

Stock discrimination of orange roughy, *Hoplostethus atlanticus*, by parasite analysis

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Abstract

The parasite fauna of the viscera of 1251 orange roughy, *Hoplostethus atlanticus*, collected in 1983 to 1986 from eight areas off southern Australia and three areas off New Zealand, was examined for evidence of discrete host populations. Fish from each area were divided into three length groups which averaged close to 28, 37 and 42 cm. Canonical multivariate analysis of data on larval nematodes (*Anisakis* spp., *Terranova* sp., and a spirurid) and larval cestodes (*Hepatoxylon trichiuri* and *Callitetrarhynchus* sp.) discriminated five Australian and three New Zealand stocks. These were for Australia: (1) Great Australian Bight, (2) South Australia/west Victoria/west and south Tasmania, (3) Cascade Plateau/Tasman Rise, (4) north-east Tasmania, (5) New South Wales; and for New Zealand: (1) north-east New Zealand, (2) south-east New Zealand, (3) west New Zealand. No significant differences in parasite fauna were detected between samples of fish taken within the spawning season and those taken outside the spawning season in the same area. In one southern Australian stock there was a north-south cline in the numbers of *Anisakis* spp. This was apparent in both small (immature) and medium-sized (mature) fish. We conclude that *Hoplostethus atlanticus* is a sedentary species with little movement between fish-management zones.

Introduction

Orange roughy *Hoplostethus atlanticus* is the basis of an established trawl-fishery in New Zealand (Robertson et al. 1984) and an emerging deep-water trawl-fishery in Australia (Wilson 1982). The fish occurs in 900 to 1 200 m. A feasible means to tag it has not yet been developed.

The New Zealand fishery is based on aggregations thought to be associated with spawning. Robertson et al. (1984) suggested that between spawnings fish were dispersed

over several management areas, and that fish on the west of New Zealand probably constituted a single spawning stock. Isoenzyme studies on New Zealand and Atlantic fish showed that the species had high heterozygosity (Smith 1986). Smith suggested that the species was widely distributed in the world at the 1 000 m isobar and that the genetic similarity between the New Zealand and North Atlantic fish could be maintained by gene flow along the slope edge and gene-hopping between ocean ridges and sea mounts. He was unable to distinguish any stocks around New Zealand.

The use of parasites for separating marine stocks is a well established technique (MacKenzie 1983, 1987, Sindermann 1983). Parasites, particularly larval stages, survive for extended periods in fish and some persist until the fish dies. As parasite species are rarely distributed uniformly over the host range, juveniles in one area will acquire a parasite species but not those in another. Thus, the parasite fauna of adult fish reflects the environment in which it has grown. Margolis (1965) separated sockeye salmon in the north Pacific Ocean into those of North American or Asian origin using parasites acquired during the fishes' juvenile freshwater phase. In 1939, Dogiel and Bykhovski distinguished two stocks of sturgeon in the Caspian Sea using parasites common in the northern less saline waters but largely absent from the south (in: Dogiel 1961).

We used the natural parasite fauna of orange roughy to determine if there were consistent differences between fish from different geographical areas around Australia and New Zealand.

Materials and methods

Orange roughy, *Hoplostethus atlanticus*, were collected from eight areas off southern Australia and three areas off eastern and western New Zealand (Fig. 1): Great Australian Bight (Area 1), South Australia (Area 2), west Tasmania (Areas 3 to 5), Cascade Plateau and Tasman Rise (Area 6), east Tasmania (Area 7), New South Wales (Area 8), Challenger

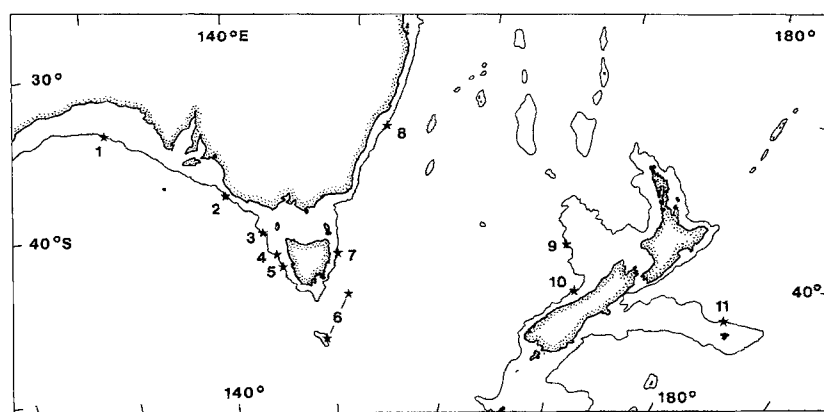


Fig. 1. Origins of eleven samples of *Hoplostethus atlanticus* from Australia and New Zealand; 1000 m isobath is shown

Plateau (Area 9), combined Cook and Moeraki Canyons (Area 10), and the Chatham Rise (Area 11). Of the 1 422 fish examined, 874 were provided by the Tasmanian Department of Sea Fisheries, 74 by the New South Wales Department of Agriculture Fisheries Division, and 474 by the New Zealand MAF Fisheries Research Centre. Fish were either gutted at sea or held in chilled brine for a maximum of 3 d and gutted immediately on landing. The viscera were stored frozen after being placed in a plastic bag with a label giving the fish caudal fork length (LCF), cruise number and haul number. They were later thawed and separated into their component parts for parasitological examination.

Parasites (Table 1) were recorded using the following methods. Prevalence of *Sphaeromyxa* sp. was assessed by searching for spores in gall-bladder fluid using a compound microscope ($\times 40$ objective) for a maximum of 5 min. Trypanorhynch larvae (*Hepatoxylon trichiuri*, *Tentacularia* sp., *Sphyricephalus* sp. and *Callitetrarhynchus* sp.), the larval anisakid nematodes (*Anisakis* spp. and *Terranova* sp.) and an unidentified species of larval spirurid were found in the mesentery and gut wall using the naked eye and a dissecting microscope with transmitted light. Digenea (*Glomeriscirrus amadai* and *Pseudopascoelus* sp.), Acanthocephala (*Echinorhynchus* sp.), the nematode *Ascarophis* sp., and tetraphyllidean larvae (scolex polymorphus), were found in the washings from the lumen of the stomach and intestine using a dissecting microscope. Representative specimens of these parasites have been lodged in the Queensland Museum; for accession numbers and a listing of the raw data see Sewell and Lester (1988).

The data were analysed in three ways: summary statistics, investigation into the similarities and dissimilarities of the parasite fauna between areas, and investigation of seasonal differences in average parasite numbers between areas.

Fish from each sample were divided into three size groups, small (20 to 34 cm LCF), medium (35 to 39 cm LCF) and large (40 to 48 cm LCF). Short or long fish were removed from each size group until the average length of each group was approximately 28, 37 and 42 cm LCF, respectively, except for New Zealand samples where the average length of the small category was 29.8 cm LCF. Of the total number of fish dissected (1 422), 1 251 were used in the

analyses. For each size group, the similarities and dissimilarities between areas were examined using canonical multivariate analysis (Mardia et al. 1979). The method was essentially as described by Lester et al. (1985) for their analysis of data from skipjack tuna. A single transformation of the natural logarithm of the number of parasites plus one, was used on all parasite numbers. To further remove bias due to associations between parasite numbers and fish length within each fish size group, transformed counts were adjusted for fish length. For each parasite species, a regression of transformed parasite number on fish length was undertaken, and the resulting relationship used to adjust the parasite numbers to that expected for a fish of 28, 37 or 42 cm LCF. No adjustment was made if the parasite number was zero.

A random number between -0.05 and $+0.05$ was added to all parasite data. This allowed matrix inversion in the canonical variate analysis which was otherwise impossible as some parasites were absent from some samples. The small addition did not significantly affect the outcome. The results of the canonical analyses were displayed as plots of the first, second and third canonical axes. Confidence limits (99%) for the points are presented in the relevant figures as circles with radius equal to the square root of 9.21 divided by the number of fish in the sample. Confidence limits at 95% were visualised as circles with radius equal to the square root of 5.99/no. of fish in sample (Mardia et al. 1979).

The differences in average log (parasite number + 1) between fish taken during the spawning season and those taken from the same site outside the spawning season were investigated on four separate pairs of samples by an analysis of that variance which remained after each of a series of five models had been fitted to the data. Model 1 was the total variability about the mean in the 237 fish tested. Unexplained variability was progressively reduced by successive models as follows: Model 2 removed simple linear length effects; Model 3, average differences between sites; Model 4, common seasonal differences between sites; and Model 5, seasonal differences between sites. Using hierarchical and other analyses of variance constructed from the results of these models, it was possible to determine whether evidence existed for the presence of seasonal differences, either as common differences over all sites or as differences at particular sites.