

The study of parasite populations and communities has led to a higher comprehension of fish biology for nearly one century. Due to the fact that the biology of deep sea fish is still scarcely known, parasites could represent high potential biological tags. The family Moridae is the best-represented family in terms of biomass in the Balearic deep-sea. *Lepidion lepidion* (Risso, 1810) it is the most abundant morid and the dominant fish species in this area at depths between 1,000-1,500m but knowledge about its biology and ecology is still scarce. The objectives of this study were: first to identify and describe the parasite fauna of *L. lepidion* in the Balearic Sea; secondly, to perform a quantitative characterisation of the parasite populations; thirdly to describe the composition and structure of parasite communities in *L. lepidion* at Barcelona and Mallorca and assess the variations in infracommunity richness, abundance and similarity with depth; and finally to evaluate the natural geographical variability of parasite infracommunities and the effect of depth on parasite community composition and structure. A total of 1,043 metazoan parasites was found in the 89 *L. lepidion* collected from two localities off the Balearic Sea (Barcelona and Mallorca) at 2 depths (1,000-1,399 m and 1,400-1,900 m). The metazoan parasite fauna of *L. lepidion* in the Balearic Sea appear to be rich and comprises 12 species (3 adult vs 9 larval stages): *Echinorhynchus trachyrinchi*, *Lepidapedon desclersae*, *Capillostrongyloides* sp., *Scolex pleuronectis*, *Bothriocephalidae* gen. sp., *Trypanorhyncha* fam. gen. incertae sedis, *Otodistomum* sp., *Anisakis* type II, *Hysterothylacium aduncum*, *Anisakidae* gen. sp. and *Raphidascaris* sp. All these species which are transmitted via food ingestion, represent new host records for *L. lepidion* and the first record of *E. trachyrinchi* and *Capillostrongyloides* sp. from the Mediterranean Sea. The complete checklist of helminth parasites of *Lepidion* spp. developed during the course of the study that contains a total of 18 species and 35 host-parasite-area records revealed that only three species found in *L. lepidion* are shared with the North Atlantic codling, *L. eques*: *H. aduncum*, *L. desclersae* and the larval cestode complex, *Scolex pleuronectis*. This study represents the first quantitative characterisation of the parasite populations and the first description of the composition, structure and diversity of parasite communities in *L. lepidion* and has revealed that 4 helminth communities in this host are relatively rich, abundant and diverse for a deep-sea species with the dominance of a species, *L. desclersae*. This is also the first study on the use of parasite communities of a deep-sea fish as indicators of natural variability (geographical and related to depth). The results suggest that parasite communities of this host could be used as indicators of fish populations. It is also remarkable that the parasite species that appear to be the most important in the discrimination of fish populations at two depths and two localities are the only three species (*L. desclersae*, *E. trachyrinchi*, *Capillostrongyloides* sp.) which use *L. lepidion* as definitive host. A part of natural factors of variability, such as a different topography (e.g.canyons) and possible effects of anthropogenic impact have been suggested as a factor contributing to the differences found between parasite communities from the two localities studied.