

## **Complex satellite DNA reshuffling in the cattle 1;29 translocation: A two-step model of the dynamic evolution of the 1;29 chromosome**

R. Chaves<sup>a</sup>, F. Adegas<sup>a</sup>, J.S. Heslop-Harrison<sup>b</sup>, H. Guedes-Pinto<sup>a</sup> and J. Wienberg<sup>c</sup>

<sup>a</sup>Center of Genetics and Biotechnology – CGB/UTAD, Vila Real (Portugal);

<sup>b</sup>Department of Biology, Leicester University, Leicester (UK);

<sup>c</sup>Institute of Human Genetics, Munich University, Munich (Germany)

We have analyzed and mapped satellite I, III (subunits pvu and sau) and IV DNA sequences in cattle using *in situ* hybridization. Four breeds (Alentejana, Barrosã, Mirandesa and Alistana-Sanabresa) were analyzed including 2n = 60 individuals and individuals with the widespread t(1;29) in the homozygous (2n = 58) and heterozygous state (2n = 59). All three satellite DNA families were mainly present at the centromeres of autosomes; but absent in the sex chromosomes. On the translocated chromosome t(1;29), the satellite DNA families displayed a different pattern from that expected simply by fusion of the acrocentric autosomes and loss of satellite sequences and showed no variation among breeds. Moreover, restriction enzyme banding with MspI revealed a polymorphism in the centromeric regions of 1;29 translocations in Barrosã breed, suggesting a recurrent origin for the translocation. Based on these results, a two-step model of the dynamic centromere evolution of the 1;29 translocation, is presented. Knowledge on mechanisms occurring at the centromere during translocation formation is essential, not only for the functional understanding of centromere and satellites, but also for the investigation of chromosomal abnormalities and understanding of the chromosomal fusion during evolution of other bovids.