

## Gut Patterns of the Acanthuridae and Zanclidae

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**Abstract** The gut patterns of one or more species of all six genera of the family Acanthuridae, and of the single genus of the family Zanclidae, are described and the phylogenetic significance of the patterns is considered. An advanced pattern, placement of the end of the b loop to the left side of the stomach, is shared by Zanclidae and all acanthurids, suggesting that they are a monophyletic group. The gut patterns of the acanthurids contain little intrafamilial phylogenetic information.

### Introduction

In studying the form of acanthopterygian gastrointestinal tracts as exemplified by the patterns of intestinal convolution, I found a simple gut pattern in *Zanclus cornutus* and *Zebrasoma flavescens*. This seems at first glance to be an advanced character (see discussion below), indicating that *Zanclus* might be the sister group of *Zebrasoma*. The gut patterns of one or more species of all genera in the family Acanthuridae were studied in order to find evidence to test this hypothetical relationship.

The form of the intestinal convolution is a useful feature that provides information on the phylogenetic relationships of fishes of the orders Tetraodontiformes (Mok, 1974), and Pleuronectiformes (personal observations). Other gut characters, such as gross external morphology of the stomach and the foldings of the mucous membranes of the gastrointestinal tract, are considered too variable to be interpretable. Therefore, the present paper deals only with the gut pattern as an approach to clarifying the interrelationships of the acanthurids and zanclids. The comparative gross anatomy of the acanthurid gastrointestinal tract was studied by Breder and Clark (1947), and Jones (1968).

### Material and methods

Specimens I examined are at the American Museum of Natural History (AMNH), the Academy of Natural Sciences of Philadelphia (ANSP), the Bernice P. Bishop Museum

(BPBM), and the Zoology Museum, National Taiwan University (ZMNTU).

Dissections were made on one to several individuals of each species studied, with special attention being given to *Acanthurus bahianus* and *Zanclus cornutus* to determine intraspecific consistency of the pattern. Gut patterns of the specimens of these two species are similar. As a consequence, I generalize that reliable information can be derived from examination of a limited number of specimens of any particular species. Intraspecific gut pattern was also found to be consistent in another group of teleosts, the Pomacentridae (Fukusho, 1969).

Species examined are listed with the number of specimens dissected in parentheses. *Acanthurus bahianus* (Castelnau) (4), *A. nigrofuscus* (Forsskål) (1), *A. thompsoni* (Fowler) (1), *Ctenochaetus striatus* (Quoy & Gaimard) (1), *Naso annulatus* (Quoy et Gaimard) (3), *N. hexacanthus* (Bleeker) (1), *Paracanthurus hepatus* (Linnaeus) (3), *Prionurus microlepidotus* (Lacépède) (1), *Zebrasoma flavescens* (Bennett) (4), *Z. rostratum* (Günther) (1), *Z. scopas* (Cuvier) (1), *Z. veliferum* (Bloch) (1), *Zanclus cornutus* (Linnaeus) (5), *Gerres* sp. (1), *Heniochus acuminatus* (Linnaeus) (1), *Kyphosus* sp. (1), *Melanochromis johannii* (1), and *Siganus restratus* (Valenciennes) (1).

Drawings are based on dissections made on the left side of the body, with the exception of *Paracanthurus hepatus*, a specimen of which was dissected on the right side. The gut pattern of this specimen was redrawn in a left side view to facilitate comparison.

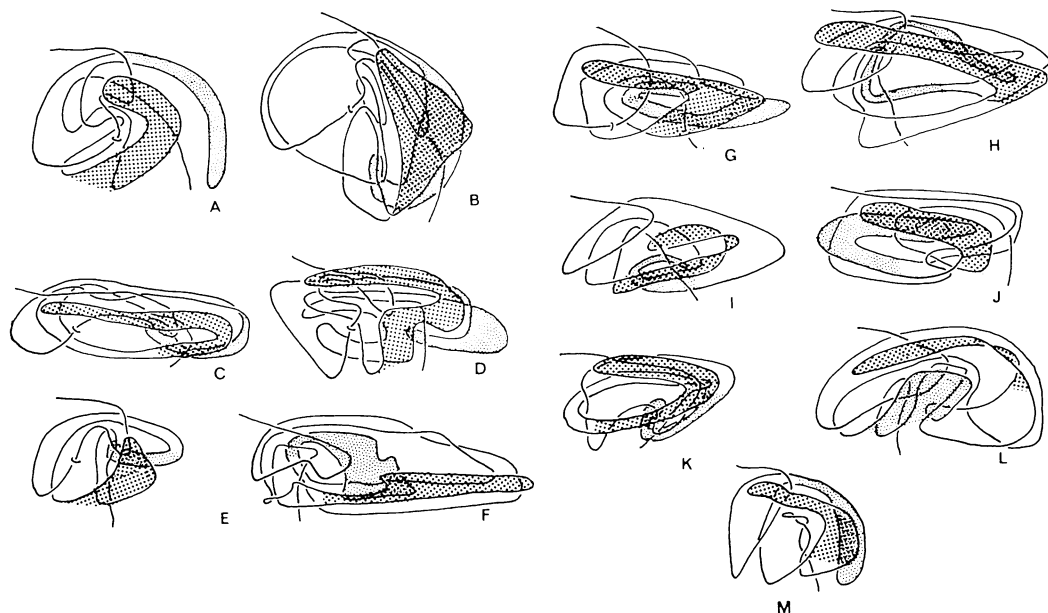


Fig. 1. Gut patterns of 13 species of Acanthuridae and Zanclidae. A, *Zebrasoma flavescens*, AMNH 29301, 108 mm S.L.; B, *Z. scopas*, BPBM 7652, 135 mm S.L.; C, *Z. veliferum* BPBM 7824, 95 mm S.L.; D, *Z. rostratum*, BPBM 12847, 135 mm S.L.; E, *Naso annulatus* AMNH 18461, 55 mm S.L.; F, *N. hexacanthus* BPBM 8519, 218 mm S.L.; G, *Ctenochaetus striatus*, AMNH 30915, 132 mm S.L.; H, *Acanthurus nigrofuscus*, AMNH 1778, 40 mm S.L.; I, *A. bahianus*, AMNH 5284, 26 mm S.L.; J, *A. thompsoni*, BPBM 9430, 96 mm S.L.; K, *Prionurus microlepidotus*, AMNH 34784, 170 mm S.L.; L, *Paracanthurus hepatus*, ANSP 131125, 87 mm S.L.; M, *Zanclus cornutus*, AMNH 13515, 35 mm S.L. In some figures, (- indicates junction between the stomach and intestine. Fine stippling: loop a; heavy stippling: loop b.

### Results

The gut patterns of twelve acanthurid species and of one species of *Zanclus* are shown in Fig. 1. The homologous loops a and b are recognized in these species (Fig. 1, A~M).

A feature unique to acanthurids and zanclids among all acanthopterygian groups I have studied is the placement of the end of loop b to the left side of the stomach (Fig. 1, A~M). A loop resembling loop b, but with its end placed to the right of the

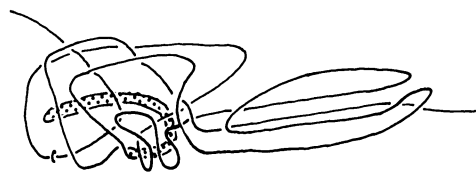


Fig. 2. Gut pattern of *Kyphosus* sp. AMNH, uncatalogued, 230 mm S.L.

stomach, occurs in other teleosts, for example, the rudderfish, *Kyphosus* sp. (Fig. 2).

Loop a commonly occurs in the rear part of the abdominal cavity in many teleosts besides the acanthurids and zanclids, for example, *Melanochromis johannii* (Cichlidae), the mojarras, *Gerres* sp. (Gerridae), *Heniochus acuminatus* (Chaetodontidae), and *Siganus rostratus* (Siganidae) (Fig. 3, A~D).

Among all acanthurids and in *Zanclus cornutus*, loop a shows different degrees of winding complexity. In *Zanclus cornutus* and *Zebrasoma flavescens*, loop a is extremely simple and similar (Fig. 1, A, M). *Naso hexacanthus*, at the other extreme, has a very complex loop a (Fig. 1, F). However, there is no trend of progressive development of complexity of this loop that can be traced within these two families.

The gross morphology of the stomach of

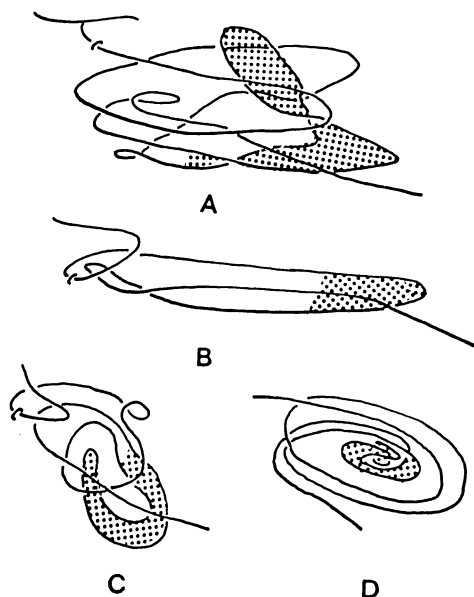


Fig. 3. Gut patterns of (A): *Melanochromis johannii*, Michael Oliver uncataloged specimen, 65 mm S.L., (B): *Gerres* sp. AMNH 3878, 67 mm S.L., (C): *Heniochus acuminatus*, ZMNTU, uncatalogued, 51 mm S.L., (D): *Siganus rostratus*, AMNH 14918, 131 mm S.L.

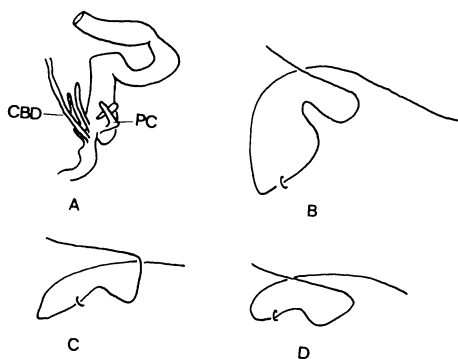


Fig. 4. (A). Gross stomach morphology of *Zebrasoma flavescens*, (B). Anterior section of the gut pattern of *Zebrasoma flavescens*, (C). Anterior section of the gut pattern of *Naso annulatus*, (D). Anterior section of the gut pattern of *Naso hexacanthus*. CBD: common bile duct; PC: pyloric caecum.

*Zebrasoma* and *Naso* is similar, giving the anterior section of the gut pattern an easily recognizable W-shape (Fig. 4) as seen in lateral view. In *Paracanthurus hepatus*, the stomach is more elongate than in other acanthurids, extending to the rear part of

the abdominal cavity.

### Discussion

*Zebrasoma* has two character states of loop a; the simple state as found in *Zebrasoma flavescens* and the complex state seen in all other species of this genus. The similarity in the unusually simplified state of loop a in *Zebrasoma flavescens* and *Zanclus cornutus* is of particular interest. This shared character state might be the result of convergence, or it might be synapomorphic, and hence evidence for the relationship of these two genera because other possibly related fishes have a complex loop a, for example, siganids (Fig. 3, D). The Zanclidae traditionally is considered a sister group of the Acanthuridae (e.g., Greenwood et al., 1966; Herald, 1961: 208; McAllister, 1968: 143). Two phylogenetic hypotheses can be proposed, as outlined (Fig. 5). There are eight possible evolutionary changes of loop a in either one of these two hypotheses. When the possible sister group such as Siganidae (Greenwood et al., 1966) is taken into account, sixteen possible evolutionary changes can be assumed for each of these hypotheses. However, there is no minimum evolutionary change unique to only one of these hypothetical events in both cases. It is, therefore, not possible to ascertain whether the simple character state

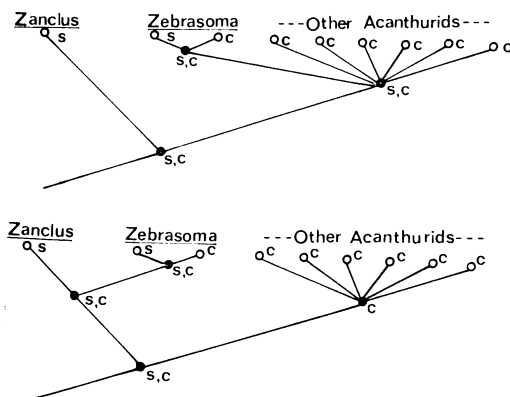


Fig. 5. Two hypotheses regarding the relationship of the acanthurids and *Zanclus*. The possible character states of loop a in the living groups and hypothetical ancestors are indicated. S—simple state; C—complex state.

of loop **a** is primitive or advanced by the criterion of parsimony.

The patterns of the four species of *Zebrasoma* dissected in this study are basically similar. Except for *Zebrasoma flavescens*, loop **a** of the other three species (*Z. rostratum*, *Z. scopas*, and *Z. veliferum*) winds antero-dextrally to the right side of the rectum (Fig. 1, B,C,D). Barlow (1974) equates *Zebrasoma scopas* with *Z. flavescens* without explanation. At Enewetak, *Z. flavescens* is rare and *Z. scopas* is common and the species hybridize. It is likely that the establishment of a hybrid population at this locality has led Barlow to this conclusion (Randall, personal communication). The difference in complexity of loop **a** in the gut pattern of these two species suggests that *Zebrasoma flavescens* and *Z. scopas* are best retained as separate species.

A final observation involves the number of pyloric caeca. All acanthurids dissected, except *Naso annulatus*, have five pyloric caeca. In *Naso annulatus*, a juvenile specimen (55 mm S.L.) has six pyloric caeca, while adult specimens (124~137 mm S.L.) have only five. Because of the limited number of specimens available, the significance of this variability in number of pyloric caeca is not known. It is possible that the number becomes reduced during ontogeny. A low number of pyloric caeca may be evidence of specialization and hence close intrarelationship of the acanthurids. In contrast to the acanthurids, *Zanclus cornutus* has seven to ten pyloric caeca. Consideration of a low number of pyloric caeca as an advanced character state is based on the assumption that a primitive feature is to be found early in ontogeny and an advanced feature later (Nelson, 1970).

Compared to carnivorous fishes, herbivorous species are generally characterized by having a longer digestive tract which might as a result generate a more complex looping pattern. Whether the complexity of the pattern will appear depends on the volume and shape of the abdominal cavity. In acanthurids, for example, an increase in the length of the digestive tract might lead to a more complex loop **a** or loop **b**, to initiation of a new loop not found in its relatives,

or to a combination of these strategies. The interesting question is, why do certain groups of fishes develop a specific combination of loops. This potential variability implies the significance of gut patterns in providing useful data for the reconstruction of phylogenies.

*Zebrasoma flavescens* and *Z. veliferum* are filamentous-algae feeders (Jones, 1968), but differ in complexity of their gut patterns. The plankton feeders, *Paracanthurus hepatus*, *Naso hexacanthus*, *Acanthurus hexacanthus*, and *A. thompsoni* (Jones, 1968; Randall, personal communication), and the algae feeders, *Naso annulatus* (personal observation) and *Acanthurus nigrofuscus* (Jones, 1968), have similar gut patterns. These observations suggest that, for acanthurids, there is no correlation between feeding habit (plankton versus algae feeders) and gut pattern.

To summarize, the gut pattern of the Acanthuridae and Zanclidae, specifically the occurrence of the unique condition of loop **b** on the left side of the stomach, provides evidence for their monophyly. The intra-familial phylogeny of acanthurid genera, however, cannot be deciphered from the data obtained in this study.

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ニザダイ科とツノダシ科の腸型

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ニザダイ科6属とツノダシ科1属の腸型を記載し、系統的意味を論じた。特化していると考えられるbループが胃の左側に存在するパターンは、これら全ての魚に認められた。このことから、上記の魚類は単一系統群に属すると考えられる。ニザダイ科内の相互類縁関係に対する情報は、腸型からは殆んど得られなかった。