O1-02 Divergence and genomic evolution of repetitive elements in the sole *Solea senegalensis*

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The Senegalese sole, *Solea senegalensis*, is a flatfish of major interest in fisheries and aquaculture with a high market value, mainly in Europe. Due to its high interest, genomic studies on this species have been increasing in the last decade, leading finally to the publication of its genome[1,2]. However, from the published genome, there are no specific studies of the distribution, abundance or chromosomal evolution of repetitive elements. These elements play a fundamental role in the evolution of genomes and their adaptation to changing environmental conditions. Therefore, in this work, an analysis of transposable elements (TEs) and satellite DNA, as the main components of the repeat fraction of the genome, has been carried out in *S. senegalensis*. The results have shown that the repetitive elements coverage in its genome is 35.0%. In addition, the coverage of the main TE families has been analysed in 7 other flatfish species belonging to 4 families, and two other species outside this group, *Seriola aureovittata* and *Sparus aurata*, with the latter having the highest coverage (47.29%) of repetitive elements and *Cynoglossus semilaevis* (Pleuronectiforme, Cynoglossidae) the lowest. However, *S. senegalensis* has the highest number of annotated loci per Mb of genome (NL/Mb=3373) of all the species analysed. A more detailed analysis of the TEs in Senegalese sole revealed that the most abundant elements are LINEs (LINE-L2) followed by Class II transposons (hAT-Ac) and helitrons. The study of centromeric satellite families has also revealed a high concentration of helitron families around the centromeres of a large number of chromosomes. Divergence studies of TE families by chromosomes have been carried out, as well as phylogenomic studies of subfamilies mapped in the genome. A bimodal distribution in the divergence of TEs on the 21 chromosomes of the species has been observed, indicating differences in genome evolution of transposon families.

1. De la Herrán et al. (2023). Mol Ecol Resour. 00:1–19
2.- Guerrero-Cózar et al. (2021). Scientific Reports, 11, 13460