PRESS RELEASE

Singapore-led Consortium Deciphers the Genome of Asian Seabass: First Major Tropical Food Fish with its ‘Genetic Blueprint’ Assembled and Read

16 April 2016, Singapore – Temasek Life Sciences Laboratory (TLL) is pleased to announce the successful sequencing and assembly of the genome of Asian seabass (also known as barramundi). This is the first major tropical food fish to have its genome completed. The article reporting these data has been published online today in the international journal *PLoS Genetics*.

The Asian Seabass Genome Consortium was set up in 2013 and it was spearheaded by a research team led by Prof. László Orbán, Senior Principal Investigator at TLL based in Singapore. The consortium comprises an international team of scientists from 20 organizations, including the South African National Bioinformatics Institute (SANBI-UWC; South Africa), the Max Planck Institute for Molecular Genetics (Germany), and the Cold Spring Harbor Laboratory (USA).

The research interest of Prof. Orbán’s team is to study fishes using sophisticated genomics and molecular genetics tools to understand their physiology, with special emphasis on their reproduction. Since 2004, TLL has been working with the Agri-Food and Veterinary Authority of Singapore on a selective breeding program to produce superior Asian seabass lines with increased growth rate and disease resistance. The species, popular as a seafood source, was chosen for genome sequencing due to its economic importance. These valuable data are expected to open up new opportunities for the first time in research and the selection of desirable traits of Asian seabass.

“I am proud to be part of this project. I am thankful to my mentor for giving me opportunities to learn as well as for his courage to embrace alternative genome sequencing strategies.” said Dr. Shubha Vij, Research Fellow at TLL and the first author of the publication.

“As a consortium we can be proud of setting a new standard for genome sequencing projects. This project challenged our gene prediction paradigm and reminded us that the biology of the organism drives the data analytics strategy.” - added Prof. Alan Christoffels, Director of SANBI-UWC (South Africa).

“This project is an important incremental step for routine assembly of ever larger genomes, such as in the development of our centre’s pipeline for *de novo* assembly of clinical cohorts to identify genomic determinants of autism.” – commented Dr. Si Lok, Head of Technology Development, The Centre for Applied Genomics, The Hospital for Sick Children (Toronto, Canada).

“It is highly satisfying to finish a giant, four year-long collaborative project on such a high note. The use of this excellent reference genome will allow us to shift our approach from marker-assisted selection to a more efficient genome-based process thereby moving faster towards a better fish for the farmer and consumer.” - commented Prof. Orbán, the lead PI for the project.

“TLL places heavy emphasis on pursuing research that can create positive impact to the wider scientific community and mankind. We are proud to be part of this challenging project that involved international collaboration across several well-known research organizations. I believe that these findings will translate into greater productivity and growth for the aquaculture industry which will in turn benefit the community in the near future.” - commented Prof. Yu Hao, TLL Executive Director and Temasek Senior Investigator.

This research was supported in part by the Singapore National Research Foundation (under NRF Award No. NRF-CRP7-2010-01).

Enclosed:
Brief Summary of Research

About Temasek Life Sciences Laboratory (TLL)

TLL, established in 2002, is a beneficiary of the Temasek Trust and affiliated to the National University of Singapore and Nanyang Technological University. The research institute focuses primarily on understanding the cellular mechanisms that underlie the development and physiology of plants, fungi and animals. Such research provides new understanding of how organisms function, and also provides foundation for biotechnology innovation. For more information, please visit www.tll.org.sg.

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Brief Summary of Research

The advent of new technologies has made the sequencing (i.e. reading) of large vertebrate genomes possible. To date, over three dozen fish genomes have been sequenced and assembled (i.e. read and pasted together), but at a much lower resolution, and none represent commercial species utilized in tropical marine aquaculture production.

In an article that appears online in *PLoS Genetics*, researchers from Temasek Life Sciences Laboratory (TLL, Singapore) - in collaboration with scientists from several international institutions - report on the first chromosome-level genome assembly in fish: the Asian seabass (*Lates calcarifer*), the major tropical aquaculture species in South East Asia.

The species has a genome size of ~700 million base pairs (or letters) and the karyotype is represented by 24 pairs of chromosomes. A partially inbred individual from the Asia-Pacific region was selected for sequencing. The genome sequence information was generated using high coverage of long sequence reads totaling over 65 billion letters produced with the SMRT™ whole-genome shotgun sequencing technology. The sequence reads were scaffolded using a multi-step process resulting in a high quality assembly at chromosomal resolution for the first time. This is the first fish genome and the second vertebrate genome after that of the gorilla (published last week) that was assembled exclusively from such long sequence reads, with a resulting quality that far exceeds that of any other *‘de novo’* fish genome to date (i.e. those genomes that were put together without any help from a template derived from another species).

The assembled genome allowed for the prediction of over 22,000 protein-coding genes. The long sequencing reads spanned repeat-rich regions, found in centromeres and telomeres. These regions are the most complex parts of a genome and are typically missing from most genome assemblies. The completeness of the Asian seabass genome offers an opportunity to study these structures.

Besides its commercial value as a food fish species, the Asian seabass also has a very interesting biology. It is able to tolerate a wide range of salinities from freshwater to seawater and changes its sex from male to female after maturation. The team at TLL has been studying the latter process, called sequential hermaphroditism or natural sex reversal, for over a decade using the zebrafish as a model. They hope that the availability of the reference genome will allow for faster progress towards the understanding of this fascinating biological phenomenon.