# GENETIC DIVERSITY STUDY OF SEVEN BOVINE BREEDS BY THE USE OF SSR MARKERS

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The genetic diversity available for selection will affect the success of future cattle breeding strategies. Selective breeding programs aiming the improvement of desirable traits result in genetic erosion and, inevitably, in a reduction of the genetic base from which to select phenotypes in the future and eventually affecting the whole cattle populations. Such genetic erosion can occur for many different reasons, mainly by: 1) extensive use of semen and embryos from the same sources by means of artificial insemination and embryo transfer; 2) use of a restricted number of improved breeds, as a result for the commitment of high input farming that forces the use of high yielding breeds. The reduced genetic base would limit the opportunities to select production related traits which could be important in the future. It is, therefore, important that the genetic diversity is maintained to provide a base from which new desirable traits can be selected.

Early work to measure genetic diversity used blood groups to show differences between breeds and diversity analysis. More recently, minisatellite probes have been used to generate genetic fingerprints which have been used to show differences between individuals. Such fingerprints have been used to estimate genetic diversity - the greater the number of bands revealed by the fingerprint being equated with greater diversity. Simple sequence DNA motifs, also known as microsatellites (or SSR's) are at present the most usual and useful molecular markers for human and most domestic species. The availability of genetic markers on different chromosomes and high polymorphism allows them to be used in different studies including paternity testing, molecular taxonomy, evolution and population genetics, evaluation of the genetic divergence among different populations or breeds, and the search for genes responsible for diseases and other traits (BOTSTEIN et al., 1980; BOWCOCK et al., 1994; GEORGES & ANDERSSON, 1996; MacHUGH et al., 1998; ALMEIDA et al., 2000). SSR are reproducible from one laboratory to the other allowing comparisons to be made between breeds analyzed in different studies, bringing up the possibility of developing an efficient diversity monitoring program. These short repetitive DNA sequences display length polymorphism which segregates in a discrete Mendelian fashion among individual organisms. The distribution and patterns of variation at these genetic loci therefore reflects genealogical associations and ultimately phylogenetic affinities between related populations and taxa. Population genetic analysis may therefore provide a predictive model for future investigations of heterosis between divergent cattle breeds.

In the present study, we evaluate the genetic diversity among 250 unrelated animals belonging to seven cattle breeds: Charolais-CH (30), Nellore-NE (50), Guzerat -GU (30), Caracu-CU

(30), Santa Gertrudis-SG (20), Canchim-CA (30) and Gyr-GI (60), using a set of seven SSR markers (BM8246 – Chrom. 1, CSFM50 – Chrom. 2, BMS963 – Chrom. 3, BM1224 – Chrom. 4, TEXAN15 – Chrom. 5, BMS483 – Chrom. 6 E INRA112 – Chrom.7).

Polymorphic Information Content (PIC) was estimated according to BOTSTEIN et al. (1980). The software TFPGA v. 1.3 (Miller, 1997) was used to estimate allele frequencies, Nei's genetic distance (1972), expected and observed heterozygosities and to evaluate Hardy-Weinberg equilibrium for the seven loci. $G_{ST}$ values (Nei, 1987), which measure the degree of genetic variation within and among populations were estimated by the use of the BioSys-2 computer package (Swofford & Selander, 1981).

Our results suggest that the different breeds have a similar degree of genetic diversity, although different levels of diversity were observed for the evaluated loci. The fixation index estimates ranged from 0.07 to 0.26, being higher for GU and SG (0.21 e 0.26, respectively) suggesting a lower proportion of heterozigous genotypes for the evaluated loci, in relation to the ones expected under Hardy-Weinberg equilibrium. As expected for this kind of markers, the analyzed loci showed a high level of PIC, with mean values ranging from 0.639 to 0.806. The cluster analysis results based on the estimated genetic distances distributed the populations into two distinct groups (Figure 1): Group I – CH, CN, CA, SG, and Group II – NE, GU and GI (taurine and indicine origins, respectively). Note that CN (3/8 Zebu and 5/8 Charolais) and SG (3/8 Brahman and 5/8 Shorthorn) breeds are knowm as "synthetic".

The pattern revealed by the polymorphism of these markers is consistent with the one expected from previous information concerning the breeds origin and breeding genealogy highlighting the efficiency of this kind of approach in population genetics studies.

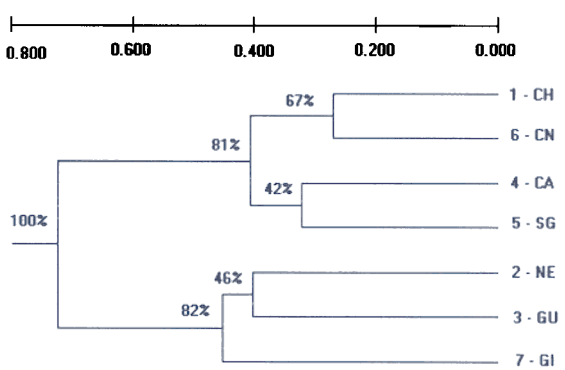


**Figure 1** - UPGMA phenogram: based upon Nei's genetic distance (1972) and node consistency (Coelho, 2000).

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