

1.2. 1.709 satellite IV DNA sequences evolution in the Bovini and Tragelaphini tribes – Molecular and cytogenetic analysis

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The centromeric satellite DNA of the Bovidae as well as the other mammals is organised as a complex of tandem repeats. Only closely related species share homologous satellite sequences. One of these satellite DNA families is the 1.709 satellite IV, who has no resemblance to other satellites and is considered by several authors as being the evolutionarily youngest repeat studied until now, only present in the Bovini tribe, having something about 5 MYBP. Previous studies of this sequence were made using, as probe, a PCR amplified product from cattle genome. Previous studies of this sequence were made using, as probe, a PCR amplified product from cattle genome. This probe was specifically hybridized (Southern blot / Fluorescent *In situ* Hybridization FISH) only to DNA or chromosomes of members of the tribe Bovini from all the Bovidae tribes analyzed.

The scope of this work was the isolation, cloning and sequencing of the 1.709 satellite IV DNA sequences from five species belonging to the tribes Bovini (*Bos taurus*, *Bos indicus* and *Bubalus bubalis*) and Tragelaphini (*Taurotragus oryx* and *Tragelaphus strepsiceros*) of the Bovidae family. The sequences were analyzed in terms of its genome organization, chromosome localization and distribution by Southern blot hybridization and FISH.

The differences at the molecular organization level and chromosome distribution between these five sequences and between species allowed us to make evolutionary and phylogenetic inferences.