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Letter

Synergistic Integration of Genomics and Ecoevolutionary Dynamics for Sustainable Fisheries: A Reply to Kuparinen and Uusi-Heikkilä

Louis Bernatchez[1,*] and Maren Wellenreuther[2]

The reply by Kuparinen and Uusi-Heikkilä [1] on our review paper about 'Harnessing the power of genomics to secure the future of seafood' [2] suggested that our plea for a more rigorous implementation of genomics-informed approaches to fisheries management needs to be 'digested with consideration'. Their main point of contention is that to realistically account for the multiple drivers underpinning fish population abundances, ecosystem-based management is the future for assessing and managing fisheries. They also pointed out that a practical implementation of ecosystem-based fisheries management has been lagging behind relative to the ever-growing conceptual and methodological developments in this field. This is identical to our argument about genomic approaches; namely, that despite the solid demonstration of the usefulness of genomics to inform seafood production and conservation (e.g., [3]), genomic tools are seldom applied and integrated into management decisions. In other words, the path that would allow the implementation of genomics and ecosystem-based management is riddled with similar problems. Consequently, we do not see our review [2] and the views of Kuparinen and Uusi-Heikkilä [1] as fundamentally opposed. Instead, we can only agree that ecosystem-based and genomic approaches should be integrated tightly to maximize synergistic benefits. Kuparinen and Uusi-Heikkilä [1] also partly disagreed with our conclusion that genomics is urgently needed to improve fisheries management. This is because they were apparently left with the impression that we argued that maintenance of genetic diversity is more important than keeping populations at sufficient abundances to ensure productivity, ecological functionality, and resilience. While it is true that we argued that adaptive genetic diversity is essential towards maintaining the evolutionary potential of species in the face of new challenges (e.g., overfishing, environmental change) [4], we certainly did not deny that a sufficient abundance has to be the primary focus to ensure sustainable fishing practices. Quite the contrary, we argued that careful management and production strategies are required to secure a sustainable future for the seafood industry. To reach this goal, we pressed that the best scientific knowledge must be used and implemented to inform decision making. Application of genomics-informed methods allows the definition of 'real' as opposed to merely administrative units and thus would provide crucial biological information necessary for the accurate identification of fisheries management units, which is fundamental to enable proactive population management [5]. For instance, traditional scientific fisheries management relies on stock assessment models to predict variability in stock–recruitment relationships to determine abundance and sustainable catch limits for the corresponding management units. These management units are still predominantly based on 'administrative' units, which are often loosely connected with the true population structure of a species, despite the demonstrated ability of genomic data to delineate populations accurately [6]. This contradicts the very basis of fisheries science whereby the maximum sustainable yield (MSY) can be achieved only by the efficient management of distinct populations. There is little doubt that relying on administrative rather than real biological units is suboptimal towards the goal of maintaining healthy fisheries. Hence, our main point of proposing a more rigorous integration of genomics into fisheries management practices was essentially about helping to keep (real) populations at sufficient abundances to ensure their productivity and resilience in the long term, consistent with Kuparinen and Uusi-Heikkilä's [1] arguments.

We would further like to argue that the integration of the two approaches should be seen as a desirable goal that can yield more powerful information. According to Kuparinen and Uusi-Heikkilä [1], the successful implementation of ecosystem-based management requires development projections about fish population abundances under alternative harvesting scenarios. Here, a basic requirement towards predicting fish population abundances is obviously to first define what a population is and then to quantify the extent of demographic connectivity among these populations. Arguably, this will be best achieved by a better integration of the genomics tools that are already available. We can also only agree with Kuparinen and Uusi-Heikkilä's [1] statement that genomic approaches, namely metagenomics and metabarcoding, can provide immense help in constructing realistic food webs and by allowing the identification of 'all' species in a community. Indeed, our review does propose exactly that; namely, that environmental DNA (eDNA) and metabarcoding methods should be used to improve our ability to monitor environmental variation or exploited species, thereby representing another way that genomics can improve fisheries management practices. By proposing to use these genomic tools to analyze food-web structures and dynamics, detect rare or invasive species, or characterizing prey composition in gut contents, Kuparinen and Uusi-Heikkilä [1] are adding further arguments to our claim that genomic approaches are crucially needed to inform fisheries management. Other suggested applications of genomics are also aligned with what we originally proposed or nicely extend our view to the context of ecosystem-based management; namely, the need to understand the genomic basis of adaptation to anthropogenic and environmental challenges or the genetic architecture of adaptive traits. For instance, our 'Outstanding Questions' section included

questions such as 'Will genomics allow establishing clear links between genotype, phenotype, and fitness, and hence robustly ascertain the functional effects of observed genomic changes?' Or 'What can we learn from a more comprehensive understanding of the genomic basis of fisheries induced evolution?'

To conclude, while Kuparinen and Uusi-Heikkilä [1] had the impression that we were solely advocating the use of genomics at the expense of other approaches, this was certainly not our goal and we would like to highlight that we are embracing an interdisciplinary perspective as much as they do. We deeply recognize the need for a science-based integrated ecosystem approach, which necessitates innovative holistic monitoring to obtain data to determine the health of aquatic ecosystems and adjust management decisions accordingly. We also made the point that immediate involvement of all stakeholders, including policy-makers, social scientists, fisheries scientists, and managers, is urgently needed. Consequently, we concur with Kuparinen and Uusi-Heikkilä's [1] claim for an interdisciplinary pilot initiative, 'which would bring together fisheries scientists, ecologists, and evolutionary biologists'. However, we would certainly propose that Kuparinen and Uusi-Heikkilä consider adding population genetics and genomics to their list of expertise required. Finally, while an ecoevolutionary dynamics framework in the context of fisheries management is a commendable goal, we must warn that this also needs to be 'digested with consideration'. As for genomics, it may well be that the value of an ecoevolutionary dynamics framework towards supporting sustainable fisheries does not need to be further demonstrated. However, to achieve integration one needs to remove structural roadblocks and propose solutions that would support the incorporation of ecosystem-

based methods into fisheries management, just as we have argued for the integration of genomics. Three of the solutions that we have outlined to pave the way for the integration of genomic tools to inform sustainable seafood management may therefore also apply, and we hence list them here in relation to ecosystem-based approaches. First, to achieve an integration of ecosystem-based methods, communication skills among academic ecoevolutionary dynamics experts, managers, and end-users will likely require training and structuring. Second, as for genomics, the current lag in implementing ecosystem-based information into fisheries management suggests that historical settings and political considerations may impede integration of this alternative scientific framework when defining policies and management strategies, and these need to be overcome. Third, this will be achieved only if the traditional structures are modernized, and this can be best achieved by updating the training of fisheries and aquaculture scientists and including evolutionary biology in the curriculum. Once a new cohort of trained scientists has been recruited, rapid progress in the integration of genomic data in the management of capture fisheries can be expected. Taken together, the future of fisheries management is not about competition or an arms race between new emerging disciplines, but more about modernizing the traditional structures that are in place so that we can all benefit from the full advantage of the best scientific knowledge that such approaches can synergistically generate to inform decision making.

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Letter

Cryptic Species – Conceptual or Terminological Chaos? A Response to Struck *et al.*

Michael Heethoff[1],[*]

In a recent article, Struck *et al.* [1] aimed at finding evolutionary processes hidden in cryptic species. They provided a broad overview on the different usage of the term 'cryptic species' and called for a more rigorous definition by comparing phenotypic (morphological) disparity with the degree of genetic differentiation. They conclude 'if biologists cannot even agree on what to consider different species, then how can we reach consensus on what represents cryptic species?' I argue that there is only one solution to both of these issues and that cryptic species represent nothing more than an incompatibility of species 'concepts' in applied taxonomy. Hence, 'cryptic species' can neither be defined nor are they outcomes of an evolutionary process like 'cryptic speciation'.

Species delimitation has been confused with species conceptualization, leading to a controversy on what the species category is and how species can be delineated [2]. The evolutionary species concept [3] represents a general primary concept, however, without much value for applied taxonomy. Applied taxonomy mostly refers to the morphological species concept, although there is no clearly defined workflow for species delineation [4]. In this context, Struck *et al.* suggest that 'morphological variation needs to be explicitly quantified', and I could not agree more. The biological species concept [5] is often used to confirm or reject morphospecies hypotheses, but is only applicable to sexually reproducing organisms. Using genetic differences for species delineation has also been proposed (e. g., [6]), and has recently been applied to split giraffes into four distinct species despite them interbreeding in captivity [7]. Hence, whether a species is cryptic or not depends on nothing else than the underlying species concept. Struck *et al.* implicitly used the morphological species concept and 'tested' it against genetic divergence. Hence, they compared two classes of species concepts (morphological vs. genetical) regarding their compatibility (i.e., supporting the same boundaries of species), and 'define' species to be cryptic when they are morphologically similar but genetically distinct (which is here taken as a proxy for 'reduced gene flow' and 'reproductive isolation' and would thus confirm the biological species hypothesis). This approach prioritizes the 'evolutionary truth' of genetic over morphological species concepts – probably a valid approach in many if not most cases. Ten years ago, Bickford and colleagues defined cryptic species as 'two or more distinct species classified as a single species' [8], rendering 'cryptic' species as nothing more than grouping artifacts. I agree and conclude that cryptic species do not exist as a concept, but that the term 'cryptic' is only used to prioritize one species concept over others. Eventually, it may turn out that cryptic species are not so cryptic at all [9].

Hence, we should not aim at defining what 'cryptic species' are, but what species concept we believe to represent evolutionary entities that we can use as fundamental units in biology – even if such a concept may lack clear instructions for applied taxonomy.

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Letter

Cryptic Species – More Than Terminological Chaos: A Reply to Heethoff

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