



A136 Population Studies and Proposed Nomenclature for 16 Bovine STR Loci for Forensic Purposes

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After attending this presentation, attendees will understand population studies and proposed nomenclature for 16 bovine STR loci for forensic purposes.

This presentation will impact the forensic community by showing that repeat - based nomenclature is highly relevant to the field of animal forensics.

As a consequence of the close integration of cattle into the food chain of humans, forensically relevant cases involving cattle, such as identity forgery or cattle theft, are relatively common. Bovine STR loci are extensively used for parentage verification by the animal breeding industry and the first description of cattle microsatellites in the 1990s has eventually led to international recommendations for these loci in 1998 by the International Society for Animal Genetics (ISAG). While ISAG recommends certain STR loci for bovine parentage testing purposes, large scale population data reporting the information content of the loci remains scarce.

Population studies were performed on 16 polymorphic STR loci (BM1824, BM2113, ETH10, ETH225, INRA023, SPS115, TGLA122, TGLA126, TGLA227, ETH3, TGLA53, BM1818, CSRM66, CSSM66, HAUT27, and ILSTS006) on 9,738 randomly selected cattle (*Bos taurus*), representing 22 distinct breeds. The power of parental exclusion (PE 1 and PE 2), the expected heterozygosity (HE), the observed heterozygosity (HO), probability of identity (HW P_{ID} and sib P_{ID}) as well as null allele frequencies were calculated. Here we show that, when using microsatellite loci for forensic purposes, major differences exist in the information content of bovine genotyping between different cattle breeds. The 16 loci provide sufficient power for forensic analysis.

Furthermore, the efficacy of the loci in assigning unknown individuals to the correct breed based on genotype data, an application which has considerable use in forensic casework was studied. The individual assignment tests provided excellent success in several breeds.

For the purpose of legal casework a universal nomenclature system was established for the sixteen markers which is based on the principles of human repeat-based nomenclature according to the recommendations of International Society of Forensic Genetics (ISFG). To propose this repeat-based nomenclature in cattle, a selection of most frequent alleles was sequenced for the polymorphic dinucleotide STR loci. In the sixteen STR-markers the variable repeat structure revealed simple or compound variable nuclear tandem repeats (VNTRs); only one intermediate allele was found. The proposed nomenclature for the sixteen bovine STR markers investigated herein enabled us to successfully adopt the ISAG nomenclature to the recommendations of the ISFG for the nomenclature of human STRs.

Bovine Short Tandem Repeats, Repeat Number-Based Nomenclature, STR Population Studies