

Cucullanus (Rhabditida, Cucullanidae) parasitizing the thinlip conger *Gnathophis mystax* (Delaroche, 1809) (Congridae) from the coast of Calabria (Italy)

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INTRODUCTION & AIM

The thinlip conger *Gnathophis mystax* (Delaroche, 1809) is a benthic marine teleost inhabiting muddy and sandy substrates of the continental shelf and upper continental slope, generally at depths between 80 and 400 m. The species is widely distributed throughout the Mediterranean Sea and the eastern Atlantic Ocean, where it plays an important ecological role as a predatory fish feeding primarily on benthic invertebrates and small fishes. Although its flesh is considered to be of good quality, *G. mystax* is not a primary target of commercial fisheries and is usually caught incidentally by deep trawl nets or longlines (palangres), resulting in limited availability in fish markets.

Despite its broad distribution, knowledge of the parasitic fauna of *G. mystax* is extremely scarce, with no previous parasitological studies specifically addressing this host species. In particular, data on helminth parasites of benthic deep-water fishes from the southern Tyrrhenian Sea remain fragmentary. Nematodes of the genus *Cucullanus* Müller, 1777 are common gastrointestinal parasites of marine teleosts and are characterized by high morphological similarity among species, making accurate identification challenging and emphasizing the importance of detailed morphological investigations.

The objectives of the study were to investigate the presence and prevalence of nematodes of the genus *Cucullanus* in *G. mystax* from the southern Tyrrhenian Sea (Calabria, Italy); to provide a morphological characterization of the recovered specimens using light microscopy and scanning electron microscopy (SEM); to evaluate infection parameters (prevalence and mean intensity); to explore potential relationships between parasite abundance and host biometric parameters (length and weight); and to compare parasitological data between two different sampling areas along the Calabrian coast.

METHOD

A total of 41 specimens of *Gnathophis mystax* (Fig. 1) were examined in this study. Fish were collected from the southern Tyrrhenian Sea along the Calabrian coast, specifically in the areas of Vibo Valentia and Gioia Tauro, and were provided by local professional fishermen. All specimens were measured (total length) and weighed prior to parasitological examination.

The gastrointestinal tract of each fish was carefully dissected and examined under a stereomicroscope for the presence of helminths. Recovered nematodes were isolated, washed in physiological saline, and processed according to standard parasitological protocols. Specimens were fixed and preserved for morphological identification, mounted on slides, and photographed using light microscopy.

Selected specimens were further prepared for scanning electron microscopy (SEM) to obtain detailed observations of external morphological features relevant for taxonomic identification, including the cephalic region, cuticular structures, and caudal morphology. Identification was performed based on available taxonomic keys and original species descriptions for the genus *Cucullanus*.

Parasitological indices, including prevalence and mean intensity, were calculated following standard definitions. Differences in host biometric data between sampling sites and correlations between parasite abundance and host length or weight were statistically analyzed.



Fig.1: *Gnathophis mystax* [1].

RESULTS & DISCUSSION

Nematodes recovered from the gastrointestinal tract of *G. mystax* were morphologically assigned to the genus *Cucullanus*. This represents the first record of *Cucullanus* spp. infecting *Gnathophis mystax*. Infection parameters showed measurable prevalence and mean intensity values, confirming that *G. mystax* serves as a suitable definitive host for cucullanid nematodes in the study area.

Morphological observations obtained through light microscopy and SEM (Fig. 2) revealed diagnostic characters consistent with the genus *Cucullanus*, including the typical cephalic structure and cuticular features. However, species-level identification was constrained by the lack of comparative material and the absence of previous parasitological records from this host species.

Comparisons between the two sampling areas indicated differences in host biometric parameters, while analyses of parasite abundance suggested possible relationships with host size (length and/or weight). These findings are consistent with patterns reported for cucullanid infections in other marine teleosts, where larger or older hosts often harbor higher parasite loads.

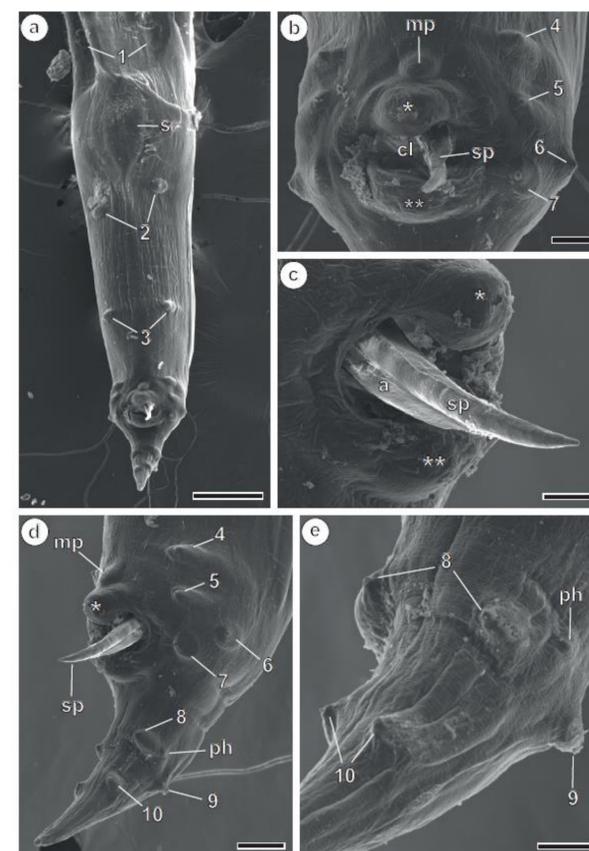


Fig.2: SEM of *Cucullanus* (Scale bars: a=200 µm; b=30 µm; c=20 µm; d=50 µm; e=20 µm)

*: median outgrowth of anterior cloacal lip; **: median outgrowth of posterior cloacal lip; 1-10: pairs of cloacal papillae; a: specular ala; cl: cloaca; mp=median precloacal papilla-like formation; ph=phasmid; s: ventral sucker; sp=spicule

The absence of previous studies on the parasitic fauna of *G. mystax* highlights the novelty and relevance of the present work. The results contribute to the growing body of knowledge on Mediterranean helminth biodiversity and underscore the importance of investigating non-commercial and deep-water fish species, which remain largely overlooked in parasitological research.

CONCLUSION

This study provides the first parasitological assessment of *Gnathophis mystax* from the southern Tyrrhenian Sea and documents the first record of *Cucullanus* spp. infecting this host species. The findings expand current knowledge of host–parasite associations in Mediterranean marine ecosystems and contribute valuable morphological data for the taxonomy of cucullanid nematodes.

Given the limited information available on the helminth fauna of deep-water benthic fishes, further studies incorporating larger sample sizes and molecular analyses are strongly recommended. Such approaches will be essential for resolving species-level identification and for improving our understanding of the ecological and biogeographical patterns of marine nematode parasites.

REFERENCES

[1] <http://www.mondomarino.net/ricerca/index.asp?view=zoom&q=&p=1&idb=155>