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Localization of the tryptophanyl tRNA synthetase gene (*WARS*) on human and bovine chromosomes by in situ hybridization

Alexander Graphodatsky,¹ Ludmila Frolova,² Larisa Biltueva,¹ Violetta Eremina,¹ Tamara Lushnikova,¹ Marina Sudomoina,² Olga Zinovieva,² and Lev Kisselev²

¹Laboratory of Animal Cytogenetics, Institute of Cytology and Genetics, Academy of Sciences, Siberian Branch, Novosibirsk, 630090, Russia; ²Engelhardt Institute of Molecular Biology, Academy of Sciences, Moscow, Russia

Received September 20, 1991; accepted October 30, 1992

Bovine tryptophanyl-tRNA synthetase (ECC 6.1.1.2.; *WARS*) is one of the best studied synthetases from multicellular organisms. Previous assignment of the *WARS* gene to the long arm of human Chromosome (Chr) 14 has been made by somatic cell hybrid techniques (Denney and Craig 1976; Shimizu et al. 1976). Francke and co-workers (1977) mapped it on 14q21-q32. We describe here the localization of the *WARS* gene to the bovine and human chromosomes with specific cDNA probes (Frolova et al. 1991) for in situ hybridization. Detailed protocols for the in situ hybridization, chromosome staining, and silver grain distribution analysis have been given previously (Graphodatsky et al. 1992). Standard nomenclatures of the human and cattle chromosomes were used (ISCN 1985; ISCNDA 1989).

Our results confirm the previously reported assignment of the tryptophanyl-tRNA synthetase gene to Chr 14 (Denney and Craig 1976; Shimizu et al. 1976; Francke et al. 1977). Twenty-four percent of all grains (202 grains from 104 total metaphases) were mapped on Chr 14 ($\chi^2 = 185.0$; $P < 0.001$). Sixty-three percent of the grains over Chr 14 were localized to the 14q23-q31 region; 33% to the 14q24 band. These results demonstrate the location of the *WARS* gene in the 14q23Lq31 region and presumably more precisely in the 14q24 band. Unexpected results were obtained with bovine chromosomes probed with cloned human cDNA. Thirteen percent of all the grains (353 grains per 103 metaphases) were mapped on Chr 3 ($\chi^2 = 53.6$; $P < 0.001$). However, these grains were not condensed in one locus but were concentrated in two separate loci: 38% of grains on BTA3 were found over the q11–q21 region and 36% over the q42–45 region.

Figure 1 shows the G- and RBG-banding patterns of cattle 3 (BTA3) Chr and human Chr 14 (HSA14).

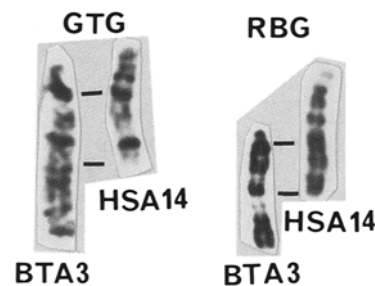


Fig. 1. A comparison of the GTF- and RBG-banding patterns of human Chr 14 (HSA14) and bovine Chr 3 (BTA3) in the region of possible homology.

The region within each chromosome with similar banding patterns is bordered. In the cow, the banding region is centromeric; in humans it is telomeric. This may represent a conserved region among human and cattle chromosomes, although additional genes must be mapped to determine real borders of this region.

Acknowledgments. This work was supported by research grants from the Russian Human Genome and Genetics Projects.

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