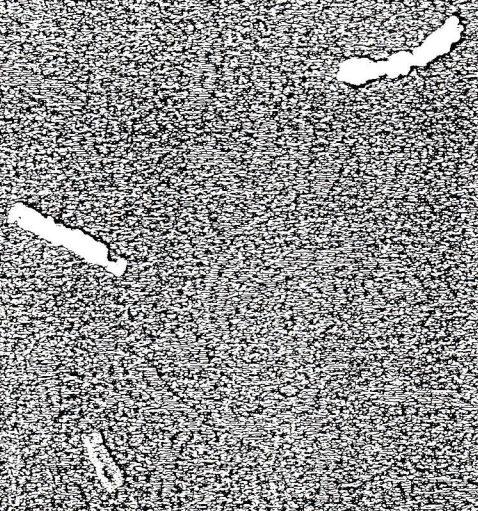
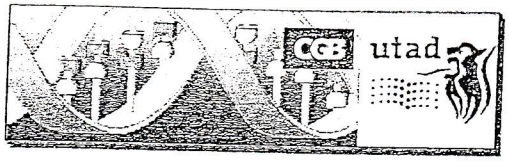
17th European Colloquium on Animal Cytogenetics and Gene Mapping

Book of Abstracts



18-21 June 2006

Auditorium of Calouste Gulbenkian Foundation, Lisbon, Portugal



CENTRE OF GENETICS AND BIOTECHNOLOGY
OF THE UNIVERSITY OD TRAS-OS-MONTES AND ALTO DOURO

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Lisbon, Portugal**

POSTERS SESSION

"Gene Mapping and Chromosome Maps"

P1

Cytogenetic localization of *FMR1* gene in farm animals

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We have localized trinucleotide repeats of the *FRMI* gene in cattle, sheep and pigs karyotypes using in situ PCR method with primers flanking CCG repeats located in the 5'UTR regulatory region of the human FMR1 mRNA. The primers: GCTCAGCTCCGTTTCGGTTTCACTTCCCG T (forward) and AGCCCCGCACTTCCACCACCAGCTCCTCC A (reverse) were used for in situ PCR and biotin-16 dUTP labeling of CGG containing *FRMI* gene fragment (1 cycle: 94° C - 3 min, 65° C – 1 min, 72° C – 1 min; 30 cycles: 94° C – 1 min, 65° C – 1 min, 72° C – 1 min) on QFQ- and GTG-banded metaphase chromosomes slides. Fluorescent amplification signals were detected by avidin-conjugated FITC and mapped on cattle, sheep and pig X chromosome at BTA Xp13, OAR Xq22 and SSC Xq26 regions, respectively.

In conclusion, the results obtained suggest that there are similarities of regulatory sequences in CGG region of *FRMI* gene in different species. The identified locus-specific sequence can be applied in comparative and evolutionary studies.

This work was conducted as part of NRIAP statutory activity, project no. 3210.1

P2

Karyotyping prometaphase chromosomes of alpaca (*Lama pacos*, family *Camelidae*)

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As known, the alpaca (*Lama pacos,2n=74,XY*) belongs to the family Camelidae, suborder Tylopoda, which includes the vicugna (*Lama vicugna*), llama (*Lama glama*), guanaco (*Lama guanicoe*) and the two camels, bactrian (*Camelus bactrianus)* and dromedary (*Camelus dromedarius*). Despite the increasing worldwide economical interest in the peculiar characteristics of its wool (extremely fine, unallergic and naturally stained), the alpaca species has been –so far- almost forgotten from a cytogenetic point of view. In order to contribute to the clarification of the chromosomal constitution of this species, we decided to undertake a detailed cytogenetic investigation, thus providing, for the first time, the QFQ-C-GTG-RBG and RBA banded karyotypes and the GTG-RBG ideograms, at a resolution of nearly 400 bands. Based on centromeric index and relative chromosome length measurements, the alpaca karyotype can been arranged in four groups of chromosomes, as follows: group A, subtelocentrics, from pair 1 to 10; group B, telocentrics, from pair 11 to 20; group C, submetacentrics, from pair 21 to 29; group D, metacentrics, from pair 30 to 36. Six pairs of nucleolar organizer chromosomes have been also identified by using a sequential RBA/silver staining technique as n. 6 (A group), 28 (C group), 31, 32, 33 and 34 (D group). The

present karyotypes and the GTG/RBG-banded ideograms can be used for clinical cytogenetics, karyotype standardization, gene mapping, cytotaxonomy, comparative studies and genetic improvement programs within the family Camelidae.

P3
Chromosomal mapping of ribosomal genes in venerid clams (Bivalvia: Veneridae)

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The family Veneridae is a group of bivalve molluscs found in all the world seas. Although the family includes some 500 species, many of which are of commercial importance and subjected to intensive exploitation, no data on chromosomal mapping of DNA sequences on species of Veneridae was reported to date.
In order to localize both the major and the 5S rDNA gene clusters, fluorescent *in situ* hybridization (FISH) experiments were performed on mitotic chromosomes and surface spread synaptonemal complexes of the venerid clams *Dosinia exoleta*, *Ruditapes decussatus*, *Ruditapes phillipinarum* and *Venerupis pullastra*. Species specific probes were generated by PCR amplification of both the internal transcribed spacers and the 5.8 rDNA of the major rDNA gene cluster and the whole repeat unit of the 5S rDNA cluster.
The repeats of the major rDNA genes are clustered in only one chromosome pair in all the species analyzed, the NOR is terminal in two of the species and intercalary in the other two. The also unique 5S rDNA gene cluster appears - intercalary or terminal - in a different chromosome pair in three of the four clam species but co-localizes with the major rDNA cluster in *Ruditapes decussatus*. The co-location was confirmed by FISH on extended chromatin fibres.

P4
Recurent airway obstruction (RAO) in horse: chromosomal an RH mapping of three candidate genes

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Recurrent airway obstruction (RAO) of the horse is likely a polygenetic disorder and shares many characteristic features with human asthma and chronic obstructive pulmonary disease (COPD). RAO and asthma are characterized by airway bronchospasm, coughing, airway hyperreactivity, inflammation and mucus accumulation. Select genes: *EGFR, CLCA1, BLC2* are of interest in respiratory disorders with chronic mucus overproduction, including asthma. In our study, we mapped these four genes by FISH on equine metaphase spreads. Equine BAC librarys (CHORI, INRA) were screened with equine gene-specific primers and positive clones were labelled with digoxigenin and then used for FISH on GTG-banded chromosomes. The BAC clones harbouring these three genes were mapped to the following chromosomes: *EGFR*- ECA4p12, *CLCA1*-ECA5q15, *BLC2*-ECA8q22. Additionally, we confirmed the results with the RH-mapping on the TAMU radiation hybrid panel. The mapping data, which confirm the established conservation of synteny between equine and human chromosomes, provide a resource for further association studies of these genes in equine RAO.