

**LOCAL BREEDS AND THEIR POTENTIAL FOR PROGRESS
IN ANIMAL BREEDING****P. Dovc***Introduction*

Management of animal genetic resources became more and more important issue worldwide during the last decade. The rapid reduction of the population size and in some cases even extinction of local breeds are the most commonly used arguments to support fund raising for preservation of animal genetic resources at national and international level. Although not always well documented, the common belief is that with the reduction of the number of local breeds, the common genetic base of a species is reduced. The economic pressure towards more productive breeds supports introduction of modern highly productive breeds in traditional environments and rapid reduction of population size in local breeds. In addition, the modern reproductive techniques, i.e. artificial insemination, cloning, and embryo transfer, contribute significantly to the reduction of the number of superior parents needed for normal reproduction in highly productive cosmopolitan breeds. Both processes contribute to the erosion of biodiversity at the global level and represent potential threat for further advances in animal breeding. Rapid development of molecular genetics and progress in genome mapping and sequencing in numerous species, among them also traditional farm animal species, offer the possibility to tackle this problem more efficiently than ever before.

Survey of biodiversity

Traditionally the description of different breeds was based on morphological and production traits. Since prominent phenotypic traits are often determined with only a few genes and production traits strongly affected by environmental factors, the real extent of biodiversity may remain hidden using only traditional methods for characterization of animal breeds and populations. Therefore molecular markers were successfully introduced in genetic characterization of animal genetic resources during the last decade.

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This approach revealed important genetic relationships among populations and shed new light into the estimation of global genetic diversity. This information can significantly support decisions related to different preservation activities and help to preserve global biodiversity in amore efficient way. However, there is not only scientific argumentation driving such programs, different political and economic arguments play also an important role in allocation of financial support for preservation of animal genetic resources. Unfortunately, the distribution of global biodiversity and financial support available for preservation of animal genetic resources show clear bias towards extreme low financial resources in the regions with the highest level of biodiversity. Even in the case when scientific argumentation plays an important role it is not always clear how to use this information. Driven by phenotypic extremes, people often tend to support preservation of extreme genotypes, believing that they represent the majority of the common genetic pool. However, in some cases genetically most distant populations are the consequence of genetic drift and fixation of some alleles, which are rare in the main population. Therefore such populations are not suitable for restoration of the entire genetic pool of the species. On the other side some rare alleles may be favorable in special environments and represent selective adaptive advantage of the certain population in a special environment. Much more than production traits, play an important role in this context traits related to animal health and resistance to different diseases.

Identification of candidate gene regions

The progress in genomic research enabled whole genome screening with the high number of molecular markers (microsatellites or SNPs) for reasonable costs. This made it feasible to perform association studies for a number of traits, among them also susceptibility for important pathogens, mainly spread in certain geographical regions. Nice examples for such traits are *Trypanosoma* tolerance in cattle in central Africa and susceptibility to *Leishmania sp.* in dogs in Mediterranean basin. In the case of *Trypanosoma* tolerance the observation was made that certain African breeds (mainly N'Dama and West African Shorthorn, but also *Bos indicus*) are trypanosomiasis resistant (Stewart *et al.*, 1951; Letenneur *et al.*, 1978). Therefore the potential value of these breeds for crossing with *Bos taurus* were explored (Cunningham *et al.*, 1987). Newly molecular approach for mapping QTLs affecting trypanotolerance was applied (Hanotte *et al.*, 2003). Further research of the candidate regions is needed on order to identify potential candidate genes having an impact on trypanotolerance.

In the case of susceptibility to *Leishmania* sp in dogs in the Mediterranean countries a high proportion of dogs in this area is infected with *Leishmania* sp., representing a major dog health problem in this area (Amela et al., 1995; Cabral et al., 1998; Fisa et al., 1999). The extent of infection already represents a global health threat (Desjeux, 2001). However, there is a number of local dog breeds with significantly lower susceptibility to *Leishmania* infection in Mediterranean area (Kramer et al., 2006). The application of molecular genetic methods and genomic information available, allowed identification of the candidate locus *Nramp1* which may have an impact on susceptibility to infection (Sanchez et al., 2005).

Both examples show that valuable alleles are already present in some animal breeds, probably assuring selective advantage to animals traditionally exposed to specific pathogens. Molecular genetics so offers completely new strategies for identification of causal genes and, combined with genomic information, strategies for targeted introduction of these valuable alleles into genetic background of more productive breeds can be developed.

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