

A FIRST SURVEY OF THE GENOMIC ORGANIZATION OF THE T-CELL RECEPTOR GAMMA LOCUS IN *TURSIOPS TRUNCATUS*

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The dolphin is one of the species whose genome is being sequenced as part of a comparative genomic analysis aimed to identify functional elements conserved across mammals.

The phylogenetic position of the bottlenose dolphin within the mammals is still uncertain, but recent molecular morphological and paleontological studies suggest that Cetacea share a close relationship with Artiodactyla, so it has been proposed that these two orders should be combined into a single new order, the Cetartiodactyla.

Artiodactyls (i.e. ruminants and pigs) occupy a particular immunological niche with regard to the cell-mediated immune response. They are defined “ $\gamma\delta$ high species”, referring to the high level (20 to 50%) of $\gamma\delta$ T cells present in blood rather than in epithelial cell-rich tissues. On the other hand, species such as human and mouse are “ $\gamma\delta$ low species” because only 5% of their peripheral T-cell pool is composed of $\gamma\delta$ T cells.

The wide and diversified repertoire of the $\gamma\delta$ chains certainly depends by the genomic organization of γ and δ loci.

In particular, the TRG locus of sheep and cattle, was apparently originated by reiterated duplication of functional gene cassettes, and is split into two cassette arrays localized in different chromosomal regions.

Here, we report data about the genomic TRG locus organization in dolphin.

The comparison of the sequence retrieved from HGSG Genome Data with human and cattle has resulted in two adjacent but non-contiguous contigs (96017 bp and 91079bp). The 5' and 3' boundaries of the locus are defined by the AMPHU and STARD3 genes and its putative length is at least 138 kb. Only two variable genes (TRGV) orthologous to human V9 and V11 are present in the first contig while three joining (TRGJ) and one constant (TRGC) genes orthologous to the sheep cassette C5, were found in the second contig.

Genome walking and Long PCR experiments indicate that the dolphin TRG locus is organized in a single V-J-C cassette. This gene organization is reminiscent of cattle and sheep, whose TRG loci consist, at each chromosomal region, of four or three tandemly repeated V-J-C cassettes, arranged in the same transcriptional orientation. The main difference between Bovidae and Cetacea we observed is the very low number of TRG genes found in dolphin.