

Cytogenetic and radiation hybrid mapping of the bovine *interleukin 4 induced 1 (IL4I1)* gene to cattle chromosome 18 (Brief Report)*

Zytogenetische und Radiation-Hybrid-Kartierung des bovinen *Interleukin 4 Induced 1 (IL4I1)* Gens auf Rinderchromosom 18 (Brief Report)

ALBRECHT RIEF¹, MANFRED SCHWERIN¹ and TOM GOLDAMMER²

¹Research Group Functional Genome Analysis and ²Research Unit Molecular Biology, Research Institute for the Biology of Farm Animals, Dummerstorf, Germany

Background

The *interleukin 4 induced 1 (IL4I1)* gene, also known as *FIG1*, encodes a lysosomal protein in B cells with L-amino oxidase (EC 1.4.3.2) property and a high preference for aromatic amino acid substrates implicating a fundamental role in antigene processing and presentation (MANSON *et al.* 2004). In human, *IL4I1* has been assigned to chromosome 19q13.3-19q13.4, a hot spot for susceptibility to several autoimmune diseases (CHAVAN *et al.* 2002). Based on comparative genome data between human and cattle (GOLDAMMER *et al.* 2002), an assignment of *IL4I1* to *Bos taurus* chromosome 18 (BTA18) has been predicted within a quantitative trait locus for somatic cell score (KÜHN *et al.* 2003). This prediction is supported by the putative bovine sequence for *IL4I1*, LOC520692, which has been assigned to BTA18 close to 56.1 megabases within the annotated bovine sequence (NCBI build Btau-4.0). Therefore, we started positional cloning of bovine *IL4I1*, as a candidate gene related to adaptive immunity, i.e. during udder infections in cattle. Here we present the physical assignment of the bovine *IL4I1* gene by fluorescence *in situ* hybridization (FISH) and radiation hybrid (RH) mapping.

Material and methods

The primer sequences IL4I1-F 5'-CCA TCG CGT ACC GACTTT-3' and IL4I1-R 5'-ACT TGA CTG CCG TCT CCA C-3' have been designed from the putative *IL4I1* sequence LOC520692 (GenBank acc. no. XR_028168) and have been used for RH mapping in a bovine 5 000 rad RH panel (WOMACK *et al.* 1997). A BLAST search within the NCBI genome database (<http://www.ncbi.nlm.nih.gov>) identified the ovine BAC clone CH243-207017 as genomic DNA sequence corresponding partially to bovine *IL4I1*. This BAC from CHORI library CH243 (<http://bacpac.chori.org>) has been used for FISH in cattle. Amplification of *IL4I1* specific DNA within the BAC by PCR has been performed at an annealing temperature of 58°C using the described primers. Automated sequencing of the 216 bp long amplicon followed by a BLAST search with the resulting DNA sequence within the NCBI genome database showed 95% similarity between the bovine and ovine sequences for *IL4I1*.

*To our knowledge, this is the first physical chromosome assignment of this gene in cattle.

GOLDAMMER *et al.* (2002, 2009) describe further methodical steps such as PCR, preparation of the BAC DNA as probe for FISH, cytogenetic procedures for preparation of bovine metaphase chromosomes, the hybridization procedure and probe visualization in more detail. The position of *IL4I1* in the ILTX-2005 RH map (EVERTS-VAN DER WIND *et al.* 2005) has been calculated with the software Carthagene 1.0R (DE GIVRY *et al.* 2005).

Results

The BAC CH243-207O17, containing the *IL4I1* gene, has been used as probe for FISH and was assigned to BTA18q25-q26 (Figure 1). PCR with the *IL4I1* primers in the RH₅₀₀₀ panel resulted in a retention frequency of 0.13. The data vector obtained was 0000000010 0000001001 0000001000 0000100100 0000000000 0000000001 0000100000 0010010000 0000010010 (1=present in cell line; 0=not present in cell line). Two-point linkage analysis connected *IL4I1* with a LOD score of 8.8 in a distance of 26.5 cR₅₀₀₀ to RH marker BF440193 (map position 596 cR₅₀₀₀). Our data confirm the predicted gene sequence position for the bovine *IL4I1* alias sequence LOC520692 and anchor the corresponding genome region (NCBI component acc. no. AAF03010410) to BTA18q25-q26.

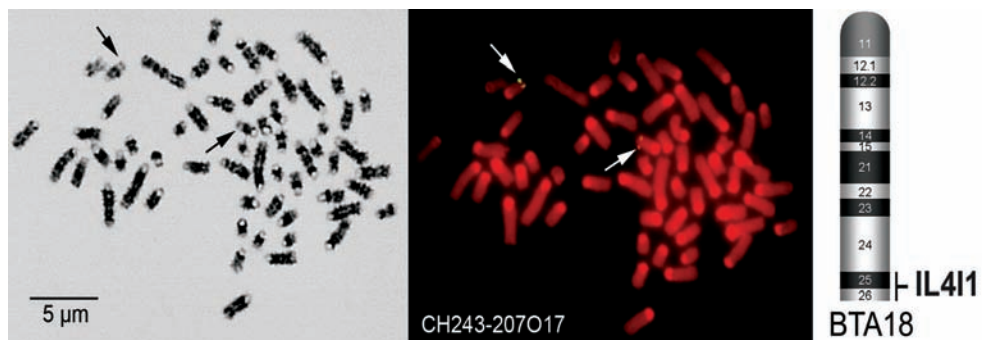


Figure 1
Assignment of *IL4I1* to cattle chromosome 18q25-q26
Kartierung des Gens IL4I1 auf Rinderchromosom 18q25-q26

Acknowledgements

We thank Jim Womack (Texas A&M University, TX, USA) for providing the RH panel and Harris Lewin and Annelie Everts-van der Wind (University of Illinois, IL, USA) for providing the RH marker raw data set of the ILTX-2005. Funds for this work came from DFG (GO-896/6-3), BMBF, and FBF (Förderverein Biotechnologieforschung e.V., AZ 0313381).

References

- Chavan SS, Tian W, Hsueh K, Jawaheer D, Gregersen PK, Chu CC (2002) Characterization of the human homolog of the *IL-4* induced gene-1 (*Fig1*). *Biochim Biophys Acta* 1576, 70-80
- De Givry S, Bouchez M, Chabrier P, Milan D, Schiex T (2005) CARHTA GENE: multipopulation integrated genetic and radiation hybrid mapping. *Bioinformatics* 21, 1703-4

- Everts-van der Wind A, Larkin DM, Green CA, Elliott JS, Olmstead CA, Chiu R, Schein JE, Marra MA, Womack JE, Lewin HA (2005) A high-resolution whole-genome cattle-human comparative map reveals details of mammalian chromosome evolution. *Proc Natl Acad Sci USA* 102, 18526-31
- Goldammer T, Brunner RM, Rebl A, Wu CH, Nomura K, Hadfield T, Maddox JF, Cockett NE (2009) Cytogenetic anchoring of radiation hybrid and virtual maps of sheep chromosome X and comparison of X chromosomes in sheep, cattle, and human. *Chromosome Res* [accepted]
- Goldammer T, Kata SR, Brunner RM, Dorroch U, Sanftleben H, Schwerin M, Womack JE (2002) A comparative radiation hybrid map of bovine chromosome 18 and homologous chromosomes in human and mice. *Proc Natl Acad Sci USA* 99, 2106-11
- Kühn C, Bennewitz J, Reinsch N, Xu N, Thomsen H, Looft C, Brockmann GA, Schwerin M, Weimann C, Hiendleder S, Erhardt G, Medjugorac I, Förster M, Brenig B, Reinhardt F, Reents R, Russ I, Averdunk G, Blümel J, Kalm E (2003) Quantitative trait loci mapping of functional traits in the German Holstein cattle population. *J Dairy Sci* 86, 360-8
- Manson JM, Naidu MD, Barcia M, Porti D, Chavan SS, Chu CC (2004) *IL-4-Induced Gene-1* is a Leukocyte L-Amino acid oxidase with an unusual acidic pH preference and lysosomal localization. *J Immunol* 173, 4561-7
- Womack JE, Johnson JS, Owens EK, Rexroad CE^{III}, Schläpfer J, Yang YP (1997) A whole-genome radiation hybrid panel for bovine gene mapping. *Mamm Genome* 8, 854-6

Received 6 March, accepted 4 May 2009.

Corresponding author:

Dr. TOM GOLDAMMER

email: tomgoldammer@fhn-dummerstorf.de

Research Unit Molecular Biology, Research Institute for the Biology of Farm Animals (FBN), Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany
