

Summary of genetic stock identification studies in the Bering Sea

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Early studies of allozyme variation in walleye pollock (Iwata 1975; Grant and Utter 1980) reported differentiation across broad spatial scales in the Bering Sea. A more recent study using mitochondrial DNA restriction fragment length polymorphism (RFLP) provided some evidence for population substructure at smaller spatial scales in the eastern Bering Sea (Mulligan et al. 1992). However, other studies examining mtDNA (Shields and Gust 1995; Kim et al. 2000), nuclear microsatellite DNA (O'Reilly et al. 2004), or a combination of allozyme and mtDNA variation (Olsen et al. 2002) have failed to resolve stock discretion in the eastern Bering Sea. A study of variation at the pantophysin (Pan I) locus (Canino et al. in press), a gene that appears to be influenced by natural selection (Canino and Bentzen 2004), showed a clear distinction between a sample from the central Bering Sea and the Unimak Pass area (Fig. 1). However, the central Bering Sea sample was taken in September, thus the potential for stock admixture can not be ruled out. Gene frequency distributions at the Pan I locus were correlated with water temperatures (Fig.2) suggesting the effects of temperature-mediated selection over moderate geographic scales. Table 1 summarizes various genetic studies on pollock, the areas covered, methods used, and key results.

Currently, there is no conclusive evidence for genetic discretion of the Donut Hole stock component in the Bering Sea. Results from Mulligan et al. (1992) showed a sample from Adak Island to be distinct from samples in the Donut Hole or from Bogoslof Island but the Donut Hole sample did not show significant differentiation from Bogoslof Island in the eastern Bering Sea. Sample sizes from the two studies that included the Donut hole area (Mulligan et al. 1992, n = 50; Shields and Gust 1995, n = 8) are too small, and mtDNA variation may not be sufficiently polymorphic to resolve expected weak levels of population structuring in walleye pollock. Future efforts should be directed towards collecting larger samples (e.g. 100 - 200 individuals) from spawning aggregates and the use of highly polymorphic markers (e.g. microsatellites).

General conclusions from recent genetic studies

- Evidence for subpopulation structuring within the Bering Sea (Olsen et al. 2002; Canino et al. in press) and between the Bering Sea and the Gulf of Alaska (Olsen et al. 2002; O'Reilly et al 2004;
- No evidence for genetic discretion of the Donut hole stock component

Possible reasons:

- small sample sizes (Mulligan et al. 1992, n = 50; Shields & Gust 1995, n = 8)
- samples taken from non-spawning individuals



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Table 1. Studies of genetic population structure in walleye pollock since 1998

Study	Area	Marker	Results
Kim et al. 2000	Korea -Bogoslov	mtDNA RFLP	<ul style="list-style-type: none"> • no significant genetic heterogeneity
Olsen et al. 2002	Western north Pacific, Eastern BS, GOA, PWS	mtDNA RFLP allozyme microsatellites	<ul style="list-style-type: none"> • east -west heterogeneity between Asian and N American populations • regional heterogeneity among GOA samples (PWS vs SHEL) • Discordant results between BS and GOA - significant differentiation observed with allozymes and mtDNA but in different years
O'Reilly et al. 2004	Western north Pacific, North Central BS, Eastern BS, GOA, Puget Sound	microsatellites	<ul style="list-style-type: none"> • weak structuring (global $F_{ST} = 0.004$) • genetic isolation by distance over moderate scales (~1500 km) • sign. genetic differentiation between NCBS and GOA
Canino et al. In press	Western north Pacific, North Central BS, Eastern BS, GOA, Puget Sound	pantophysin (Pan I) locus	<ul style="list-style-type: none"> • stronger differentiation than observed with microsatellites (global $F_{ST} = 0.038$) • north-south cline in Pan I allele frequencies correlated with water temperature • North Central BS sample differentiated from Eastern BS and PWS sample
Grant In review	reanalysis of data from Mulligan et al. 1992 Kim et al. 2000 Olsen et al. 2002	mtDNA	<ul style="list-style-type: none"> • nested clade analysis indicated 3 phylogroups within data in Mulligan et al. 1992 and Olsen et al. 2002 studies • mosaic patterns in subpopulation diversity over moderate geographic scales but no clear pattern in range-wide diversity • patterns best explained by metapopulation dynamics

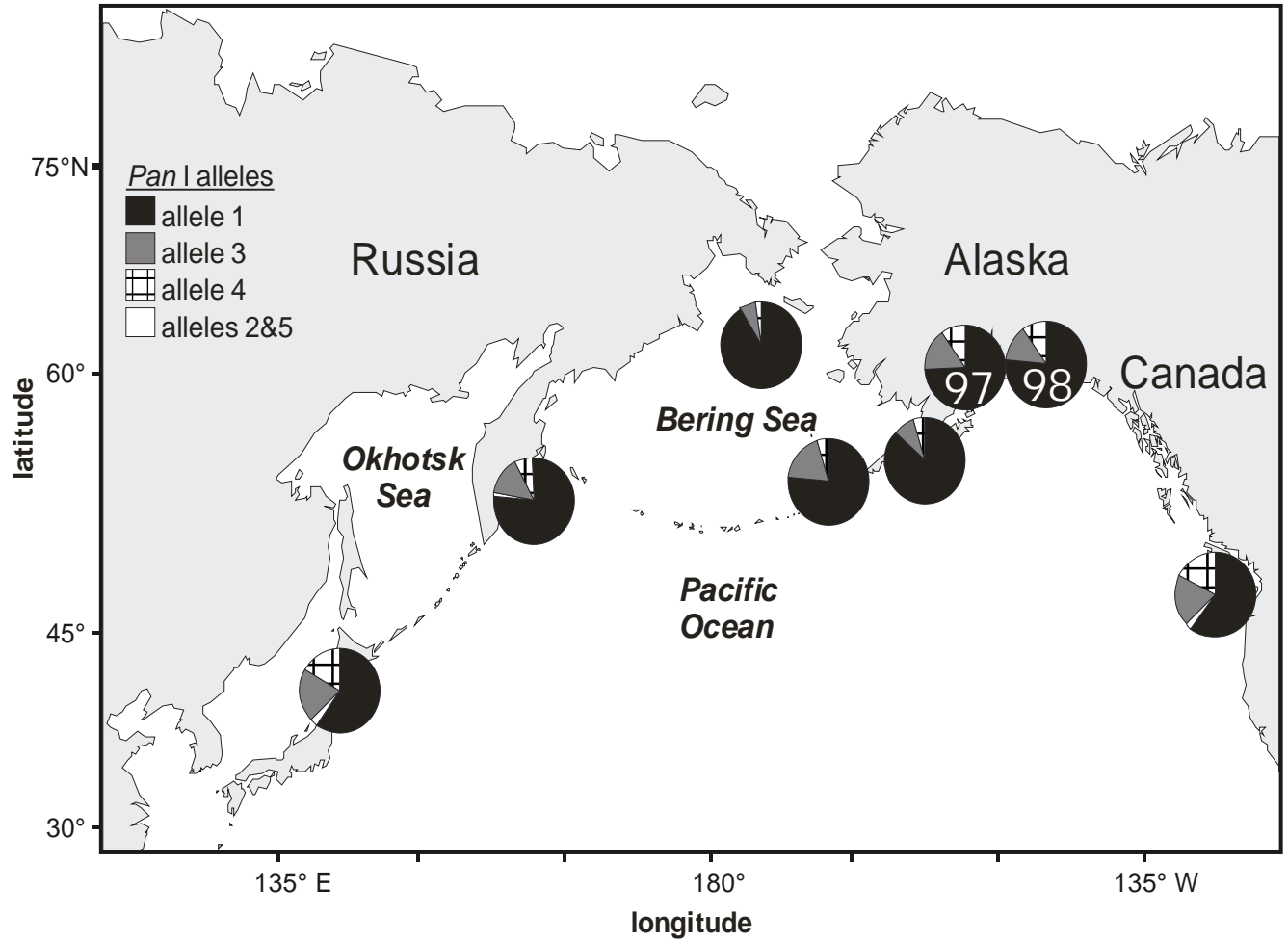


Figure 1. Frequencies of *Pan I* alleles in walleye pollock (*Theragra chalcogramma*). Samples taken in Prince William Sound in 1997 and 1998 are indicated by year. (Canino et al. in press).

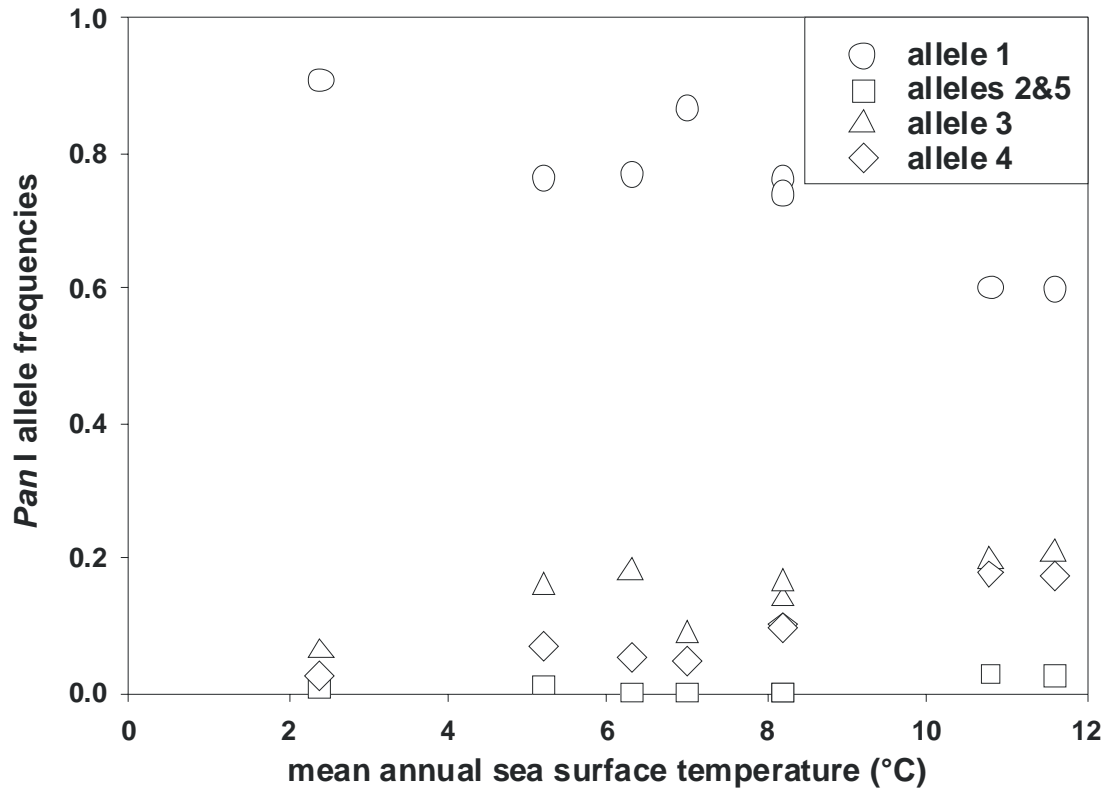


Figure 2. Frequency occurrence of Pan I alleles in walleye pollock (*Theragra chalcogramma*) versus estimated annual mean surface temperature. (Canino et al. in press).