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Characterization of energy metabolism in antarctic fishes

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Fish fauna of the antarctic seas are unusual in both species composition and the chronically cold water temperatures south of the Antarctic Convergence where they spend their entire life cycle. DeWitt (1971) has estimated that more than 70 percent of the fish genera populating antarctic waters are members of the family Nototheniidae unique to the southern ocean. For approximately 40 million years this species group has been geographically isolated and evolving independently in the frigid waters surrounding the antarctic continent.

Antarctic fishes are a major food item for many endothermic predators and, as a group, are estimated to consume annually some 100 million tons of krill (Everson 1984), a figure 30 percent greater than combined world fisheries landings. Commercial fishing pressure on antarctic finfish is now significant and projected to increase in the years ahead. Little is known about the basic physiology and biochemistry of energy metabolism in this group, despite the importance of this information to understanding mechanisms that enable life at cold body temperature and the role played by antarctic fishes in the trophic structure of the southern oceans.

Our project is focusing on two major unresolved questions in this area:

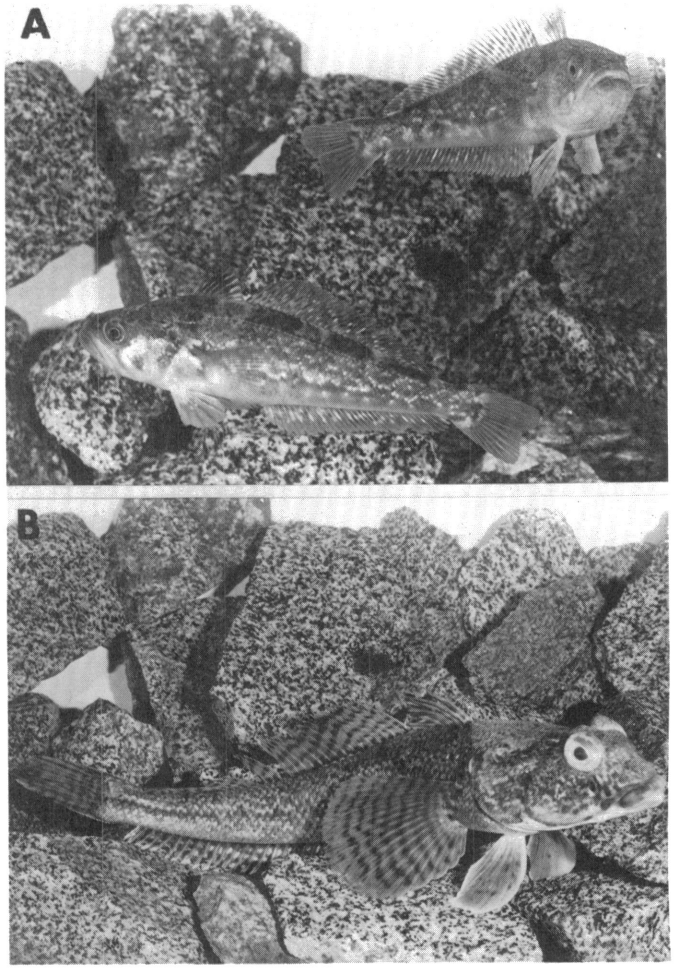
- Do antarctic fishes possess cellular/biochemical adaptations that enable a higher rate of energy metabolism (and therefore, activity) than would be expected by temperate zone animals at equally cold body temperature?
- What are the relative roles of alternative metabolic fuels (carbohydrate vs. lipid) in energy metabolism of antarctic fish tissues?

The latter question is particularly interesting because notothenioid fishes accumulate unusually large stores of corporeal lipid (Clarke et al. 1984). These low-density lipid deposits are known to contribute buoyant advantage to notothenioids which lack swimbladders (Eastman and DeVries 1981). Although some biologists have suggested that lipids are also the primary fuel for energy metabolism in this group, this hypothesis has not been tested directly.

Our initial year's field activities at Palmer Station were carried out during February and March 1987 by a research team consisting of Lisa Crockett, Kelly Edwards, and Bruce Sidell of the University of Maine. Three separate fishing efforts were conducted by bottom trawling from ;sdR/V *Polar Duke* at locations in the vicinity of Low Island and off Astrolabe Needle in Dallman Bay. We were able to obtain numerous specimens of several fish species, including *Notothenia gibberifrons, Trematomus newnesi, Chaenocephalus aceratus,* and *Parachaenicthys charcoti.* Animals were transported in tanks aboard *Polar Duke* to Palmer Station where they were maintained in aquaria until needed for experiments. Although collecting data from each species, our experiments are emphasizing *N. gibberifrons* and *T. newnesi* (figure) because of differences in their life histories and food habits. *N. gibberifrons* is a relatively sluggish benthic species whose primary dietary items are benthic invertebrates with small amounts of krill taken opportunistically. In contrast, *T. newnesi* is a more active pelagic species that displays greater dietary preference for krill.

We have measured the activities of several key enzymes of energy metabolism from muscular tissues of both *N. gibberifrons* and *T. newnesi.* Some of these data are presented in the table. Enzymes which are not stable to freezing (cytochrome oxidase, hexokinase, and 6-phosphofructokinase) were assayed at Palmer Station using freshly prepared samples while others were measured from frozen tissues transported to our laboratory at the University of Maine. All measurements were made at an assay temperature of 1°C, within the normal physiological range of each species.

Overall capacity for aerobic metabolism (cytochrome oxidase, citrate synthase) and anaerobic metabolism of carbohydrate (6-phosphofructokinase) appears roughly equivalent in homologous tissues of the two species. Highly aerobic tissues (heart and pectoral muscle) of *T. newnesi* consistently show a greater capacity for oxidation of fatty fuels (carnitine palmitoyltransferase activity) than those of *N. gibberifrons.* Preferred substrate for this enzyme in both species is the coenzyme A ester of monounsaturated palmitoleic acid (16 to 1). The marker enzyme for aerobic metabolism of carbohydrate, hexokinase, is higher in activity in cardiac muscle of *N. gibberifrons* while pectoral muscle of the more active *T. newnesi* displays greater hexokinase activity than the homologous tissue from *N. gibberifrons.* These preliminary data suggest an overall pattern of fuel preference geared more toward fat oxidation in *T. newnesi* than *N. gibberifrons* consistent with their known dietary preferences. Although more detailed comparisons are required for definitive conclusions, the absolute levels of enzyme activities



Representative examples of the primary fish species under study, *Trematomus newnesi* (A) and *Notothenia gibberifrons* (B).

found in cardiac muscle of antarctic species at 1°C are similar to those measured in hearts from temperate zone fishes at much warmer assay temperatures (e.g., see Sidell et al. 1987).

During austral summer 1987–1988 field activities, we will concentrate on direct measurements of the rate of oxidation of various radiolabeled substrates by tissues isolated from each species. In the interim, gas chromatographic analyses of the fatty acyl composition of plasma and tissue lipids are continuing in our laboratory to determine which specific lipid fuels are accessible to the metabolic machinery of antarctic fishes. Electron micrographs of tissues fixed during last field season also are being prepared for quantitative ultrastructural analyses which may reveal unique aspects of cellular organization tailored to life at subzero body temperature.

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Maximum activities of key enzymes of energy metabolism from muscular tissues of antarctic fishes[a]

	Activity (micromoles per minute per gram wet weight)				
	6-PFK	CS	CYTOX	HK	CPT[b]
Trematomus newnesi					
Heart	2.12 ± 0.16 (12)	9.13 ± 0.54 (8)	13.73 ± 1.01 (12)	0.94 ± 0.05 (12)	0.29 ± 0.01 (8)
Pectoral muscle (oxidative)	1.50 ± 0.15 (12)	25.71 ± 1.88 (8)	19.84 ± 0.98 (12)	0.37 ± 0.03 (12)	0.73 ± 0.01 (8)
White skeletal muscle (glycolytic)	1.96 ± 0.18 (12)	1.46 ± 0.10 (8)	1.70 ± 0.08 (12)	ND (5)	0.05 ± 0.01 (8)
Notothenia gibberifrons					
Heart	2.10 ± 0.10 (12)	13.69 ± 0.91 (8)	15.12 ± 1.05 (12)	1.32 ± 0.09 (12)	0.18 ± 0.01 (8)
Pectoral muscle (oxidative)	1.48 ± 0.10 (12)	23.47 ± 1.78 (8)	16.77 ± 0.79 (12)	0.20 ± 0.02 (12)	0.34 ± 0.02 (8)
White skeletal muscle (glycolytic)	1.53 ± 0.07 (12)	0.77 ± 0.12 (8)	1.07 ± 0.10 (12)	ND (8)	0.02 ± 0.00 (8)

[a] All assays were conducted at 1° ± 0.5°C; data presented are mean ± standard error measure for number of individual samples indicated parenthetically; "ND" denotes "not detectable"; "6-PFK" denotes "6-phosphofructokinase"; "CS" denotes "citrate synthase"; "CYTOX" denotes "cytochrome oxidase"; "HK" denotes "hexokinase"; "CPT" denotes "carnitine palmitoyltransferase."

[b] CPT activity reported is that determined with palmitoleoyl CoA as substrate.