

{rokbox title=|Map of the Mediterranean Sea and surrounding area with three larvae sampling sites: A) Strait of Sicily, B) Ionian Sea and C) Levantine Sea :: Figure: Authors| thumb=|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-identificacion-molecular-larvas-atun-rojo-francisco-alemany-puncher-et-al-2015-thumb.jpg|images/stories/ieo/imagenespublicaciones/centro-oceanografico-baleares-identificacion-molecular-larvas-atun-rojo-francisco-alemany-puncher-et-al-2015.jpg{/rokbox}

Gregory Neils Puncher, Haritz Arrizabalaga, **Francisco Alemany**, Alessia Cariani, Isik K. Oray, F. Saadet Karakulak, Gualtiero Basilone, Angela Cuttitta, Salvatore Mazzola, Fausto Tinti, 2015.

[Molecular](#)

[identification of atlantic bluefin tuna \(\*Thunnus thynnus\*](#)

[, Scombridae\) larvae and development of a DNA character-based identification key for Mediterranean scombrids.](#)

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**Abstract:** The Atlantic bluefin tuna, *Thunnus thynnus*, is a commercially important species that has been severely over-exploited in the recent past. Although the eastern Atlantic and Mediterranean stock is now showing signs of recovery, its current status remains very uncertain and as a consequence their recovery is dependent upon severe management informed by rigorous scientific research. Monitoring of early life history stages can inform decision makers about the health of the species based upon recruitment and survival rates. Misidentification of fish larvae and eggs can lead to inaccurate estimates of stock biomass and productivity which can trigger demands for increased quotas and unsound management conclusions. Herein we used a molecular approach employing mitochondrial and nuclear genes (CO1 and ITS1, respectively) to identify larvae (n = 188) collected from three spawning areas in the Mediterranean Sea by different institutions working with a regional fisheries management organization. Several techniques were used to analyze the genetic sequences (sequence alignments using search algorithms, neighbour joining trees, and a genetic character-based identification key) and an extensive comparison of the results is presented. During this process various inaccuracies in related publications and online databases were uncovered. Our results reveal important differences in the accuracy of the taxonomic identifications carried out by different ichthyoplanktologists following morphology-based methods. While less than half of larvae provided were bluefin tuna, other dominant taxa were bullet tuna (*Auxis rochei*), albacore (*Thunnus alalunga*) and little tunny (*Euthynnus alletteratus*). We advocate an expansion of expertise for a new generation of morphology-based taxonomists, increased dialogue between morphology-based and molecular taxonomists and increased scrutiny of public sequence databases.

Keywords: Larvae, Sequence databases, Tuna, Sequence alignment, BLAST algorithm, DNA sequence analysis, Fisheries, Mediterranean Sea