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Poster Abstract - F.27

THE ROB(1;29) IN CATTLE: INCIDENCE IN SOME ITALIAN AND PORTUGUESE CATTLE AND POSSIBLE ORIGIN AS DEMONSTRATED BY BOTH HIGH RESOLUTION CHROMOSOME BANDING AND DUAL-COLOUR FISH WITH SPECIFIC MOLECULAR MARKERS

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Autosomal numerical aberrations have a few importance in the animal breeding since the carriers have an abnormal body conformation and are directly eliminated by the breeders. Sex numerical and structural (balanced) chromosome abnormalities are more tolerate by the species but, very often, are correlated with reduced fertility or sterility. These abnormalities escape the normal breeding selection because the body conformation is generally normal and, without a cytogenetic control, can easily been spread in the progeny, especially when artificial insemination is applied. Centric fusions translocations are the most common chromosome abnormalities in cattle, especially in meat breeds. In particular, that involving chromosomes 1 and 29 has been found in more than 70 different breeds in all the world with different frequencies, reaching 70% of carriers in Barrosa breed (Portugal).

In this study we show the frequency of this translocation in some Italian and Portuguese cattle breeds and its impact on the reproduction. Furthermore, by combining both high resolution chromosome banding and the dual-colour FISH technique with specific markers, we demonstrated that: (**a**) this translocation is of ancient origin being monocentric; (**b**) it occurred by apparent loss of the centromere of chromosome 29 and retention of that of chromosome 1, as revealed by C- R- and G-banding techniques; (**c**) the translocation originated by complex chromosome rearrangements is different step which required centric fusions, pericentric inversions or transpositions with loss of heterochromatic material as demonstrated by the use of specific chromosome markers of BTA29 (*INRA143*) and bovine satellites I, III and IV. The possible role of this famous chromosome polymorphism in cattle as a possible evolutionary mechanism which tries to reduce the diploid number from 60 to 58 so to obtain new genetic advantages derived from both the new genetic linkage between syntenic groups U10 (BTA1) and U7 (BTA29) and the chromosome rearrangements occurred in the pericentromeric regions, is discussed in light of other species (*sheep, river buffalo*) which used the centric fusion translocations as autosome evolutionary mechanism.