Accelerated rates of climate change and other growing anthropogenic pressure challenge the persistence of many plant and animal populations. Faced with drastically altered environmental conditions, natural populations may either go extinct locally or respond by: 1) dispersing to areas with more favorable conditions; 2) modifying their trait expression to better fit with new local conditions through phenotypic plasticity; or 3) adapt genetically in response to selection. A better understanding of the relative importance of these different coping mechanisms and the interactions between them in different settings will be crucial for making reliable predictions about the future distribution of biodiversity. The present thesis uses genomic analysis of historical and contemporary DNA samples to retrospectively assess how populations of Atlantic cod, Gadus morhua, have responded to environmental and human-induced changes over the past century. Capitalizing on unique collections of archived samples and recently developed genomic resources, we study temporal and spatial variation at both microsatellite loci and up to 1047 gene-associated single nucleotide polymorphisms (SNPs) over a period of 80 years. The extensive sampling in time and the – for a non-model species – high genomic coverage provide unprecedented resolution for disentangling effects of drift, migration and selection. This elucidation generates novel insights about how cod previously have responded microevolutionarily to changed conditions. Focusing on two different cod population complexes, our overarching objectives have been to assess 1) whether levels of genetic diversity, population structure and distribution patterns have remained stable over time despite large demographic changes, 2) if we could detect molecular signatures of selection over decadal time scales and if so, how widespread such signatures would be, 3) if recent changes in selection pressures have been gradual or abrupt and what factors may have driven them, 4) how temporal and spatial variation in selection pressure have interacted, and 5) if signatures of recent selection are parallel between adjacent populations and across different geographic regions.

The thesis is divided into six chapters that report on different efforts to address these objectives. It opens with a general introduction and synopsis that lays out the context for the research, summarizes the main findings and discusses perspectives for future research (Chapter 1). Chapter 2 presents a baseline study demonstrating temporal stability at microsatellite loci over an 80-year period in a Canadian cod population. This result sets the stage for two SNP-based spatiotemporal population genomics studies that search for signatures of recent selection and examine the stability of population structure in Canadian (Chapter 3) and Greenlandic (Chapter 4) cod populations. The final two chapters elaborate on methodological developments that were implemented to reach the primary research goals: Chapter 5 evaluates the quality of SNP genotyping in our historical samples and demonstrates high reproducibility of our presented data while Chapter 6 proposes a new statistical approach to detecting loci under selection based on temporal variation in allele frequencies. Our results provide important insights about the recent dynamics at both study locations. In Canada, the population structure appears to have remained intact over the study period, whereas in Greenland the temporal analyses reveal large changes in the spatial distribution and mixing of different populations. Against this backdrop of contrasting neutral evolutionary patterns, we observe widespread signatures of selection in both systems, reflected in substantial locus-specific divergence in space and time. This suggests ongoing adaptation in response to temporally and spatially varying selection pressures, and nonparallel patterns between adjacent areas indicate that populations may react differently to environmental variation. Both dispersal and adaptation hence appear to be important responses to environmental change in cod populations, depending on local conditions. These findings have important implications for our understanding of local adaptation and evolutionary potential in high gene flow organisms and underscore the need to carefully consider all dimensions of biocomplexity for evolutionarily sustainable management of biodiversity and natural resources.