

RELATIONSHIP BETWEEN ANCIENT AND NATIVE PIGS ON JEJU ISLAND

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Ancient pig bones were collected from three archaeological sites on Jeju Island, Korea which have been estimated to date from A.D. 0 to A.D. 500, and phylogenetically analyzed. The obtained CR fragments were identified as the species, *Sus scrofa*. On the neighbor-joining tree, ancient CR sequences were localized to two distinct subclusters, indicating that there were two kinds of animals present on Jeju in ancient times, domestic pigs and wild boars. Thus, the ancient CR sequences were divided into two pig breeds and were maternally distinct, although both were indigenous to the Asian pig lineage. Thus, contrary to our original prediction, there must have been two kinds of pig breeds on Jeju Island in ancient times, domestic and wild. These would have been used by the islanders for various reasons at that time and notably included domestic pigs that are different to those currently present on this island.

SINGLE NUCLEOTIDE POLYMORPHISM WITHIN EXON 4 OF THE BOVINE PROLACTIN GENE IN THREE IRANIAN NATIVE CATTLE

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Prolactin stimulates mammary development and promotes the formation and action of the corpus luteum during the female reproductive cycle in some mammals. Hence the PRL gene is a potential quantitative trait locus and genetic marker of production traits in dairy cattle. The gene and genotypic frequencies of bovine prolactin (bPRL) in Iranian Sarabi, Golpayegani and Sistani cattle (268 blood samples in total) was investigated using PCR-RFLP analyses. Three genotypes of AA, AB and BB were observed. The frequencies of A and B alleles were 0.3 and 0.7 for Sistani and 0.73 and 0.27 for Sarabi and Golpayegani cows, respectively. The χ^2 test confirmed the Hardy-Weinberg equilibrium in these populations. Different allele frequency may be explained by the reason of Sistani is beef cattle nevertheless Sarabi and Golpayegani are dairy cattle.

Keywords: Sarabi, Golpayegani, Sistani, Prolactin, Genetic polymorphism

Keywords: PRL gene, RFLP, genetic polymorphism, SNP, quantitative trait locus, Adipocyte

ANALYSIS OF M... FOR POTEN...

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This study was conducted in various regions on carcasses of 67 proven steers of chromosome 14 with a view to identifying QTL effects. The estimated breeding value (EBV) for carcass weight (CW) and breeding value (BV) for individual allele frequencies showed a potential

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Variance components (DG), metabolic feed conversion ratio. Data were analyzed for maternal associations comprising direct and maternal effects significantly (P < 0.05). Heritability estimates for carcass weight (0.45±0.03, 0.3) and RFI, respectively, were zero for only covariances of...
Keywords: G...