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Editorial: Population genomics and adaptation to novel environments: challenges and opportunities

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Editorial on the Research Topic
Population genomics and adaptation to novel environments: challenges and opportunities

Understanding how organisms adapt to novel environments is an active Research Topic in ecological and evolutionary studies. Most ecological and evolutionary studies focus on how organisms find food (utilization of ecological resources), how they avoid being the food (avoidance of predators), or form the next generation (reproductive strategies) in changing environmental conditions. Yet, some novel environments may present with extreme challenges that organisms may need to evolve novel metabolic pathways even just to exist. Population genomics methods can offer reliable estimates of basic population characteristics such as effective population size, inbreeding, demographic history, and population structure, all of which are also important for conservation efforts. Furthermore, population genomics studies can pinpoint specific genetic loci and variants that are under selection for a populations' ability to evolve and adapt in response to environmental change and manage adaptive variation. The last 10 years have seen a rise in the study of population genetics of non-model organisms, and the findings of this research are increasingly being applied to the conservation and management of wildlife. To understand population genetics and adaptations, it is equally crucial to share and disseminate the research done using these techniques.

Adaptation to novel environments is a key driver of evolutionary processes, leading to differentiation in the genome as long as selection pressure is present. Red clover is an economically relevant crop that has undergone rapid climatic and anthropogenic changes, requiring identification of genetically diverse stock populations for breeding programs. A study by Gemeinholzer et al. proposed mRNA-GBS as a rapid, cost-effective method for studying populations' adaptation to novel environments. Gemeinholzer et al. used an mRNA based genotyping by sequencing (mRNA-GBS) approach to analyze patterns of genetic differentiation between natural populations of red clover (*Trifolium pratense*) in three regions of the Biodiversity Exploratory sites in Germany, and evaluated how their approach correlated with previous genomic diversity reports. They propose mRNA-GBS as a rapid, cost-effective, and technically relatively simple method that can simultaneously screen for genetic diversity while identifying expression of specific candidate genes involved in the response to certain species-specific environmental interactions. They conclude that although more sequencing depth and fewer divergent populations are needed for comparison, mRNA-GBS is a potential method for studying populations' adaptation to novel environments.

Domestication of wild animals can be seen as an artificial selection experiment, imposing extreme selection on natural populations and forcing them to adapt to "novel" un-natural environments. Cattle adapted to their local environments forming diverse ecotypes, and through further selective breeding many different agrotypes were generated. Hybridization of divergent genomes selected on very different conditions can produce genomes capable of adapting to new habitats. The Jersey cattle, a British island breed, is an example of an economically important agrotype. In Africa, introduced agrotypes are bred with local ecotypes aiming to create genetically productive local breeds adapted to local environments. Opoola et al. presents an extensive review on the breeding history, fertility, fecundity, and agricultural performance characteristics of Jersey breed in Africa. The success of crosses between Jersey and indigenous exotic breeds is compelling. These observations suggest that hybridization of divergent genomes that have been selected on very different conditions can produce genomes capable of adapting to new habitats.

Environmental influence may have a greater contribution than we anticipated in shaping the structure of populations in epigenetic evolutionary processes. Ecological epigenetic studies have become popular areas for detailed investigations in recent years. Differences at the nucleotide level studied through epigenome research have the potential to make such studies more effective. Combining stress and behavioral data could be effective in conservation, ecology, and biology, aiding our ability to recognize species that require management and propose viable intervention measures. Lamka et al. also suggests that combining stress and behavioral data could be effective in conservation, ecology, and biology. Our ability to recognize species that require management and propose viable intervention measures may be aided by a deeper comprehension of epigenetic mechanisms, along with their evolutionary rates and trajectories.

Differentiation, investigation of the effects of environmental factors, and the identification of their genomic signatures can be observed not only in terrestrial fauna but also in aquatic environments without sexual selection pressures. Chen et al. demonstrated differentiation and genomic signatures in different brittle star colonies found in cold seep fields, attributed to ecological factors. They suggested that positive selection in the ND4 gene could play a role in environmental adaptation. They also provided clues that colonization could occur through different mechanisms, indicating potential diversification.

Adaptation to fast changing acidity and low pH environments is largely unexplored. Sezgin and Tekin investigated the molecular evolution and population genetics of glutamate decarboxylase (GAD) pathway in lactic acid bacteria thriving in high acid environments. The study showed that, GAD pathway genes in lactic acid bacteria exhibit a dynamic molecular evolutionary history shaped by gene loss, gene transfer, negative and positive selection to maintain its active role in acid resistance mechanism, and enable organisms to thrive in high acid environments. The study showed that adaptive protein evolution and the acquisition of novel genes during adaptation to low pH conditions, followed by the conservation of protein function and activity, are the driving forces behind the evolution of acid resistance in LABs.

In summary, adaptation to novel environments can be observed through differentiation in the genome resulting from environmental events and selection pressure. This Research Topic of five papers presents different methods utilized in different non-models. Red clover is a crop that requires genetically diverse stock populations for breeding programs due to fast climatic and anthropogenic changes. Gemeinholzer et al. proposed mRNA-GBS as a potential method for studying populations' adaptation to novel environments as it is rapid, cost-effective, and can screen for genetic diversity while identifying expression of specific candidate genes. Domestication of wild animals can also impose extreme selection and force them to adapt to un-natural environments, leading to the formation of diverse ecotypes and agrotypes. Hybridization of divergent genomes can produce genomes capable of adapting to new habitats. Ecological epigenetic studies have become popular in investigating the effects of environmental factors and identifying genomic signatures that shape the structure of populations. Differentiation and genomic signatures in different brittle star colonies found in cold seep fields can be attributed to ecological factors. Finally, Sezgin and Tekin found that adaptive protein evolution and acquisition of novel genes are driving forces behind the evolution of acid resistance in lactic acid bacteria. We hope this Research Topic of these papers will benefit the researchers working on understanding the mechanisms behind adaptation to novel environments.

Author contributions

All authors listed have made a substantial, direct, and intellectual contribution to the work and approved it for publication.

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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