

# Genomic resources for a commercial flatfish, the Senegalese sole (*Solea senegalensis*): EST sequencing, oligo microarray design, and development of the Soleamold bioinformatic platform

Joan Cerdà <sup>a,\*</sup>, Jaume Mercadé <sup>b</sup>, Juan José Lozano <sup>c</sup>, Manuel Manchado <sup>d</sup>, Angèle Tingaud-Sequeira <sup>a</sup>, Antonio Astola <sup>e</sup>, Carlos Infante <sup>d</sup>, Silke Halm <sup>e</sup>, Jordi Viñas <sup>f</sup>, Barbara Castellana <sup>g</sup>, Esther Asensio <sup>d</sup>, Pedro Cañavate <sup>d</sup>, Gonzalo Martínez-Rodríguez <sup>e</sup>, Francesc Piferrer <sup>f</sup>, Josep V. Planas <sup>g</sup>, Francesc Prat <sup>e</sup>, Manuel Yúfera <sup>e</sup>, Olga Durany <sup>b</sup>, Francesc Subirada <sup>b</sup>, Elisabet Rosell <sup>b</sup>, and Tamara Maes <sup>b</sup>

<sup>a</sup> *Institut de Recerca i Tecnologia Agroalimentàries (IRTA), Barcelona, 08003, Spain*

<sup>b</sup> *Oryzon Genomics, Barcelona, 08028, Spain*

<sup>c</sup> *CIBERehd, Barcelona, 08036, Spain*

<sup>d</sup> *IFAPA Centro El Toruño, El Puerto de Santa María, Cádiz, 11500, Spain*

<sup>e</sup> *Instituto de Ciencias Marinas de Andalucía (CSIC), Puerto Real, Cádiz, 11510, Spain*

<sup>f</sup> *Institut de Ciències del Mar (CSIC), Barcelona, 08003, Spain*

<sup>g</sup> *University of Barcelona, Barcelona, 08028, Spain*

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## Abstract

The Senegalese sole, *Solea senegalensis*, is a flatfish of growing commercial interest for aquaculture in Southern Europe. However, despite the industrial production of Senegalese sole being hampered primarily by lack of information on the physiological mechanisms involved in reproduction, growth and immunity, very limited genomic information is available on this species. The international consortium Pleurogene was aimed to improve this knowledge by using functional genomics and proteomics approaches. Sequencing of a *S. senegalensis* multi-tissue normalized cDNA library, from adult tissues, larval and juvenile stages, and undifferentiated gonads, generated 10,185 expressed sequence tags (ESTs). Clones were sequenced from the 3'-end to identify isoform specific sequences. Assembly of the entire EST collection into contigs gave 5,208 unique sequences of which 1,769 (34%) had matches in GenBank, thus showing a low level of redundancy. The sequence of the 5,208 unigenes was used to design an oligonucleotide microarray representing 5,087 unique sole transcripts. This platform was validated and employed to determine global patterns of gene expression

during gonad growth and maturation, sex differentiation and larval development. Proteomic analysis during spermatogenesis, and of specific larval stages, was also carried out using conventional 2-DE methods and 2-D DIGE. Finally, a novel interactive bioinformatics platform, named Soleamold, which integrates EST sequences, microarray and in situ hybridization data on an anatomical basis, has been developed. These resources will help elucidate transcriptional regulation in wild and captive Senegalese sole for optimization of its production under intensive culture conditions.

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\* Corresponding author. Tel.: +34 932309531; fax: +34 932309555.

E-mail address: [joan.cerda@irta.es](mailto:joan.cerda@irta.es) (J. Cerdà).