Confusion in the deep: morphology and taxonomy of Lantern Sharks (Elasmobranchii: Etmopteridae)

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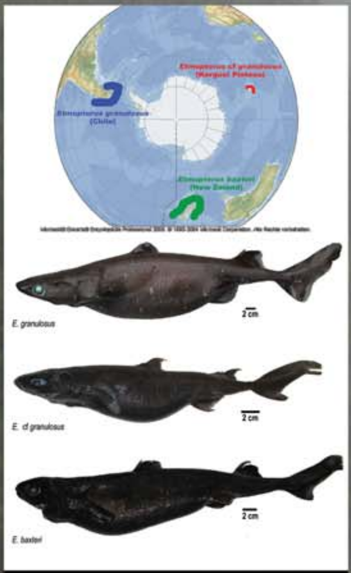

Figure 1: Distribution map and photographs of freshly caught specimens of *Etmopterus granulosus*, *Etmopterus* cf *granulosus* and *Etmopterus baxteri*.

Introduction

The speciose family of Lantern Sharks, Etmopteridae, comprises 43 described extant and several undescribed species in five genera. All inhabit the subphotic zone from 100 to more than 2500 m depth. Etmopterids are found in all oceans at continental shelves and insular or seamount slopes. Eponymous for this family of Squaliform or Dogfish sharks is the ability to emit light using photophores located in clearly defined body areas: bioluminescent organs are situated at the ventral side of the body, at flanks and caudal fins. The genus *Etmopterus* is the largest within Etmopteridae with described 33 species.
External morphological characters are highly important for species identification, e.g. dorsal fin spine morphology, dentition or shape of flank and caudal markings, body regions appearing dark black, carrying photophores in skin, etc. Some of these characters exhibit high intraspecific variation such as tooth morphology.
Flank markings are probably the most important characters for species identification, but seem to be specific for some and highly variable in shape and/or conspiciousness for other species.
One example for a species which is hard to identify with traditional characters is *Etmopterus granulosus*, originally described from Cape Horn (South America). The species then was synonymized, but later separated again from *Etmopterus baxteri*, described from New Zealand waters (Tachikawa et al. 1989, Comapgno et al. 1998).
Today, distribution patterns (fig. 1) of *E. granulosus* are not satisfactorily clarified, and it is still unclear, if specimens from the Kerguelen Plateau, are either individuals of *E. granulosus* or *E. baxteri* - a possible hint for cryptic diversity?

Material and Methods

42 body measurements (table 1) were attained from 12 specimens of *E. granulosus* caught in Chilean waters, 10 specimens of *E. baxteri*, caught off New Zealand, and 48 specimens of *E.* cf *granulosus* from the Kerguelen Plateau in the southern Indian Ocean. Principal component analysis (PCA) was used for identifying morphometric differences of specimens.
For preliminary molecular phylogenetic analyses of Etmopteridae, tissue samples of representatives of the different locations (Chile, Patagonian fjord region, New Zealand, Chatham Rise, and slope of the Kerguelen Plateau) were added to the sampling and used for DNA extraction and sequencing of a portion of the nuclear RAG1 gene (1200 bp). *Squalus megalops* was defined as outgroup, since Squalidae are considered to be sister family of Etmopteridae (Compagno et al. 2005). For a preliminary analysis, a branch and bound search was conducted resulting in a 50% majority rule consensus tree of 24 trees. Currently the data set consists of 1217 characters, 1119 of which are constant, 54 parsimony uninformative, and 44 parsimony informative. Additional sequences from other genomic regions as well as additional samples will be included in the near future.

Total length	Pre pelvic length
Pre caudal length	Pectoral pelvic distance
Pre first dorsal fin length	Interdorsal distance
Pre second dorsal fin length	Dorsal caudal distance
Head length	Pelvic caudal distance
Pre branchial length	Pectoral fin anterior margin length
Pre spiracle length	Pectoral fin inner margin length
Pre orbital length	Pectoral fin posterior margin length
Pre narial length	Pectoral fin base length
Pre oral length	First dorsal fin maximal length
Eye length	First dorsal fin base length
Eye height	First dorsal fin inner margin length
Spiracle length	First dorsal fin height
Eye- spiracle distance	First dorsal fin spine length
Mouth width	Second dorsal fin maximum length
Nostril width	Second dorsal fin base length
Snout width	Pelvic fin length
Head width	Pelvic fin anterior margin length
Head height	Caudal fin dorsal caudal margin
Interorbital distance	Caudal fin preventral margin length
Pre pectoral length	Caudal fin subterminal margin length

Table 1: body measurements taken for further analyses.

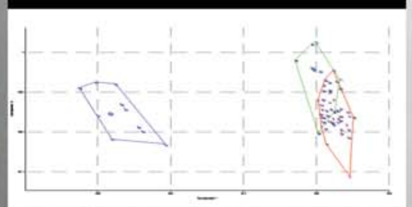

Figure 2: PCA plot of PCs 1 and 2 showing separation of Chilean *E. granulosus* (N=12, blue) from *E. baxteri* from New Zealand (N= 10, green), and *E.* cf *granulosus* (N= 48, red) from the Kerguelen Plateau. Specimens of *E. baxteri* and *E.* cf *granulosus* strongly overlap.

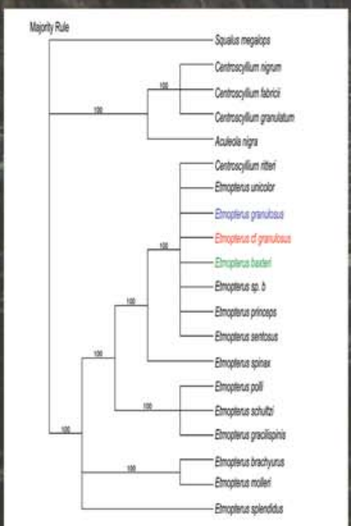

Figure 3: 50% majority rule consensus tree of 24 parsimonius trees based on portion of RAG1 gene (1200 bp).

Results and Discussion

Morphometrics: The PCA plot of PCs 1 and 2 (fig. 2) shows a clear spatial separation of specimens of *E. granulosus* caught in Chile from specimens of *E.* cf *granulosus* from the Kerguelen Plateau and *E. baxteri* stemming from Chatham Rise, New Zealand. Loadings of the different variables reveal the distance between second dorsal fin and origin of caudal fin as the most decisive factor in separation of specimens. *E. baxteri* and specimens from the Kerguelen Plateau strongly overlap. Other variables must be taken into consideration for analysis, meristic characters, e.g. number of vertebrae, are of great interest for supporting results of PCA.
Phylogeny: As preliminary analysis, the consensus parsimony tree shows *E. granulosus* from Chile, *E. baxteri* from New Zealand, and *E.* cf *granulosus* from the Kerguelen Plateau together with *E. unicolor*, *E.* sp. B, *E. princeps*, *E. sentosus*, and *Centroscyllium ritteri* in a polytomic clade, but the RAG1 gene is apparently not informative to species level within the clade. All seven species are closely related, their relationships are not fully resolved.
The position of *C. ritteri* within the genus *Etmopterus* is surprising, since phylogenetic analyses based on morphological characters place *C. ritteri* in the *Centroscyllium – Aculeola* clade (Shirai & Nakaya 1990). However, *C. ritteri* is the only *Centroscyllium* showing light organs and may be a specialized species of *Etmopterus*. Further analyses will test the position of this species more rigourously, and will shed new light on the importance of various morphological character sets for the phylogenetic analysis and generic classification of etmopterid sharks.

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