

within the nuclear interior, while acquirement of a definite spatial chromatin configuration accompanies karyosphere formation in late oocytes. In contrast to interphase nucleus, germinal vesicles are enriched with polymerized actin. Intranuclear compartments were detected using antibodies against RNA-polymerase II, splicing factors, heterogeneous nuclear RNPs (hnRNPs) and coilin along with microinjections of fluorescently tagged RNAs. HnRNPs were found to concentrate within intranuclear domains corresponding to transcription units associated with specific chromosomal loci. It is noteworthy that in all avian species investigated, with the only exception of pigeon, the germinal vesicles do not reveal any extrachromosomal RNA-enriched domains. It seems to be an exclusive example of transcriptionally active nucleus lacking such a universal subnuclear structure as Cajal body. In chicken oocytes, the absence of Cajal bodies was found to correlate with ribosomal and histone gene inactivation. Nucleolated cells of follicular epithelium surrounding oocytes comprise Cajal bodies and SC35-domains. This work was supported by RFBR (project 08-04-01328-à).

O11

Genomic organization of *Camelus dromedarius* TRD locus as drawn from the T-cell receptor delta chain repertoire

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The dromedary or one-humped camel has been considered as one of the most popular domesticated animal in North African, Middle East and in South American countries. The productive potential of this species as sources for milk, meat and wool together with its suitability for transport highlight its socio-economic value.

The literature on the dromedary is scarcely compared with other domestic animals. Even the relative phylogenetic placement of *Camelidae* within Cetartiodactyla remains unresolved.

However, *Camelidae* species occupy an important immunological niche within the humoral immune response. As a matter of fact, these animals contain in their serum a unique class of antibodies that lack L-chain, in addition to the conventional antibodies. The functional properties of the Heavy-chain-only antibodies are of fundamental

interest for the engineering of the antigen-binding subunits of the human antibodies.

On this scenario, we started investigating the dromedary TRD genes, which are involved in cell mediated-immunity. To identify the delta chain repertoire, studies on RNA from different lymphoid tissues were performed. Results on *Variable*, *Joining* and *Constant* genes allowed us to deduce the TRD locus genomic organization. Our preliminary data seem to confirm the *Camelus dromedarius* as an outstanding model for the immune system.

O12

An extended river buffalo (*Bubalus bubalis*, 2n=50) cytogenetic map: assignment of 68 new autosomal loci by FISH-mapping and R-banding, and comparative mapping with human chromosomes

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An extended river buffalo (*Bubalus bubalis*, 2n = 50) cytogenetic map with 388 loci is reported, including 68 new autosomal loci that were assigned in the present study by fluorescent *in situ* hybridisation (FISH). Ovine and caprine BAC clones containing both type I (known genes) and type II (SSRs/microsatellite marker/STSs) loci, previously assigned to sheep chromosomes, were FISH-mapped on R-banded river buffalo chromosomes (BBU), thus expanding the cytogenetic map of this important domestic species and increasing our knowledge on the physical organization of the genome. Loci mapped in the present study were also localized on homologous cattle and sheep chromosomes and chromosome bands, further confirming the high degree of conserved synteny among bovids. Comparison between integrated cytogenetic maps of BBU2p/BBU10 and BBU5p/BBU16 with HSA6 and HSA11, respectively, identified at least 9 conserved chromosome segments among species along with complex rearrangements differentiating river buffalo and cattle from human chromosomes.