

Supplementary Material

Male reproductive dysfunction in *Solea senegalensis*: new insights into an unsolved question

Marta F. Riesco^A, David G. Valcarce^A, Juan Manuel Martínez-Vázquez^A, Ignacio Martín^A, Andrés Ángel Calderón-García^B, Verónica Gonzalez-Nunez^B and Vanesa Robles^{A,C}

^ASpanish Institute of Oceanography (IEO), Planta de Cultivos el Bocal, Barrio Corbanera, Monte, Santander, Spain.

^BInstituto de Neurociencias de Castilla y León (INCyL), Department of Biochemistry and Molecular Biology, Faculty of Medicine, University of Salamanca, Institute of Biomedical Research of Salamanca (IBSAL), E-37007 Salamanca, Spain.

^CCorresponding author. Email: robles.vanesa@gmail.com

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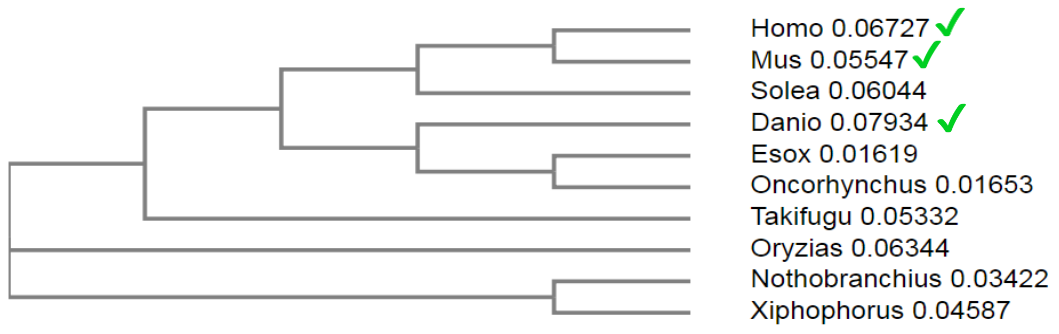
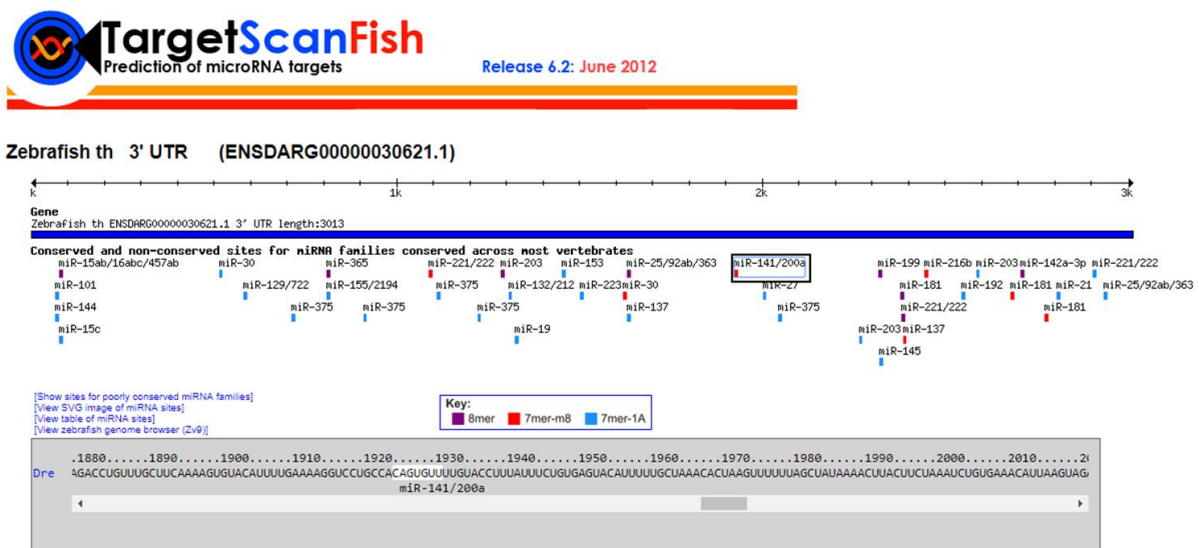


Fig. S1. (A) Multiple sequence alignment of Th proteins from the obtained sequenced of *Solea senegalensis* (Solea), *Homo sapiens* (Homo), NP_954987.2, *Mus musculus* (Mus), NP_033403.1, *Danio rerio* (Danio), NP_571224.1, *Esox lucius* (Esox), XP_010896475.1, *Oncorhynchus mykiss* (Oncorhynchus), XP_021419922.1, *Takifugu rubripes* (Takifugu), XP_003967406.1, *Oryzias latipes* (Oryzias), NP_001265797.1, *Nothobranchius furzeri* (Nothobranchius), XP_015820360.1, and *Xiphophorus maculatus* (Xiphophorus), XP_023199811.1, performed with Clustal Omega. Legend: * (asterisk) - fully conserved residue; : (colon) – amino acid substitution between groups of strongly similar properties; . (period) – amino acid substitution between groups of weakly similar properties. Note the high degree of sequence similarity among proteins, which supports broad range of species reactivity and supports the specific recognition of Solea Th. (B) Neighbour-joining phylogenetic cladogram without distance corrections for the previous alignment generated with Clustal Omega. Ticks represent proven species reactivity for AB152 antibody.



Target sites

	predicted consequential pairing of target region (top) and miRNA (bottom)	seed match	site-type contribution	3' pairing contribution	local AU contribution	position contribution	TA contribution	SPS contribution	context+ score	context+ score percentile
Position 1924-1930 of th 3' UTR	5' ...GAAAAGGUCCUGCCACAGUGUUU... dre-miR-200a 3' UGUAGCAAUGGUCUGACACAAU	7mer-m8	-0.120	0.003	-0.036	0.092	0.015	0.020	-0.03	27
Position 1924-1930 of th 3' UTR	5' ...GAAAAGGUCCUGCCACAGUGUUU... dre-miR-141 3' CGUAGCAAUGGUCUGACACAAU	7mer-m8	-0.120	0.003	-0.036	0.092	0.015	0.020	-0.03	27

Fig. S2. Screen capture of miR target analysis for *th* transcript using Target Scan Fish 6.2 program (http://www.targetscan.org/fish_62/).