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BIOCHEMICAL POLYMORPHISMS IN THE PACIFIC HAKE (*MERLUCCIUS PRODUCTUS*)

By

FRED M. UTTER and HAROLD O. HODGINS

National Marine Fisheries Service, Biological Laboratory, 2725 Montlake Boulevard East Seattle, Washington 98102, U.S.A.

Since 1966, scientists of the National Marine Fisheries Service Biological Laboratory in Seattle, Washington, have studied genetic features of commercially important teleost species indigenous to the northeastern Pacific Ocean, mainly to detect polymorphisms for use as genetic markers. We will summarize here some findings on the Pacific hake, *Merluccius productus*.

Four polymorphic loci have been found in Pacific hake coding for an esterase of vitreous fluids, serum transferrin, lactate dehydrogenase, and a protein of the skeletal muscle (UTTER, 1969a, b; UTTER and HODGINS, 1969; Table 46). Five alleles were detected at the esterase locus-four at the transferrin locus and two each at the muscle protein and LDH A loci. Typical patterns of these four systems, as demonstrated by starch gel electrophoresis, are seen in Figure 32. In the LDH phenotypes, the most cathodal migrating bands of each homozygous type represent the A_4 and the A'_4 bands respectively. All five combinations of the two A locus subunits are seen in the AA′ phenotype although the A_4 band, as seen here, is typically very weak.

Large concentrations of Pacific hake are found in the Pacific Ocean between Baja California, Mexico, and Vancouver Island, Canada and in Puget Sound, Washington, U.S.A. Ocean stocks have distinct seaso-

Table 46. Gene frequency of skeletal muscle protein phenotypes in Pacific hake from Puget Sound and the Pacific Ocean

Location and date of capture	Phenotype[1] AA	AB	BB	B allele frequency	No. of fish	Age Composition
Near Blaine, Wash. 11–10–68	1 (·7)	6 (6·7)	16 (15·6)	·823	23	Adults, 3 years and older
Near Everett, Wash. 10–3–68	2 (2·4)	16 (15·2)	23 (23·4)	·756	41	
10–7–68	3 (1·7)	8 (10·6)	18 (16·7)	·759	29	
10–23–68	7 (4·6)	17 (21·8)	28 (25·6)	·702	52	
5–22–69	7 (9·2)	48 (43·6)	50 (52·2)	·705	105	
Puget Sound totals	20 (18·2)	95 (98·6)	135 (133·2)	·730	250	
Off northern Oreg. 10–68	0 (0)	1 (1·0)	15 (15·0)	·969	16	Adults, 3 years and older
2–25–69	0 (0·1)	5 (4·8)	84 (84·1)	·972	89	First year fish
5–27–69	0 (0)	2 (1·9)	118 (118·1)	·992	120	Adults, 3 years and older
Pacific Ocean totals.....	0 (0·1)	8 (7·9)	217 (217·0)	·982	225	

[1] Frequency of observed and (in parentheses) expected phenotypes. Expected phenotypes based on Hardy-Weinberg distribution.

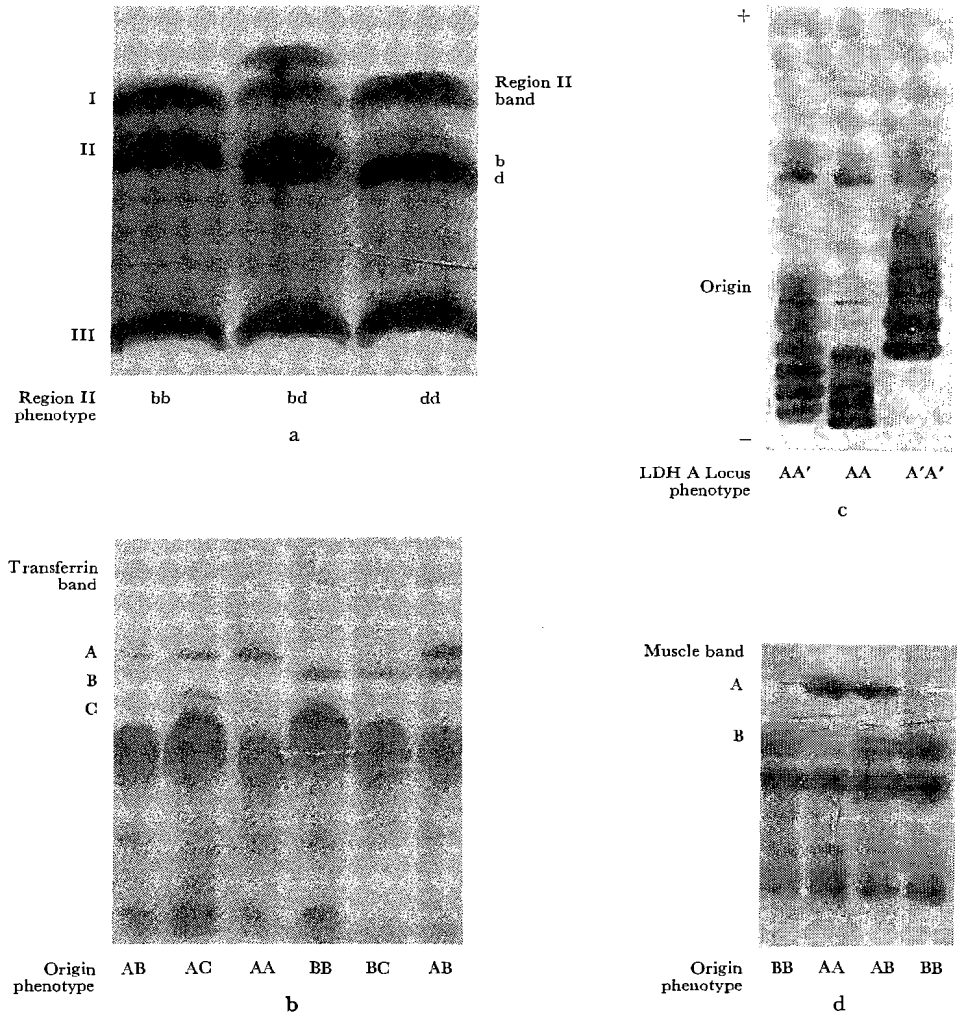

Figure 32. Representative phenotypes of four polymorphic systems in Pacific hake demonstrated by starch gel electrophoresis. a. B esterase in vitreous fluids. Second band in region I represents rare phenotype in about 1 % of all individuals tested (2× magnification).[1] b. Serum transferrin (1×).[1] c. LDH isozymes of the liver (1×).[1] d. Muscle protein variants (1×).[2]

[1] Buffer systems described by UTTER (1969).
[2] Buffer system consists of 0.2 M tris (hydroxymethylaminomethane) and 0.1 M boric acid, undiluted for electrode compartments and diluted 10 fold for gel preparation.

nal distributions and growth patterns as opposed to Puget Sound stocks (NELSON, 1967). Sampling areas of our studies are indicated in Figure 33: ocean fish were taken in areas 1 and 2, Puget Sound fish in area 3.

Samples from both areas in the Pacific Ocean were tested for LDH and esterase phenotypes and no evidence was found for heterogeneity of stocks within or between these two areas.Transferrin and muscle protein data similarly indicated no heterogeneity between different samples taken from area 1. Significant deviation within Puget Sound from expected frequencies (assuming a Hardy-Weinberg distribution of phenotypes) was found only in the esterase system. This difference appeared to be an effect of sex rather than a reflection of heterogeneity; when males and females were considered separately, the males deviated significantly from expected ratios, whereas the females did fit closely (UTTER, 1969).

Gene frequencies of each system differentiated samples taken from the Pacific Ocean and Puget Sound. The sample means, ranges, and standard deviations for the gene frequencies of the most frequent alleles in each system are shown in Figure 34, in which samples from Puget Sound and the Pacific Ocean are compared.

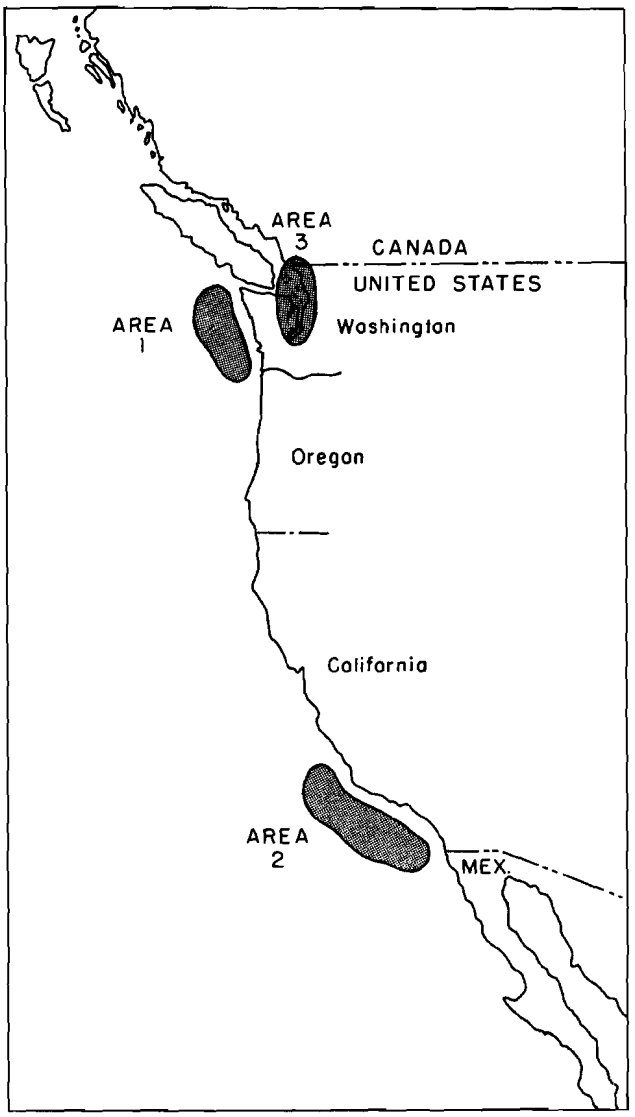

Figure 33. Areas of sampling in the Pacific Ocean and Puget Sound.

The distribution of the alleles of these systems provides genetic evidence of the reproductive isolation of these two groups of Pacific hake.

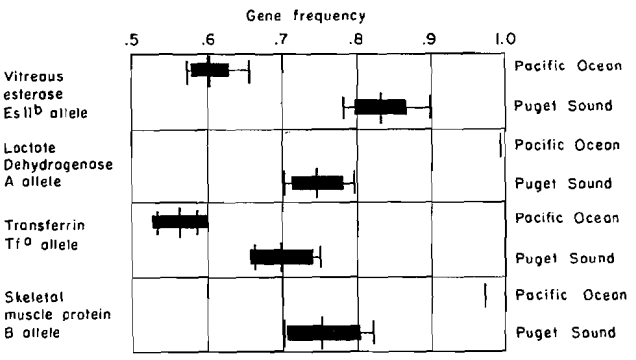

Figure 34. A comparison between sample means, ranges, and standard deviations of gene frequencies of the most common alleles of four polymorphic systems in Pacific hake from Puget Sound and the Pacific Ocean. In the lactate dehydrogenase and muscle protein systems, only the means are presented for the Pacific Ocean samples because of the low frequencies of the alternate alleles.

Parallel phenotypes between the vitreous fluid and the serum were observed in the esterase and transferrin systems. The vitrous fluids were unmodified for detection of the esterase systems but required four-fold concentration by dialysis for reliable identification of the transferrin bands. The finding of serum proteins in vitreous fluids of Pacific hake suggests that these fluids may be applied more generally in the study of serum proteins, which may be of practical significance because of the difficulties encountered in obtaining blood samples in fishes.

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