

New insights into Bovidae satellite III evolutionary history

F. Adega¹, R. Chaves¹, J. Heslop-Harrison², J. Wienberg³ and H. Guedes-Pinto¹

¹Department of Genetics and Biotechnology, Centre of Genetics and Biotechnology, Vila Real, Portugal;

²Department of Biology, University of Leicester, UK; ³Institute of Human Genetics, University of Munich, Munich, Germany

Repeats like satellite DNA sequences constitutes a rich palaeontological record, holding crucial clues about evolutionary events. As in the others mammalian orders, the Bovidae centromere is greatly composed of satellite DNA families. Satellite 1.706 (satIII) is a long unit of 2350 bp composed of complex and altered repetitions of two related and homogeneous 23-mer tandem subrepeats, the Pvu and the Sau motifs. The scope of this work was the isolation, sequencing and analysis of the genome organization and physical distribution (by Southern Blot and Fluorescent *in situ* Hybridization) of these satellite sequences in several Bovidae species. The procedures used showed that the presence of this satellite family was not restricted to the Bovini (*Bos taurus*, *Bos indicus* and *Bubalus bubalis*), as described in previous works; instead we detected satellite III on the Tragelaphini (*Tragelaphus euryceros*). This ending could be revealing of an earlier appearance or formation of 1.706 satellite III DNA, prior to the Bovini and Tragelaphini divergence. Although the existence of satellite III in water buffalo (*Bubalus bubalis*) had been reported, it was noticed to only one autosomal pair. In the present work we were able to observe signal hybridization in the majority of the autosomes, and remarkably, in the sex chromosome X, in contrast with the absence of satIII in *Bos* chromosome X. These observations are revealing of a different evolutionary mechanism for the sex chromosome X of this species.