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Salmon Sequence Gives Information On Mechanisms of Genome Evolution

Fish products, including farmed salmon, account for 7% of Norway's yearly export behind oil (50%) and natural gas (35%). A recent Nature paper (1) by CIGENE scientists at Ås and their partners signals the next step in using molecular methods to improve salmon aquaculture. Not only is the salmon genome sequenced and assembled, this paper also contributes new findings on the evolution of genomes, generally.

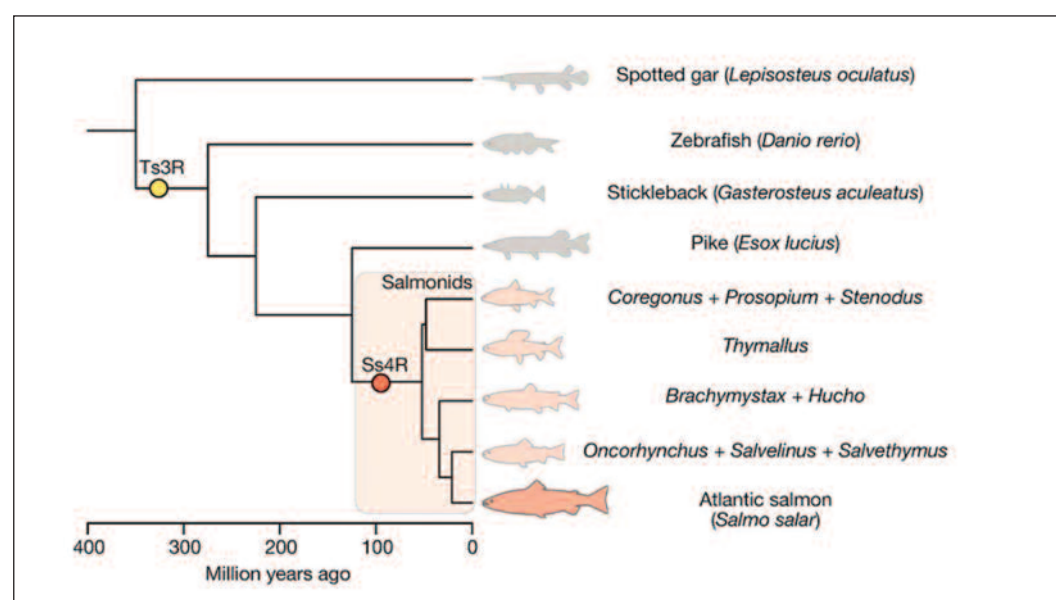


Fig. 1. The lineage leading up to modern-day salmon experienced two episodes of whole-genome duplication. The first episode (designated Ts3R) occurred approximately 320 million years ago while the second episode (designated Ss4R) occurred approximately 125 million years ago. This Figure is from reference 1 and is available for use via a Creative Commons license.



Determining the sequence of the salmon genome took approximately 10 years (2) and involved 45 authors from 6 different countries, including Norway, USA, Canada, Sweden, Chile and China. Two scientists from Canada plus Sigbjørn Lien and Stig Omholt were key people when the project started. Initially sequencing was done using Sanger technology but eventually most sequencing was accomplished with high-throughput

Comparative studies of the sequences of salmon and several of its relatives from other labs indicate that the lineage preceding salmon



Sigbjørn Lien

experienced two rounds of whole-genome duplication (WGD) 320 million and 125 million years ago, respectively (Fig. 1). With each WGD, one would expect that functionally diploid individuals became tetraploid individuals with associated problems of sterility resulting from improper chromosome separation at meiosis. So, how has the salmon genome solved problems tied to WGD?

According to the Nature paper, two mechanisms appear to be involved in 'rediploidization':

- Bursts of transposon element expansion in the genome combined with large chromosomal rearrangements obstruct pairing of inappropriate chromosomes.
- Corresponding genes after WGD evolve different expression patterns, guaranteeing that both of them will be retained in the genome.

In a recent article in a national newspaper (3), three of the authors of the Nature paper point out that they wouldn't have succeeded in publishing their work in such a high-profile journal if they hadn't interpreted the salmon genome as a way to understand general mechanisms involved in genome evolution. Given the fact that most funding by NFR involves applied research, they recommend that researchers interested in Nature should write grant proposals combining both applied as well as basic objectives.

References:

1. Lien, S et al.: The Atlantic salmon genome provides insights into rediploidization. Nature, published online 18 April 2016
2. Davidson WS et al.: Sequencing the genome of the Atlantic salmon (Salmo salar). Genome Biology 1 (2010) 403-409
3. Omholt SW, Sandve SR, Lien S: Laksens genom er kartlagt. Dagens Næringsliv, 18 April 2016



Stig Omholt

Illumina technology at several different sites. The published sequence consists of 2.97 Gbp DNA divided among 29 chromosomes with approximately 60% repeat sequence content which is one of the highest found in any vertebrate.