World Fisheries Congress in Adelaide, Australia

Symposium organisers: Maren Wellenreuther^{1,2}, Luciano Beheregaray³ and Louis Bernatchez⁴

¹The New Zealand Institute for Plant & Food Research Ltd, Nelson, New Zealand, ²School of Biological Sciences, University of Auckland, Auckland, New Zealand, ³Molecular Ecology Laboratory, Flinders University, Adelaide, SA, Australia, ⁴Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval, Québec, QC, Canada

Email: <u>Maren.wellenreuther@plantandfood.co.nz</u> Email: <u>Luciano.Beheregaray@flinders.edu.au</u> Email: <u>Louis.Bernatchez@bio.ulaval.ca</u>

Symposium title: Advances in genomics for sustainable fisheries and aquaculture

Suggested length of session: 1 day

Description: The ongoing development of sequencing technologies has the potential to significantly advance fisheries management, biosecurity, conservation and aquaculture applications. The ability to generate genome-wide sequence data has enabled researchers to assemble full genome sequences, scan for marker and structural variation across the entire genome, and to test for genome-wide differences in gene expression patterns both at an everdiminishing cost and in any species desired. Further, rapid development in the field of eDNA holds immense promise to improve the way we bio-monitor fisheries and biotic factors impacting them. Genomic tools can potentially revolutionize the management and conservation of marine and freshwater aquatic resources by: (i) scaling-up genome coverage for non-model species, leading to improved estimates of demographic parameters, which is particularly critical for the many weakly structured marine species; (ii) identifying markers under selection to clarify management units and characterize local adaptation; (iii) finding causal relationships between genetic variation, gene expression, phenotypes and the environment to predict future dynamics of selectively important variation and to forecast the potential for adaptation to changing environments (e.g. global warming, ocean acidification, coastal pollution, selective harvesting, etc.). These methods may also allow improved genetic tagging to identify fish of unknown origins and their associated pathogens, estimation of "real time" migration rates and dispersal, as well as informing restocking strategies. These tools further offer to advance aquaculture production by means of genomic selection. Finally, they also provide a powerful and less costly means to document assemblages and even stock biomass, or tracking the spread of invasive species and pathogens that may negatively impact fisheries. This session will aim to evaluate the progress of these exciting advances by bringing together contributors in the field of fisheries genomics working in marine or freshwater systems.