Assignment¹ of bovine submaxillary mucin (BSM1) gene homologues to bubaline, caprine, and ovine chromosomes by comparative mapping

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¹ To our knowledge this is the first time this gene has been mapped in river buffalo, goat and sheep.

Rationale and significance

BSM1 gene encodes for bovine submaxillary mucin, which is a member of a group of macromolecular glycoproteins present in mucous secretions of mammalian respiratory, gastrointestinal, and urogenital tracts (Roussel et al., 1988). The central domain of the BSM1 gene consists of approximately 55 tandem repeats of 329 amino acids and shows high peptide sequence similarity with porcine and ovine submaxillary mucins (Jiang et al., 2000; Eckhardt et al., 1997). The BSM1 gene was previously mapped to bovine chromosome 5q2.2→q2.3 by Jiang et al. (2000). We used the PCR-generated BSM1 probe for comparative FISH mapping. The assigned positions of BSM1 homologues in river buffalo (4q2.2→q2.3), sheep (3q2.2→q2.3), and goat (5q2.2→q2.3) genomes confirm the high linkage conservation in these species.

Materials and methods

The probe for bovine submaxillary mucin gene BSM1 was prepared from bovine genomic DNA by the PCR method using primer pair 5'-AGG AAG TGG TGC AGG TTC AGG-3' and 5'-CTC CTT GTG TTG AGC CAG

GC-3' designed on the basis of bovine gene sequence from the GenBank. Cloned PCR product was labeled with biotin-11-dUTP by nick-translation. The hybridization mixture contained 50% formamide, 2× SSC, 10% dextran sulphate, 10 µg of salmon sperm DNA, and 100 ng of probe. The probe was hybridized for two days to normal metaphase chromosomes from cultured lymphocytes of river buffalo, domestic sheep, and goat, and of cattle (overnight, as control). Localization of signals was performed after incubation with FITC conjugated antibodies on DAPI-banded chromosomes, using image analysis.

Probe name: BSM1

Probe type: cloned PCR product

Insert size: 971 bp

Vector: pGEM

Proof of authenticity: size and restriction analysis

Gene reference accession no: AF178428

Results

Mapping data: river buffalo (*Bubalus bubalis* L.)

Location: 4q2.2→q2.3

Number of cells examined: 30

Number of cells with specific signal: 30

1 (1), 2 (5), 3 (8), 4 (16) chromatids per cell

Location of background signals (sites with >2 signals): none observed

Mapping data: sheep (*Ovis aries* L.)

Location: 3q2.2→q2.3

Number of cells examined: 20

Number of cells with specific signal: 19

1 (5), 2 (7), 3 (4), 4 (3) chromatids per cell

Location of background signals (sites with >2 signals): none observed

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Fig. 1. Chromosomal localization of the BSM1 homologue in river buffalo. A metaphase showing specific signals on both chromosomes 4q2.2→q2.3.

Fig. 2. Chromosomal localization of the BSM1 homologue in sheep. A metaphase showing specific signals on both chromosomes 3q2.2→q2.3.

Fig. 3. Chromosomal localization of the BSM1 homologue in goat. A metaphase showing specific signals on both chromosomes 5q2.2→q2.3.

Mapping data: goat (*Capra hircus* L.)

Location: 5q2.2→2.3

Number of cells examined: 32

Number of cells with specific signal: 32

1 (2), 2 (5), 3 (12), 4 (13) chromatids per cell

Location of background signals (sites with >2 signals): none observed

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