Introduction to genetics of subpolar fish and invertebrates

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This 20th Wakefield Symposium, ‘The genetics of subpolar fish and invertebrates’, is the successor of the 11th Wakefield Symposium, ‘Genetics of subarctic fish and shellfish’, which was held in Juneau, Alaska in 1993. In the introduction to that symposium (Gharrett & Smoker 1994), it was noted that: ‘beginning in the 1960s, modern tools of genetic analysis began to be broadly applied in fisheries science’, and that ‘within the past decade (referring to the 1980s), fisheries genetics had entered the mainstream of fisheries resource utilization’. That observation may be an understatement in today’s world of fisheries science. Once-vigorous fisheries in many parts of the world have failed, growing demand for fisheries products has led to full utilization of many remaining capture resources and is driving an increase in aquaculture productivity, and the role of aquaculture has increased dramatically (FAO 2002). Looming over concerns of lost stocks and persistent erosion of genetic variability are predictions of global warming, which may further tax genetic resources. One of the consequences of these developments is an increased interest in and reliance on genetic applications to many aspects of fisheries management, aquaculture, and conservation.

In addressing those concerns, fisheries scientists have increased their attention to the genetics of fish and fish populations; the number of fish genetics citations has increased fourfold in the last decade (Figure 1). In addition to the increased attention, the application of sophisticated genetic analysis tools, such as studies of mitochondrial DNA (mtDNA) and microsatellites, have nearly caught up with the more traditional allozyme studies in annual citations (Figure 1).

One of the predominant themes of both symposia was the descriptive study of population structure. Descriptive studies are an important step in developing management or conservation plans because they can provide markers for use in stock identification programs and because they can identify distinct productivity units (the geographical scale of such units) in species that do not have convenient or obvious geographical boundaries, such as many marine species. Analyses of allozyme variation, which dominated early fisheries genetics research, still provide valuable
**Information and Methods**

![Genetics citations](image1)

**Methods**

![Number of citations](image2)

*Figure 1*. The number of genetics citations from a search of BIOSIS® using combinations of the words and terms (pisces, osteichthyes, or fish) and (genetics or cytogenetics or mtDNA or allozyme or electrophoresis or microsatellite) for papers published each year from 1969 to 2001 (upper). The number of citations for specific molecular methods from a search of BIOSIS Previews (BIOSIS 2001) using combinations of the words and terms (pisces, osteichthyes, or fish) with (1) mtDNA or mitochondrial DNA for mtDNA analyses, (2) allozyme or electrophoresis for allozyme analyses, or (3) microsatellite for microsatellite analyses in papers published each year from 1969 to 2001 (lower). BIOSIS® Previews, BIOSIS, Philadelphia, PA. 20 May 2001. http://www.biosis.org.

As geneticists address more complicated – and more interesting – questions, descriptive studies are becoming increasingly sophisticated. A.R. Templeton’s keynote address presented an approach to descriptive studies that uses the temporal information inherent in gene and haplotype trees in combination with the