APPLICATION ESSAYS

Promoting collaboration between livestock and wildlife conservation genetics communities

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Abstract The collaboration between livestock and wild-life conservation genetics communities has the potential to help promote shared priorities, with respect to emerging technologies and new analytical approaches such as next generation sequencing incorporating adaptive variation. The GLOBALDIV Consortium recently organized an international workshop held at the Ecole Polytechnique Fédérale de Lausanne (Switzerland) including a whole-day session with contributions aimed at taking stock of the situation regarding the extent of information and methodology exchange between the two communities. Discussions permitted the identification of potential benefits of further promoting cooperation in the context of genetic monitoring in particular, a central concept to current concerns for both the livestock and wildlife conservation communities.

A 2-day international workshop was recently held at the Ecole Polytechnique Fédérale de Lausanne (EPFL, Switzerland), as the closing event of a four-year European Project "A global view of livestock biodiversity and conservation—GLOBALDIV". The main goals of the project were (1) to improve the conservation, characterization, collection and utilization of farm animal genetic resources in agriculture in EU and beyond (Ajmone-Marsan and GLOBALDIV Consortium 2010), (2) to complement and promote actions previously undertaken in the Community

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Member States at a global level, and (3) to facilitate co-ordination of international activities on animal genetic resources in agriculture.

The first day of the workshop was dedicated to contributions aimed at taking stock of the situation regarding the extent of information and methodology exchange between the livestock and wildlife conservation genetics communities, to identify possible common research interests, in particular in the domain of genetic monitoring, and to discuss perspectives, challenges and, above all, potential benefits of further promoting collaboration between the two scientific communities. During the second day of the workshop, the main results obtained during the GLOB-ALDIV project were presented. This review gives a short overview of the major issues raised during the workshop by focusing on contributions related to the promotion of collaboration between livestock and wildlife scientists and aims to stimulate further discussion useful to both communities.

Pierre Taberlet (CNRS/University of Grenoble, France) presented an overview of farm animal history. Cattle, sheep and goats were domesticated in the Middle East about 10,000 years ago, spread out of the domestication centers, and resulted in many populations well adapted to local conditions. After a period of 'soft' selection during thousands of years, the situation changed dramatically 200 years ago with the emergence of the breed concept. The selection pressure strongly increased, and genetic exchange among breeds was seriously reduced, leading to the fragmentation of the initial gene pool. About 50 years ago, the selection pressure was increased again via the use of artificial insemination, leading to a few industrial breeds with very high performance, but with low effective population sizes and the associated risk of genetic drift and inbreeding. Beside this performance improvement of industrial breeds, genetic resources are being lost, first because of the replacement of traditional breeds by high performance industrial breeds at a worldwide level, and second because of the loss of genetic diversity in these industrial breeds (Taberlet et al. 2008, 2011). Many breeds are already extinct, and genetic resources in cattle, sheep, and goats are thus highly endangered, particularly in developed countries. The recent development of next generation sequencing technologies opens new avenues for properly characterizing the remaining genetic resources, not only in diverse domestic breeds, but also in their wild ancestors where they still exist. Based on sound genetic characterization, urgent conservation measures must be taken to avoid an irremediable loss of farm animal genetic resources, integrating economical, sociological, and political parameters.

This raises the need to assess and monitor diversity, a theme central to the Convention on Biological Diversity

(CBD), which equally applies to livestock and wildlife. Irene Hoffmann (FAO, Food and Agriculture Organization) explained the complexities of monitoring biological diversity in livestock. She pointed out that besides having to take into account the three levels addressed by CBD—i.e. ecosystems, species and genes—in livestock it also needs to take into account the breed concept, an entity often defined on the basis of cultural aspects as much as morphology or genetics. Hoffmann stressed the difficulties that livestock community is facing, including the uneven availability of information and tools for characterization, inventory and monitoring of livestock biodiversity at the gene, species and ecosystem level. Despite the effort spent during the last years, characterization at the agro-ecosystem level still remains a big challenge, as it requires interdisciplinary approaches and the evaluation of complex long-term ecological relationships. Such analysis is very much needed for future sustainable ecosystem management, particularly related to emerging diseases and zoonoses often deriving from wild or domesticated animals. A key element is also the collection of information on breed phenotypes and performance to create linkages to the gene level of diversity. For molecular genetics, livestock characterization is far more advanced than in nearly other non-human, non-model animal species: molecular tools are at the forefront of genomic research and efforts have been made to establish standards (FAO 2011) and to create global databases to run meta-analyses of diversity. Due to its deep cultural and ethical significance, preserving livestock resources also becomes an institutional/public service rather than a purely scientific challenge. Because of the multifaceted drivers and threats affecting breed diversity, it is therefore crucial to monitor equally both agro-ecosystem and gene level drivers.

The importance of genetic monitoring for wildlife conservation was highlighted by the contribution of Fred Allendorf (University of Montana, USA). His presentation highlighted the fact that, on one hand, the recent rapid advances in molecular techniques made genetic monitoring relatively easy and inexpensive to quantify temporal changes in the genetics of populations over tens or even hundreds of years. But on the other hand, the existing plans for the implementation of the CBD at the national level only rarely recognize the need for monitoring the levels of genetic variation through time. This, besides undermining efforts to maintain genetic diversity at all levels, also endangers economically exploited wildlife species through genetic risks associated with population augmentation, and hampers the recognition of ongoing processes of adaptation to changing climates, selective harvesting effects and human-driven landscape alterations. Instead, monitoring is foreseen for these adaptive responses as a future valuable tool in conservation biology, for identifying populations

unable to evolve at sufficiently high rates and for identifying possible donor populations for genetic rescue. The realization of these potentials will be further augmented by technological advances, notably next generation sequencing technologies that may allow for monitoring at the level of whole genomes (Allendorf et al. 2010).

The same message, i.e. the importance of recognizing adaptive genetic variation, was emphasised by Aurélie Bonin (University of Grenoble, France) through the description of a Population Adaptive Index (PAI) (Bonin et al. 2007). The PAI accounts for the adaptive uniqueness of a given population among a set. Its estimation relies upon a population genomics approach which aims to detect loci with atypically high population differentiation compared to the rest of the genome, as a distinctive signature of divergent selection (Luikart et al. 2003). Bonin illustrated the use of PAI in two case studies, one on the common frog (*Rana temporaria*) and the second on the Austrian dragonhead (*Dracocephalum austriacum*) and the investigation of four different conservation strategies to identify the one most suitable to protect the maximum amount of either neutral or adaptive genetic diversity. She also stressed that a range of empirical case studies are now required to assess the impact of different parameters on PAI estimation before the index can be used to steer management decisions in wildlife or in livestock conservation.

The usefulness of genomic data to evaluate the adaptive potential of livestock breeds was also highlighted by Olivier Hanotte (University of Nottingham, UK). He presented an approach for which the basis—landscape genomics—was developed at the intersection of livestock and wildlife sciences (Joost et al. 2007), illustrating the powerful potential of joining efforts to develop new methods to study adaptation. Hanotte et al. (2010) stated that livestock landscape genomics offers a new start for the sustainable improvement of African livestock productivity. Combined with selection based on genome-wide analyses, this approach might offer the opportunity to tailor individual indigenous African livestock genotypes to current needs, while taking into account future environmental conditions. In this respect, livestock may represent a unique model for the study and the understanding on how animal species may be adapted to future changes of the environment such as climatic ones. This new field of livestock landscape genomic selection is building upon the outcomes of past research aiming to characterize and to understand the distribution of indigenous livestock diversity (e.g. Hanotte et al. 2002), illustrating the importance of such work in the today context of the study of adaptation. Interestingly, genome-wide screening of polymorphisms will provide also a fine map of genome introgression pattern in crossbreeds taurine × zebu, populations commonly found across most of sub-Saharan Africa. It may provide an interesting model for understanding the introgression pattern across the genome which follows hybridization of wild species (Fitzpatrick et al. 2010).

The risk due to introgression also affects wildlife species, as Iris Biebach (University of Zürich, Switzerland) pointed out. Together with her colleagues, she investigated the Major Histocompatibility Complex (MHC), a gene family known to be important for the immune response in vertebrate, in Alpine ibex *Capra ibex*, and Iberian ibex *Capra pyrenaica*. Both species showed low genetic diversity at this gene, which is likely to be a consequence of their recent demographic history. Populations of both ibex, in fact, experienced severe bottlenecks due to strong hunting pressure during the last century and were subsequently subject to reintroduction/restocking starting from the few nuclei of individuals still surviving in the wild. Similarly, the two species exhibit low genetic diversity at neutral microsatellites loci (Biebach and Keller 2009) and, unexpectedly, possess alleles that were identical to those found in domestic goats. According to Linkage Disequilibrium analyses, a likely explanation for this is introgression between domestic goat and ibex which probably took place by chance during the recent evolutionary past of both ibex species.

Even though there is no complete agreement on the issue, it is generally accepted that introgression may represent a factor of endangerment from the point of view of the conservation of genetic diversity. This was exemplified by Mike Bruford (University of Cardiff, UK) through the description of the recent events which led to the removal of the ban to the bull semen import to the island of Jersey. Besides highlighting the risks of genetic erosion in similar cases, Bruford also highlighted the underlying lack of implementation of recommendations using real genetic data in conservation actions. According to his view, there is a general and widespread antipathy towards genetic data in the conservation community. This probably derives from the lack of a clear legislative and policy framework for genetic diversity in countries outside of North America and negatively affects both wildlife and livestock conservation efforts. As Bruford explained, to help improve this situation in the European Union, an EU FP7 support action project, CONGRESS "Conservation Genetic Resources for Effective Species Survival", has recently been launched to provide information and resources for biodiversity managers and policy makers to encourage the use of genetic data in biodiversity projects.

Conclusion

Genetic monitoring appears to be central to current concerns and priorities for both the livestock and wildlife

conservation communities. The difference is that, for the former, monitoring is mainly applied at the ecosystem and species levels, which are usually well represented in conservation and management policies but difficult to implement in the field for the monitoring of real farm animal genetic data. While for the latter, genetic monitoring already constitutes a valuable tool for the management and conservation of wildlife populations (Schwartz et al. 2007). Here, the concept is directly applicable by specialized research teams interested in the evolution and conservation of a given species or community. The number of actors is often reduced (scientists, states, NGOs) compared to livestock conservation, and most stakeholders have the same ultimate interest: to conserve biodiversity. In livestock science, the problem can be more complicated since it involves often many actors with different and often conflicting interests, among which preserving biodiversity is seldom the most important. As leader of the CBD's programme for Work on Agricultural Biodiversity, FAO has the delicate task of trying to reconcile unsustainable pure production concerns with biodiversity conservation worries (Hoffmann 2011).

However, the genomic revolution is under way, and sequencing complete genomes is becoming a realistic option in the context of forthcoming research programs. Such data and knowledge will soon be available to wildlife and livestock conservation communities, and both of them will greatly benefit from the sharing of methods and experiences according, perhaps, to a model potentially offered by the CONGRESS project. This approach will most probably permit a faster implementation of novel approaches suitable for obtaining a more balanced picture of adaptive and neutral genetic variation in threatened species or populations (Allendorf et al. 2010). Even if wildlife and livestock conservation genetics have different priorities and some important differences will always remain, many of the same principles apply. Therefore, common research has to be stimulated at the intersection of wildlife and livestock science, since—as the tools presented during this workshop by Aurélie Bonin and Olivier Hanotte ably demonstrated—biodiversity conservation as a whole will greatly benefit from these joint efforts.

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