STRATEGIES AND TOOLS FOR CONSERVATION OF LIVESTOCK GENETIC RESOURCES

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Most livestock are believed to have originated from very few, often a single domestication event per species, from which large-scale radiation, genetic change and adaptation has occurred. Natural and artificial selection has created enormous genetic diversity among breeds, with examples of adaptation to extreme and fluctuating environments, resistance to many of the most important livestock diseases, and highly developed and specialised production capacity. Most wild ancestors are extinct, and where surviving, do so in limited numbers and/or geographical range with limited genetic diversity. Thus, in contrast to many agricultural plant species, most or all genetic diversity in livestock resides within and between existing domesticated stocks. While most of the more than 5000 breeds of livestock remain very poorly characterised, it is estimated that two breeds per week are lost through extinction. Ex situ cryopreservation methods are not available for most livestock species, and will rarely be practical even where technically feasible. In situ conservation through utilization, and ensuring that AnGRs remain functioning parts of the production system, seems the most practical solution for widespread conservation of diversity. Community based approaches seem essential for sustainable *in-situ* programs, and open nucleus breeding schemes provide a practical model for genetic improvement. It is likely, however, that there will also be need for *in situ* and *ex situ* conservation without immediate utilisation. Conservation decisions will involve difficult choices with important long-term consequences, and will thus need to be based on reliable information and frameworks for objective decision making. Considerable, but still inadequate effort is underway to characterise livestock at the phenotypic and molecular genetic levels, and to document their production environments, uses and status. Research is also underway to evaluate methods of valuing livestock breeds and for developing frameworks for decision making based on information on phenotype, value, molecular diversity, status and cost of conservation. It is hoped that such information and tools will enhance both the quality of conservation decisions and the amount of conservation activity.