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This is the author's manuscript

Original Citation:

Availability:

This version is available <http://hdl.handle.net/2318/150207> since

Published version:

DOI:10.1007/s10577-014-9435-7

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UNIVERSITÀ DEGLI STUDI DI TORINO

The final publication is available at Springer via <http://dx.doi.org/10.1007/s10577-014-9435-7>

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/cgi-bin/bovmmap/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.

Acknowledgements. This study was in part supported by CISIA-VARIGEAV project and in part by RARECA-project, PSR, Misure 214 e2 of Campania region.