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The indel polymorphism in cattle amelogenin gene (AMEL) and its significance for the identification and evolutionary studies

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Abstarc :

Nucleotide and amino acid sequences of cattle amelogenin, the major protein of forming enamel, were analysed by screening 1547 samples collected from cattle of various breeds. Sequenced was the part of cattle exon six of the AMEL gene (codons from 107 to 186) encompassing so-called hot spot of mutation in the mammals amelogenin gene. The analysis showed the presence of characteristic repeats of 9-nucleotide motifs (triplet PXQ) that makes its structure similar to STR sequences. In Polish Red (PR) cattle (37 cows and 6 bulls) a novel variant of 271 bp was detected on chromosome X. The alignment of sequences obtained showed that a novel variant of the amelogenin gene in PR cattle – AMEL-X(271) – is caused by deletion of one 9-nucleotide motif in position 485-493 (numbering according to Gibson et al. 1991). Irrespectively of the use of length polymorphism in the AMEL gene in early sex determination, the new possibilities in evolutionary and identificatory research are created by analysis of sequence structure. In the amelogenin gene the insertion-deletion of 9-nucleotide motifs can be localized in different sequence positions. As a result, sequences can differ by the number of tandem repeats as well as by the position of indels. Comparison of the AMEL-X gene sequences of Bos/Bison and Bubalus species revealed that distinguishing between the two is feasible not only based on the size of the PCR amplicon but also by the presence of additional 9-nucleotide motif in certain repeat region.

Key Word :
amelogenin, bovine species, cattle, gene polymorphism, sequence variation, sex determination

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