

MOLECULAR VERIFICATION OF TRACEABILITY: OPPORTUNITIES FOR ASSESSING BOVINE GENETIC DIVERSITY

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Summary

Molecular traceability verification (MTV) in bovines may be expected to provide useful data for genetic diversity studies. Examination of protocols and simulations of MTV plans on a sample of Italian breeds were used to assess the value of the MTV data and identify problems. A coordinated, national program is necessary; limited savings should be compensated by effective monitors of major breeds. Minor breeds need specific studies.

Keywords

Traceability, microsatellites, sampling, bovines, cost analysis

Contribution

The extensive implementation of traceability system for bovines offers several opportunities for assessing and managing genetic resources. Assessment (and monitoring) of genetic resources is needed for the conservation and sustainable exploitation of biodiversity. Molecular tools have been extensively used for assessment, but require significant funding. Notably, traceability systems often include molecular traceability verification (MTV) plans that employ similar molecular methods. Animals may be sampled at marking, or later, and the extracted DNA may be compared with samples bearing the same identification number and thus supposedly belonging to the same individual. Such MTV plans may be extensive. The aim of our study was to assess, based on FAO guidelines [4], available protocols and Italian breed population data, the extent, obstacles and economic impact of the potential use of MTV data for genetic diversity (GD) data gathering. To this purpose, we examined published and unpublished sources, applied FAO guidelines, developed a sample MTV plan for Italy and simulated various cost scenarios. We found that, as evidenced in some MTV protocols, sampling for GD and MTV are inherently different. While the individual is the primary sampling unit for both MTV and GD, GD studies require sampling stratified by breed whereas random sampling appears an adequate strategy for MTV. In fact, examined protocols do not include breed as a sampling criterion. Also, MTV is often applied at slaughter (blood) and at retail (meat) only, resulting in the exclusion of animals not used for meat, such as milk producers. However, sample size is a significant benefit of MTV compared with most GD studies; some MTV plans sample thousands and analysed hundreds of individuals (theoretically, if a 0-3% traceability failure is considered acceptable, around 250 individuals should be sampled). Under a hypothetical national MTV plan, run regionally, among 24 Italian breeds taken for a simulation (16 of which considered rare), 4 important Italian breeds would be expected to yield a full GD sample every year. Within five years, two other breeds could be characterized. This group includes economically important breeds such as

Piemontese, Chianina, Maremmana, Marchigiana, Podolica. On average, however, rare breeds would not be included in the sample for years.

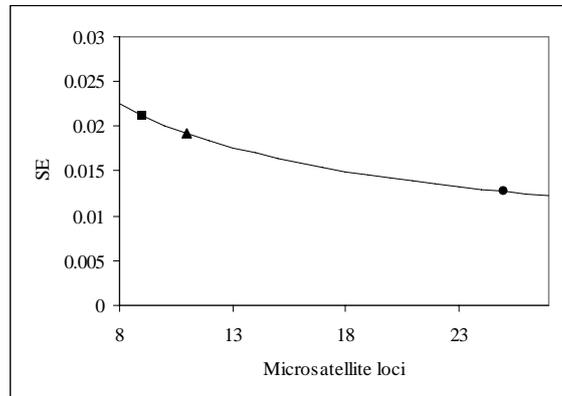


Figure 1 Standard error of genetic distance as a function of microsatellite loci analyzed, with two traceability studies chosen as an example and according to FAO guidelines (square, study 1; study 2; circle, FAO guidelines [1]).

Data recording may also be inadequate in MTV. Traceability systems generally record breed affiliation but phenotypic qualities of the individual and confirmation of stated affiliation remains outside the scope of MTV.

At the lab level, procedures are similar. However, MTV studies have shown that, at least in some context, adequate discriminative power may be obtained with 9 microsatellite loci, with some having less than 2 alleles. For GD purposes, on the other hand, more microsatellite loci (up to 25), with at least 4 alleles, are suggested [1]. Increasing microsatellite loci to GD levels for a whole MTV sample may triple costs. Yet, it should be noted that, for the purpose of measuring genetic distances, low standard errors (suggested 0.025 [1]) can be obtained with 9 loci or 11 loci (figure 1). Handling MTV in labs that also study GD (by sending samples to a breed reference labs) may be cost-effective if more extensive genome characterization is employed only on a breed-specific subsample. Most savings will be accrued to sampling and fixed lab costs, while analytical savings can be expected to be low.

MTV may provide much needed data for bovine genetic resource assessment and monitoring. A nation-wide coordinated effort is necessary; extensive information will be available for breeds numbering in the thousands (depending on sampling scheme for MTV), making year-to-year monitoring and identification of diversity hot-spots possible. More targeted monitoring and independent resources will be needed for minor breeds.

REFERENCE LIST

[1] FAO, Secondary Guidelines for Development of National Farm Animal Genetic Resources Management Plans–Measurement of Domestic Animal Diversity (MoDAD): Original Working Group Report. Available at <http://dad.fao.org/en/refer/library/guidelin/workgrp.pdf>