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PROTEIN VARIATION IN *NOTOTODARUS GOULDI* FROM SOUTHEASTERN AUSTRALIA

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Twenty seven sample sets, each consisting of pieces of mantle muscle and digestive gland from 100 animals, were collected from a series of sampling stations in Bass Strait and off S.E. Tasmania and South Australia. A total of 30 different specific proteins were surveyed using standard cellulose acetate and starch gel electrophoretic techniques. Twelve digestive gland enzymes and two muscle enzymes showed inter-animal variability.

The phosphoglucomutase (PGM) variation in muscle had the appearance expected of a genetic polymorphism at this locus while the lactate dehydrogenase (LDH) variation could be so interpreted, though the patterns were different from those seen in vertebrates.

The variation observed in the digestive gland proteins was different from that described in any other group of organisms. Six or more band positions were found in the variable proteins and from one to six bands in all combinations were observed. The band strengths varied markedly and all band positions could be strong, weak or absent. There was no regular association of patterns in one enzyme with patterns in other enzymes. The genetic and/or environmental basis of this variation is unknown but clearly complex. Though the patterns observed varied widely from sample set to set, within any set only a limited number of the possible patterns were observed.

Further studies were restricted to the muscle LDH and PGM loci and to the variation in digestive gland, LDH, PGM and glutamate oxaloacetate transaminase (GOT). The effects of a range of environmental factors on these proteins was examined:

1. Organ heterogeneity

Five samples taken from different points along the length of the digestive gland of each of ten animals expressed similar phenotypes within each animal and the inter-animal variation could not be ascribed to the varying proportions of the various tissues found in different parts of this organ.

2. Sample deterioration

Ten animals were sampled on capture and resampled after 1, 2, and 4 hours at ambient temperature. There was no change in pattern. Samples retyped after extended periods of storage typed correctly.

3. Animal size, general condition (i.e. mantle thickness) and reproductive condition

There was no systematic effect of these variables on the patterns observed.

4. Food type

The ability of squid to transfer incompletely digested food to the digestive gland raises the possibility that the enzymes of the prey species were being typed as well as the squid proteins. However, analysis of protein patterns within schools by food type showed this was not so.

5. Feeding state

There were differences in the patterns observed between individuals with full and empty stomachs within a sample set. However, which electrophoretic patterns were related to which feeding state changed from set to set.

There was no systematic between-area variation in the frequencies of the muscle enzyme patterns.

The geographical distribution of the digestive gland variation in PGM and GOT was random while the LDH variation was nonrandomly distributed between areas. A series of sets from the eastern edge of the study area (namely, the set taken off Maria Is., a set from Flinders Is.

and sub-sets from Storm Bay and Lakes Entrance) consisted of squid with only a fast LDH pattern. Only 4 of these animals were found throughout the rest of the sets studied. The other bands observed for this enzyme occurred in all combinations throughout the region.

There was no evidence in this study of the presence of more than one *Notododarus* species in the fishery. S. Collins (Personal Communication) was able to ascribe some of the sample sets studied to the proposed spring brood and others to the winter brood. There were no systematic differences between the observed electrophoretic patterns of these groups; however, the absence of a good series of allelic polymorphisms in the species made it difficult to obtain significant evidence on the number of stocks in the fishery.