Poster

Preliminary comparative RH mapping between river buffalo chromosome 6 (BBU6) and bovine chromosome 3 (BTA3)

N. Bonvino Stafuzza¹, P. Ianella¹, M. Nunes Miziara¹, R. Agarwala², A.A. Schäffer², P. K. Riggs³, J.E. Womack⁴, M.E.J. Amaral¹

 ¹UNESP - São Paulo State University, IBILCE, Dept. Biologia, São Jose Rio Preto, Brazil
²National Center for Biotechnology Information, National Institutes of Health, Department of Health and Human Services, Bethesda, Maryland, USA

³Department of Animal Science, Texas A&M University, College Station, TX, USA ⁴Department of Veterinary Pathobiology, Texas A&M University, College Station, USA

Corresponding author: M.E.J. Amaral, Universidade Estadual Paulista (UNESP-São José do Rio Preto, São Paulo, Brazil). E-mail: eamaral@ibilce.unesp.br

ABSTRACT: We present the first radiation hybrid map of BBU6 developed from a recently constructed river buffalo whole-genome radiation hybrid panel (BBURH $_{5000}$). The preliminary map contains 33 cattle-derived markers, including 12 microsatellites, 19 coding genes and two ESTs, distributed in two linkage groups. The retention frequency of individual markers ranged from 14.4% to 40.0%. Most of the marker order within the linkage groups is consistent with the cattle sequence and RH maps. This preliminary BBU6 RH map is the starting point for comparing gene order between both species, presenting an opportunity for examination of micro-rearrangements of these chromosomes and, thereby enhancing the possibility of positional candidate cloning in river buffalo.