site is located along the north Pacific Ocean and subject to the southwestern flowing Oyashio current.

Future Research

The northwestern Alaska collections were genetically homogenous, although it is unlikely those collections are from a single large stock because dispersal distances probably do not span the entire northwestern Alaska range that was sampled. Although the northwestern Alaskan populations appear genetically similar, as little as 10% exchange between populations can disrupt the population dynamics enough to result in two independently behaving populations (Hastings 1993). To further address stock structure, it might be useful to use isotope analyses. Stable isotope ratios present in otoliths have been compared to the signature isotope ratio profiles of water masses to identify potential origins and movements of fishes across water gradients (Trueman et al. 2012). Another approach might be to examine elements (barium, strontium, and calcium) and rare earth elements that are abundant in freshwater and are often incorporated into larval otolith compositions. This elemental composition of otoliths has been used to determine fish residency within specific water masses (McCulloch et al. 2005) and to resolve larval dispersal distances within ranges of < 500km (Miller and Shanks 2004). The presence of elements abundant in freshwater at the center of an otolith can indicate the natal estuarine origin of an individual fish, and can be compared to the signature where the fish was sampled to determine whether the fish has moved or been transported from its place of origin. Otolith chemistry in conjunction with microsatellite analyses have also been used to examine the extent of genetic overlap among populations of black rockfish (*Sebastes melanops*) (Miller et al. 2009). Chemical analysis of otolith composition in tandem with analyses of additional microsatellites could be used to examine population structure of estuarine spawning saffron cod in apparently genetically homogenous regions with strong freshwater inflow—such as nearshore northwestern Alaska—at a finer geographic scale.

The extent of Saffron Cod movement within the regions should also be examined because movements provide a demographic and genetic buffer to potential habitat changes or losses. The contemporary coastline along the north Pacific and Arctic oceans has changed substantially since the LGM, and the potential habitat available to Saffron Cod has been altered as well. A study by Partlow and Munk (2015) reported evidence of Saffron Cod from middens in archaeological sites along the Gulf of Alaska, dating back 500 years, and remains were recovered in middens from 7,000 years ago in the Aleutian Islands. Further research of contemporary populations as well as past populations through midden analysis may prove useful in establishing time frames of habitation and the movement of Saffron Cod within the study regions.

Further research should be conducted to establish the ranges of Saffron Cod groupings in these regions and how far they disperse within those ranges. Studies of adult and young-of-year Pacific Ocean Perch (*Sebastes alutus*) have reported genetic structure as a result of their restricted dispersal in the Gulf of Alaska (Kamin et al. 2014). To better understand larval dispersal and how it is influenced by oceanographic currents, the location of adult Saffron Cod distribution and the sites in which the demersal eggs are laid must be identified. This would provide further insight into whether the larvae travel from their natal origins, how far they are able to travel, and their survival as they are transported along currents.

Another question is the divergence times among areas and regions of Saffron Cod. Coalescence analyses of mitochondrial DNA sequence data has been used to estimate separation times of populations of marine fishes. A study conducted by Schwenke et al. (2018) examined the potential time frame of hybridization among three species of rockfish in the Salish Sea, Washington, USA. They were able to estimate divergence timelines as well as identify areas experiencing varying extents of hybridization. It is possible that these methods could be used to scrutinize the northwestern Alaska and Gulf of Alaska lineages of Saffron Cod.

In addition, examination of divergence between the Gulf of Alaska and northwestern Alaska lineages should be extended to intervening areas and include mitochondrial variation. The northwestern Alaskan waters (the Bering Sea) and the Gulf of Alaska are connected through the flow of the Alaska Coastal Current (ACC) through Unimak Pass. It is possible that the ACC could convey Gulf of Alaska fish through the passage ways into the northwestern Alaska region. Consequently, samples from the waters near the eastern passes through the Aleutian Islands may provide information about the contact zone between the two lineages.

Figure Legends

Figure 1. Saffron Cod collection sites (white filled circles) along the contemporary coast line with approximate current patterns (black arrows) in the north Pacific and Arctic Oceans ($n = 40$) (Stabeno et al. 1998; Reithdorf et al. 2013; Takahashi et al. 2016). The map was constructed in ArcView (ESRI 2011) from ETOPO1 1 arc-minute data (Amante and Eakins 2009). The gray section describes land, the white section describes water, the thick solid line describes 50 m depth contours, and thin solid line describes 1000 m depth contours.

Figure 2. Maximum-likelihood tree of eight regional groups estimated from chord distances. The solid line separates two distinct lineages (Table 2). The dashed line encircles areas that do not differ significantly; all of the other nodes are significant ($P < 0.0001$).

Figure 3. Paleoceanographic map depicting contemporary Saffron Cod collection sites (white filled circles) and approximate paleocurrents (black arrows) (Katsui and Takahashi 2005; Lambeck et al. 2014). The gray section describes land, the white section describes water, and the boundary line between the sections describes a 50 m depth contour. The map was constructed in ArcView (ESRI 2011) from ETOPO1 1 arc-minute data (Amante and Eakins 2009).

Figures

Figure 1

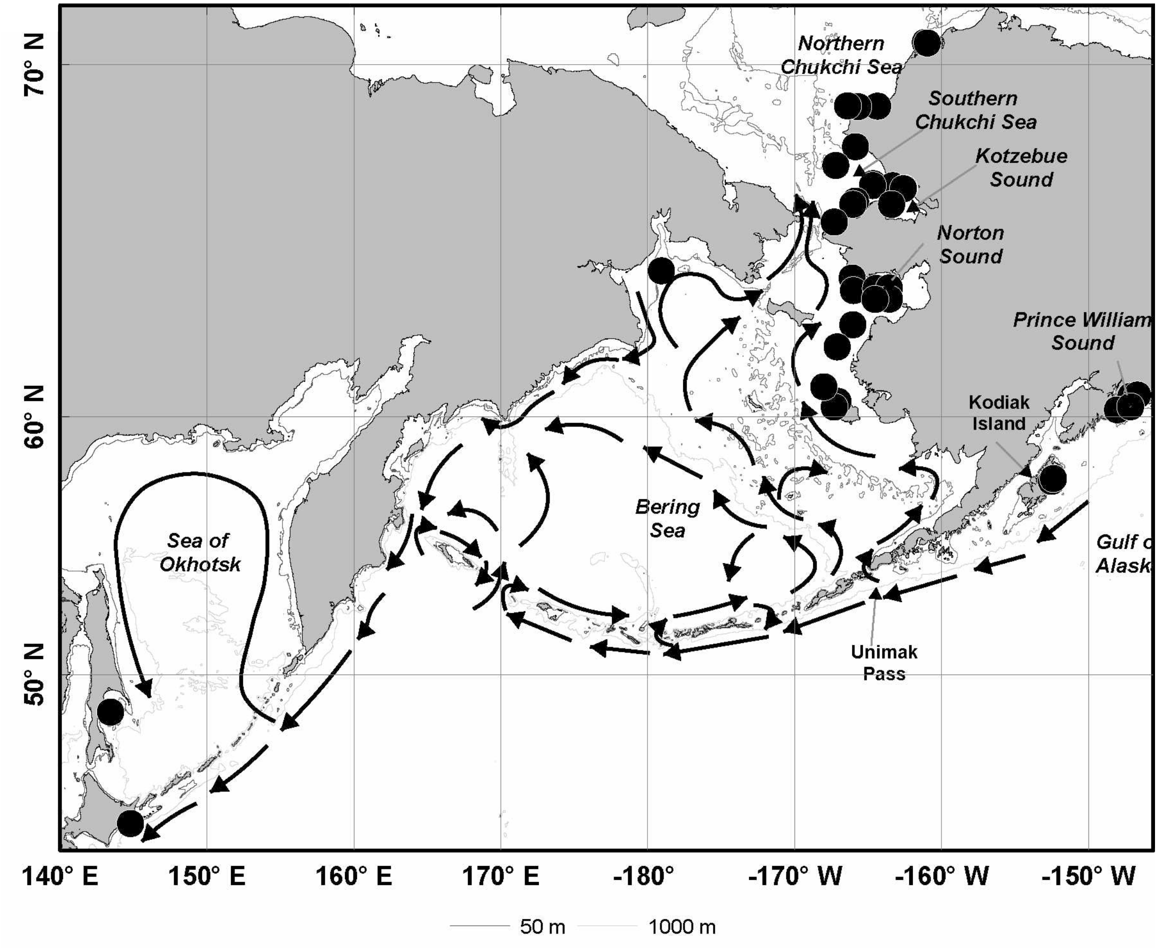


Figure 2

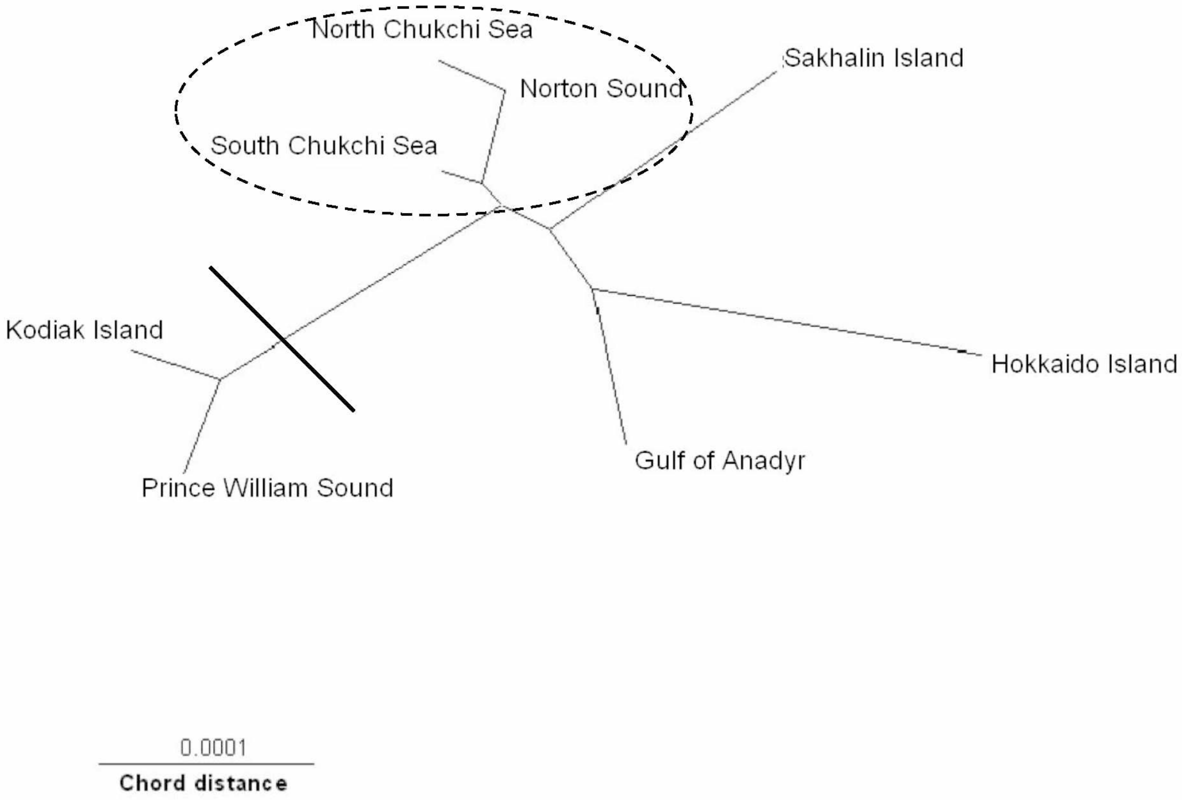
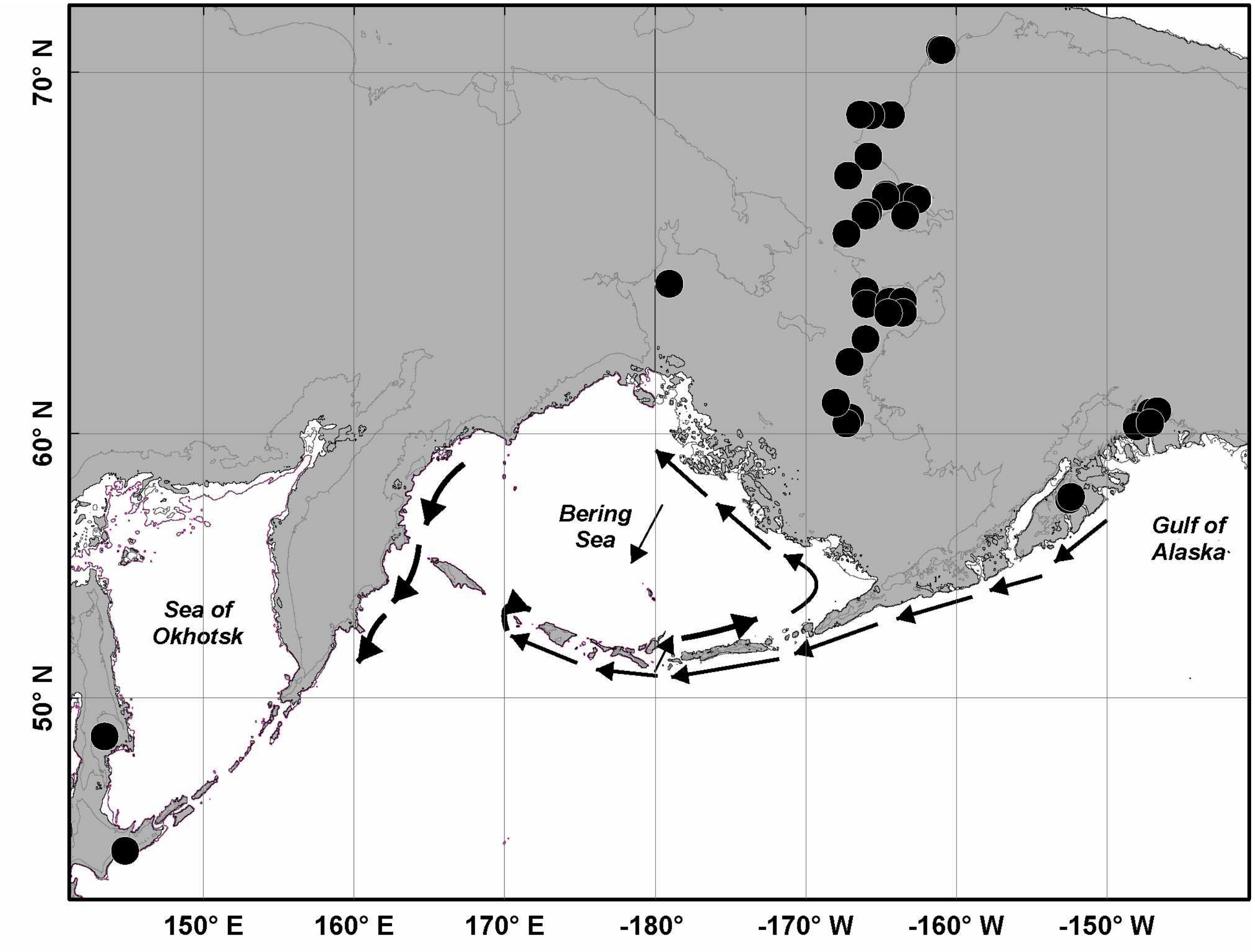

North Chukchi Sea
Norton Sound
South Chukchi Sea
Sakhalin Island
Kodiak Island
Hokkaido Island
Prince William Sound
Gulf of Anadyr
0.0001
Chord distance

Figure 3



70° N
60° N
50° N
150° E
160° E
170° E
-180°
-170° W
-160° W
-150° W
Bering Sea
Sea of Okhotsk
Gulf of Alaska

Tables

Table 1. Number of samples ≥150 mm (*n*), geographic regions, sample date (month/year or year), and coordinates for each Saffron Cod collection.

Collection	*n*	Geographic Region	Date	Latitude	Longitude
J06B	1	North Chukchi Sea	08/12	70.51°N	161.09°W
J06A	1	North Chukchi Sea	08/12	70.50°N	160.96°W
G04	4	North Chukchi Sea	08/12	69.01°N	164.34°W
G03A	2	North Chukchi Sea	08/12	69.00°N	165.69°W
E03A	16	South Chukchi Sea	08/12	68.00°N	165.84°W
C04A	10	South Chukchi Sea	08/12	67.04°N	164.66°W
CH3	50	South Chukchi Sea	08/12	66.99°N	164.69°W
CH2	99	South Chukchi Sea	08/12	66.98°N	163.32°W
KZ11	36	South Chukchi Sea	10-11/2011	66.90°N	162.59°W
KZ12	74	South Chukchi Sea	04/12	66.90°N	162.59°W
B05	6	South Chukchi Sea	08/12	66.48°N	163.40°W
B03A	6	South Chukchi Sea	08/12	66.57°N	165.84°W
B03B	4	South Chukchi Sea	08/12	66.48°N	166.03°W
A02A	4	South Chukchi Sea	08/12	66.00°N	167.29°W
R04	1	Norton Sound	09/12	64.40°N	166.07°W
S04	21	Norton Sound	09/12	64.03°N	165.99°W
S05	21	Norton Sound	09/12	64.09°N	164.44°W
S06B	6	Norton Sound	09/12	63.77°N	163.54°W
S06A	11	Norton Sound	09/12	64.10°N	163.54°W
U04	37	Norton Sound	09/12	62.99°N	166.03°W
MW21	43	Norton Sound	09/12	62.18°N	167.06°W
Y02	5	Norton Sound	09/12	61.01°N	168.00°W
Z03	7	Norton Sound	09/12	60.52°N	167.05°W
CH1B	4	Norton Sound	06/12	60.33°N	167.30°W
KODA	79	Kodiak Island	06-07/2013	57.73°N	152.51°W
KODB	16	Kodiak Island	08/13	57.83°N	152.38°W
PWSD	3	Prince William Sound	07/12	61.00°N	147.57°W
PWSE	49	Prince William Sound	07/12	60.87°N	147.18°W
PWSF	1	Prince William Sound	12/13	60.73°N	146.65°W
PWSC	4	Prince William Sound	07/12	60.69°N	147.10°W
PWSB	16	Prince William Sound	07/12	60.65°N	147.44°W
PWSA	24	Prince William Sound	07/12	60.41°N	148.08°W
PWSH	1	Prince William Sound	12/13	60.34°N	147.13°W
PWSG	9	Prince William Sound	12/13	60.24°N	148.01°W
CPAB	49	Gulf of Anadyr	2012	64.61°N	180.95°E
JLA	115	Sea of Okhotsk	2012	43.03°N	144.80°E
SCSI	113	Sakhalin Island	2012	48.33°N	143.44°E
≤150mm					
G02	100	North Chukchi Sea	08/13	69.02°N	166.39°W
D02	86	South Chukchi Sea	08/13	67.52°N	167.19°W
T05	84	Norton Sound	09/12	63.76°N	164.52°W

Table 2. Probabilities of hierarchical homogeneity tests of allele frequency distribution for collections within geographic areas, collections among areas within regions, and collections among regions. Fixation indices (θ) are in parentheses. *Denotes uncorrected significant values.

Region	**Area**	**Within Areas**	**Within regions**	**Among regions**	$\boldsymbol{\theta}$
NW Alaska	North Chukchi Sea	0.458			0.027
	South Chukchi Sea	0.091			0.001
	South Chukchi Sea	0.015			0.003
			0.281		0.001
Gulf of Alaska	Kodiak Island	0.403			-0.005
	Prince William Sound	0.290			0.001
			<0.0001*		0.025
Sea of Okhotsk	Sakhalin Island				
	Hokkaido Island				
			<0.0001*		0.006

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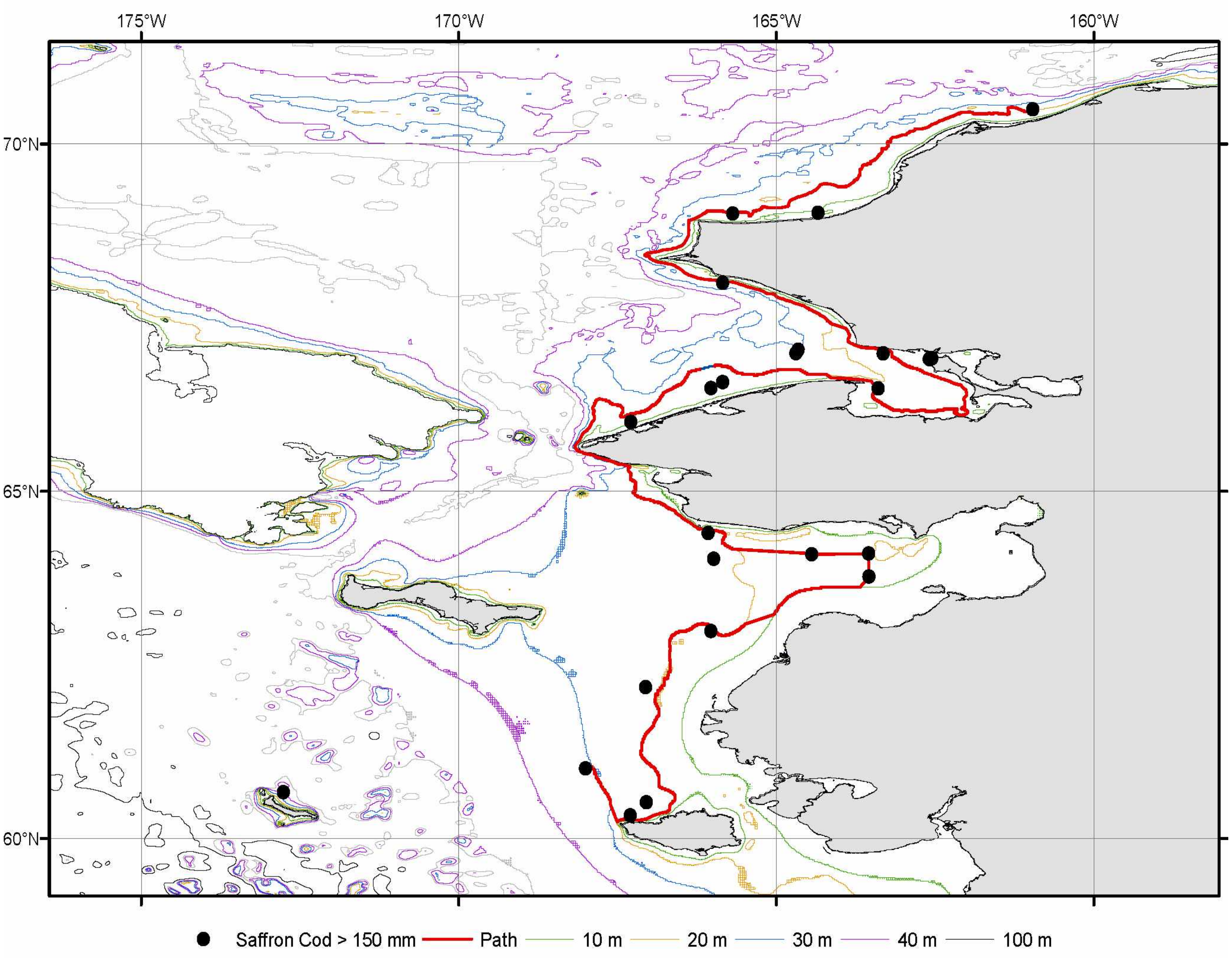
Supplements

Supporting Figure 1. Distances (km) between collections in northwestern Alaska.



Supporting Table 1. Allele frequencies at each locus (*n*=9) and each collection (*n*=40).

Elgr07

	Collection														
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A	R04
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000
119	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
123	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
127	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.015	0.014	0.014	0.000	0.000	0.000	0.000	0.500
131	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.007	0.000	0.000	0.000	0.000	0.000
135	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.025	0.028	0.000	0.083	0.000	0.000	0.000	0.000
139	0.000	0.000	0.000	0.000	0.031	0.000	0.010	0.005	0.000	0.020	0.000	0.083	0.000	0.000	0.000
143	0.000	0.000	0.000	0.000	0.063	0.200	0.040	0.020	0.042	0.030	0.083	0.000	0.125	0.125	0.000
147	0.000	0.000	0.000	0.250	0.063	0.050	0.030	0.066	0.111	0.040	0.000	0.083	0.000	0.000	0.000
151	0.000	0.500	0.125	0.250	0.125	0.050	0.080	0.126	0.097	0.101	0.167	0.167	0.125	0.125	0.000
155	0.000	0.000	0.250	0.250	0.188	0.300	0.150	0.146	0.236	0.200	0.000	0.083	0.000	0.000	0.000
159	0.000	0.500	0.250	0.000	0.063	0.100	0.190	0.177	0.153	0.182	0.167	0.000	0.250	0.375	0.000
163	0.000	0.000	0.375	0.000	0.188	0.100	0.250	0.278	0.181	0.196	0.333	0.417	0.125	0.125	0.000
167	0.000	0.000	0.000	0.000	0.063	0.050	0.080	0.025	0.042	0.081	0.000	0.000	0.375	0.000	0.500
171	0.500	0.000	0.000	0.250	0.094	0.000	0.070	0.025	0.014	0.061	0.083	0.167	0.000	0.125	0.000
175	0.500	0.000	0.000	0.000	0.031	0.150	0.070	0.056	0.069	0.041	0.083	0.000	0.000	0.000	0.000
179	0.000	0.000	0.000	0.000	0.031	0.000	0.010	0.010	0.000	0.020	0.000	0.000	0.000	0.125	0.000
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000
187	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.007	0.000	0.000	0.000	0.000	0.000
191	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
195	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
199	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
235	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
331	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	49	98	36	72	6	6	4	4	1

Supporting Table 1 (continued)

Elgr07

	Collection													
Allele	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE	PWSF
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
119	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
123	0.000	0.050	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
127	0.000	0.000	0.000	0.000	0.014	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
131	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
135	0.024	0.000	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
139	0.000	0.000	0.000	0.046	0.014	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
143	0.095	0.050	0.083	0.182	0.054	0.058	0.000	0.071	0.000	0.000	0.000	0.000	0.000	0.000
147	0.048	0.050	0.000	0.000	0.027	0.023	0.100	0.071	0.125	0.000	0.000	0.000	0.010	0.000
151	0.119	0.143	0.167	0.045	0.149	0.116	0.100	0.357	0.000	0.055	0.036	0.000	0.010	0.000
155	0.238	0.113	0.250	0.183	0.176	0.209	0.100	0.143	0.625	0.143	0.143	0.167	0.092	0.000
159	0.095	0.153	0.083	0.136	0.162	0.081	0.500	0.214	0.125	0.250	0.321	0.000	0.235	0.000
163	0.190	0.220	0.000	0.227	0.203	0.198	0.000	0.000	0.000	0.500	0.464	0.667	0.602	0.000
167	0.095	0.050	0.167	0.046	0.054	0.093	0.100	0.000	0.000	0.004	0.000	0.000	0.041	0.000
171	0.000	0.073	0.083	0.046	0.054	0.023	0.100	0.071	0.125	0.025	0.000	0.167	0.010	0.000
175	0.095	0.050	0.083	0.091	0.068	0.081	0.000	0.071	0.000	0.006	0.000	0.000	0.000	0.000
179	0.000	0.025	0.000	0.000	0.027	0.023	0.000	0.000	0.000	0.018	0.036	0.000	0.000	0.000
183	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
187	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
191	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
195	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
199	0.000	0.000	0.083	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
235	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
331	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	21	21	6	11	37	43	5	7	4	75	14	3	49	0

Supporting Table 1 (continued)

Elgr07

	Collection										
Allele	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
115	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
119	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
123	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
127	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000
131	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.025	0.000
135	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.013	0.015	0.017	0.000
139	0.000	0.000	0.000	0.000	0.000	0.041	0.043	0.009	0.010	0.006	0.012
143	0.000	0.000	0.000	0.000	0.000	0.071	0.052	0.071	0.045	0.047	0.012
147	0.000	0.000	0.000	0.000	0.000	0.041	0.091	0.119	0.045	0.035	0.024
151	0.000	0.000	0.021	0.000	0.000	0.122	0.161	0.124	0.050	0.093	0.042
155	0.375	0.156	0.146	0.000	0.125	0.133	0.174	0.208	0.250	0.198	0.107
159	0.125	0.125	0.333	0.000	0.313	0.153	0.152	0.133	0.210	0.145	0.244
163	0.250	0.719	0.500	0.500	0.500	0.224	0.157	0.155	0.175	0.215	0.167
167	0.125	0.000	0.000	0.500	0.063	0.061	0.065	0.066	0.065	0.064	0.214
171	0.000	0.000	0.000	0.000	0.000	0.041	0.052	0.040	0.020	0.050	0.060
175	0.125	0.000	0.000	0.000	0.000	0.082	0.026	0.035	0.075	0.065	0.024
179	0.000	0.000	0.000	0.000	0.000	0.010	0.004	0.000	0.010	0.012	0.065
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.005	0.012	0.018
187	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.004	0.000	0.000	0.006
191	0.000	0.000	0.000	0.000	0.000	0.010	0.004	0.009	0.000	0.006	0.006
195	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
199	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000
235	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
267	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000
331	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
n	4	16	24	1	8	49	115	113	99	85	84

Supporting Table 1 (continued)

Elgr11

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
192	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.050	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
200	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
204	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
208	0.000	0.000	0.000	0.250	0.219	0.050	0.080	0.111	0.139	0.175	0.083	0.250	0.250	0.150
212	0.000	0.000	0.000	0.000	0.219	0.150	0.190	0.106	0.125	0.128	0.167	0.000	0.375	0.250
216	0.000	0.500	0.125	0.250	0.031	0.150	0.070	0.071	0.125	0.065	0.083	0.000	0.125	0.000
220	0.000	0.000	0.500	0.250	0.313	0.250	0.260	0.308	0.250	0.265	0.167	0.250	0.250	0.000
224	0.500	0.500	0.000	0.000	0.031	0.050	0.060	0.066	0.069	0.087	0.000	0.000	0.000	0.150
228	0.000	0.000	0.000	0.000	0.094	0.000	0.040	0.035	0.069	0.081	0.083	0.000	0.000	0.150
232	0.000	0.000	0.000	0.000	0.063	0.050	0.050	0.091	0.025	0.034	0.000	0.167	0.000	0.000
236	0.000	0.000	0.125	0.000	0.000	0.050	0.010	0.066	0.045	0.000	0.083	0.083	0.000	0.000
240	0.000	0.000	0.125	0.000	0.000	0.050	0.040	0.015	0.027	0.041	0.083	0.000	0.000	0.000
244	0.000	0.000	0.000	0.250	0.031	0.000	0.070	0.020	0.056	0.034	0.083	0.083	0.000	0.000
248	0.500	0.000	0.125	0.000	0.000	0.100	0.040	0.045	0.042	0.041	0.083	0.000	0.000	0.150
252	0.000	0.000	0.000	0.000	0.000	0.000	0.060	0.010	0.000	0.013	0.000	0.083	0.000	0.000
256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.014	0.000	0.000	0.000	0.000
264	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.005	0.014	0.005	0.000	0.083	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.014	0.000	0.000	0.000	0.000	0.000
276	0.000	0.000	0.000	0.000	0.000	0.050	0.000	0.010	0.000	0.013	0.083	0.000	0.000	0.000
280	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.150
284	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
288	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	50	99	35	74	6	6	4	4

Supporting Table 1 (continued)

Elgr11

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
192	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
200	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010
204	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.010
208	0.000	0.119	0.095	0.083	0.125	0.125	0.093	0.200	0.143	0.000	0.513	0.525	0.667	0.622
212	0.000	0.214	0.143	0.167	0.125	0.125	0.225	0.300	0.286	0.250	0.025	0.125	0.000	0.061
216	0.000	0.095	0.071	0.000	0.215	0.043	0.053	0.100	0.000	0.000	0.125	0.110	0.333	0.255
220	0.000	0.286	0.381	0.417	0.215	0.225	0.198	0.200	0.286	0.250	0.082	0.058	0.000	0.031
224	0.500	0.000	0.095	0.000	0.050	0.068	0.070	0.000	0.071	0.250	0.000	0.000	0.000	0.010
228	0.000	0.048	0.048	0.083	0.000	0.095	0.093	0.000	0.000	0.250	0.025	0.000	0.000	0.000
232	0.000	0.048	0.071	0.083	0.050	0.054	0.058	0.000	0.143	0.000	0.100	0.125	0.000	0.000
236	0.000	0.000	0.024	0.083	0.000	0.054	0.012	0.000	0.071	0.000	0.000	0.000	0.000	0.000
240	0.000	0.048	0.000	0.000	0.000	0.027	0.047	0.000	0.000	0.000	0.075	0.058	0.000	0.000
244	0.500	0.024	0.048	0.000	0.000	0.068	0.070	0.000	0.000	0.000	0.005	0.000	0.000	0.000
248	0.000	0.048	0.024	0.000	0.120	0.068	0.047	0.000	0.000	0.000	0.000	0.000	0.000	0.000
252	0.000	0.048	0.000	0.083	0.050	0.038	0.012	0.100	0.000	0.000	0.000	0.000	0.000	0.000
256	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.025	0.000	0.000	0.000
264	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.024	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
276	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
280	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
284	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
288	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	21	6	9	36	42	5	7	4	70	12	3	49

Supporting Table 1 (continued)

Elgr11

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
192	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006
196	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
200	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
204	0.000	0.000	0.063	0.042	0.000	0.111	0.000	0.017	0.025	0.025	0.006	0.000
208	0.000	0.750	0.500	0.583	1.000	0.444	0.102	0.152	0.035	0.025	0.140	0.119
212	0.000	0.125	0.125	0.063	0.000	0.000	0.133	0.035	0.035	0.125	0.087	0.143
216	1.000	0.125	0.219	0.188	0.000	0.278	0.102	0.057	0.062	0.100	0.105	0.071
220	0.000	0.000	0.031	0.042	0.000	0.111	0.163	0.113	0.248	0.240	0.302	0.232
224	0.000	0.000	0.000	0.000	0.000	0.000	0.061	0.217	0.137	0.075	0.081	0.071
228	0.000	0.000	0.000	0.000	0.000	0.000	0.051	0.091	0.035	0.100	0.087	0.101
232	0.000	0.000	0.000	0.000	0.000	0.000	0.092	0.109	0.075	0.050	0.058	0.036
236	0.000	0.000	0.063	0.063	0.000	0.056	0.041	0.030	0.048	0.053	0.029	0.042
240	0.000	0.000	0.000	0.021	0.000	0.000	0.031	0.022	0.040	0.020	0.017	0.030
244	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.035	0.053	0.055	0.047	0.036
248	0.000	0.000	0.000	0.000	0.000	0.000	0.112	0.057	0.088	0.053	0.023	0.054
252	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.030	0.031	0.025	0.006	0.042
256	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.022	0.025	0.006	0.000
260	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.018	0.000	0.000	0.006
264	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.027	0.025	0.000	0.006
268	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.005	0.000	0.000	0.006
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
276	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.005	0.005	0.000	0.000
280	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
284	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000
288	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
n	1	4	16	24	1	9	49	115	111	99	86	84

Supporting Table 1 (continued)

Elgr13

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
214	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
218	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
222	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
226	0.000	0.000	0.000	0.000	0.000	0.000	0.030	0.010	0.000	0.007	0.250	0.000	0.000	0.000
230	0.000	0.000	0.000	0.000	0.031	0.000	0.010	0.035	0.050	0.000	0.083	0.167	0.000	0.000
234	0.000	0.000	0.125	0.000	0.000	0.000	0.020	0.051	0.028	0.054	0.000	0.000	0.000	0.000
238	0.500	0.000	0.250	0.000	0.094	0.050	0.200	0.136	0.125	0.135	0.000	0.083	0.250	0.000
242	0.500	0.000	0.000	0.000	0.094	0.050	0.070	0.062	0.050	0.074	0.000	0.167	0.000	0.375
246	0.000	0.000	0.125	0.500	0.063	0.150	0.140	0.100	0.167	0.176	0.083	0.167	0.000	0.125
250	0.000	0.000	0.125	0.000	0.156	0.200	0.210	0.172	0.195	0.162	0.250	0.000	0.375	0.375
254	0.000	1.000	0.250	0.250	0.188	0.200	0.170	0.207	0.167	0.196	0.083	0.083	0.125	0.000
258	0.000	0.000	0.000	0.000	0.156	0.050	0.020	0.076	0.075	0.054	0.083	0.000	0.125	0.000
262	0.000	0.000	0.000	0.000	0.031	0.150	0.020	0.030	0.014	0.034	0.000	0.167	0.000	0.000
266	0.000	0.000	0.000	0.000	0.063	0.000	0.010	0.030	0.080	0.007	0.000	0.083	0.000	0.000
270	0.000	0.000	0.000	0.250	0.031	0.100	0.020	0.040	0.000	0.034	0.083	0.000	0.125	0.000
274	0.000	0.000	0.000	0.000	0.031	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000	0.125
278	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.025	0.025	0.020	0.083	0.083	0.000	0.000
282	0.000	0.000	0.125	0.000	0.000	0.050	0.040	0.015	0.000	0.034	0.000	0.000	0.000	0.000
286	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000
294	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
298	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	50	99	34	72	6	6	4	4

Supporting Table 1 (continued)

Elgr13

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
214	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.000	0.000	0.000	0.000	0.000
218	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
222	0.000	0.024	0.000	0.000	0.000	0.014	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000
226	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000
230	0.000	0.024	0.000	0.000	0.000	0.014	0.058	0.000	0.000	0.000	0.044	0.031	0.000	0.000
234	0.000	0.024	0.024	0.000	0.000	0.014	0.012	0.000	0.000	0.125	0.000	0.000	0.000	0.000
238	0.000	0.119	0.119	0.125	0.182	0.203	0.174	0.000	0.125	0.125	0.030	0.031	0.000	0.071
242	0.000	0.024	0.119	0.375	0.091	0.108	0.070	0.000	0.125	0.000	0.013	0.000	0.000	0.000
246	0.000	0.095	0.095	0.125	0.136	0.149	0.128	0.000	0.225	0.125	0.076	0.000	0.000	0.000
250	0.000	0.286	0.095	0.125	0.364	0.081	0.081	0.400	0.225	0.000	0.295	0.469	0.500	0.388
254	0.500	0.167	0.238	0.125	0.091	0.149	0.233	0.200	0.000	0.125	0.285	0.250	0.500	0.408
258	0.000	0.143	0.190	0.125	0.045	0.014	0.070	0.000	0.075	0.000	0.076	0.063	0.000	0.041
262	0.000	0.024	0.048	0.000	0.000	0.122	0.070	0.000	0.000	0.000	0.000	0.000	0.000	0.000
266	0.000	0.024	0.000	0.000	0.091	0.081	0.012	0.000	0.075	0.000	0.000	0.000	0.000	0.000
270	0.000	0.048	0.024	0.000	0.000	0.000	0.023	0.200	0.075	0.000	0.000	0.000	0.000	0.000
274	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.076	0.063	0.000	0.010
278	0.500	0.000	0.048	0.000	0.000	0.000	0.035	0.000	0.075	0.000	0.000	0.000	0.000	0.000
282	0.000	0.000	0.000	0.000	0.000	0.014	0.023	0.000	0.000	0.375	0.055	0.063	0.000	0.061
286	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.025	0.031	0.000	0.020
294	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
298	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	21	4	11	36	43	3	5	4	78	16	3	49

Supporting Table 1 (continued)

Elgr13

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
214	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.004	0.000	0.006	0.000
218	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.006	0.012
222	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.006
226	0.000	0.000	0.000	0.000	0.000	0.000	0.055	0.000	0.000	0.000	0.029	0.006
230	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.020	0.029	0.012
234	0.000	0.000	0.000	0.000	0.000	0.000	0.051	0.009	0.000	0.020	0.017	0.012
238	0.500	0.000	0.094	0.104	0.000	0.000	0.102	0.096	0.097	0.130	0.105	0.101
242	0.000	0.000	0.000	0.000	0.000	0.056	0.122	0.078	0.146	0.045	0.047	0.101
246	0.000	0.000	0.031	0.000	0.000	0.444	0.122	0.165	0.177	0.095	0.145	0.119
250	0.000	0.750	0.438	0.313	0.500	0.445	0.184	0.126	0.164	0.205	0.169	0.161
254	0.500	0.250	0.344	0.396	0.500	0.000	0.112	0.174	0.181	0.220	0.186	0.208
258	0.000	0.000	0.063	0.104	0.000	0.000	0.071	0.113	0.071	0.075	0.070	0.065
262	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.065	0.027	0.040	0.064	0.060
266	0.000	0.000	0.000	0.000	0.000	0.000	0.033	0.035	0.035	0.045	0.058	0.048
270	0.000	0.000	0.000	0.000	0.000	0.000	0.055	0.043	0.031	0.025	0.023	0.024
274	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.026	0.009	0.020	0.029	0.012
278	0.000	0.000	0.000	0.000	0.000	0.056	0.010	0.013	0.031	0.025	0.012	0.018
282	0.000	0.000	0.031	0.063	0.000	0.000	0.020	0.017	0.009	0.010	0.000	0.030
286	0.000	0.000	0.000	0.021	0.000	0.000	0.000	0.022	0.009	0.005	0.000	0.006
294	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.006	0.000
298	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.004	0.000	0.000	0.000
n	1	4	16	24	1	8	46	115	113	100	86	81

Supporting Table 1 (continued)

Elgr14

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
310	0.000	0.000	0.000	0.250	0.000	0.000	0.000	0.005	0.000	0.007	0.000	0.167	0.125	0.000
314	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.000	0.000	0.000	0.000	0.000
318	0.000	0.000	0.125	0.000	0.000	0.000	0.000	0.030	0.000	0.007	0.000	0.000	0.000	0.125
322	0.000	0.000	0.125	0.000	0.035	0.050	0.050	0.030	0.075	0.054	0.083	0.083	0.000	0.250
326	0.000	0.000	0.000	0.000	0.095	0.150	0.070	0.025	0.076	0.081	0.000	0.000	0.000	0.000
330	0.000	0.000	0.125	0.250	0.098	0.000	0.090	0.081	0.025	0.081	0.167	0.167	0.125	0.000
334	0.000	1.000	0.125	0.250	0.035	0.000	0.070	0.101	0.056	0.088	0.250	0.250	0.375	0.375
338	0.000	0.000	0.125	0.000	0.000	0.000	0.060	0.076	0.028	0.027	0.000	0.167	0.250	0.000
342	0.000	0.000	0.125	0.250	0.095	0.150	0.070	0.111	0.056	0.047	0.000	0.000	0.000	0.000
346	0.000	0.000	0.250	0.000	0.095	0.300	0.150	0.167	0.181	0.169	0.167	0.083	0.000	0.125
350	0.500	0.000	0.000	0.000	0.300	0.100	0.120	0.157	0.190	0.182	0.083	0.083	0.125	0.125
354	0.500	0.000	0.000	0.000	0.063	0.100	0.070	0.045	0.043	0.027	0.083	0.000	0.000	0.000
358	0.000	0.000	0.000	0.000	0.063	0.150	0.120	0.076	0.069	0.108	0.167	0.000	0.000	0.000
362	0.000	0.000	0.000	0.000	0.060	0.000	0.080	0.040	0.125	0.061	0.000	0.000	0.000	0.000
366	0.000	0.000	0.000	0.000	0.063	0.000	0.050	0.040	0.025	0.061	0.000	0.000	0.000	0.000
370	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.000	0.000
374	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
378	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000
n	1	1	4	2	15	10	46	99	33	70	6	6	4	4

Supporting Table 1 (continued)

Elgr14

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
310	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
314	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.250	0.000	0.375	0.000	0.000	0.000	0.000
318	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.250	0.071	0.000	0.000	0.000	0.000	0.000
322	0.000	0.024	0.050	0.000	0.045	0.041	0.081	0.000	0.000	0.000	0.000	0.000	0.000	0.000
326	0.000	0.095	0.071	0.150	0.136	0.135	0.081	0.000	0.000	0.000	0.010	0.000	0.000	0.000
330	1.000	0.071	0.093	0.450	0.045	0.054	0.070	0.000	0.071	0.125	0.000	0.000	0.000	0.000
334	0.000	0.095	0.000	0.000	0.045	0.027	0.070	0.250	0.357	0.125	0.183	0.136	0.167	0.239
338	0.000	0.071	0.050	0.000	0.000	0.000	0.012	0.000	0.286	0.375	0.077	0.136	0.000	0.000
342	0.000	0.095	0.071	0.000	0.045	0.014	0.105	0.125	0.071	0.000	0.279	0.364	0.500	0.466
346	0.000	0.167	0.095	0.275	0.136	0.216	0.233	0.000	0.000	0.000	0.125	0.182	0.000	0.000
350	0.000	0.119	0.250	0.000	0.182	0.230	0.140	0.000	0.000	0.000	0.163	0.136	0.000	0.000
354	0.000	0.024	0.050	0.000	0.045	0.068	0.000	0.125	0.071	0.000	0.000	0.000	0.000	0.000
358	0.000	0.095	0.095	0.000	0.045	0.122	0.128	0.000	0.071	0.000	0.000	0.000	0.000	0.023
362	0.000	0.095	0.125	0.125	0.045	0.054	0.035	0.000	0.000	0.000	0.077	0.045	0.333	0.227
366	0.000	0.048	0.000	0.000	0.136	0.014	0.012	0.000	0.000	0.000	0.077	0.000	0.000	0.045
370	0.000	0.000	0.050	0.000	0.091	0.027	0.023	0.000	0.000	0.000	0.010	0.000	0.000	0.000
374	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
378	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	19	5	11	37	43	4	7	4	52	11	3	44

Supporting Table 1 (continued)

Elgr14

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
310	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
314	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.006	0.000
318	0.000	0.000	0.000	0.000	0.000	0.000	0.021	0.000	0.014	0.000	0.006	0.000
322	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.070	0.041	0.033
326	0.000	0.000	0.000	0.000	0.000	0.000	0.052	0.017	0.055	0.085	0.070	0.059
330	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.074	0.036	0.070	0.035	0.053
334	0.000	0.125	0.267	0.326	0.500	0.222	0.115	0.109	0.132	0.100	0.105	0.059
338	0.000	0.000	0.000	0.022	0.000	0.000	0.021	0.030	0.050	0.040	0.052	0.086
342	0.500	0.375	0.233	0.261	0.500	0.333	0.125	0.091	0.064	0.095	0.081	0.099
346	0.000	0.000	0.000	0.000	0.000	0.111	0.135	0.122	0.132	0.160	0.169	0.066
350	0.000	0.000	0.000	0.000	0.000	0.000	0.260	0.187	0.195	0.160	0.186	0.184
354	0.000	0.125	0.000	0.000	0.000	0.000	0.042	0.091	0.073	0.030	0.029	0.125
358	0.000	0.000	0.000	0.000	0.000	0.056	0.083	0.104	0.109	0.095	0.145	0.092
362	0.000	0.375	0.267	0.283	0.000	0.222	0.094	0.096	0.086	0.045	0.047	0.079
366	0.500	0.000	0.200	0.109	0.000	0.056	0.021	0.052	0.032	0.020	0.012	0.033
370	0.000	0.000	0.033	0.000	0.000	0.000	0.010	0.013	0.005	0.030	0.017	0.033
374	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.009	0.000	0.000	0.000
378	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
n	1	4	15	23	1	9	48	115	110	100	86	76

Supporting Table 1 (continued)

Elgr23

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
138	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.000
142	0.000	0.000	0.000	0.000	0.000	0.050	0.010	0.000	0.014	0.013	0.000	0.000	0.000	0.000
146	0.000	0.000	0.000	0.000	0.031	0.050	0.010	0.035	0.014	0.026	0.083	0.083	0.125	0.000
150	0.000	0.000	0.000	0.250	0.000	0.100	0.080	0.040	0.029	0.030	0.000	0.083	0.000	0.125
154	1.000	0.500	0.500	0.000	0.094	0.150	0.100	0.100	0.086	0.109	0.083	0.083	0.500	0.125
158	0.000	0.000	0.000	0.000	0.031	0.050	0.090	0.135	0.071	0.090	0.167	0.250	0.000	0.125
162	0.000	0.000	0.000	0.000	0.219	0.100	0.090	0.115	0.100	0.128	0.167	0.000	0.000	0.000
166	0.000	0.500	0.250	0.250	0.344	0.150	0.210	0.220	0.214	0.205	0.083	0.250	0.250	0.250
170	0.000	0.000	0.000	0.250	0.156	0.250	0.160	0.145	0.171	0.122	0.167	0.167	0.000	0.125
174	0.000	0.000	0.000	0.000	0.031	0.000	0.090	0.040	0.057	0.058	0.000	0.000	0.000	0.125
178	0.000	0.000	0.000	0.250	0.000	0.000	0.050	0.040	0.043	0.045	0.083	0.000	0.000	0.000
182	0.000	0.000	0.125	0.000	0.000	0.000	0.040	0.045	0.000	0.026	0.083	0.000	0.000	0.000
186	0.000	0.000	0.000	0.000	0.000	0.050	0.000	0.015	0.043	0.026	0.000	0.000	0.000	0.000
190	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.010	0.029	0.030	0.000	0.000	0.000	0.000
194	0.000	0.000	0.125	0.000	0.094	0.050	0.030	0.040	0.086	0.061	0.083	0.000	0.125	0.000
198	0.000	0.000	0.000	0.000	0.000	0.000	0.030	0.015	0.029	0.007	0.000	0.000	0.000	0.125
202	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.083	0.000	0.000
206	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	50	99	35	74	6	6	4	4

Supporting Table 1 (continued)

Elgr23

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
138	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
142	0.000	0.000	0.024	0.000	0.045	0.028	0.035	0.000	0.000	0.000	0.000	0.000	0.000	0.000
146	0.000	0.024	0.000	0.000	0.045	0.056	0.047	0.000	0.071	0.000	0.000	0.000	0.000	0.000
150	0.000	0.048	0.048	0.000	0.000	0.028	0.035	0.000	0.143	0.000	0.000	0.000	0.000	0.000
154	0.000	0.095	0.214	0.100	0.000	0.139	0.163	0.300	0.071	0.000	0.000	0.000	0.000	0.020
158	1.000	0.048	0.024	0.300	0.091	0.069	0.070	0.000	0.071	0.000	0.007	0.000	0.000	0.051
162	0.000	0.119	0.143	0.000	0.091	0.083	0.070	0.000	0.000	0.250	0.120	0.067	0.000	0.102
166	0.000	0.286	0.190	0.200	0.273	0.278	0.186	0.500	0.214	0.500	0.313	0.367	0.333	0.265
170	0.000	0.167	0.119	0.200	0.182	0.167	0.140	0.100	0.214	0.000	0.553	0.533	0.667	0.520
174	0.000	0.000	0.071	0.000	0.045	0.014	0.058	0.000	0.071	0.000	0.000	0.033	0.000	0.031
178	0.000	0.048	0.048	0.100	0.045	0.056	0.035	0.000	0.071	0.000	0.000	0.000	0.000	0.010
182	0.000	0.071	0.000	0.000	0.000	0.014	0.047	0.100	0.071	0.000	0.000	0.000	0.000	0.000
186	0.000	0.000	0.024	0.000	0.000	0.028	0.035	0.000	0.000	0.125	0.000	0.000	0.000	0.000
190	0.000	0.048	0.024	0.000	0.091	0.000	0.012	0.000	0.000	0.000	0.007	0.000	0.000	0.000
194	0.000	0.048	0.071	0.100	0.045	0.014	0.047	0.000	0.000	0.000	0.000	0.000	0.000	0.000
198	0.000	0.000	0.000	0.000	0.045	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000
202	0.000	0.000	0.000	0.000	0.000	0.028	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
206	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.125	0.000	0.000	0.000	0.000
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	21	5	11	36	43	5	7	4	75	15	3	49

Supporting Table 1 (continued)

Elgr23

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
138	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.018	0.000	0.000	0.000	0.012
142	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.004	0.010	0.006	0.006
146	0.000	0.000	0.000	0.000	0.000	0.000	0.051	0.053	0.009	0.035	0.012	0.018
150	0.000	0.000	0.000	0.000	0.000	0.000	0.122	0.031	0.049	0.040	0.030	0.018
154	0.000	0.000	0.000	0.042	0.000	0.000	0.102	0.092	0.071	0.110	0.090	0.098
158	0.000	0.000	0.031	0.042	0.000	0.056	0.061	0.114	0.080	0.080	0.114	0.110
162	0.000	0.125	0.031	0.104	0.000	0.167	0.153	0.145	0.164	0.135	0.090	0.122
166	0.500	0.125	0.250	0.250	1.000	0.278	0.143	0.162	0.146	0.185	0.193	0.201
170	0.500	0.750	0.656	0.542	0.000	0.500	0.133	0.118	0.133	0.160	0.193	0.152
174	0.000	0.000	0.031	0.021	0.000	0.000	0.041	0.070	0.128	0.040	0.060	0.061
178	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.079	0.066	0.055	0.066	0.067
182	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.053	0.031	0.065	0.018	0.043
186	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.035	0.058	0.020	0.036	0.030
190	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.018	0.022	0.020	0.024	0.012
194	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.004	0.031	0.040	0.054	0.037
198	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.009	0.000	0.006	0.006
202	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.006	0.006
206	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
210	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	4	16	24	1	9	49	114	113	100	83	82

Supporting Table 1 (continued)

Elgr31

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
179	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
183	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.083	0.000	0.000
187	0.000	0.000	0.000	0.000	0.000	0.000	0.023	0.020	0.000	0.007	0.000	0.000	0.000	0.125
191	0.000	1.000	0.500	0.750	0.313	0.300	0.349	0.283	0.292	0.316	0.167	0.167	0.375	0.250
195	0.000	0.000	0.000	0.000	0.156	0.200	0.058	0.101	0.125	0.079	0.000	0.000	0.000	0.125
199	0.000	0.000	0.375	0.250	0.188	0.200	0.186	0.268	0.292	0.191	0.417	0.083	0.250	0.250
203	0.000	0.000	0.000	0.000	0.219	0.150	0.279	0.237	0.222	0.289	0.250	0.417	0.375	0.125
207	0.500	0.000	0.125	0.000	0.063	0.150	0.081	0.061	0.042	0.066	0.083	0.250	0.000	0.000
211	0.500	0.000	0.000	0.000	0.031	0.000	0.023	0.020	0.028	0.007	0.083	0.000	0.000	0.125
215	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.020	0.000	0.000	0.000	0.000
219	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
323	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
327	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	43	99	36	72	6	6	4	4

Supporting Table 1 (continued)

Elgr31

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
179	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
183	0.000	0.000	0.024	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000
187	0.000	0.024	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.250	0.000	0.000	0.000	0.010
191	0.000	0.429	0.190	0.375	0.227	0.243	0.360	0.167	0.286	0.125	0.513	0.500	0.667	0.490
195	0.000	0.143	0.190	0.250	0.136	0.135	0.116	0.333	0.000	0.125	0.120	0.188	0.000	0.071
199	0.000	0.167	0.214	0.125	0.273	0.216	0.163	0.500	0.286	0.250	0.323	0.281	0.000	0.184
203	0.000	0.167	0.310	0.125	0.227	0.216	0.244	0.000	0.286	0.000	0.044	0.000	0.333	0.153
207	0.000	0.071	0.048	0.125	0.091	0.108	0.035	0.000	0.071	0.250	0.000	0.031	0.000	0.061
211	0.000	0.000	0.024	0.000	0.000	0.081	0.047	0.000	0.000	0.000	0.000	0.000	0.000	0.031
215	0.000	0.000	0.000	0.000	0.045	0.000	0.000	0.000	0.071	0.000	0.000	0.000	0.000	0.000
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
323	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
327	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	0	21	20	4	11	37	43	3	7	4	79	16	3	49

Supporting Table 1 (continued)

Elgr31

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
179	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000
183	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.009	0.000	0.010	0.000	0.012
187	0.000	0.000	0.000	0.021	0.000	0.000	0.000	0.004	0.027	0.000	0.023	0.006
191	0.500	0.167	0.550	0.479	0.500	0.667	0.521	0.580	0.385	0.247	0.285	0.331
195	0.000	0.000	0.000	0.021	0.000	0.000	0.063	0.053	0.102	0.108	0.151	0.072
199	0.000	0.500	0.100	0.104	0.000	0.167	0.177	0.257	0.243	0.263	0.256	0.235
203	0.500	0.333	0.350	0.375	0.500	0.167	0.156	0.062	0.097	0.247	0.209	0.193
207	0.000	0.000	0.000	0.000	0.000	0.000	0.042	0.018	0.102	0.093	0.041	0.078
211	0.000	0.000	0.000	0.000	0.000	0.000	0.031	0.018	0.040	0.031	0.029	0.066
215	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.006
219	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
227	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
323	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
327	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	3	10	24	1	9	48	113	113	97	86	83

Supporting Table 1 (continued)

Elgr38

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.014	0.000	0.000	0.000	0.000	0.000
116	0.000	0.000	0.000	0.250	0.031	0.000	0.080	0.071	0.069	0.068	0.125	0.000	0.125	0.125
120	0.000	0.000	0.000	0.250	0.031	0.000	0.220	0.172	0.208	0.243	0.188	0.000	0.000	0.000
124	0.000	0.000	0.625	0.000	0.156	0.100	0.140	0.197	0.222	0.176	0.156	0.250	0.000	0.125
128	0.000	0.500	0.125	0.000	0.250	0.200	0.230	0.237	0.181	0.223	0.125	0.417	0.375	0.250
132	0.000	0.500	0.000	0.000	0.219	0.100	0.020	0.040	0.014	0.041	0.063	0.000	0.125	0.125
136	0.500	0.000	0.000	0.000	0.188	0.250	0.100	0.071	0.097	0.054	0.156	0.000	0.000	0.000
140	0.000	0.000	0.250	0.500	0.031	0.000	0.180	0.192	0.181	0.162	0.156	0.333	0.375	0.375
144	0.000	0.000	0.000	0.000	0.063	0.100	0.010	0.010	0.014	0.020	0.031	0.000	0.000	0.000
148	0.500	0.000	0.000	0.000	0.000	0.200	0.020	0.015	0.000	0.014	0.000	0.000	0.000	0.000
152	0.000	0.000	0.000	0.000	0.031	0.050	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	50	99	36	74	6	6	4	4

Supporting Table 1 (continued)

Elgr38

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
112	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
116	0.000	0.167	0.100	0.000	0.091	0.000	0.058	0.100	0.071	0.000	0.000	0.000	0.167	0.010
120	0.000	0.238	0.125	0.200	0.136	0.000	0.186	0.200	0.000	0.250	0.000	0.000	0.167	0.153
124	0.500	0.214	0.275	0.200	0.091	0.054	0.221	0.200	0.357	0.375	0.000	0.000	0.167	0.612
128	0.000	0.119	0.125	0.100	0.091	0.216	0.233	0.300	0.214	0.250	0.000	0.000	0.167	0.051
132	0.000	0.000	0.075	0.200	0.045	0.176	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.010
136	0.500	0.048	0.075	0.000	0.182	0.257	0.047	0.000	0.000	0.125	0.000	0.000	0.000	0.122
140	0.000	0.214	0.225	0.200	0.227	0.027	0.221	0.200	0.286	0.000	0.000	0.000	0.333	0.000
144	0.000	0.000	0.000	0.100	0.045	0.041	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.041
148	0.000	0.000	0.000	0.000	0.045	0.189	0.012	0.000	0.071	0.000	0.000	0.000	0.000	0.000
152	0.000	0.000	0.000	0.000	0.045	0.027	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
156	0.000	0.000	0.000	0.000	0.000	0.014	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	20	5	11	37	43	5	7	4	0	0	3	49

Supporting Table 1 (continued)

Elgr38

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
112	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.004	0.000	0.000	0.006
116	0.000	0.000	0.000	0.022	0.000	0.000	0.143	0.026	0.013	0.071	0.047	0.107
120	0.500	0.125	0.094	0.239	0.500	0.222	0.163	0.298	0.261	0.230	0.244	0.202
124	0.500	0.625	0.625	0.370	0.500	0.500	0.153	0.307	0.190	0.219	0.221	0.155
128	0.000	0.000	0.000	0.087	0.000	0.056	0.204	0.175	0.195	0.112	0.186	0.202
132	0.000	0.000	0.000	0.022	0.000	0.000	0.051	0.127	0.133	0.020	0.023	0.042
136	0.000	0.125	0.156	0.174	0.000	0.000	0.133	0.044	0.080	0.071	0.064	0.101
140	0.000	0.000	0.031	0.065	0.000	0.056	0.112	0.017	0.093	0.260	0.180	0.167
144	0.000	0.125	0.094	0.022	0.000	0.167	0.010	0.004	0.027	0.010	0.000	0.012
148	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.005	0.029	0.006
152	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.006	0.000
156	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
176	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
n	1	4	16	23	1	9	49	114	113	98	86	84

Supporting Table 1 (continued)

Elgr44

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
208	0.000	0.000	0.000	0.000	0.000	0.050	0.000	0.000	0.000	0.027	0.083	0.000	0.000	0.000
212	0.500	0.000	0.125	0.250	0.000	0.000	0.031	0.056	0.028	0.088	0.000	0.000	0.000	0.000
216	0.000	0.000	0.000	0.000	0.000	0.000	0.051	0.040	0.042	0.034	0.083	0.000	0.000	0.000
220	0.000	0.000	0.125	0.000	0.031	0.000	0.031	0.005	0.028	0.014	0.083	0.000	0.125	0.000
224	0.000	0.000	0.000	0.000	0.031	0.050	0.010	0.025	0.028	0.014	0.000	0.000	0.000	0.000
228	0.000	0.000	0.125	0.000	0.063	0.000	0.071	0.076	0.097	0.068	0.167	0.000	0.125	0.125
232	0.000	0.000	0.000	0.000	0.219	0.150	0.143	0.152	0.125	0.162	0.083	0.250	0.000	0.000
236	0.000	0.000	0.250	0.000	0.125	0.100	0.184	0.131	0.083	0.115	0.250	0.083	0.000	0.125
240	0.000	0.000	0.125	0.000	0.188	0.150	0.082	0.121	0.111	0.108	0.000	0.000	0.000	0.125
244	0.000	0.000	0.000	0.000	0.031	0.150	0.071	0.076	0.042	0.047	0.000	0.083	0.375	0.250
248	0.500	0.500	0.125	0.250	0.125	0.100	0.092	0.056	0.153	0.095	0.083	0.083	0.250	0.000
252	0.000	0.000	0.125	0.000	0.000	0.050	0.020	0.071	0.083	0.047	0.167	0.083	0.000	0.000
256	0.000	0.000	0.000	0.000	0.094	0.000	0.102	0.096	0.083	0.101	0.000	0.167	0.125	0.125
260	0.000	0.500	0.000	0.500	0.063	0.100	0.041	0.030	0.056	0.054	0.000	0.083	0.000	0.250
264	0.000	0.000	0.000	0.000	0.031	0.100	0.041	0.035	0.042	0.007	0.000	0.083	0.000	0.000
268	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.020	0.000	0.000	0.000	0.083	0.000	0.000
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.007	0.000	0.000	0.000	0.000
276	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.007	0.000	0.000	0.000	0.000
280	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.005	0.000	0.007	0.000	0.000	0.000	0.000
284	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
288	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
292	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
296	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
304	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
316	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	49	99	36	74	6	6	4	4

Supporting Table 1 (continued)

Elgr44

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
208	0.000	0.000	0.000	0.000	0.091	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
212	0.000	0.048	0.068	0.000	0.045	0.068	0.012	0.000	0.000	0.250	0.006	0.000	0.000	0.000
216	0.000	0.071	0.000	0.000	0.000	0.054	0.035	0.000	0.000	0.000	0.000	0.000	0.000	0.000
220	0.000	0.048	0.000	0.000	0.045	0.014	0.035	0.000	0.000	0.000	0.006	0.000	0.000	0.000
224	0.000	0.048	0.000	0.000	0.000	0.000	0.000	0.100	0.071	0.000	0.006	0.031	0.000	0.010
228	0.000	0.095	0.045	0.083	0.091	0.014	0.047	0.300	0.214	0.125	0.104	0.125	0.333	0.250
232	0.000	0.071	0.136	0.083	0.091	0.108	0.198	0.100	0.143	0.000	0.078	0.063	0.000	0.031
236	0.500	0.119	0.114	0.250	0.000	0.149	0.128	0.100	0.000	0.125	0.032	0.000	0.000	0.000
240	0.500	0.119	0.273	0.083	0.136	0.108	0.128	0.100	0.214	0.000	0.026	0.031	0.000	0.000
244	0.000	0.071	0.068	0.083	0.091	0.068	0.058	0.100	0.143	0.125	0.000	0.094	0.000	0.000
248	0.000	0.024	0.045	0.083	0.136	0.068	0.128	0.100	0.000	0.125	0.506	0.375	0.500	0.396
252	0.000	0.048	0.023	0.000	0.045	0.068	0.105	0.000	0.000	0.125	0.143	0.125	0.167	0.313
256	0.000	0.143	0.091	0.083	0.182	0.135	0.058	0.000	0.143	0.125	0.000	0.000	0.000	0.000
260	0.000	0.048	0.000	0.083	0.000	0.068	0.035	0.100	0.000	0.000	0.006	0.000	0.000	0.000
264	0.000	0.048	0.068	0.083	0.000	0.000	0.012	0.000	0.000	0.000	0.078	0.156	0.000	0.000
268	0.000	0.000	0.023	0.000	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
272	0.000	0.000	0.023	0.000	0.000	0.014	0.012	0.000	0.071	0.000	0.006	0.000	0.000	0.000
276	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
280	0.000	0.000	0.000	0.083	0.045	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
284	0.000	0.000	0.000	0.000	0.000	0.000	0.012	0.000	0.000	0.000	0.000	0.000	0.000	0.000
288	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
292	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
296	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
304	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
316	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	21	6	11	37	43	5	7	4	77	16	3	48

Supporting Table 1 (continued)

Elgr44

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
208	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.006
212	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.088	0.062	0.040	0.052	0.036
216	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.009	0.035	0.017	0.012
220	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.000	0.025	0.029	0.006
224	0.000	0.000	0.063	0.021	0.000	0.063	0.020	0.044	0.027	0.030	0.017	0.054
228	0.500	0.500	0.344	0.333	0.500	0.313	0.051	0.062	0.102	0.090	0.041	0.065
232	0.000	0.000	0.094	0.021	0.000	0.000	0.286	0.341	0.296	0.115	0.192	0.131
236	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.124	0.124	0.130	0.151	0.137
240	0.000	0.000	0.000	0.000	0.000	0.000	0.143	0.080	0.133	0.090	0.145	0.149
244	0.000	0.000	0.000	0.021	0.000	0.000	0.041	0.053	0.049	0.070	0.087	0.089
248	0.500	0.375	0.188	0.417	0.000	0.438	0.082	0.044	0.049	0.105	0.041	0.095
252	0.000	0.125	0.313	0.167	0.500	0.188	0.051	0.027	0.027	0.065	0.047	0.060
256	0.000	0.000	0.000	0.021	0.000	0.000	0.071	0.022	0.013	0.120	0.076	0.060
260	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.040	0.027	0.040	0.029	0.036
264	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.018	0.022	0.030	0.052	0.024
268	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.013	0.031	0.005	0.012	0.024
272	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.013	0.005	0.006	0.000
276	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.013	0.000	0.000	0.000
280	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.006	0.012
284	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.006
288	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
292	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.004	0.000	0.000	0.000
296	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
304	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
316	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000
n	1	4	16	24	1	8	49	113	113	100	86	84

Supporting Table 1 (continued)

Elgr45

	Collection													
Allele	J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12	B05	B03A	B03B	A02A
185	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
193	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
197	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.007	0.000	0.000	0.000	0.000
201	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.005	0.000	0.035	0.083	0.083	0.000	0.000
205	0.000	0.000	0.000	0.000	0.031	0.100	0.060	0.101	0.083	0.123	0.333	0.000	0.000	0.125
209	0.000	0.000	0.125	0.000	0.094	0.100	0.160	0.076	0.125	0.082	0.083	0.000	0.667	0.000
213	0.000	0.500	0.375	0.250	0.031	0.150	0.140	0.172	0.264	0.137	0.167	0.250	0.000	0.125
217	0.000	0.000	0.125	0.750	0.281	0.300	0.240	0.172	0.181	0.158	0.083	0.333	0.000	0.375
221	0.000	0.000	0.250	0.000	0.063	0.000	0.070	0.126	0.056	0.130	0.083	0.167	0.167	0.000
225	0.000	0.000	0.125	0.000	0.094	0.100	0.030	0.051	0.069	0.103	0.083	0.000	0.000	0.125
229	0.500	0.000	0.000	0.000	0.250	0.000	0.080	0.076	0.042	0.075	0.083	0.167	0.167	0.000
233	0.000	0.500	0.000	0.000	0.063	0.050	0.030	0.051	0.069	0.027	0.000	0.000	0.000	0.000
237	0.000	0.000	0.000	0.000	0.000	0.050	0.010	0.040	0.028	0.034	0.000	0.000	0.000	0.125
241	0.000	0.000	0.000	0.000	0.000	0.050	0.070	0.035	0.028	0.034	0.000	0.000	0.000	0.000
245	0.000	0.000	0.000	0.000	0.000	0.000	0.040	0.056	0.014	0.027	0.000	0.000	0.000	0.125
249	0.500	0.000	0.000	0.000	0.000	0.100	0.010	0.005	0.014	0.000	0.000	0.000	0.000	0.000
253	0.000	0.000	0.000	0.000	0.063	0.000	0.010	0.010	0.014	0.007	0.000	0.000	0.000	0.000
257	0.000	0.000	0.000	0.000	0.031	0.000	0.000	0.005	0.000	0.021	0.000	0.000	0.000	0.000
261	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.000	0.000	0.000	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.000	0.014	0.000	0.000	0.000	0.000	0.000
277	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000
n	1	1	4	2	16	10	50	99	36	73	6	6	3	4

Supporting Table 1 (continued)

Elgr45

	Collection													
Allele	R04	S04	S05	S06B	S06A	U04	MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE
185	0.000	0.000	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000
189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
193	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
197	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000
201	0.000	0.024	0.048	0.000	0.000	0.000	0.023	0.000	0.000	0.000	0.000	0.000	0.000	0.000
205	0.500	0.095	0.119	0.000	0.092	0.095	0.034	0.000	0.214	0.250	0.000	0.031	0.000	0.000
209	0.000	0.095	0.119	0.167	0.092	0.149	0.170	0.100	0.000	0.000	0.348	0.406	0.167	0.388
213	0.000	0.071	0.286	0.500	0.361	0.216	0.205	0.100	0.143	0.375	0.418	0.406	0.667	0.500
217	0.500	0.238	0.310	0.167	0.136	0.230	0.148	0.300	0.214	0.250	0.215	0.125	0.167	0.061
221	0.000	0.214	0.048	0.083	0.092	0.095	0.114	0.100	0.000	0.125	0.019	0.000	0.000	0.041
225	0.000	0.071	0.048	0.000	0.136	0.081	0.045	0.000	0.143	0.000	0.000	0.031	0.000	0.010
229	0.000	0.071	0.024	0.083	0.045	0.068	0.125	0.100	0.143	0.000	0.000	0.000	0.000	0.000
233	0.000	0.000	0.000	0.000	0.000	0.014	0.011	0.100	0.071	0.000	0.000	0.000	0.000	0.000
237	0.000	0.000	0.000	0.000	0.000	0.000	0.068	0.000	0.000	0.000	0.000	0.000	0.000	0.000
241	0.000	0.024	0.000	0.000	0.045	0.027	0.034	0.000	0.071	0.000	0.000	0.000	0.000	0.000
245	0.000	0.024	0.000	0.000	0.000	0.027	0.000	0.100	0.000	0.000	0.000	0.000	0.000	0.000
249	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
253	0.000	0.071	0.000	0.000	0.000	0.000	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000
257	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
261	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
277	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	21	21	6	11	37	43	5	7	4	79	16	3	49

Supporting Table 1 (continued)

Elgr45

	Collection											
Allele	PWSF	PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI	G02	D02	T05
185	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
189	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.000	0.000	0.000	0.000
193	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
197	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.004	0.000	0.015	0.000	0.000
201	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.013	0.009	0.010	0.012	0.000
205	0.000	0.000	0.000	0.000	0.000	0.000	0.173	0.135	0.111	0.120	0.081	0.083
209	0.000	0.250	0.281	0.333	0.500	0.389	0.102	0.117	0.124	0.100	0.093	0.065
213	1.000	0.500	0.406	0.479	0.000	0.444	0.153	0.178	0.173	0.255	0.209	0.226
217	0.000	0.250	0.219	0.104	0.500	0.111	0.194	0.104	0.164	0.110	0.186	0.244
221	0.000	0.000	0.063	0.063	0.000	0.056	0.041	0.078	0.071	0.110	0.116	0.095
225	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.035	0.049	0.055	0.070	0.048
229	0.000	0.000	0.000	0.000	0.000	0.000	0.102	0.148	0.142	0.075	0.076	0.071
233	0.000	0.000	0.031	0.021	0.000	0.000	0.051	0.043	0.031	0.020	0.023	0.042
237	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.043	0.058	0.065	0.058	0.054
241	0.000	0.000	0.000	0.000	0.000	0.000	0.020	0.043	0.004	0.030	0.035	0.048
245	0.000	0.000	0.000	0.000	0.000	0.000	0.041	0.004	0.022	0.015	0.035	0.018
249	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.018	0.005	0.000	0.000
253	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.013	0.013	0.010	0.000	0.000
257	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.009	0.009	0.000	0.000	0.006
261	0.000	0.000	0.000	0.000	0.000	0.000	0.010	0.004	0.004	0.005	0.006	0.000
265	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
277	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
n	1	4	16	24	1	9	49	115	113	100	86	84

Supporting Table 2. Summary statistics of Saffron Cod microsatellite data. Includes sample size (*n*), inbreeding coefficient (F_{IS}), expected heterozygosity (H_E), effective number of alleles (n_{eff}), and number of alleles (n_a) for each of the 40 collections. Summary over all collections include estimates of heterozygosity (H_T) and fixation indices (F_{ST}). Uncorrected probabilities are: *<0.05; **<0.01; ***<0.001.

		Locus									
Collection	Value	*Elgr07*	*Elgr11*	*Elgr13*	*Elgr14*	*Elgr23*	*Elgr31*	*Elgr38*	*Elgr44*	*Elgr45*	Total
J06B	n	1	1	1	1	1	1	1	1	1	
	F_{IS}	---	---	---	---	---	---	---	---	---	---
	H_E	---	---	---	---	---	---	---	---	---	---
	n_{eff}	---	---	---	---	---	---	---	---	---	---
	n_a	2	2	2	2	1	2	2	2	2	
J06A	n	1	1	1	1	1	1	1	1	1	
	F_{IS}	---	---	---	---	---	---	---	---	---	---
	H_E	---	---	---	---	---	---	---	---	---	---
	n_{eff}	---	---	---	---	---	---	---	---	---	---
	n_a	2	2	2	1	2	1	2	2	2	
G04	n	4	4	4	4	4	4	4	4	4	
	F_{IS}	-0.263	0.053	-0.091	-0.044	0	-0.125	-0.286	0.25	0.143	0.007
	H_E	0.821	0.786	0.929	0.964	0.75	0.679	0.607	0.964	0.857	0.833
	n_{eff}	5.6	4.67	14.08	28	4	3.11	2.55	28	7	6
	n_a	4	5	6	7	4	3	3	7	5	
G03A	n	2	2	2	2	2	2	2	2	2	
	F_{IS}	0	0	-0.333	0	0	0	-0.333	0.5	0	0.043
	H_E	1	1	0.833	1	1	0.5	0.833	0.833	0.5	0.043
	n_{eff}	---	---	6	---	---	2	6	5.99	2	6
	n_a	4	4	3	4	4	2	3	3	2	
G02	n	99	99	100	100	100	97	98	100	100	
	F_{IS}	**0.051****	**0.005***	-0.03	0.003	0.06	-0.03	-0.043	-0.015	0.121	0.017
	H_E	0.851	0.879	0.874	0.902	0.894	0.791	0.812	0.917	0.876	0.854
	n_{eff}	6.72	8.26	7.94	10.25	9.41	4.79	5.33	12.02	8.06	6.86
	n_a	15	16	18	13	15	7	9	17	16	

Supporting Table 2 (continued)

E03A	*n*	16	16	16	15	16	16	16	16	16	
	F_{IS}	0.043	0.005	0.043	-0.065	-0.077	-0.157	-0.077	-0.051	0.345	0.024
	H_E	0.913	0.817	0.913	0.878	0.815	0.815	0.815	0.893	0.849	0.854
	n_{eff}	11.54	5.45	11.54	8.21	5.39	5.39	5.39	9.36	6.61	6.84
	n_a	13	8	13	11	8	7	8	11	9	
C04A	*n*	10	10	10	10	10	10	10	10	10	
	F_{IS}	0.077	-0.104	0.094	0.198	0.006	0.16	0.083	-0.078	0.1	0.034
	H_E	0.863	0.911	0.879	0.863	0.905	0.826	0.868	0.932	0.884	0.833
	n_{eff}	7.31	11.18	8.26	7.31	10.56	5.76	7.6	14.62	8.64	6
	n_a	8	11	9	7	10	5	7	10	9	
CH3	*n*	49	50	50	46	50	43	50	49	50	
	F_{IS}	-0.07	-0.007	**0.128***	0.094	0.037	-0.036	-0.075	0.014	0.093	0.004
	H_E	0.859	0.874	0.893	0.911	0.892	0.764	0.838	0.911	0.882	0.85
	n_{eff}	7.07	7.92	9.37	11.25	9.29	4.23	6.16	11.21	8.45	6.68
	n_a	12	14	16	12	14	7	9	17	16	
CH2	*n*	98	99	98	97	94	98	99	99	99	
	F_{IS}	-0.002	0.001	0.022	**0.089****	-0.051	-0.062	-0.066	-0.007	0.088	-0.006
	H_E	0.845	0.86	0.917	0.875	0.884	0.78	0.834	0.913	0.896	0.865
	n_{eff}	6.46	7.13	12	8.03	8.59	4.55	6.04	11.51	9.66	7.4
	n_a	15	21	17	14	15	8	8	19	18	
KZ11	*n*	36	35	34	33	35	36	36	36	36	
	F_{IS}	0.004	0.024	-0.008	0.086	-0.051	-0.006	-0.061	0.035	0.076	-0.005
	H_E	0.865	0.878	0.876	0.894	0.898	0.773	0.839	0.921	0.871	0.858
	n_{eff}	7.39	8.19	8.05	9.45	9.78	4.41	6.2	12.59	7.72	7.05
	n_a	12	13	12	14	15	6	9	14	14	
KZ12	*n*	75	75	73	72	75	73	75	75	74	
	F_{IS}	-0.038	-0.071	0.007	0.055	-0.008	-0.035	0.042	**-0.030****	0.104	-0.015
	H_E	0.861	0.872	0.883	0.897	0.9	0.768	0.835	0.906	0.904	0.865
	n_{eff}	7.17	7.83	8.55	9.67	9.99	4.31	6.06	10.67	10.39	7.39
	n_a	14	16	17	15	16	10	9	18	16	

Supporting Table 2 (continued)

B05	n	6	6	6	6	6	6	6	6	6	
	F_{IS}	0	0.074	-0.091	0.107	-0.132	0.375	-0.111	-0.132	-0.111	-0.022
	H_E	0.833	0.833	0.924	0.924	0.879	0.773	0.909	0.894	0.909	0.907
	n_{eff}	6	6	13.2	13.2	8.25	4.4	11	9.43	11	10.8
	n_a	7	8	8	7	8	4	7	7	7	
B03A	n	6	6	6	6	6	6	6	6	6	
	F_{IS}	-0.02	0.074	-0.071	0.091	-0.132	0.167	-0.191	0.123	-0.225	-0.011
	H_E	0.818	0.894	0.939	0.909	0.894	0.788	0.712	0.939	0.833	0.87
	n_{eff}	5.5	9.43	16.5	11	9.43	4.71	3.47	16.5	6	7.72
	n_a	6	7	8	8	7	5	3	9	5	
B03B	n	4	4	4	4	4	4	4	4	4	
	F_{IS}	0.143	-0.263	-0.2	-0.2	0	0.368	-0.333	-0.2	-0.263	-0.065
	H_E	0.857	0.821	0.857	0.857	0.75	0.75	0.786	0.857	0.821	0.852
	n_{eff}	7	5.6	7	7	4	4	4.67	7	5.6	6.75
	n_a	5	4	5	5	4	3	4	5	4	
A02A	n	4	4	4	4	4	4	4	4	4	
	F_{IS}	-0.143	-0.044	0.4	-0.2	-0.044	-0.091	-0.2	0.217	0.182	-0.065
	H_E	0.893	0.964	0.786	0.857	0.964	0.929	0.857	0.929	0.893	0.889
	n_{eff}	9.33	28	4.67	7	28	14	7	14	9.33	9
	n_a	6	7	4	5	7	6	5	6	6	
D02	n	85	86	86	86	83	86	86	86	86	
	F_{IS}	0.056	-0.008	-0.069	0.007	-0.073	-0.048	-0.133	-0.063	0.076	-0.025
	H_E	0.872	0.854	0.892	0.889	0.887	0.788	0.822	0.898	0.881	0.889
	n_{eff}	7.8	6.85	9.23	9.04	8.87	4.72	5.6	9.77	8.39	8.97
	n_a	17	15	17	15	16	8	9	17	13	
R04	n	1	1	1	1	1	0	1	1	1	
	F_{IS}	---	---	---	---	---	---	---	---	---	---
	H_E	---	---	---	---	---	---	---	---	---	---
	n_{eff}	---	---	---	---	---	---	---	---	---	---
	n_a	2	2	2	1	1	0	2	2	2	

Supporting Table 2 (continued)

S04	n	21	21	21	21	21	21	21	21	21	
	F_{IS}	0.02	-0.057	0.082	0.17	0.128	-0.078	0.022	-0.073	0.08	0.016
	H_E	0.875	0.857	0.88	0.914	0.871	0.753	0.827	0.934	0.878	0.836
	n_{eff}	7.97	7	8.36	11.63	7.76	4.04	5.78	15.11	8.2	6.1
	n_a	9	11	12	11	11	6	6	14	11	
S05	n	21	21	21	19	21	20	20	21	21	
	F_{IS}	-0.062	**0.132****	0.243	0.003	0.088	-0.07	0.052	-0.086	0.056	0.038
	H_E	0.898	0.82	0.876	0.898	0.887	0.796	0.842	0.879	0.806	0.822
	n_{eff}	9.78	5.55	8.05	9.76	8.88	4.91	6.34	8.28	5.16	5.63
	n_a	12	10	10	11	12	6	7	13	8	
S06B	n	6	6	4	5	5	4	5	6	6	
	F_{IS}	0.107	0	-0.143	-0.25	-0.143	0.143	-0.111	0.138	-0.136	-0.123
	H_E	0.924	0.833	0.893	0.822	0.889	0.857	0.911	0.955	0.742	0.898
	n_{eff}	13.2	6	9.33	5.62	9	7	11.25	22	3.88	9.81
	n_a	8	7	6	4	6	5	6	10	5	
S06A	n	11	9	11	11	11	11	11	11	11	
	F_{IS}	0.188	-0.008	**0.184****	0.024	0.091	-0.099	-0.005	0.024	0.14	0.055
	H_E	0.887	0.882	0.883	0.931	0.896	0.831	0.905	0.931	0.84	0.836
	n_{eff}	8.88	8.5	8.56	14.44	9.62	5.92	10.5	14.44	6.24	6.1
	n_a	9	9	11	12	11	6	10	11	8	
U04	n	37	36	37	37	36	37	37	37	37	
	F_{IS}	0.045	-0.046	0.025	0.129	0.039	-0.153	0.016	-0.061	0.089	-0.016
	H_E	0.876	0.903	0.887	0.867	0.866	0.822	0.824	0.918	0.859	0.861
	n_{eff}	8.09	10.35	8.86	7.52	7.47	5.62	5.69	12.17	7.11	7.2
	n_a	12	13	15	12	14	6	9	14	10	
MW21	n	43	42	43	43	43	43	43	43	43	
	F_{IS}	-0.075	-0.002	-0.082	**0.080***	-0.055	-0.077	0.033	0.043	0.105	-0.023
	H_E	0.888	0.879	0.882	0.884	0.905	0.778	0.817	0.898	0.883	0.871
	n_{eff}	8.89	8.28	8.48	8.64	10.5	4.5	5.47	9.83	8.52	7.72
	n_a	15	13	14	13	15	6	9	15	14	

Supporting Table 2 (continued)

Y02	n	5	5	3	4	5	3	5	5	5	
	F_{IS}	0.25	0.111	0.2	0.217	0.172	0.111	0.086	-0.081	-0.081	-0.011
	H_E	0.778	0.889	0.8	0.929	0.711	0.733	0.867	0.933	0.933	0.765
	n_{eff}	4.5	9	5	14	3.46	3.75	7.5	15	15	4.25
	n_a	6	6	4	6	4	3	5	8	8	
Z03	n	7	7	5	7	7	7	7	7	7	
	F_{IS}	-0.014	-0.2	0.18	-0.044	0.241	**0.486****	-0.091	0.053	0.053	0.077
	H_E	0.846	0.846	0.956	0.824	0.923	0.802	0.791	0.901	0.901	0.803
	n_{eff}	6.5	6.5	22.5	5.69	13	5.06	4.79	10.11	10.11	5.08
	n_a	7	6	8	7	9	5	5	7	7	
T05	n	74	84	81	78	82	83	84	84	84	
	F_{IS}	-0.087	-0.051	-0.004	**0.169***	0.017	-0.057	-0.011	0.008	**0.142****	-0.029
	H_E	0.846	0.884	0.885	0.909	0.893	0.787	0.848	0.912	0.86	0.856
	n_{eff}	6.51	8.62	8.73	10.95	9.35	4.69	6.57	11.31	7.12	6.93
	n_a	14	15	18	14	17	9	10	17	12	
CH1B	n	4	4	4	4	4	4	4	4	4	
	F_{IS}	-0.2	-0.2	0.455	-0.125	0	-0.143	-0.263	-0.044	0.1	0.007
	H_E	0.643	0.857	0.857	0.679	0.75	0.893	0.821	0.964	0.821	0.833
	n_{eff}	2.8	7	7	3.11	4	9.33	5.6	28	5.6	6
	n_a	4	4	5	3	4	5	4	7	4	
KODA	n	75	70	76	52	75	79	0	74	79	
	F_{IS}	-0.115	-0.098	-0.084	-0.042	-0.176	**-0.080***	---	**0.111*****	0.14	-0.088
	H_E	0.634	0.638	0.801	0.831	0.579	0.586	---	0.684	0.662	0.713
	n_{eff}	2.73	2.76	5.03	5.92	2.38	2.42	---	3.16	2.96	3.49
	n_a	7	10	10	8	5	4	0	10	4	
KODB	n	14	12	16	11	15	16	0	15	16	
	F_{IS}	0.06	0.022	-0.035	0.111	-0.077	-0.25	---	0.164	0.074	-0.075
	H_E	0.683	0.681	0.726	0.814	0.559	0.655	---	0.793	0.673	0.686
	n_{eff}	3.15	3.14	3.65	5.37	2.27	2.9	---	4.83	3.06	3.19
	n_a	5	6	8	6	3	4	0	7	5	

Supporting Table 2 (continued)

PWSD	n	3	3	3	3	3	3	3	3	3	
	F_{IS}	-0.143	-0.333	0.5	0.111	0.111	-0.333	-0.091	-0.5	-0.143	-0.098
	H_E	0.6	0.533	0.6	0.733	0.733	0.533	0.933	0.733	0.6	0.704
	n_{eff}	2.5	2.14	2.5	3.75	3.75	2.14	15	3.75	2.5	3.37
	n_a	3	2	2	3	3	2	5	3	3	
PWSE	n	49	49	48	44	49	49	49	48	49	
	F_{IS}	-0.132	__0.215**__	-0.16	-0.004	-0.121	-0.109	0.04	0.064	0.186	-0.023
	H_E	0.578	0.57	0.666	0.679	0.656	0.7	0.637	0.689	0.6	0.65
	n_{eff}	2.37	2.33	2.99	3.12	2.91	3.34	2.76	3.22	2.5	2.86
	n_a	7	7	6	5	7	7	7	5	5	
PWSF	n	0	1	1	1	1	1	1	1	1	
	F_{IS}	---	---	---	---	---	---	---	---	---	---
	H_E	---	---	---	---	---	---	---	---	---	---
	n_{eff}	---	---	---	---	---	---	---	---	---	---
	n_a	0	1	2	2	2	2	2	2	1	
PWSC	n	4	4	4	4	4	3	4	4	4	
	F_{IS}	-0.2	-0.091	-0.2	0.4	0.5	-0.5	-0.2	0.294	-0.059	-0.074
	H_E	0.857	0.464	0.429	0.786	0.464	0.733	0.643	0.679	0.714	0.639
	n_{eff}	7	1.87	1.75	4.67	1.87	3.75	2.8	3.11	3.5	2.77
	n_a	5	3	2	4	3	3	4	3	3	
PWSB	n	16	16	16	15	16	10	16	16	16	
	F_{IS}	0.046	-0.075	-0.171	-0.015	0.04	-0.189	-0.071	-0.157	0.054	-0.104
	H_E	0.458	0.7	0.698	0.789	0.52	0.595	0.585	0.76	0.726	0.688
	n_{eff}	1.84	3.33	3.31	4.73	2.08	2.47	2.41	4.17	3.65	3.2
	n_a	3	6	6	5	5	3	5	5	5	
PWSA	n	24	24	24	23	24	23	23	24	24	
	F_{IS}	0.009	-0.204	-0.003	0.015	-0.305	-0.16	0.053	-0.134	-0.079	-0.129
	H_E	0.63	0.626	0.707	0.75	0.643	0.602	0.78	0.7	0.658	0.732
	n_{eff}	2.71	2.67	3.41	4	2.8	2.51	4.54	3.34	2.92	3.74
	n_a	4	7	6	5	6	4	8	7	5	

Supporting Table 2 (continued)

PWSH	n	1	1	1	1	1	1	1	1	1	
	F_{IS}	---	---	---	---	---	---	---	---	---	---
	H_E	---	---	---	---	---	---	---	---	---	---
	n_{eff}	---	---	---	---	---	---	---	---	---	---
	n_a	2	1	2	2	1	2	2	2	2	
PWSG	n	8	9	8	9	9	9	9	8	9	
	F_{IS}	-0.12	-0.219	**0.627****	**0.051***	-0.333	-0.053	-0.109	-0.05	0.01	-0.086
	H_E	0.675	0.739	0.642	0.817	0.68	0.529	0.706	0.717	0.673	0.701
	n_{eff}	3.08	3.82	2.79	5.46	3.12	2.12	3.4	3.53	3.06	3.34
	n_a	4	5	4	6	4	3	5	4	4	
CPAB	n	49	49	46	48	49	47	49	49	49	
	F_{IS}	0.052	0.015	-0.018	0.021	-0.01	0.051	0.036	-0.018	0.102	0.014
	H_E	0.882	0.911	0.893	0.872	0.909	0.695	0.867	0.883	0.885	0.844
	n_{eff}	8.46	11.26	9.39	7.84	11	3.27	7.53	8.52	8.71	6.41
	n_a	13	16	14	14	16	7	10	18	14	
JLA	n	115	115	115	115	114	113	114	113	115	
	F_{IS}	-0.029	-0.077	0.036	0.039	-0.011	**0.006***	-0.01	0.091	0.087	0.011
	H_E	0.879	0.889	0.893	0.896	0.902	0.597	0.773	0.837	0.895	0.827
	n_{eff}	8.28	8.99	9.36	9.61	10.21	2.48	4.4	6.14	9.5	5.76
	n_a	15	18	16	14	15	8	8	19	19	
SCSI	n	113	111	113	110	113	113	113	113	113	
	F_{IS}	0.031	0.018	0.017	0.034	-0.015	-0.078	-0.059	-0.009	0.062	0.003
	H_E	0.877	0.89	0.873	0.893	0.898	0.763	0.828	0.86	0.886	0.862
	n_{eff}	8.11	9.08	7.86	9.35	9.78	4.23	5.81	7.14	8.8	7.23
	n_a	16	20	16	15	15	8	10	18	16	
Total	n	1197	1198	1197	1153	1200	1187	1118	1208	1218	
	n_a	26	24	22	17	19	11	12	25	22	
	H_T	0.827	0.84	0.863	0.876	0.846	0.735	0.811	0.863	0.844	
	F_{IS}	-0.009	-0.021	0.004	0.05	-0.021	-0.048	-0.032	0.004	0.093	
	F_{ST}	0.03	0.052	0.021	0.027	0.034	0.028	0.026	0.046	0.028	

Supporting Table 3. Pairwise F_{ST} (above diagonal) and homogeneity tests (below diagonal) between all pairs of collections after correction for multiple testing (False Discovery Rate). [(-) = no test was conducted due to small sample size; (ns) = not significant after correction; * $P < 0.01$; ** $P < 0.001$; *** $P < 0.0001$)].

		N. Chukchi				S. Chukchi					
		J06B	J06A	G04	G03A	E03A	C04A	CH3	CH2	KZ11	KZ12
N. Chukchi	J06B		-	-	-	0.05	0.01	0.03	0.04	0.04	0.03
	J06A	-		-	-	0.03	0.01	0.02	0.03	0.02	0.02
	G04	-	-		-	0.01	0.01	0.01	0.01	0.00	0.01
	G03A	-	-	-		0.02	-0.05	0.00	0.01	-0.01	0.00
S. Chukchi	E03A	ns	ns	ns	ns		0.00	0.01	0.00	0.00	0.00
	C04A	ns	ns	ns	ns	ns		-4E-03	3E-03	-0.01	-1E-03
	CH3	ns	ns	ns	ns	ns	ns		2E-03	-2E-04	-1E-03
	CH2	ns	ns	ns	ns	ns	ns	ns		-7E-05	2E-03
	KZ11	ns	ns	ns	ns	ns	ns	ns	ns		-2E-03
	KZ12	ns	ns	ns	ns	ns	ns	ns	ns	ns	
	B05	-	-	ns	-	ns	ns	ns	ns	ns	ns
	B03A	-	-	ns	-	ns	ns	ns	ns	ns	ns
	B03B	-	-	-	-	ns	ns	ns	ns	ns	ns
	A02A	-	-	-	-	ns	ns	ns	ns	ns	ns
Norton	R04	-	-	-	-	ns	ns	ns	ns	ns	ns
	S04	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	S05	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	S06B	-	-	ns	-	ns	ns	ns	ns	ns	ns
	S06A	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	U04	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	MW21	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	Y02	-	-	-	-	ns	ns	ns	ns	ns	ns
	Z03	-	-	ns	-	ns	ns	ns	ns	ns	ns
	CH1B	-	-	-	-	ns	ns	ns	ns	ns	ns
Kodiak	KODA	***	**	***	***	***	***	***	***	***	***
	KODB	***	ns	***	***	***	***	***	***	***	***
PWS	PWSD	-	-	-	-	ns	ns	ns	*	ns	ns
	PWSE	***	**	***	***	***	***	***	***	***	***
	PWSF	-	-	-	-	ns	ns	ns	ns	ns	ns
	PWSC	-	-	-	-	*	*	**	***	ns	**
	PWSB	***	**	***	***	***	***	***	***	***	***
	PWSA	***	ns	***	***	***	***	***	***	***	***
	PWSH	-	-	-	-	ns	ns	ns	ns	ns	ns
	PWSG	-	-	***	***	***	***	***	***	***	***
Anadyr	CPAB	ns	ns	ns	ns	ns	ns	ns	**	ns	ns
Okhotsk	JLA	ns	ns	ns	ns	***	***	***	***	***	***
	SCSI	ns	ns	ns	ns	***	ns	***	***	***	***

Supporting Table 3 (continued)

		Norton									
		B05	B03A	B03B	A02A	R04	S04	S05	S06B	S06A	U04
N. Chukchi	J06B	-	-	-	-	-	0.06	0.03	-	0.02	0.02
	J06A	-	-	-	-	-	0.02	0.03	-	0.02	0.02
	G04	0.01	0.03	-	-	-	0.00	0.00	0.00	0.01	0.01
	G03A	-	-	-	-	-	-0.02	0.01	-	-0.01	-3E-03
S. Chukchi	E03A	0.00	0.01	0.02	0.01	0.08	0.00	0.00	0.00	-0.01	3E-04
	C04A	-0.01	0.01	0.02	-0.02	0.04	-0.01	-4E-05	-0.01	-0.01	-0.01
	CH3	-3E-04	4E-03	0.01	-0.01	0.06	-3E-03	5E-03	-6E-04	-2E-03	-2E-03
	CH2	4E-03	1E-03	0.02	4E-03	0.07	3E-03	3E-03	0.01	-2E-03	5E-04
	KZ11	-1E-03	0.01	0.02	-2E-03	0.06	-3E-03	-3E-05	-4E-03	-0.01	-2E-03
	KZ12	-1E-03	0.01	0.02	7E-04	0.06	-1E-03	3E-03	4E-03	-4E-03	-5E-04
	B05		0.02	0.02	3E-03	-	-0.01	-3E-03	-3E-03	-0.01	0.01
	B03A	ns		0.03	0.01	-	0.02	0.01	0.01	8E-05	-4E-03
	B03B	ns	ns		-	-	0.02	0.02	0.03	7E-04	0.02
	A02A	ns	ns	-		-	-3E-03	5E-03	-0.01	-0.02	-5E-03
Norton	R04	-	-	-	-		0.06	0.04	0.06	0.05	0.05
	S04	ns	ns	ns	ns	ns		3E-03	-4E-03	-0.01	2E-03
	S05	ns	ns	ns	ns	ns	ns		-0.01	-2E-03	1E-03
	S06B	ns	ns	ns	ns	ns	ns	ns		-0.02	-5E-03
	S06A	ns	ns	ns	ns	ns	ns	ns	ns		-5E-03
	U04	ns	ns	ns	ns	ns	ns	ns	ns	ns	
	MW21	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	Y02	ns	ns	-	-	-	ns	ns	ns	ns	ns
	Z03	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	CH1B	ns	ns	-	-	-	ns	ns	ns	ns	ns
Kodiak	KODA	***	***	***	***	***	***	***	***	***	***
	KODB	***	***	***	***	***	***	***	***	***	***
PWS	PWSD	ns	ns	ns	ns	ns	ns	ns	ns	ns	***
	PWSE	***	***	***	***	***	***	***	***	***	***
	PWSF	ns	ns	ns	ns	ns	ns	ns	ns	ns	ns
	PWSC	ns	***	**	*	ns	*	**	*	ns	***
	PWSB	***	***	***	***	***	***	***	***	***	***
	PWSA	***	***	***	***	***	***	***	***	***	***
	PWSH	ns	ns	ns	ns	ns	ns	ns	-	ns	ns
	PWSG	***	***	***	***	***	***	***	***	**	***
Anadyr	CPAB	ns	ns	ns	ns	ns	ns	ns	ns	ns	**
Okhotsk	JLA	***	***	***	***	***	*	***	***	ns	***
	SCSI	ns	**	**	ns	ns	***	**	ns	**	***

Supporting Table 3 (continued)

						Kodiak		PWS		
		MW21	Y02	Z03	CH1B	KODA	KODB	PWSD	PWSE	PWSF
N. Chukchi	J06B	0.03	-	-	-	0.24	0.22	-	0.27	-
	J06A	0.01	-	-	-	0.12	0.11	-	0.16	-
	G04	0.01	-	3E-03	-	0.10	0.09	-	0.12	-
	G03A	0.01	-	-	-	0.10	0.10	-	0.18	-
S. Chukchi	E03A	5E-04	0.01	-0.01	0.01	0.10	0.07	0.07	0.12	2E-03
	C04A	-4E-03	0.01	-0.02	0.03	0.11	0.08	0.08	0.15	-1E-03
	CH3	2E-04	0.01	-3E-03	0.04	0.09	0.07	0.06	0.12	0.01
	CH2	5E-03	0.01	-0.01	0.03	0.10	0.08	0.08	0.12	0.03
	KZ11	-1E-03	0.01	-0.01	0.02	0.08	0.06	0.05	0.10	-0.01
	KZ12	-2E-04	0.01	-0.01	0.03	0.09	0.08	0.06	0.11	0.02
	B05	2E-03	-1E-03	-0.01	0.06	0.12	0.09	0.08	0.13	1E-03
	B03A	0.01	0.04	-0.01	0.05	0.12	0.11	0.08	0.16	0.04
	B03B	0.01	-	0.01	-	0.12	0.09	0.11	0.16	0.09
	A02A	4E-03	-	-0.03	-	0.12	0.08	0.09	0.16	0.06
Norton	R04	0.06	-	0.07	-	0.28	0.26	0.28	0.28	0.62
	S04	-8E-04	1E-03	-0.01	0.03	0.10	0.07	0.06	0.12	0.01
	S05	4E-03	0.01	-0.01	0.03	0.11	0.09	0.08	0.13	0.01
	S06B	-4E-03	0.01	-0.01	0.03	0.13	0.10	0.09	0.15	0.02
	S06A	4E-03	5E-04	-0.02	0.02	0.08	0.05	0.04	0.11	-0.03
	U04	-6E-04	0.01	-4E-03	0.02	0.10	0.08	0.08	0.13	0.02
	MW21		0.02	-3E-03	0.04	0.10	0.08	0.06	0.11	-6E-04
	Y02	ns		-4E-03	-	0.12	0.08	-	0.15	-
	Z03	ns	ns		0.02	0.12	0.09	0.08	0.15	-
	CH1B	**	-	ns		0.17	0.15	-	0.19	-
Kodiak	KODA	***	***	***	***		-0.01	-3E-03	0.02	0.06
	KODB	***	***	***	***	ns		-0.01	0.02	0.05
PWS	PWSD	ns	-	*	-	ns	ns		-0.02	-
	PWSE	***	***	***	***	***	***	ns		-0.01
	PWSF	ns	-	-	-	ns	ns	-	ns	
	PWSC	***	-	**	-	ns	ns	-	ns	-
	PWSB	***	***	***	***	***	***	ns	ns	ns
	PWSA	***	***	***	***	***	***	ns	ns	ns
	PWSH	ns	-	-	-	ns	ns	-	ns	-
	PWSG	***	***	***	***	*	ns	ns	ns	ns
Anadyr	CPAB	*	ns	ns	*	***	***	ns	***	ns
Okhotsk	JLA	***	ns	**	**	***	***	*	***	ns
	SCSI	***	ns	*	*	***	***	*	***	ns

Supporting Table 3 (continued)

								Anadyr	Okhotsk
		PWSC	PWSB	PWSA	PWSH	PWSG	CPAB	JLA	SCSI
N. Chukchi	J06B	-	0.29	0.25	-	-	0.03	0.06	0.04
	J06A	-	0.19	0.11	-	-	-1E-03	9E-04	0.02
	G04	-	0.11	0.10	-	0.07	0.02	0.02	0.02
	G03A	-	0.17	0.15	-	0.11	-3E-03	0.02	0.01
S. Chukchi	E03A	0.09	0.11	0.10	-0.01	0.08	0.01	0.02	0.01
	C04A	0.10	0.13	0.12	0.01	0.09	-2E-03	0.02	4E-03
	CH3	0.10	0.10	0.09	-0.01	0.07	4E-03	0.02	0.01
	CH2	0.10	0.10	0.09	0.01	0.08	0.01	0.02	0.01
	KZ11	0.07	0.09	0.08	-0.01	0.06	4E-03	0.02	0.01
	KZ12	0.10	0.10	0.09	-0.01	0.08	4E-03	0.02	0.01
	B05	0.10	0.12	0.10	-0.04	0.08	4E-03	0.02	4E-03
	B03A	0.13	0.13	0.12	0.02	0.12	0.02	0.04	0.03
	B03B	0.14	0.16	0.13	0.05	0.11	0.02	0.05	0.04
	A02A	0.11	0.14	0.13	-0.01	0.10	1E-03	0.03	0.01
Norton	R04	0.27	0.27	0.26	0.57	0.23	0.06	0.06	0.06
	S04	0.09	0.10	0.09	-0.04	0.07	3E-03	0.02	0.01
	S05	0.10	0.11	0.10	0.01	0.09	0.01	0.03	0.01
	S06B	0.11	0.14	0.12	-	0.09	0.01	0.02	0.01
	S06A	0.06	0.09	0.08	-0.03	0.06	2E-03	0.03	0.01
	U04	0.11	0.11	0.10	0.01	0.09	0.01	0.02	0.01
	MW21	0.10	0.10	0.09	2E-03	0.08	0.01	0.02	0.01
	Y02	-	0.14	0.11	-	0.08	0.02	0.03	0.02
	Z03	0.09	0.12	0.12	-	0.09	-2E-03	0.02	0.01
	CH1B	-	0.19	0.18	-	0.16	0.04	0.05	0.03
Kodiak	KODA	0.04	0.04	0.03	0.02	3E-03	0.09	0.10	0.10
	KODB	0.02	0.03	0.03	-0.02	-0.01	0.07	0.08	0.09
PWS	PWSD	-	-0.01	-0.03	-	-0.04	0.06	0.09	0.09
	PWSE	0.02	0.01	0.01	-0.04	-0.01	0.12	0.12	0.12
	PWSF	-	-6E-04	-0.02	-	-0.05	0.02	0.03	0.03
	PWSC		0.01	0.02	-	-4E-03	0.10	0.11	0.11
	PWSB	ns		0.01	-0.03	-4E-03	0.10	0.11	0.11
	PWSA	ns	ns		-0.03	-0.01	0.09	0.10	0.10
	PWSH	-	ns	ns		-0.06	0.00	0.01	0.02
	PWSG	ns	ns	ns	ns		0.07	0.08	0.08
Anadyr	CPAB	*	***	***	ns	***		0.01	4E-03
Okhotsk	JLA	***	***	***	ns	***	***		0.01
	SCSI	***	***	***	ns	***	***	***	

Supporting Table 4. Estimation of effective population size of each location based on linkage disequilibrium, heterozygote excess, and molecular coancestry. Estimates of harmonic mean (*n*), lower (LCI) and upper (UCI) confidence intervals for effective population size (>0.01) are also included.

			N_e Linkage disequilibrium			N_{eb} Heterozygote excess			N_{eb} Molecular coancestry		
Region	Collection	*n*	Estimate	LCI	UCI	Estimate	LCI	UCI	Estimate	LCI	UCI
N. Chukchi		8	Infinite	Infinite	Infinite	Infinite	9.3	Infinite	Infinite	Infinite	Infinite
	J06A/J06B	2	Infinite	Infinite	Infinite	Infinite	3.6	Infinite	Infinite	Infinite	Infinite
	G04	4	Infinite	6.6	Infinite	56.5	6.4	Infinite	25.7	1.9	80
	G03A	2	Infinite	Infinite	Infinite	Infinite	5.2	Infinite	Infinite	Infinite	Infinite
S. Chukchi		297.8	2006.6	1092.8	9490.6	Infinite	Infinite	Infinite	593.7	0.6	2980.1
	E03A	15.7	Infinite	115.9	Infinite	Infinite	16.3	Infinite	42	0	210.8
	CH3/C04A	57.8	321.6	179.7	1217.6	Infinite	363.7	Infinite	22.2	10.4	38.4
	CH2	95.3	Infinite	1158.8	Infinite	Infinite	37.1	Infinite	237.7	0.2	1193.1
	KZ11/KZ12	107.5	892.9	424.9	Infinite	Infinite	65.7	Infinite	Infinite	Infinite	Infinite
	B05	6	Infinite	18.6	Infinite	27.4	7	Infinite	12.6	8.1	18
	B03A/B03B	10	3864.6	29.6	Infinite	47.4	8.2	Infinite	Infinite	Infinite	Infinite
	A02A	4	Infinite	Infinite	Infinite	Infinite	8.2	Infinite	Infinite	Infinite	Infinite
Norton		151.1	1667.7	706.3	Infinite	Infinite	Infinite	Infinite	161.5	0.2	810.9
	R04	1	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite
	S04	21	Infinite	146.6	Infinite	Infinite	31.1	Infinite	Infinite	Infinite	Infinite
	S05	20.2	273.5	70	Infinite	Infinite	21.9	Infinite	9.1	5.4	13.9
	S06A/S06B	15.3	Infinite	106.5	Infinite	Infinite	17.6	Infinite	45.2	0	227
	U04	36.5	Infinite	1091.5	Infinite	Infinite	22.4	Infinite	Infinite	Infinite	Infinite
	MW21	42.8	1877.1	276.8	Infinite	Infinite	22	Infinite	Infinite	Infinite	Infinite
	Y02	4.2	Infinite	Infinite	Infinite	Infinite	16.9	Infinite	Infinite	Infinite	Infinite
	Z03	6.4	Infinite	32.4	Infinite	Infinite	16.3	Infinite	Infinite	Infinite	Infinite
	CH1B	4	Infinite	3.7	Infinite	21.7	4.8	Infinite	Infinite	Infinite	Infinite

Supporting Table 4 (continued)

			N_e Linkage disequilibrium			N_{eb} Heterozygote excess			N_{eb} Molecular coancestry		
Region	Collection	*n*	Estimate	LCI	UCI	Estimate	LCI	UCI	Estimate	LCI	UCI
Kodiak		75.5	148.9	89	353	72.9	11.5	Infinite	Infinite	Infinite	Infinite
	KODA	62.1	163.1	85.3	725.9	61.6	10.1	Infinite	Infinite	Infinite	Infinite
	KODB	12.5	Infinite	53.4	Infinite	Infinite	8.5	Infinite	Infinite	Infinite	Infinite
Prince William Sound		101.7	836.2	246.7	Infinite	73.9	10	Infinite	Infinite	Infinite	Infinite
	PWSD	3	Infinite	2.8	Infinite	9.5	3.1	Infinite	Infinite	Infinite	Infinite
	PWSE	47.7	1831.8	140.6	Infinite	141	11	Infinite	29	0	145.6
	PWSF	1	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite
	PWSC	3.8	Infinite	7.7	Infinite	Infinite	4.2	Infinite	Infinite	Infinite	Infinite
	PWSB	14.8	232.8	23	Infinite	15.4	5.5	Infinite	21.3	0.5	78.8
	PWSA	23.4	Infinite	116.5	Infinite	11.5	6	310.4	Infinite	Infinite	Infinite
	PWSH	1	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite
	PWSG	8.4	Infinite	14.7	Infinite	38.8	4.2	Infinite	8.6	2.4	18.9
Anadyr Bay	CPAB	47.8	1176.5	290	Infinite	Infinite	83.2	Infinite	Infinite	Infinite	Infinite
Hokkaido Island	JLA	113.8	Infinite	929.7	Infinite	Infinite	Infinite	Infinite	204.8	0.2	1027.9
Sakhalin Island	SCSI	111.7	Infinite	886.2	Infinite	Infinite	47.8	Infinite	Infinite	Infinite	Infinite
N. Chukchi small	G02	98.9	1804.6	557.1	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite	Infinite
S. Chukchi small	D02	85	Infinite	753.9	Infinite	270.7	20.6	Infinite	97.2	0.1	487.9
Norton small	T05	79	Infinite	Infinite	Infinite	Infinite	63.5	Infinite	Infinite	Infinite	Infinite

Supporting Table 5. Results from the pooled collection Bottleneck analysis using the two-phase model (TPM; 95% SMM, 12% variance). Significantly small heterozygosity (-) and no significant difference (ns) for the observed value relative to the simulated value.

Area	Sign Test	Standardized Differences Test	Wilcoxon Test	Distribution
Kodiak Island	ns	-	ns	L-shaped
Prince William Sound	-	-	-	L-shaped
N. Chukchi Sea	ns	ns	ns	L-shaped
S. Chukchi Sea	ns	ns	ns	L-shaped
Norton Sound	ns	ns	ns	L-shaped

Supporting Table 6. Pairwise relatedness and variance in pairwise relatedness in pooled collections. Significant P values ($P < 0.05$) are bold. Estimates are based on the Lynch and Ritland (L-R)'s method (1999) or identity (Belkhir et al. 2002) values from the data and “per” describes the average (L-R or Identity) or variance (var) after 1000 allele permutations.

Pool	L-R	per	*P*	var	per	*P*	Pool	Identity	per	*P*	var	per	*P*
N. Chukchi	-0.143	-0.143	1.000	4.18E-03	7.07E-03	0.939	N. Chukchi	0.252	0.253	0.532	8.50E-03	1.05E-02	0.761
S. Chukchi	-0.003	-0.003	0.594	8.00E-03	7.85E-03	**0.042**	S. Chukchi	0.216	0.218	0.989	1.01E-02	1.03E-02	0.892
Norton	-0.007	-0.007	0.801	8.33E-03	8.17E-03	0.146	Norton	0.218	0.223	0.996	1.06E-02	1.05E-02	0.344
G02	-0.010	-0.010	0.238	8.15E-03	8.05E-03	0.295	G02	0.217	0.220	0.885	9.94E-03	1.01E-02	0.742
D02	-0.012	-0.012	0.820	7.76E-03	7.74E-03	0.430	D02	0.233	0.229	**0.033**	9.77E-03	1.04E-02	0.969
T05	-0.012	-0.012	0.682	7.88E-03	8.32E-03	0.964	T05	0.215	0.219	0.963	1.04E-02	1.06E-02	0.756
Kodiak	-0.014	-0.012	-	3.03E-02	2.85E-02	**0.047**	Kodiak	0.485	0.479	0.153	2.05E-02	2.15E-02	0.813
PWS	-0.010	-0.010	0.983	2.18E-02	2.17E-02	0.443	PWS	0.517	0.509	**0.045**	1.57E-02	1.61E-02	0.682
Anadyr	-0.021	-0.021	0.124	6.99E-03	7.06E-03	0.557	Anadyr	0.209	0.213	0.881	9.95E-03	9.99E-03	0.528
Hokkaido	-0.009	-0.009	0.764	8.08E-03	7.86E-03	0.116	Hokkaido	0.229	0.232	0.879	1.10E-02	1.05E-02	**0.042**
Sakhalin	-0.009	-0.009	0.152	7.92E-03	7.71E-03	0.140	Sakhalin	0.228	0.229	0.697	1.08E-02	1.04E-02	0.092

Supporting Table 7. Fixation indices (F_{ST}) estimates and probabilities (P) for nine loci and total estimates over all loci among pooled areas (North Chukchi Sea, South Chukchi Sea, Norton Sound, Kodiak Island, Prince William Sound, Gulf of Anadyr, Hokkaido Island, and Sakhalin Island).

Locus	F_{ST}	P
Elgr07	0.038	3.83E-07
Elgr11	0.075	4.13E-07
Elgr13	0.029	4.57E-07
Elgr14	0.038	2.80E-07
Elgr23	0.051	3.64E-07
Elgr31	0.036	2.27E-07
Elgr38	0.036	2.00E-07
Elgr44	0.066	4.00E-07
Elgr45	0.040	4.09E-07
Overall	0.046	3.48E-07

Supporting Table 8. Fixation indices (F_{ST}) estimates and probabilities (P) for nine loci and total estimate over all loci among pooled areas with the exception of the Gulf of Alaska region (North Chukchi Sea, South Chukchi Sea, Norton Sound, Gulf of Anadyr, Hokkaido Island, and Sakhalin Island).

Locus	F_{ST}	P
Elgr07	0.002	5.70E-03
Elgr11	0.016	1.24E-07
Elgr13	0.001	3.24E-04
Elgr14	0.003	8.61E-08
Elgr23	0.006	1.16E-06
Elgr31	0.030	1.10E-07
Elgr38	0.017	9.85E-08
Elgr44	0.014	1.25E-07
Elgr45	0.003	5.18E-03
Overall	0.010	1.24E-03