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Comparing single-, multi-trait approaches to identify best wild candidate species for aquaculture

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Results show multi-trait approach is the most suitable to identify higher domestication potential

This study evaluated single- and multi-trait approaches through a larviculture trial to assess the domestication and aquaculture potential of wild species using the European perch as a model. Results showed the multi-trait approach as the most suitable to identify higher domestication potential. Photo by Christa Rohrbach, CC BY-SA 2.0 via Wikimedia Commons.

Domestication – one of the most important evolutions in human history – is the process in which groups of individual animals are bred in a human-controlled environment and modified across succeeding generations from their wild ancestors in ways that they become more useful to humans, who increasingly control their food supply and reproduction. This process ranges from the first trials of acclimatization to the setting up of selective-breeding programs. The main wave of domestication for fishes only started at the beginning of the 20th century to develop aquaculture, notably to mitigate provisioning service disruptions due to fishery collapse.

Evaluating the ability of a species/population to be successfully domesticated and commercially produced requires an initial assessment of its expression of key trait(s). Looking back at past domestication programs, two alternative paradigms can be used to identify suitable species or population(s) for further production development: the (1) single-trait and (2) multi-trait approaches.

The single-trait assessment is the traditional approach which consists of studying a single phenotypic [observable] trait and consequently a single biological function, to identify population(s) with desirable expression of the trait for further production development. This approach has been widely applied at the beginning or at advanced stages of the domestication process in agriculture of animals. Single-trait assessments often focus on an easily measurable trait, the expression of which is involved in the domestication process and/or production profitability. Most of the time, growth rate is considered as a premium criterion. This was, for instance, the case with Nile tilapia (*Oreochromis niloticus*), for which domestication programs initially focused on the growth rate. However, other traits are often considered.

The multi-trait approach has recently been considered as an alternative method to the single-trait assessment, as a promising way to overcome domestication bottlenecks. First applied in land agriculture, this approach is now promoted in fish aquaculture, especially at advanced stages of domestication, for selective breeding programs. At these advanced stages, growth performance, morphology, disease resistance, flesh quality traits, age at sexual maturation and feed efficiency have been considered. Although the multi-trait approach is the focus of increasing research in aquaculture, an explicit assessment of its advantages and its pitfalls has not been performed to date. Indeed, no comparison between single-trait and multi-trait approaches to highlight best wild populations for fish aquaculture is currently available.

This article – adapted and summarized from the **original publication** (https://doi.org/10.1038/s41598-020-68315-5) [Toomey, L. et al. 2020. Comparison of single- and multi-trait approaches to identify best wild candidates for aquaculture shows that the simple way fails. *Sci Rep* 10, 11564] – provides the first assessment of the consequences of using single-trait or multi-trait approaches in aquaculture development. We compared the potential suitability for aquaculture of four wild allopatric [a mode of speciation that occurs when biological populations become geographically isolated from others and which interferes with or prevents gene flow] populations of a test-case species, the European perch (*Perca fluviatilis*), during the larval period using the two different models.

“**Shrimp postlarvae: Know your starting point (https://www.aquaculturealliance.org/advocate/shrimp-postlarvae-know-your-starting-point/?__hstc=236403678.410916e450568f89c8cee49ec81f09c6.1680753528083.1680753528083.1680753528083.1&__hssc=236403678.1.1680753528084&__hs**

Study setup

The European perch is a common, widely spread Eurasian species living in freshwater and brackish habitats. Its economic (high market value) and recreational (i.e., fishing) interests have led to the development of its culture in recirculating aquaculture systems since the 1990s and it is considered among the most interesting species for the development of inland aquaculture in Europe. However, despite its economic potential, the production is still limited. This is mainly due to major bottlenecks, especially in first-life stages, such as low growth rate, low survival rate and high cannibalism rate, which emphasizes the potential interest of re-starting new domestication programs.

We collected *E. fluviatilis* egg ribbons (one ribbon corresponding to one female) during the spawning seasons from four lakes: Valkea-Müstajärvi (VAL) and Iso-Valkjärvi (ISO) in Finland; Geneva (GEN) in France; and Balaton (BAL) in Hungary. We chose these populations since a phenotypic differentiation is known between the Finnish and Geneva populations while genetic specificities of central Europe populations have been already observed.

After transportation there, 13 to 19 egg ribbons per lake were incubated (one population per incubator) at the Unit of Animal Research and Functionality of Animal Products, University of Lorraine, Vandœuvre-lès-Nancy, France. Each incubator had its own temperature control and recirculated water system, and water quality parameters were monitored.

Two independent experimental phases were performed: phase I from hatching until the end of weaning (i.e., transition from live feed to inert pellets; 26 days post-hatching, dph) and phase II from 27 dph until the end of nursery, at 60 dph. The larval period was split in two phases in order to ensure availability of larvae across the whole larval period since there is a very high mortality rate during first-life stages. Because wild egg ribbons are not available the same time for all populations (i.e., asynchronous spawning seasons) and in order to prevent potential pathogen transmission, all populations were reared in independent structures.

For detailed information on the experimental design and rearing protocols; larviculture performance assessments; behavioral and growth traits; and statistical analyses, refer to the original publication.

Results and discussion

Our study shows that the alternative single-trait and multi-trait approaches can lead to divergent results when identifying the best population(s) for aquaculture purpose. Overall, we detected three main limitations of the single-trait approach. First, considering a single trait can lead to neglecting the potential available in the wild biodiversity if the targeted trait does not vary between studied populations. This is particularly noticeable for the growth rate (no significant differentiation between populations despite a differential length at hatching; Fig. 1), which has traditionally been the most considered trait when assessing performances in aquaculture.

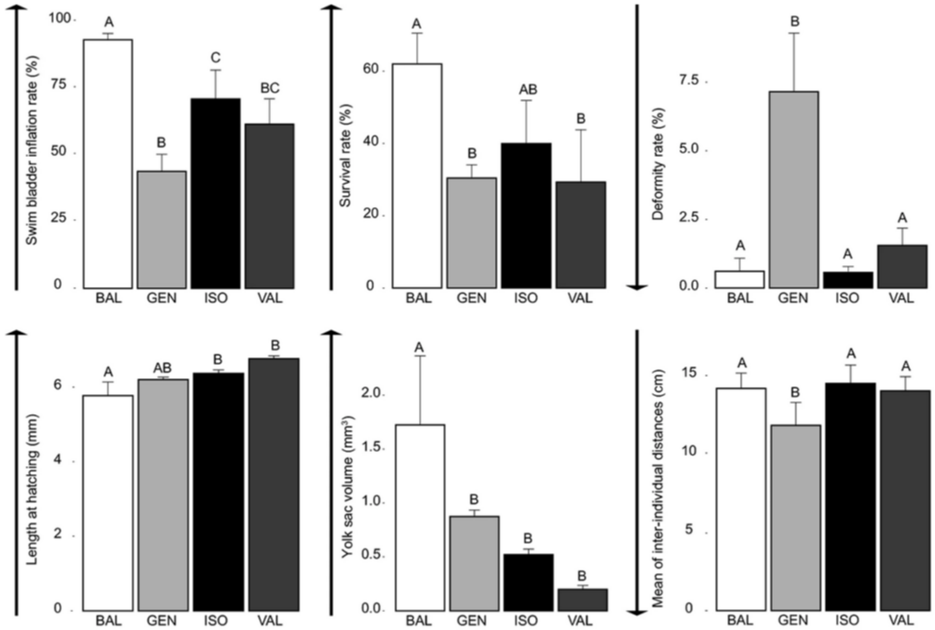

Fig. 1: Bar plots representing results obtained for several traits studied in phase I for which a statistically significant difference was found between populations (n = 3 per population except for activity and inter-individual distances for which n = 9). Different letters indicate significant differences between populations (p value < 0.05) using post-hoc [after the event] tests. The arrow represents how the expression of each trait should vary to meet stakeholder demands.

In the worst-case scenario, this could lead to starting aquaculture production with a suboptimal population that will have to be improved through costly and difficult selective breeding programs while better candidates were available in the wild.

Second, the identification of populations with the highest suitability for aquaculture can vary depending on the trait picked for evaluation. For instance, the observed differentiations for survival and deformity rates allow identifying best population(s) for aquaculture but do not converge to highlight the same best population(s) (Fig. 2).

Fig. 2: Bar plots representing results obtained for traits studied in phase II for which a statistically significant difference was found between populations (n = 3 per population except for activity and inter-individual distances for which n = 9). Different letters indicate significant differences between populations (p value < 0.05) using post hoc tests. The arrow represents how the expression of each trait should vary to meet stakeholder demands.

Furthermore, some of the conclusions obtained by the single-trait approach are completely contradictory (e.g., deformity rate would identify Lake Balaton as one of the best populations, while if activity is considered, it would qualify this population as the least suitable). This highlights the importance of the definition of the most important trait for fish production, although this is controversial because of the divergent opinions between fish farmers and the numerous traits evaluated as very important.

Third, the choice of a population based on a single trait, and consequently a single biological function, can lead to starting fish domestication/production with a population displaying deleterious expression of other key traits. Indeed, since traits are linked in complex ways, selection of only one trait will inevitably be associated with the indirect selection of other traits, including undesirable characteristics. Eventually, this leads to deleterious impacts on the species production.

The risk of co-selecting a deleterious trait which is not considered in the single-trait approach is a well-known fact in land species domestication history. For instance, continuous selection towards milk yield and growth led respectively to a decrease of (1) fertility in dairy cows and (2) reproductive and immune performances in broilers. In the same way, artificial selection in domestic turkeys for large breast size has led to the artificial insemination of females due to the inability of males to copulate naturally. Similarly, the focus on taming at the beginning of the domestication process of the silver fox led to morphological changes disadvantageous for the pelt market.

The multi-trait approach allows overcoming the single-trait method limitations. Indeed, investigating several traits minimizes the risk of missing valuable population-specific traits or choosing a population with hidden undesirable characteristics. Therefore, the growing promotion of the multi-trait approach in land and aquatic production is a timely and welcomed trend.

Moreover, it provides a more efficient and realistic assessment to start new domestication processes and to increase the sector sustainability, since they both involve several biological functions that could be studied only through the consideration of many traits. Indeed, the domestication itself involves several biological functions such as growth, nutrition, behavior and reproduction. Furthermore, the willingness to develop a more sustainable aquaculture production implies for instance to study traits involved in robustness (e.g., resistance to thermal changes, vulnerability to new pathogens/parasites) and nutrition (e.g., ability to grow with a plant-based diet). However, beyond the bright sides of multi-trait approach, three main limitations could make its implementation difficult.

First, the most obvious pragmatic issue is that workload and cost associated with this approach are much more substantial than with the single-trait approach. One potential solution to facilitate the multi-trait assessment consists of restricting the assessment framework to a limited set of traits. This could be achieved through trait correlation evaluation. Some traits could be removed from the assessment framework by considering phenotypic correlations between traits (assuming phenotypic correlations are a good proxy for genetic correlations).

However, in our study, we detected only few correlations including biological non-relevant relationships (e.g., positive correlation between length at hatching and activity in phase II). In this work, trait correlations are not helpful to restrict the evaluation to a handful of traits. Nevertheless, the complexity of multi-trait assessment should be seen as balanced by choosing the best part of the wild biodiversity before starting large-scale domestication programs which are far more expensive and time-consuming.

Second, methodological limitations could impede the relevance of the multi-trait and multi-function approach. Indeed, the lack of efficient methods to measure some traits (e.g., assessment of traits involved in the nutrition function such as food conversion ratio requiring complex protocols) and the increased risk of errors when working on multiple traits could lead to false decisions when choosing candidates for domestication/production. However, research advances are making fish trait information available, or trait analysis methods easier and cheaper.

Finally, working with multiple traits implies using a method to reach a consensus between results obtained for individual traits. Here, we propose a method that allows attributing a score to each population in order to identify the best candidate(s) for aquaculture within species. It is worth nothing that this scoring method does not reflect the differentiation degree between populations. Indeed, ranks are used to classify populations, but these ranks do not show how much differentiated populations are. However, it allows putting all traits at the same level and then uses weighting coefficient to consider trait importance divergences according to fish farmers.

Perspectives

Our results showed that the single-trait approach can (1) miss key divergences between the populations and (2) highlight different best candidate(s). Conversely, the multi-trait approach, which includes several key traits for larviculture, allowed identifying the population with the highest domestication potential thanks to several congruent lines of evidence.

This multi-trait approach is more complex and requires achieving a consensus between trait results. However, despite these limitations, it appears as the most suitable approach to identify within species populations with higher domestication potential.

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