Assignment¹ of the bovine attractin (ATRN) gene to chromosome 13q21→q22 by in situ hybridization

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¹ This is a more precise localization of a gene previously genetically mapped to bovine chromosome 13 by Edeal et al., (2000).

Rationale and significance

Attractin (ATRN, mahogany) is a gene involved in the regulation of pigmentation, body weight regulation and formation of the central nervous system in mammals (Gunn et al., 2001; He et al., 2001). Moreover, a soluble form of attractin found in humans is implicated in monocyte spreading and T-cell clustering (Duke-Cohan et al., 1998). In mice *Atrn* was mapped to MMU2, 73.9 cM (www.informatics.jax.org). By EST database searching Tang et al., (2000) mapped ATRN to human chromosome 20p13. Bovine ATRN was mapped to chromosome 13 by linkage analysis (Edeal et al., 2000). Here we report the physical mapping of bovine ATRN to BTA 13q21→22 by FISH.

Materials and methods

The coding sequence of bovine ATRN was amplified using cross-species primers and sequenced. A bovine BAC library was screened by PCR using bovine specific primers. BAC DNA was isolated using a Qiagen Plasmid Maxi Kit. BAC DNA was digested with restriction enzyme *Sau3AI* and labeled with biotin-16-dUTP (Boehringer Mannheim, GmbH) using a Prime-it Fluor[®] Fluorescence Labelling Kit (Stratagene). Chromosomal localization of the BAC clone was assigned by fluorescence in situ hybridization (FISH) on GTG and RBA banded bovine metaphases as described elsewhere (Solinas-Toldo et al., 1995; Graphodatsky et al., 2002).

Probe name: Mgex3

Probe type: bovine genomic BAC clone

Insert size: appt. 115–120 kb

Vector: pBeloBAC11

Proof of authenticity: sequencing

Gene reference: AF531101

Results

Mapping data

Most precise location: 13q21→q22

Number of cells examined: 17

Number of cells with specific signal: 0 (3), 1 (0), 2 (5), 3 (2), 4 (7) chromatids per cell

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

Mapping by FL

Number of chromosomes examined: 34

Mean location: 0.731 Bands encompassed: 13q21→q22

Range: 33% on 13q21 and 67% on 13q22

Standard deviation: ± 0.06

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Fig. 1. Assignment of ATRN to BTA13 by FISH. (left) GTG banded chromosomes before FISH; (right) the same chromosomes after FISH with bovine BAC clone containing ATRN. Location of ATRN on BTA 13q21 → q22 is in agreement with ZOO-FISH data, as human chromosome 20 paints to 13q17 → qter (Solinas-Toldo et al., 1995). Four genes were mapped closely to ATRN in cattle: PRNP (13q17), AVP (13q21 → 22), SOD1L1 (13q21 → q22), and TOP1 (13q22 → q23) (<http://locus.jouy.inra.fr>); two of these genes, PRNP and AVP, are known to be located closely to ATRN in human and mouse (www.informatics.jax.org).

References

- Duke-Cohan JS, Gu J, McLaughlin DF, Xu Y, Freeman GJ, Schlossman SF: Attractin (DPPT-L), a member of the CUB family of cell adhesion and guidance proteins, is secreted by activated human T lymphocytes and modulates immune cell interactions. *Proc Natl Acad Sci, USA* 95:11336–11341 (1998).
- Edeal B, Rumph JM, Mass R, Killinger K, Jerez N, Enlanger S, McDanel T, Aljumaah R, Pithongsiripon U, Nephawe K, Martinez G, Gladney CD, Allan MF, Pomp D: Linkage mapping of the Mahogany (attractin) locus in cattle and pigs. *J Anim Sci* 78:2479–2480 (2000).
- Graphodatsky AS, Yang F, Perelman PL, O'Brien PC, Serdukova NA, Milne BS, Biltueva LS, Fu B, Vorobieva NV, Kawada SI, Robinson TJ, Ferguson-Smith MA: Comparative molecular cytogenetic studies in the order Carnivora: mapping chromosomal rearrangements onto the phylogenetic tree. *Cytogenet Genome Res* 96:137–145 (2002).
- Gunn TM, Inui T, Kitada K, Ito S, Wakamatsu K, He L, Bouley DM, Serikawa T, Barsh GS: Molecular and phenotypic analysis of *Attractin* mutant mice. *Genetics* 158:1683–1695 (2001).
- He L, Gunn TM, Bouley DM, Lu XY, Watson SJ, Schlossman SF, Duke-Cohan JS, Barsh GS: A biochemical function for attractin in agouti-induced pigmentation and obesity. *Nature Genet* 27:40–47 (2001).
- Solinas-Toldo S, Lengauer C, Fries R: Comparative genome map of human and cattle. *Genomics* 27:489–496 (1995).
- Solinas-Toldo S, Mezzelani A, Hawkins GA, Bishop MD, Olsaker I, Mackinlay A, Ferretti L, Fries R: Combined Q-banding and fluorescence in situ hybridization for the identification of bovine chromosomes 1 to 7. *Cytogenet Cell Genet* 73:194–202 (1996).
- Tang W, Gunn TM, McLaughlin DF, Barsh GS, Schlossman SF, Duke-Cohan JS: Secreted and membrane attractin result from alternative splicing of the human ATRN gene. *Proc Natl Acad Sci, USA* 97:6025–6030 (2000).