

Taxonomic Implications of Meristic Variation in North Atlantic Cod Populations

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Abstract

It is commonly accepted that genetic differences across populations are reinforced by environmental influences on phenotypic expression, leading to gradient variation in morphological features. We evaluated the morphological features of two Atlantic cod (*Gadus morhua*) populations. When nurtured in the same laboratory setting, juveniles from the two groups showed remarkable variations in shape. Nevertheless, there was no difference in the two populations' juveniles body forms grown in the wild, showing that the genetic variances between the populations were concealed by the competing influences of the varied environmental variables faced in the wild. We hypothesize that stabilizing selection for the same ideal phenotype may account for a considerable percentage of the genetic variation in fish body structure, leading to genetic divergence throughout populations under various environmental stressors. This article summarises studies on the diversity in the mitochondrial DNA sequence found in Atlantic cod (*Gadus morhua*) in the North Atlantic and its environs. The population genetic architecture of the Barents Sea, Northeast, and Northwest Atlantics has seen significant modifications. Compared to populations from the Northwest Atlantic, which are all dominated by a single common genotype and show little diversity in haplotype and nucleotide content, samples from Norway and the Barents Sea support many genotypes at intermediate frequencies and exhibit far more genetic variety.

Keywords: Taxonomic (TT), Meristic Variation (MV), North Atlantic Cod Populations (NACP)

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Introduction

If we try to describe taxonomy in a comprehensive sense, then it will prove that it is a science that is completely based on classification. However, in actuality, it is the classification of all those organisms that are still living and those that have become extinct. Its origin was the Greek word *taxis*, meaning management, and the *nomos*, called laws. All the methods and principles of systematic botany and zoology come under the taxonomy category because they deal with different types of plants and animals, which are placed in the hierarchies of all those superior and subordinate (Sinclair & Solemdal, 1988). Among the biologists, Swedish naturalist Carolus Linnaeus developed the Linnaean system of binomial nomenclature, which is accepted internationally. The classification of living organisms is usually made to fulfil a need; sometimes, these things seem superficial. Anglo-Saxon, which usually represents worms and fish, represents the creepers in nature, like snakes and earthworms. Intestinal parasites, like paragon or dragons and other creatures that swim to their habitats, also come in this category. Nhabitats, the term fish, is usually associated with shellfish, crayfish, and starfish (Waldman, 2005). Several differences are of anatomical type between shellfish and starfish compared to bonyfish and a man. Many variations can be seen in the list of vernacular names. The robin who belongs to America but not the English robin and the ash of the mountain resemble the truth but only at the superficial level. Biologists have attempted to watch the living organisms with a complete view and then a plural classification type. A classification of formal type becomes the base of that vocabulary, which is uniform and can be understood naturally (Silva-Segundo et al., 2011). So, it will simply be cross-referencing the information of retrieval type. There is a vast difference between the terms taxonomy and systematic concerning biological

information. The evolutionist Ernst Mayer describes taxonomy as the classification of organisms. The science involving organisms' diversity comes under the systematics category. Those people who live in an environment that is very close to nature have vast knowledge about the elements of fauna and flora that are the local type and seem very important to them. They also have the capability of recognizing living organisms. This information is mostly based on the need of the hour. All anatomical features that can be counted easily, like the number of rows found on the dorsal side or the toes found on the forefoot, come under the category of Meristic. Meristic variation describes the variation in the counting of parts of organisms. We can understand this by the following example: the appearance of six digits in the hands and feet instead of the normal features, like the occurrence of 13 ribs in man compared to 12, which seems very common. All those characters are Meristic in nature; we can take the example of ribs and spines, which are the structures found in fishes and are countable in number, and their development mostly happens in serials(Árnason, 2004). Meristics are mostly the representation of all those structures that are found in the structures of the body. The examples of fin rays and vertebrae can elaborate this thing efficiently. All those structures found in fishes and can be counted easily are known as meristic features like fin spines and rays. Certain other features also come in this category, like gill rakers, lateral line scales, and branchiostegal rays. As it has elaborated, all those countries come in an undefinable category of meristic traits(Carr & Crutcher, 1998). Like vertebrae and scale counts in a fish. Threshold traits are all or none, but they are strongly affected by multiple genes and the environment, such as diabetes and schizophrenia. In the Northwest Atlantic, the range of cod is spread across Greenland to Cape Hatteras, found in North Carolina (Janssen & Metrakos, 2023). In the US, water and cod are mostly found in Georges Bank and the areas of the western Gulf. The cod population has declined as it was 13900 metric tons in 2019. Later on, it has become 12000 metric tons in 2023(Stransky et al., 2008). This decrease in number happened in 1950 from the height of 320,000MT. All the populations are undoubtedly found under the target level, but the US wild usually catches Atlantic cod, which is considered the smart seafood choice. Because its management is usually done under the level of a rebuilding plan that permits harvest, but to a limited extent. The US fisherman usually permits it. Countable fish features fall under meristic features like fin spines and rays. Gill rakers, lateral line scales, and branchiostegal rays are also discussed under this category(Marteinsdóttir & Rose, 2019). Meristic counts are those determined by environmental factors during the phases of development of eggs and larvae. All those variances in the meristic phase show Geographic isolation during early life, which frequently happens in populations. This object proves quite informative for the identification of cattle. It proves quite uncomplicated for the Meristic to examine them as a sample (Polachini et al., 2022). So, it will be a commencement point for all investigations based on stock discrimination. Variation in morphological traits is assumed to reflect gradient and environmental impacts on phenotypic expression, amplifying genetic variability between populations. We evaluated the body morphologies of two separate populations of Atlantic cod (*Gadus morhua*) (Marcil et al., 2006). When reared in a comparable setting, there were notable changes in form between the juveniles of both groups. However, no significant variation in body size was seen among wild-reared juveniles of both groups. This means that genetic differences across the populations were hidden by the opposing influences of the changes in environmental variables reported within the ecosystems. It is hypothesized that much of the genetic diversity that determines the form of fish bodies might be concealed, and stabilizing selection for the same look leads to genetic variations across two populations impacted by distinct environmental conditions (Chase, 2014). Fish species may be identified, and the homogeneity or heterogeneity of a stock can be ascertained using morphometric features. Fish's length-weight connection is a helpful indicator of their overall health and their development, survival, maturity, and reproduction. It explains why fish vary in weight according to length and vice versa. When the length-frequency distribution of fish is known, it is frequently used to estimate fish biomass, identify potential variations between several unit stocks of the same species, and calculate the mean weight of fish based on length. In addition, it offers valuable insights into resource conservation. It may be used to evaluate the life history traits of fish populations, including longevity,

age at sexual maturity, and stock composition. Comparing the physiological robustness of fish on a numerical basis is possible through the condition factor, which also offers information on the general health state of the community and the species. The employment of non-scientific fishing techniques, decreased water flow, and rising pollution levels have affected fish species' morphological and physiological states recently. Despite the economic and ecological significance of many fish species from the River Ganga, little is known about their morphometric traits, length-weight connection, and condition variables. Fish morphology has traditionally been the main data source for taxonomy and evolutionary research (Martudi, 2023). Genetic, physiological, behavioural, and ecological data are valuable and readily available for these kinds of investigations, although systematic ichthyologists still rely mostly on morphology to identify taxonomic features. Different species can be recognized, identified, and classified by their outward characteristics, such as size, form, pigmentation patterns, fin arrangement, and other physical characteristics. Furthermore, significant traits lend themselves to dissection or other internal analysis. Important morphological characteristics and research techniques are described in this section. Our descriptions represent the majority of fish groups. However, hagfishes (Myxiniiformes) and lampreys (Petromyzontiformes) are not regarded as real fish because they do not have paired fins or jaws. As a result, most of the characters in this section are unsuitable for their classification.

North Atlantic Cod Populations

Fins In systematics, a variety of offline properties are significant. The number and relative placements of the fins and the kinds and quantity of rays that make them up are very helpful. The paired fins are the pectoral and pelvic (ventral) fins; the middle fins are the dorsal, caudal, anal, and adipose (found in a few groups) fins. Fin rays come in two main varieties: actual spines and soft rays. The spine is a single, midline structure with no joints or branches. Two jointed, usually branching longitudinal supports make up a ray. The anterior region of a single fin or the anterior of two distinct fins is where spines often appear. The dorsal fin can exhibit several unique variants and is seldom missing. Although cod (Gadidae) may have numerous soft-rayed dorsal fins, it is solitary in most soft-rayed fish. The dorsal fin's size, shape, relationship to other fins and body traits can all be used to identify different species or genders. Given that the gaps between fins are often constant about fin size, the degree of separation between two or more dorsal fins may be significant from a taxonomy perspective. A dorsal fin's posterior margin might be free from the back or connected to it (adnate). It is also important to consider if the dorsal fin is continuous with the caudal fin or hidden behind skin, as in the case of some eelpouts (Zoarcidae). Some species, like the tilefish, have an adipose fin on the head. In contrast, some species, like salmon and trout (Salmonidae) and characins (Characidae), may have a dorsal adipose fin on the caudal peduncle (Figure 1).

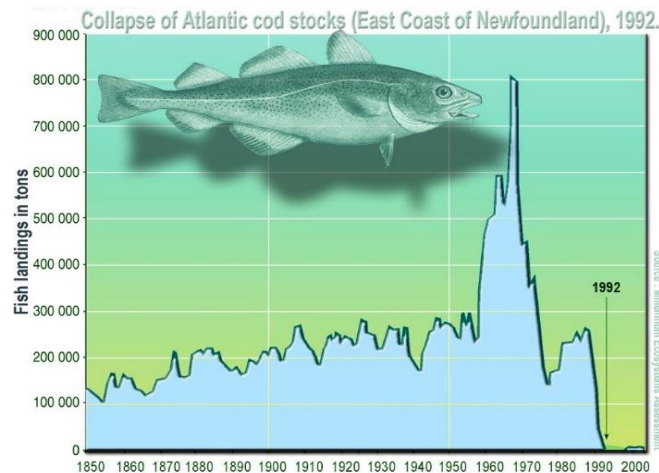


Figure 1: Collapse of Atlantic cod stocks (East Coast of Newfoundland), 1992

Research Objective

The primary purpose of this research is to understand the Taxonomic Implications of Meristic Variation in the North Atlantic Cod Population. This research proves very effective in analyzing taxonomic suggestions that usually apply to the North Atlantic cod region.

Literature Review

Researchers claim that the presence of SNP in aquatic species is determined through MSA methodology. This method allows researchers to identify the species present in the Atlantic Ocean based on the species-related genomic data. The sample from the Baltic Sea was obtained to assess the species in the mixed stock (Bekkevold et al., 2023).studies reveal that genetic codes provide evidence related to the presence of Atlantic cod species in the northern region of the sea. the deletion of cod pollution in recent years from the North Sea is due to the shifting patterns of this population(Cecapolli et al., 2023).studies claim that endemic fish species populate the nearby region of the western Antarctic peninsula. The richness of fish species in this region makes it more diverse. The great characteristic of the endemic fish species increases their chances of survival even in harsh climate conditions(Corso, 2023).studies reveal that Meristic is a countable variant. The variant in the meristic is due to certain genetic as well as environmental factors.by understanding the variation in the meristic, it becomes easier to understand the structural behavior of any population of fish species.in New Zealand, the unique species are studied to identify the impact of certain factors on their meristic(Currie et al., 2024).studies reveal that P.sophore is a species widely found in Bangladesh's freshwater ecosystem. To study the behaviour of this species, its biological characteristics or parameters are studied(Debi et al., 2023). Studies were made on the catfish species from the Nigerian sea to find out its meristic traits. The results of the studies predict that the species Arius gigas catfish were found in two rivers. The first was the caliber river, and the second was the Degema River. the species of New Camber River showed more variation in meristic features (Dienye et al., 2023).studies conclude that the population of fish species found in the aquatic ecosystem is rapidly decreasing due to certain risk factors. These factors are different for different populations of fish species.

The population of Kollera Lake is decreasing due to certain pollutants that result in the decreased biodiversity found in this lake(Gajula & Priya, 2023).studies predict that Atlantic species undergo evolutionary changes with time. The zooplanktivorous species show diversified evolutionary changes due to changes in temperature zones as well as the salinity of water. the genomic analysis-based study of zooplanktivorous reveals that these species have shown the fastest evolutionary shift(Goodall et al., 2024).studies reveal that the population of eastern Baltic cod shows great morphological changes due to the genetic evolution process. However, overfishing results in a decrease in the growth rate of this pollution over time (Han, 2024).Scholars' studies explain that the basis for species differentiation is metrics features. By assessing the role of genetics on species' meristic factors, it became easy to differentiate species. studies have revealed that the genetic basis of scophthalmus maximum species is studied to understand its merits features (Ivanova et al., 2024). Studies suggest that the European founder species are commercially important in the Baltic Sea. Information obtained regarding the founder species of the Baltic Sea revealed that this species is losing its meristic features. This information about the loss of meristic features founder fish is obtained through the fisheries monitoring system .fisheries monitoring system mostly uses microsattelites to monitor the funder specie of Baltic sea(Jakubowska-Lehrmann et al., 2023). Studies provide evidence about Atlantic cod's reproductive cycle changes due to certain climatic factors. The response of Atlantic cod species varies with the changing location of these species(Kjesbu et al., 2023).scholars' studies show that otolith species death is caused by a lack of species protection strategies. To make effective conservation plans, the cryptic

species that have higher threats are studied first. For analyzing species behavior and the impact of human and environmental activities on them, effective conservation strategies have been developed (Leonhard & Agiadi, 2023). Studies claim that the higher abundance of Atlantic cod in the sea is because of the high morphological features shown by these species, but the loss of diversity of Arctic cod species is because of habitat shift.

The warming of marine eaters is one of the factors that impacts the biodiversity and metrics features of Arctic cod (Malizia et al., 2023). Studies show that calcified morphological structures found in teleosts help them in hearing. The morphometric feature of the otolith is responsible for the shape change of the *Decapterus* species. The three species of red Finn are morphologically different from each other based on otolith meristic (Morales et al., 2023). Scholar studies explain that noise pollution is one of the reasons that species migrate. Atlantic cod species are greatly impacted by the noise pollution caused by humans through ships and other underwater instruments. The water ecosystem close to the roads is disturbed due to noise created by traffic. Aquatic disturbances cause species to migrate into ecosystems that have no aquatic disturbances. Moreover, the shift in the behaviour of Atlantic cod due to aquatic pollution is studied through research-based experimental studies (Price, 2023). A scholar suggests that classifying species based on their phenotypic and genotypic behavioural characteristics is possible using the integrative taxonomy approach. The fish management programs provide data related to the two cryptic species of freshwater using the concept of integrative taxonomy. Also, the location of species in the ecosystem, as well as patterns of the fish distribution, is explained using the taxonomic-based integrative methodology (Riley et al., 2023). Studies elaborate that the presence of many taxonomically diverse species near the coastal region of the Mediterranean Sea is determined through different approaches. One of the most important species found in the coastal region of Libya is chondrichthyans. Chondrichthyans show fluctuation in the reproductive cycle due to changes in habitat factors (Shakman et al., 2023). Researchers conclude that better environmental conditions promote faster growth of aquatic species. Many juvenile fish species survive due to certain environmental driving factors. The Baltic cod larvae belonging to zooplankton species show changes in growth patterns in different seasons. The statistic-based studies for assessing Baltic cod growth revealed that fluctuation in the growth rate of cod species is the prominent factor behind their decline (Spich & Fey, 2023). Scholars predict that *Cypselurus poecilopterus* species belongs to pelagic species. These fish species are economically and ecologically important. The structure of these species is determined using an approach based on meristic factors. The identification of this species in eastern seawater is made on the basis of their stock structure (Tuapetel et al., 2024).

Implications

During part or all of their life cycle, because the subcomponents of Atlantic cod appear to be separated in distance or time, they are classified as discrete stocks. Fisheries managers have discovered eleven similar populations on North America's continental shelf. The initial delimitation was based on vertebral counts, even though it has long been recognized that there is a considerable overlap in each region's limits. Regarding management, stocks are considered groups of individuals with similar phenotypes whose morphological and meristic homogeneity is due to environmental factors. It is indicated that a stock may be subject to overall control. Another technique for stock delimitation is genetics. A population's genetic makeup is similar for stocks and demes. Closed populations, known as stocks, are reproductively isolated from other stock populations and inhabit a particular area. Different environmental conditions can cause morphological differences between groups of genetically homogeneous fish from different sites. For example, there is an inverse link between the quantity of vertebrates and water temperature around spawning.

Morphometric and Meristic Characteristics

The investigation's conclusions showed that the fish's external morphology was severely compressed, with convex ventral and dorsal profiles that united anteriorly to form a pointed snout. The body consists of two dorsal fins, a pelvic and pectoral fin, an anal fin, and a forked caudal fin. There are seven to nine spines on the spiny dorsal fin, twenty-one to twenty-four soft rays on the second dorsal fin, seventeen to twenty-four soft rays on the pectoral fin, one to three spines and seventeen to twenty soft rays on the anal fin, two to five soft rays on the pelvic fin, thirty-seven to forty-seven-gill rakers and forty-six to sixty-two scutes on the lateral line.

Sexual Dimorphism

Demonstrates that there was congruence between the morphometric and meristic traits of the males and females of this species. The investigation's findings demonstrated very little difference in the morphometric and meristic traits of male and female *Alepes vari* fish (t-test; $p > 0.05$). The sole exception to this rule is the pectoral-fin base length (PFL), which exhibits a considerable variation (t-test; $p < 0.05$). This meant that there was no proof of sexual dimorphism in this species. Carpenter states that the number of gills rakers on *Alepes* varies first-gill arch and the number of scutes on its lateral line is two key meristic traits that may set it apart from other *Alepes* species. Furthermore, the quantity of black pigment in the dorsal, anal, and pelvic fins demonstrates sexual dimorphism in comparison to females of this species. Based on morphometric traits, they have also observed the sexual dimorphism of the carp fish species *Labeo calbasu* and the catfish species *Mystus gulio*. Therefore, one effective technique for identifying sexual dimorphism in fish may be to look at the morphometric and meristic differences between male and female fish of a particular species. Understanding population genetic structure is essential to biodiversity conservation and preservation, especially for species that face extinction. Numerous factors, including habitat loss, environmental changes, overexploitation, and the introduction of exotic species, can influence genetic structure. The overuse of resources and climate change have seriously harmed the marine ecology. For instance, the North Atlantic Ocean saw significant sea level drops, altered ocean currents, and decreased water temperatures due to the most recent Pleistocene glaciations. Significant fishing pressures have resulted in substantial population reductions in a number of marine fish species in recent times. Marine creatures typically encounter fewer and less severe physical hurdles than terrestrial and freshwater species, which commonly display considerable population genetic structure from barriers to gene flow, including rivers, waterfalls, mountains, and deserts. Large populations, high fecundity, broad gene flow, and vast ranges are common characteristics of pelagic species. When natal philopatry is absent, these species usually show a poor population structure. On the other hand, certain species—like tropical reef fishes—are constrained by their diet or habitat needs and have distinct population genetic structures. Atlantic cod are demersal omnivores that live on the continental shelves of the North Atlantic Ocean. Offshore populations typically move in immense aggregations between spawning places and feeding zones to seek capelin, their primary food source. The distribution extends south of Cape Hatteras (North Carolina), the North Sea, the Baltic and Barents Seas, and the continental shelves of Greenland and Iceland. It crosses Atlantic Canada and New England to the north as well. Particularly significant ecologically are three landlocked coastal fjords on Baffin Island, Nunavut, Canada: Lake Ogac off Frobisher Bay and Lakes Qasigialiminiq and Tariujarusiq off Cumberland. These lakes are classified as meromictic due to the different amounts of freshwater above and saltwater below. It is estimated that there are just 500–1,000 fish in each of their populations. These fish feed on echinoderms, molluscs, polychaetes, and other cod. They grow to a significantly greater size and age than their marine counterparts. They also do well in very cold, often frozen, waters (Figure 2).



Figure 2: *Alepes vari* fish

Estimates of Divergence and Coalescent Times

As pointed out, similar branch lengths were used to complete the Mr. Bailey investigation. The BEAST analysis used a tight clock and the Hasegawa, Kishino, and Yano (HKY) model with gamma-distributed rate variation and allowance for invariable sites (HKY + Γ + I). The models ran for 5,000,000 steps with a 25% burn-in, sampling every 10,000 steps. There were more than 1,000 in all ESS metrics. The trees were calibrated using a normal distribution, based on the theory that the Atlantic cod separated from the congeneric Pacific cod *G. macrocephalus* around 3.8 million years ago during the final opening of the Bering Sea. The observed mean genetic distance of 0.039 substitutions per site yields the estimated divergence rate of 1.03×10^{-8} substitutions/site/year and the temporal delay of 5,844 years between replacements. Comparable results are observed when the outgroup is Alaska pollock (*Gadus chalcogrammus*). The time interval since the expansion was estimated using pairwise mismatches and $\tau = 2\mu t$.

Meristic Variation

In zoology and botany, the term "meristic" refers to the quantitative characteristics of plants and animals, such as the number of scales or fins on fish. A meristic (countable feature) can identify an unidentified species or characterize a certain species. A meristic formula is a type of shorthand notation that is frequently used to define meristic features. Countable structures that appear in series are known as characteristic characteristics (e.g. myomeres, vertebrae, fin rays). These are some of the most often utilized population and species distinction features. Scale counts have been the most extensively used method for identifying populations within species in salmonids. The most obvious changes between populations in rainbow and steelhead trout are in the number of scales. Phenetic and cladistic analyses make advantage of meristic comparison. A meristic investigation can be a challenging undertaking. For instance, it's not as simple as it would seem to count the traits on a fish. Dead fish that have been preserved in alcohol are the subject of several meristic examinations. Even if it is conceivable, observing characteristic features in live fish is more difficult. You might need to use a microscope on very little fish. In order to eliminate as much uncertainty as possible, ichthyologists undertake meristic analyses according to a fundamental set of guidelines. However, the particular procedure may change according on the kind of fish. The expert doing the study should outline the process for meristic trait counting.

Discussion and Conclusion

The distinction between "genetically distinct" and "genetically discernable" is ultimately evident. The measured

FST for NORTH against SOUTH and the mtDNA data concur that 0.000. Only the subcomponent in the SOUTH pool (FST = 0.002) is statistically significant, compared to 0.007 for the subcomponent in the NORTH pool. These figures are similar to the differential across the Laurentian channel (0.003) that was previously noted. We suggest that, even in the case of statistical significance, this low level of genetic diversity cannot be the basis for clinically significant stock difference. Given the exceptionally high sample sizes used (average of 169 for NORTH, SOUTH, and Scotian Shelf), the ability to identify exceedingly minute variations between multivariate centroids is to be expected. Reclassifying individual cod to their place of origin based on multilocus microsatellite genotypes might not be the best option for action, though. The genetic pattern that was initially demonstrated by Cross and Payne (1978) of a significant separation of fish on the Flemish Cap and those elsewhere in the Northwest Atlantic is, in brief, supported by the mtDNA and microsatellite data. However, there is little to no genetic substructuring in this area that may be attributed to genetically distinct stocks. The genetic data confirm that the population structure of Northern Cod is not stable enough, regionally or temporally, to permit the formation of genetically different stocks because of drift in larvae and eggs. It has been suggested that Atlantic cod shows only modest population structure in trans-Atlantic comparisons and limited population structure at short geographical scales due to its wide range and pelagic environment. Although the first investigations on short mtDNA sequences discovered this, larger scale markers and local nuclear microsatellites have led to the suggestion of a more complex population structure.

The mitogenomic data show that throughout the Northwest Atlantic's commercial range, stock difference is little to nonexistent. The clock-calibrated Bayesian network reveals multiple haplogroup expansions that comprise the most prevalent haplotypes in North America at the Sangamonian interglacial/Wisconsinan glacial border, roughly 120–100 kya as well. This implies that recovery from one or more refugia in the western Atlantic happened at the same time. Nonetheless, the eastern Atlantic and nearby waters are suggested as an origin and ultimate source population by diversity metrics and the frequency of basal haplogroups. Since the varied pattern does not point to a comparable geographic origin, secondary hybridization across historically distinct tribes appears to be the most likely scenario. The lake mitogenomes of Lake Mogilnoe in the east and Lake Qasigialimiq in the west exhibit the predicted patterns in isolated populations that have arisen since the Last Glacial Maximum. To eliminate any doubts about the paths of colonization and the identification of refugia, further samples from the whole range—especially from the eastern, mid-Atlantic, and nearby seas—may be helpful. Mitogenomics offers the ability to solve these challenges because of the enormous variation observed in the cod mitogenomic sequences, which includes the isolation of Arctic fjord populations on Baffin Island and transatlantic variances. Samples collected in various years from the Gulf of Maine and Georges Bank, or even from the same spot off Newfoundland, varied just as much as samples taken from opposing sides of the Laurentian Channel. Trans-Atlantic divergence explains nearly all of the genetic variation seen in the Northwest Atlantic, whereas subdivision within samples explains a significant amount of it. There is virtually little genetic diversity among Northwest Atlantic communities, a result that is supported by reevaluating similar microsatellite data. The mtDNA data demonstrate that mtDNA haplotypes are sensitive indicators of population structure and support the theory that cod populations in the Northwestern Atlantic have undergone a bottleneck in size compared to their Old-World source populations.

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