Suez Canal University
Faculty of Veterinary Medicine
Department of Fish Diseases & Management

Studies on the Prevailing External Parasitic Diseases in Some Marine Fishes in Ismailia Governorate

Thesis Presented by

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English abstract

This study has been applied on a total number of 480 marine fishes (140 *Dicentrarchus labrax, 140 Siganus revulatus* and 200 *Moolgarda seheli)* that collected seasonally from different areas of Ismailia governorate. The parasitological examination revealed two types of crustacean parasites where 6 species of copepods (*Caligus minimus, Caligus longipedis, Caligus lichiae, Lepeophtheirus lichiae, Lernanthropus* sp. *and Lernanthropus kroyeri*) and 4 species of isopoda (*Renocila* sp., *Levonica* sp., *lironeca* sp. and *Nerocila* sp.). While the result of the monogenea was 3 species (*Pseudohaliotrema sphincteroporus, Paranella diplodae* and *Benedenia sekii*) in all examined marine fishes. The total parasitic infestation in the examined marine fishes was highest in *D. labrax* followed by *S. revulatus* then *M. seheli,* where the total crustacean infestation was highest in in *D. labrax* followed by *M. seheli* then *S. revulatus* and the monogenetic trematodes infestation was high in *S. revulatus* followed by *M. seheli* then *D. labrax.* The prevalence of copepod in *D. labrax* was high in the intermediate length than shorter and longer fish. The seasonal prevalence of total parasitic infestation in *D. labrax* and *M. seheli* was the highest in the winter and the lowest was summer, while in *S. revulatus* was the highest in the spring and the lowest was autumn. The histopathological change and the pathognomonic abnormalities in gill of infested fish with ectoparasites depend on the number of parasites to make harmful effect on fish which reflect in fish health where heavy infestation destroy the gills and threat fish life. Molecular identification of *Benedenia* sp. using PCR analysis of the 28S rRNA (mix of C1/D2 pairs) was useful tool for identification. Then sequencing and phylogenetics revealed that our sample was more closely related to *Benedenia sekii* from Australia followed by *Benedenia sciaenae* from Australia.