

Genome wide association study to identify loci for resistance to gastrointestinal nematodes in cattle

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Helminthosis is a primary factor in the productivity reduction in cattle through mortality and reduced weight gains. Quantitative trait loci (QTL), or genomic regions affecting performance traits, for parasite indicator traits in cattle are ideal targets for study of marker assisted selection; however the phenotypic data and available resource populations were not optimal for reliable QTL identification. Fecal egg count (FEC) values, which are used to measure resistance to nematodes, are not distributed normally and logarithmic transformations fail to properly normalize this data in most cases. FEC data recorded for 384 animals collected between 2001 and 2008 from Gyr x Holstein F2 populations were transformed using an extension of the Box-Cox transformation to approach normality. Samples of DNA for genetic analysis has been acquired from these animals, and a total of about 54,000 SNPs genotyped with the Illumina BovineSNP50 Bead Chip (Illumina Inc., San Diego, CA) were investigated to determine usefulness of the associated SNPs for the breeding value of resistance to gastrointestinal nematodes. For this study, a partial genome scan study was developed from chromosome 1 to chromosome 10. Any SNP with low call rate (<99%), departure from Hardy-Weinberg equilibrium (exact test $p < 0.01$), and minor allele frequency below 5 percent, were excluded from the final analysis (29,181 markers retained). Bonferroni corrected level of 0.01 were used. SNPassoc software, an R package, was used in order to detect association. For this trait, significant SNPs were found on many chromosomes, especially on BTAs 6 and 7. The presence of significant SNPs in these chromosomes suggests further SNP discovery in this region to detect causal mutations would be warranted. Financial support: CNPq, EMBRAPA, FAPEMIG, CAPES.

Keywords: dairy cattle, GWAS, nematodes, SNP.

Mitochondrial DNA diversity patterns in Pakistani buffalo

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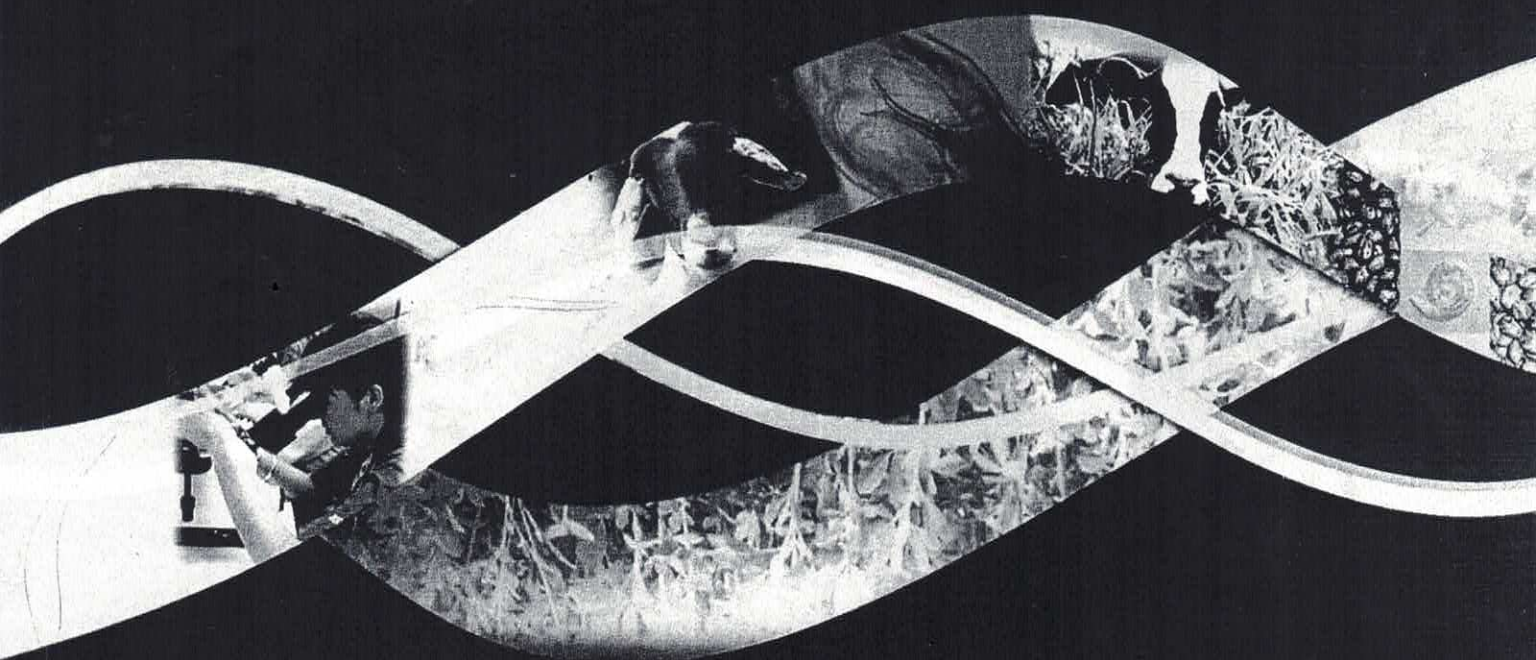
Indian subcontinent is considered the likely centre of river buffalo domestication based on population dynamics, archeological evidence and genetic diversity. Recent studies on mitochondrial DNA diversity have drawn useful conclusions about domestication history of *Bubalus bubalis*. The conclusions of these studies would however, be thought partial unless samples are also analyzed from Pakistan where exists the second largest buffalo population of the world. Here we report the results of the first

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