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POLYMORPHIC ISOZYMES IN LINGCOD, OPHIODON ELONGATUS

Lingcod, Ophiodon elongatus, support both sport and commercial fisheries in Washington State. Although stocks have not been identified, this fundamental information could be useful in developing future management plans. The purpose of this preliminary investigation was to assess the feasibility of using biochemical genetic techniques for population identification.

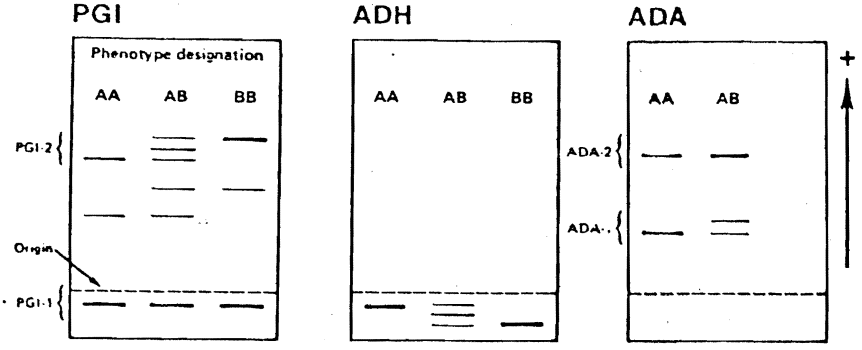
Four tissues (muscle, eye, liver and heart) were screened in the isozyme survey. Starch-gel electrophoresis procedures followed those described by Utter et al. (1974), except that an agar overlay was used to stain the isozymes. Twenty-four enzyme systems were examined.

Thirty-nine loci were hypothesized, based on the intensity and distribution of the zones of activity, three (PGI-2, ADH and ADA-1) of which (i.e. 8%) were polymorphic.

PGI (phosphoglucose isomerase) - Three phenotypes were observed for this system including one six banded and two three banded patterns. The relative mobilities and intensities of the banding patterns observed could best be interpreted as the result of two loci coding for a dimeric enzyme. Under this model both of the three banded phenotypes would reflect homozygous individuals for different allelic forms of the fast locus (AA & BB), and consist of two homodimer bands and an intermediate interlocus heterodimer. The six banded phenotype was presumed to reflect heterozygous individuals (AB); this phenotype expressed the sum of the bands of the 2 homozygous phenotypes plus an interlocus heterodimer band for the PGI-2 locus.

ADH (alcohol dehydrogenase) - The two single and one triple banded phenotypes observed for ADH were assumed to reflect a dimeric enzyme coded for by a single disomic locus.

ADA (adenosine deaminase) - Both heart and muscle tissue displayed a common zone of anodal activity. An invariant faster zone was observed in the heart only. Parallel expression of two phenotypes for the slow zone was observed in the two tissues. The common phenoytpe was represented by a single band, and the variant phenotype consisted of two bands of equal intensities with the slower band being the same mobility as the single banded phenotype. Therefore, a monomeric system coded for by one disomic locus was assummed.



The average heterozygosity (H) of this species was estimated to be 0.022. It is certainly possible that some of the zones we interpreted as monomorphic loci were actually interlocus heterodimers. Consequently, there may be fewer loci than we estimated. Therefore, our calculated heterozygosity may well be a conservative estimate.

The level of average heterozygosity (0.022) and proportion of polymorphic loci (8%) for lingcod is at the low end of the spectrum relative to surveys made over wide taxonomic ranges of organisms (e.g. Selander, 1976). Nevertheless, these values lie within ranges reported for other carnivorous marine fishes (e.g. H range in Sebastes sp. 0.004-0.06, Wishard et al., 1980). In walleye pollock, Theragra chalcogramma, 2 of 28 loci (7%) had variants in great enough frequencies to be useful in distinguishing populations (Grant and Utter 1980); lingcod are suitably polymorphic at 8% of the loci examined. Based on these comparisons, this initial study suggests that the amount of genetic variation observed in lingcod could be useful in stock identification and warrants further investigation.

Details regarding all enzymes surveyed, as well as the buffer systems utilized, can be obtained by requesting a copy of NWAFC Processed Report 81-07 from any of the authors.

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FLOW OF NUCLEAR AND MITOCHONDRIAL GENES ACROSS A HYBRID ZONE BETWEEN TWO SPECIES OF MICE

Two species of house mice, M. domesticus and M. musculus (as revised by Marshall and Sage, 1981), form a narrow hybrid zone in Denmark (Hunt and Selander, 1973). We have studied introgression of both nuclear genes (allozymes) and mitochondrial (mt) DNA in this zone. We have sampled 14 individuals from three different populations on the musculus side of the hybrid zone, and compared them with representatives of authentic musculus from Eastern Europe and authentic domesticus from Western Europe and North Africa. Our electrophoretic study of proteins encoded by 56 nuclear loci allows us to estimate that these Danish populations are about 90% musculus; i.e. they have received about 10% of domesticus genes by introgression from that species. In contrast, our analysis of 65 restriction sites in mtDNA by the method of Ferris et al. (1982) shows that these Danish mice are 100% domesticus; the musculus and domesticus types of mtDNA are easy to distinguish since they differ by 4% in nucleotide sequence. We conclude that mtDNA has moved across the hybrid zone more effectively than the average nuclear gene. This finding may indicate that a small, maternally-inherited, cytoplasmic genome can be more invasive than a nuclear gene encumbered by 10^4 kilobases of flanking DNA.

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