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## Understanding the Genetic Diversity of Livestock — An Essential Step for the Management and Improvement of Farmers’ Resources

GEROLD KIERSTEIN, DAVID N. MBURU, ANNE W. T. MUGAI, HAN JIANLIN, J. EDWARD O. REGE, OLIVIER HANOTTE

*International Livestock Research Institute (ILRI), Kenya*

### Abstract

The last 10 years has seen an explosion of genetic studies aimed at improving the understanding of the origins and genetic characteristics of livestock genetic resources. Although the focus of most of this work has been Europe, remarkable progress has also been made in the developing world, thanks to the support of development agencies. Since 1995, ILRI has developed, in collaboration with National Agricultural Research Systems in developing countries, a dynamic program on the molecular genetic characterisation of indigenous livestock of Africa and Asia. Molecular diversity information on cattle, sheep, goat, chicken, yak and Old World Camelidae are now partly available at country, regional and/or continental levels. The results show that the origin of the present day livestock diversity is more complex than previously thought with evidences for multiple origins or domestications. Livestock also show different patterns of geographic distribution of diversity in relation to the history of the domesticated species. These finding have direct applications to the design of strategies aiming to conserve diversity to maximise future utilisation. We have now the tools to understand the diversity of the genetic make-up of a livestock breed or population with direct applications to on-farm and on-station breeding programs. Genetic characterisation may also provide a genetic signature for breed uniqueness within the context of intellectual property rights. Examples of applications of molecular diversity studies in livestock conservation and utilisation are illustrated by results obtained from the ILRI-led research. We present three studies: (i) the identification of cattle diversity hotspots and priority breeds for conservation in sub-Saharan Africa; (ii) dromedary breed identification in Kenya; and (iii) the possible application of phylogenetic studies for improvement of disease resistance in cattle and sheep populations.

**Keywords:** Conservation strategy, genetic characteristics, phylogenetic studies