

## **Cytogenetic characterization, frequency and distribution of rob t(1;29) in some Italian and Portuguese cattle breeds**

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Since the discovery of rob t(1;29) (Gustavsson and Rockborn, 1964) and the demonstration of its deleterious effects on fertility (Gustavsson, 1969), it had been widely detected in more than 50 different cattle breeds (Popescu and Pech, 1991), especially in meat breeds. To date, although studies on this translocation have drastically been reduced in the last 15 years because of concentrated interest in gene mapping, they have shown an increase in the number of breeds carrying this translocation. In addition, despite various studies to characterize this common abnormality, its evolution is not completely understood. Indeed, the large block of constitutive heterochromatin (HC) almost entirely concentrated in the proximal region of the rob t(1;29) q-arm, does not agree with C-banding patterns of other centric fusion translocations in sheep and river buffalo showing very small amounts of HC. This suggests that the cattle rob t(1;29) is still evolving by progressive HC reduction. The lack of HC in the p-arm of rob t(1;29) suggests a loss of HC (and centromere) of BTA29, as demonstrated by GBA + CBA-banding, while the large block of HC in the q-arm suggests retention of HC. Previous FISH mapping studies with D29S16 (INRA143, marker of BTA29 proximal region), on chromosomes from a rob t(1;29) carrier revealed the presence of FITC-signals on the proximal q-arm region suggesting a

possible pericentric inversion following the centric fusion event (Eggen et al., 1994). We have confirmed this observation in different carriers from different breeds by FISH with the same probe although with varied positions of FITC signals from the centromere to the proximal q-arm region, possibly due to HC polymorphism. However, FISH-mapping to river buffalo chromosomes with D29S16 revealed clear FITC signals on the proximal region of BBU5p (homoeologous to BTA29). This demonstrates that these two biarmed chromosomes (BBU5 and cattle rob t(1;29)) have evolved differently, although cattle rob t(1;29) evolution is still proceeding. A recent study with molecular markers containing three different types of satellite DNA (I, III and IV) suggested a two-step model of dynamic evolution of rob t(1;29): first, a rcp between BTA1 satellite III and BTA29 satellite IV, followed by the loss of segments containing BTA1 satellite I and some BTA29 satellite III and IV repeats and second, elimination of the satellite I block from an intermediate chromosome form (Chaves et al., 2003). Data on the frequency and distribution of rob t(1;29) in some Italian and Portuguese cattle breeds is also reported.