



# ABSTRACT BOOK



# 1<sup>ST</sup> INTERNATIONAL SYMPOSIUM ON AQUATIC SCIENCES & TECHNOLOGY

CYPRUS - 2014

15 16 17 May



ORGANISED BY:

GIRNE AMERICAN UNIVERSITY - CYPRUS

KASTAMONU UNIVERSITY - TURKEY

CANAKKALE ONSEKİZ MART UNIVERSITY - TURKEY



## Intragenic Variation of *Anguillicola crassus* isolated from the European Eel (*Anguilla anguilla*) sampled from the Ceyhan River, Turkey

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### Abstract

The European Eel (*Anguilla anguilla*), is a critically endangered species with a decline level of 90-98% in the number of eels reaching Europe. Main factors related to this decline include over-fishing, barriers preventing migration, natural changes and parasites such as *Anguillicola crassus*. *A. crassus* is a parasitic swim bladder nematode which was originally endemic to East Asia. It was introduced to water bodies in Europe by its native host, the Japanese eel (*Anguilla japonica*). The nematode is found to be very successful colonizer as it already spread to four continents (Asia, Europe, Africa and America). The European Eels are infected by *A. crassus* through ingestion of third stage larvae found in crustacean intermediate hosts or by ingestion of larvae found in fish hosts. Following the infection, the nematode damages swim bladder function resulting in mortality of both farmed and wild populations. In this study, we used DNA barcoding as a molecular approach to identify the *A. crassus* isolated from eels sampled from the Ceyhan River (Adana, Turkey), which is a natural habitat of the European eel. All the nematode samples were subjected to a DNA extraction, which was followed by PCR amplifications of a fragment from mitochondrial cytochrome c oxidase I gene, known as the barcode region. Amplified fragments were sequenced and nucleotide sequences were aligned using reference sequences from the BOLD database. All sequences were successfully identified at species level. A mean intragenic distance of 0.006 was found among nematode specimens. Network analysis was performed in order to graphically visualize the genetic divergence pattern of genetic variation found in *A. crassus* specimens.

**Keywords :** *Anguillicola crassus*, *Anguilla anguilla*, nematode, COI, DNA barcoding

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