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II. ANALYSIS OF PELAGIC COLLECTIONS OF 1978 FROM THE CENTRAL AND SOUTHERN
BERING SEA (ABSTRACT OF REPORT IN PROGRESS)

by

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BIOCHEMICAL GENETIC VARIATION IN WALLEYE POLLOCK, THERAGRA CHALCOGRAMMA:

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by Fred Utter*, George Milner*, and David Teel*

This report summarizes biochemical genetic data from 324 individuals from the central and southern Bering Sea (Fig. 1), and 27 individuals from the North Pacific Ocean near Japan. The frozen storage of muscle, heart, and liver tissues from these fish for over one year resulted in significant deterioration of much enzyme activity, and precluded a definitive comparison of allelic frequencies from these collections with similar data from collections of pollock from other areas. Nevertheless, the data are valuable as a source of (1) previously undescribed genetic variation, (2) some comparative data with other studies, and (3) suggestions of structuring that require confirmation by subsequent studies.

The only useful data were from extracts of skeletal muscle, although all three tissues were extensively screened. These data included 14 monomorphic loci [fluorescent acid phosphatase (ACP), alphaslycerophosphate dehydrogenase (AGP), esterase (EST)-3, general protein (GP) - three loci, glyoxilase (GLO), isocitrate dehydrogenase (IDH), malic enzyme (ME)-1, malic dehydrogenase (MDH)-3, peptidase (PEP)-2, PEP-6, phosphoglucomutase (PGM), phosphoglucose isomerase (PGI)-2, and 11 polymorphic loci (Tables 1 and 2) adeonsine deaminase (ADA)-1, EST-1, lactate dehydrogenase (LDH)-1, LDH-2, LDH-3, MDH-1, MDH-2, ME-2, PEP-4, PEP-5, PGI-3]. Nineteen apparent or putative loci were also tentatively identified where electrophoretic expression was either indistinct, unreliable or weak [aconitase (ACON),

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ADA-2, aldolase (ALD), EST-2, fumarase (FUM), beta galactosidase (b-GAL), glyceraldehyde-3-phosphate dehydrogenase (GAP), guanine deaminase (GDA), glutamic dyhydrogenase (GLUD), glutamic-pyruvic transaminase (GPT), glutathione reductase (GR), leucine aminopeptidase (LAP), nucleoside phosphorylase (NP), 6-phosphogluconate dehydrogenase (6-PGD), phosphomannose isomerase (PMI), PEP-1, PEP-3, tetraoxolium oxidase (TO), xanthine dehydrogenase (XDH)]. Both PMI and 6-PGD in this latter category were obviously highly polymorphic and promise to be useful for population studies when analyzed from fresher materials. Iwata (1975) has reported major differences in the frequency of TO alleles between pollock populations of the eastern and western North Pacific Ocean.

Comparisons of allelic frequencies from five of the polymorphic loci (ME-1, ME-2, MDH-1, LDH-1, and LDH-2) could be made with frequencies reported by Grant and Utter (JFRBC, in press) of collections from the northeastern Pacific Ocean and the southeastern Bering Sea. Allelic frequencies at each of these loci were generally within the ranges of values reported by Grant and Utter (in press), and did not define any new population units.

Allelic frequencies at a previously unreported locus (LDH-3) differed markedly among the collections. The average allelic frequencies of most of the Bering Sea samples differed by a factor of about .50 from the average allelic frequency of the most southern Bering Sea collection (52°20'N, 178°16'E) and the Japanese sample. The preliminary nature of these data precludes further statements concerning this variation. More rigorous testing is required to confirm the genetic nature of this variation, and if confirmed, more sampling is required to determine its oceanic distribution.

It is recommended (1) that future studies include the ability to analyze the samples within a few weeks of collection because of the particularly labile nature of gadid proteins, and (2) that collection points be extended to the northwest Pacific Ocean south of 52°N.

Polymorphic Loci

Collection	N	LDH-1		LDH-2		LDH-3			EST-1		ADA-1		
		A	B	A	B	C	A	B	A	B	A	B	C
Bering Sea													
Haul 1	48	1.0	0	1.0	0	0	.86	.14	1.0	0	1.0	0	0
5	48	.99	.01	.99	.01	0	.65	.35	1.0	0	.98	.01	.01
13	48	1.0	0	.99	0	.01	.66	.34	1.0	0	1.0	0	0
33	21	1.0	0	.96	0	.04	.95	.05	1.0	0	1.0	0	0
36	47	1.0	0	.99	.01	0	.69	.31	.99	.01	.99	.01	0
40	23	1.0	0	1.0	0	0	.14	.86	1.0	0	1.0	0	0
67	48	1.0	0	1.0	0	0	.80	.20	1.0	0	1.0	0	0
78	27	1.0	0	1.0	0	0	.98	.02	1.0	0	1.0	0	0
Japanese	27	1.0	0	1.0	0	0	.32	.68	1.0	0	1.0	0	0

	N	MDH-1			MDH-2			ME-2		PEP-4			PEP-5			PGI-3	
		A	B	C	A	B	C	A	B	A	B	C	A	B	C	A	B
Haul 1	48	.99	.01	0	1.0	0	0	.47	.53	1.0	0	0	.94	.06	0	1.0	0
5	48	1.0	0	0	.99	.01	0	.41	.59	.87	.13	0	.96	.04	0	1.0	0
13	48	1.0	0	0	.99	0	.01	.42	.58	.98	0	.02	.99	.01	0	.99	.01
33	21	.95	.05	0	1.0	0	0	--	-	-	-	-	-	-	-	.98	.02
36	47	.99	.01	0	1.0	0	0	.46	.54	.97	.03	0	.98	.02	0	1.0	0
40	23	1.0	0	0	1.0	0	0	.38	.62	1.0	0	0	.95	.05	0	.98	.02
67	48	1.0	0	0	1.0	0	0	.60	.40	.98	.02	0	.86	.13	.01	1.0	0
78	27	.96	.04	0	.98	.02	0	.48	.52	1.0	0	0	-	-	-	1.0	0
Japanese	27	.96	.04	0	1.0	0	0	.43	.57	.98	0	.02	.91	.02	.07	1.0	0

Table 1.--Allelic frequencies of polymorphic systems. Allelic form designated "A" is most frequent for each system and assigned a relative mobility of 100; see Table 2 for relative mobilities of alternate allelic forms.

Locus	Alternate Allele	
	B	C
MDH-1	0.15	0.24
MDH-2	0.73	1.58
ME-2	1.10	
PEP-4	1.27	0.91
PEP-5	1.10	0.89
LDH-3	0.33	
LDH-1	0.63	
LDH-2	0.91	0.67
PGI-3	0.93	
EST-1	1.10	
ADA-1	0.62	1.14

Table 2.--Relative mobilities of alternate allelic forms.

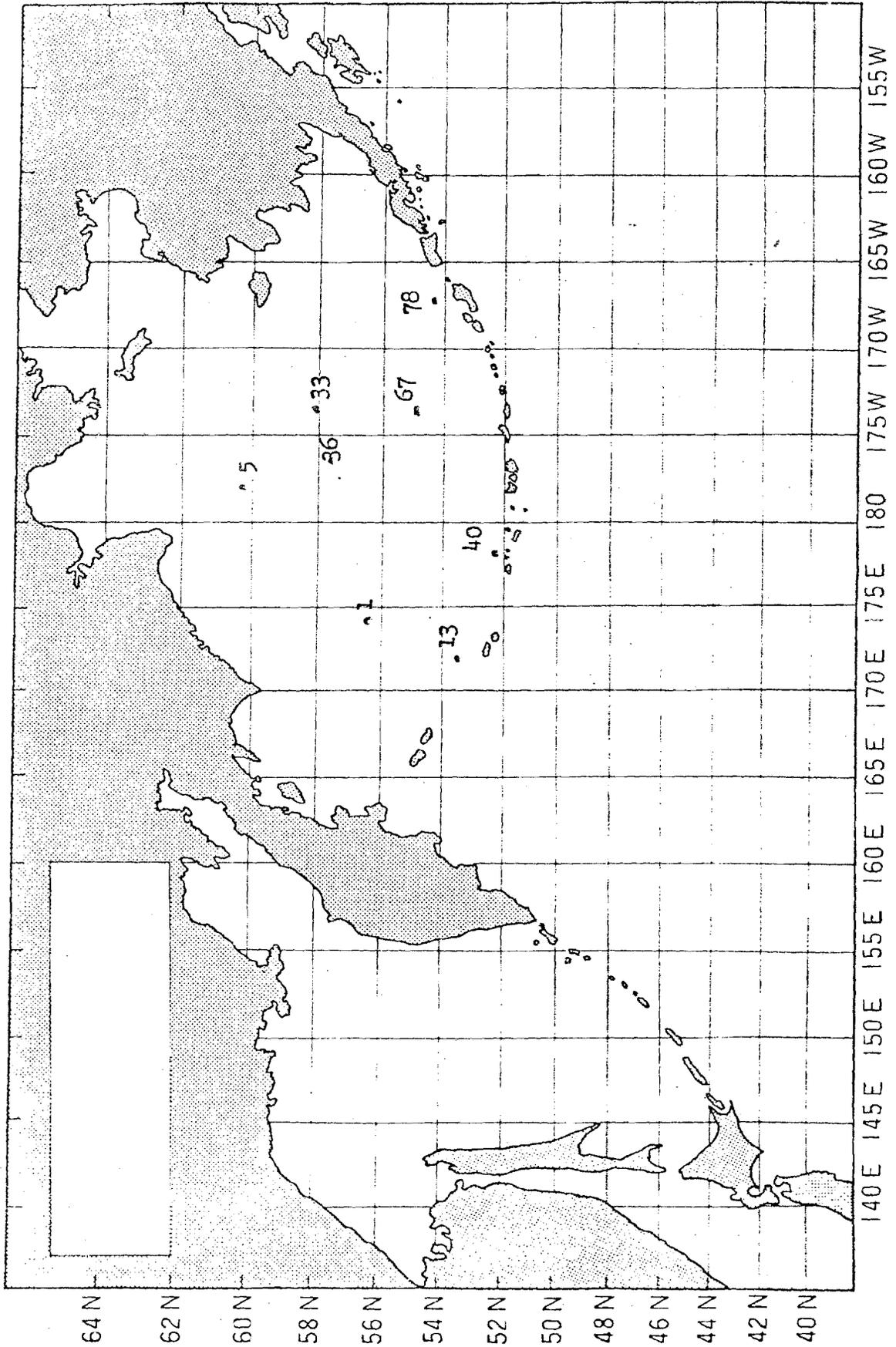


Figure 1. Locations of Bering Sea samples.