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Comparative FISH-mapping of *TNF*, *STAT5A* and *MNTR1A* fecundity genes on river buffalo, cattle, sheep and goat

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The aim of "CISIA" project, funded by National Research Council, was to improve the valorization and sustainability of Southern Italy agrifood products. One of the area of application of this project is to genotype Mediterranean Italian Buffaloes breeding in order to detect the genes involved in fertility and reproductive seasonality. For this reason, our contribute to this project has been to perform physical maps using bovine artificial chromosomes (BAC) clones containing genes related to fecundity. BACs were selected taking in account the data available on the Bov Map database (http://locus.jouy.inra.fr/cgibin/bovmap/intro2.pl), considering their physical position and the data obtained from banding experiments. Fluorescent in situ hybridization (FISH) was performed on three gene sequences: tumor necrosis factor-α (TNF), correlated to male fertility; signal transducer and activator of transcription 5A (STAT5A) important for its influence on milk production and reproduction activity; melatonin receptor 1A (MNTR1A) important for reproductive seasonality. BAC probes were hybridized on RB-banded of river buffalo (*Bubalus bubalis*, 2n=50, BBU), for the first time and to relate bovid species: cattle (Agerolese breed), sheep (Laticauda breed) and goat (Cilentana breed). TNF was assigned to BTA/CHI23q21-22, OAR20q21-22 and BBU 2p21-22; STAT5A was assigned to BTA/CHI19q17-21, OAR11q17-21 and BBU3p15-21; MTNR1A was assigned to BTA/CHI27q14-15, OAR11q17-21 and BBU1p21-22, underling the high degree of chromosome homologies among Bovids and extending the cytogenetic maps of this economically important species.

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Phylogenetic reconstruction in Phyllostomini tribe (*Chiroptera, Phyllost*omidae) based on cross-species chromosome painting

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Phyllostominae presents different rates of chromosomal evolution between genera, with *Phyllostomus* probably retaining the ancestral karyotype for this subfamily. We performed multi-directional chromosome painting, hybridizing whole chromosome paint probes from *Carollia brevicauda* (CBR) and *Phyllostomus hastatus* (PHA) onto chromosomes of *Lophostoma silvicola* (LSI, 2n=34, FN=60), *Phyllostomus discolor* (PDI, 2n=32, FN=60) and *Tonatia saurophila* (TSA, 2n=16, FN=20) from tribe Phyllostomini of Amazon region, to reconstruct the phylogenetic relationships within this tribe. LSI has 2n=34, FN=60; PDI has 2n=32, FN=60; TSA has 2n=16, FN=20. Comparative analysis using G-banding and chromosome painting show that the karyotypic complement of TSA is highly rearranged relative to LSI, PHA, while LSI, PHA and PDI have similar karyotypes, differing by only three chromosome pairs. Nearly all chromosomes of PDI and PHA were conserved in toto, except for chromosome 15 that changed by a pericentric inversion. A strongly supported phylogeny (bootstrap=100), confirms the monophyly of Phyllostomini. In agreement with molecular topologies, TSA was in basal position, while PHA and LSI formed sister taxa. A few ancestral syntenies are