CONFERENCE/WORKSHOP ORGANISER'S REPORT

7th World Fisheries Congress in Busan, Korea; Session title "Genomics for improved fisheries management and conservation: have the promises been fulfilled?"

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Brief description of what the conference/workshop was about
Session title: Genomics for improved fisheries management and conservation: have the promises been fulfilled?

New sequencing technologies have led to the recent development of potentially powerful genomic tools for fisheries management, biosecurity, conservation and aquaculture applications. These genomic tools hold the promise to revolutionize the management and conservation of aquatic resources. 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 reseeding strategies for sustainable exploitation and the restocking of natural populations. They further offer to advance aquaculture production by means of genomic selection, and identifying wild populations with the most potential for domestication. Yet, while the number of studies that have applied genomic tools has been steadily increasing, these have rarely been integrated into management decisions, both from a fishery, biosecurity and an aquaculture viewpoint. The lack of integration made it timely to hold a meeting that focussed explicitly on whether the promises offered by the new genomic methods have been fulfilled and how we can bridge the gap between the demonstrated power of these tools and their application in real life situations. This symposium aimed at evaluating these very questions by bringing together some of most important international contributors in the field of fisheries genomics working on either fish or shellfish in marine and/or freshwater systems.

Participation – details of total number of participants, countries they came from, backgrounds (academia, industry, etc.)

The session was part of a much larger event, the 7th World Fisheries Congress, which was held in Busan, Korea from the 24-27th of May 2016, under the theme "Challenge to Sustainable Fisheries and Safe Seafoods". About 1 200 people attended the Congress and our session was one of the 39 symposia that were part of the programme. Our programme comprised a total of 15 invited speakers. These represented a total of 13 OECD-member countries (Japan, U.K., Denmark, Finland, Norway, South Korea, Germany, Belgium, Canada, Chili, New Zealand, Australia and USA). In addition, 14 other non-invited presentations were included in the session programme and those participants came from eight countries (Spain, Germany, Austria, Japan, Canada, China, Thailand and South Korea). Together, the speakers represented a balanced blend of participants from Academia that are specialists in the specific field of genomics applied to fisheries (eight), but also researchers from government organisations (four) and participants representing policy makers (three). There were no representatives from the industry. The meeting lasted two days and an average of 50 people was attending the presentations at any time.

Major highlights from the presentations

Here is a summary of the major highlights from the invited speaker presentations that are of direct relevance for management and conservation of exploited species, both from a fisheries and an aquaculture perspective.

Terry Beacham (Canada) showed how genetic tools developed from genomics techniques could be efficiently used to outperform traditional physical tagging methods for estimating the cost and benefits of large-scale stocking program to enhance abundance and production in Pacific salmon.

Kerry Naish's (USA) presentation complemented this topic by illustrating how genomics can inform the success of enhancement programmes in Pacific salmon. Some of the main findings that were presented were: i) Only four generations of captive rearing is sufficient to produce rapid genetic change (as compared to the wild counterparts); ii) gene flow between natural populations and hatchery reared individuals helps to reduce this divergence and should be implemented more often; and that iii) domestication selection could be detected in several regions of the genome.

Speaker and organiser **Louis Bernatchez** (Canada) presented two successful case studies that applied genomic tools to define population structure and genetic differences among exploited stocks of the American lobster and the American Eel. In both studies, academia as well as the government and private sector joined forces to define research objectives that best meet the needs for improved management practices and for investing resources to bring these projects to successful completion. Both studies revealed unknown stock delineation patterns which will be used to design new managements units inferred from rigorous biological knowledge, rather than mere administrative considerations.

Christian Araneda (Chili) provided an illustrative example of the usefulness of genomic tools for the management and traceability of farmed Chilean blue mussel. He showed how these tools are efficiently being used in Chili for the identification of species, monitoring its distribution and elucidating patterns of hybridization between different species. He also showed how these tools have been applied to define genetic differences between mussels from different regions of Chili which in turn allows traceability of mussels when documents or tags are dubious, which will be useful especially for the international export market.

Kristi Miller (Canada) provided a powerful illustration of how genomics could also provide information about pathogens that can be devastating for both wild fisheries and aquaculture production in salmon. She developed a tool allowing to rapidly screening 45 potentially pathogenic microbes. Of these, 32 were detected in young migrating Chinook salmon, and with seven of these belonging to stocks of high conservation concern.

Nina Overgaard Therkildsen (Norway/USA) demonstrated the power of new genomic tools towards elucidating the genomic basis for rapid fisheries-induced evolution; that is change in important fish life history traits, such as growth rate and age at reproduction, that have an impact on the productivity of fisheries.

Craig Primmer (Finland) showed that such life history traits of high relevance for fisheries and conservation can be controlled by a few genes of very large effects in salmon and provided recommendations how such knowledge could assist to improve management practices.

Julia Barth (Germany/Norway) used new genomic tools to decipher the genomic basis of Atlantic cod ecotypes from northern Europe that differ in life history traits of high relevance for fisheries management (growth and migratory behaviour). She explained how such variation at the genome level must be considered towards understanding how exploited cod stocks will adapt to environmental change in the future.

Finally, **David Ashton** and **Maren Wellenreuther** (co-organiser) (New Zealand) presented their progress towards developing phenotyping and genomic resources for the management, domestication and breeding of the marine finfish *Chrysophrys auratus* (Snapper). They showed that the application of those tools will substantially improve cultured and wild production practices of this species by: i) Improving selective breeding; ii) identifying population structure and align management areas accordingly; iii) identifying breeding areas; iv) determine adaptive diversity of interest for increased production; and to v) develop cultivars adapted to production mode and location.

Major outcomes/conclusions in terms of policy relevance

The content of the following presentations best illustrates the major outcomes in terms of policy relevance.

Jann Th. Martinsohn from the European Commission's science and knowledge service provided the best illustration of how genetic information has been implemented into policies by the European Union as part of the Common Fisheries Policy (CFP). Specifically, the CFP makes explicit inferences in its regulation about the use of genetic data and analyses towards improved fisheries and management control and enforcement practices. In particular, he discussed 3 cases studies to show how genetic tools have been used in Europe to delineate fish stock structure and showed that these new structures now represent to basis for management units for fisheries regulation of these marine species. He also highlighted that the European Commission shows continued effort towards implementing a systematic genetic data collection and integrating these with the most recent genomic tools.

Jenny Ovenden (Australia) also presented a success story about working at the interface to achieve a two-way information flow between policy makers and genetic scientists. She used the "Gemfish" program to demonstrate the value of such a two-way communication between managers and researchers. In particular, she showed the clear value of scientists with broad skill sets who can assist stakeholders to: i) Clearly identify a problem; ii) evaluate what techniques are most appropriate; iii) serve as a source expertise to set up collaborative projects; and to iv) communicate and translate outcomes. At the end, she showed how scientific findings about stock structure could be implemented by policy makers towards improving management practices.

Kerry Naish (USA) also outlined some issues regarding how scientists can bridge the gap between science and policy based on lessons learned from the application of genomics: That i) translation of science to policy is best achieved by "solution driven research"; ii) an iterative process must be engaged with managers and policy makers; and that iii) it is important to share data with managers early and often, even if some components of research are not mature.

Kristi Miller (Canada) later pointed out how the information gathered from using the genomic tools she developed for screening pathogenic microbes were of relevance to policy makers, namely by; i) allowing a high throughput diagnostic method for monitoring of pathogens by regulators and industry; ii) identifying pathogens and diseases that pose biosecurity risks to salmon; iii) contributing to government agencies risk assessments associated with pathogen transmission from salmon farms and salmon enhancement hatcheries; iv) informing disease management practices on farms and in salmon enhancement hatcheries; v) informing policies on minimal testing required to release young salmon to the ocean and vi) informing policies about the placement of farms within the migratory pathways of wild salmon.

If there is one major conclusion to be drawn from the symposium, it would be that we have been exposed to the best science currently being done worldwide as far as fisheries genomics is concerned. Many of the presentations clearly demonstrated the benefits that can be gained by integrating this new knowledge with policy decisions towards improving management and conservation practice for sustainable production and yield. For instance, studies that were presented showed that i) scaling-up genome coverage for non-model species leads better estimates of population genetic parameters, especially in the many weakly structured marine species; ii) it is possible to identify genetic markers that allow to define management units based on adaptive criteria as well as markers for pathogens to manage their spread; (iii) new genomic methods allow improved genetic tagging to identify fish of unknown origins and their associated pathogens; iv) these methods also allow estimating "real time" migration rates and dispersal, and inform strategies for sustainable exploitation and the restocking of natural populations; and finally that v) these tools further offer to advance aquaculture production by means of genomic selection, and identifying wild populations with the most potential for domestication and breeding.

Another major conclusion was that apart from the examples from the European Union (Martinsohn) and Australia (Ovenden), that very few other countries have taken genomic fish data into consideration to improve management practices and regulations. This indicates that old structures and politics may still override good science when it comes to

defining policies, which is unfortunate. So clearly, this meeting and its outcomes are very timely and once published and disseminated, it should help and contribute to highlight the many benefits that modern genomics has to offer to policy makers.

To return to the initial question "Have the promises been fulfilled?", the answer is yes as far as researchers are concerned given that they do apply genomic methods in an innovative way and in a very relevant manner for fishery management. However, the answer is unfortunately no as far as policy makers are concerned because most of them are still reluctant to integrate this powerful knowledge towards improving management practices. This finding is somewhat alarming since there is an urgency to act given the alarming situation of a majority of exploited stocks.

Relevance to CRP theme(s)

This conference symposium clearly aligned with all three CRP's research themes, namely the 1) natural resources challenge, 2) sustainability in practice and 3) the food chain. The symposium related to these themes by addressing fundamental questions pertaining to the increasing global demand for protein-rich food sources and the associated challenges affecting fish and shellfish health and production. Given that wild fisheries around the world are heavily over-fished and exploited, both enhanced production of farmed seafood and improved management of wild fisheries will be increasingly needed to meet and sustain the demand. With the world's population set to increase to more than nine billion by 2050, it is estimated that managed seafood will account for 75% of the global consumption within the next 15 years. Genomic tools are rapidly changing the way by which we can potentially domesticate, manage and conserve aquatic organisms. Nevertheless, and despite the increased number of studies hinting at its usefulness, genomic information is not routinely integrated into these applied areas. This may partly be because policy makers are still largely unaware of the prospective usefulness of genomic tools towards improved management, biosecurity and production. By bringing together international leaders in genomics working on wild stocks and species relevant to aquaculture, along with several policy makers, we believe that this symposium was very successful in learning and sharing current approaches and insights gained recently in the field of fisheries genomics and initiating a much needed discussion of how genomics can inform management decisions, food security, conservation strategies, and the strategic decisions of policy makers.

Website for further details – please also indicate if the presentations are/will be available on the website
The most relevant website to obtain further information is the World Fisheries Congress website: http://www.wfc2016.or.kr/english/01_introduce/01_introduce.asp, since we have not built a specific website for our symposium.