



A14 Population Studies and Proposed Nomenclature for 17 Equine STR Loci for Forensic Purposes

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The goal of this presentation is to describe how repeat-based nomenclature is highly relevant to the field of animal forensics.

In recent years the horse industry has become a fast growing business, forensically relevant cases involving horses, such as identification of samples involved in doping control, fraud or horse theft, are relatively common. Forty-three breeds consisting of a total of 42000 horses were genotyped using 17 microsatellite markers (AHT4, AHT5, ASB2, ASB17, ASB23, CA425, HMS1, HMS2, HMS3, HMS6, HMS7, HTG4, HTG6, HTG7, HTG10, LEX3, and VHL20). To assess the power in kinship analysis and identity testing, the Power of Exclusion was calculated for 1 and 2 parents (PE (1) and PE (2)), the Expected Heterozygosity (HE), the Observed Heterozygosity (HO), probability of identity (HW P(ID) and sib P(ID)) and null allele frequencies for the 17 markers. When using microsatellite markers for equine kinship analysis, major differences exist in the reliability of the test between different horse breeds. To assess the variation between breeds, the genetic distances were calculated using Reynolds' distance F_{st} and Nei's standard G_{st} . In general, the genetic distances of the current study were similar compared to those estimated in earlier horse diversity studies. The power of individual assignment tests was assessed using the seventeen markers. Finally, based on sequencing of the most frequent alleles in the population, we propose a repeat number -based nomenclature for the 17 STR loci.

Equine Short Tandem Repeats, Repeat-Based Nomenclature, STR Population Studies