

## **Geographic distribution and frequency of a taurine *Bos taurus* and an indicine *Bos indicus* Y specific allele amongst sub-Saharan African cattle breeds**

Hanotte, O.; Tawah, C.L.; Bradley, D.G.; Okomo, M.; Ochieng, J.; Rege, J.E.O.

Date: 2000

### **Abstract**

We report for the first time, and for the whole of sub-Saharan Africa, the geographical distribution and the frequency of an indicine and a taurine Y specific allele amongst African cattle breeds. A total of 984 males from 69 indigenous African populations from 22 countries were analysed at the microsatellite locus INRA 124. The taurine allele is probably the oldest one on the continent. However, the taurine and the indicine alleles were present in 291 males (30%), and 693 males (70%), respectively. More particularly, 96% of zebu males (n = 470), 50% of taurine males (n = 263), 29% of sanga males (crossbreed *Bos taurus* × *Bos indicus*, n = 263) and 95% of zebu × sanga crossbred males (n = 56) had the indicine allele. The Borgou, a breed classified as zebu × taurine cross showed only the zebu allele (n = 12). The indicine allele dominates today in the Abyssinian region, a large part of the Lake Victoria region and the sahelian belt of West Africa. All the sanga males (n = 64) but only one from the Abyssinian region had the indicine allele. The taurine allele is the commonest only among the sanga breeds of the southern African region and the trypanotolerant taurine breeds of West Africa. In West Africa and in the southern Africa regions, zones of introgression were detected with breeds showing both Y chromosome alleles. Our data also reveal a pattern of male zebu introgression in Mozambique and Zimbabwe, probably originating from the Mozambique coast. The sanga cattle from the Lake Victoria region and the Kuri cattle of Lake Chad, cattle populations surrounded by zebu breeds were, surprisingly, completely devoid of the indicine allele. Human migration, phenotypic preferences by the pastoralists, adaptation to specific habitats and to specific diseases are the main factors explaining the present-day distribution of the alleles in sub-Saharan Africa.