Analysis of *B. taurus* and *B. indicus* admixture in Uganda as revealed by the Illumina BovineSNP50 Genotyping BeadChip.

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Introduction

The NextGen project investigates disease resistance in indigenous Ugandan cattle. Since population structure and stratification may produce biased results, we have investigated the genomic structure of sampled animals genotyped with the BovineSNP50 Genotyping Beadchip.

Materials & Methods

A total of 788 animals from 9 populations belonging to Ankole (crossbred between *B. indicus* and *B. taurus*), Zebu and Ankole-Zebu crosses have been sampled in 52 grid cells throughout the country (Table 1). We merged this data with other 400 Italian Holstein Cattle, genotyped in the framework of SELMOL project to seek for a likely introgression of European *B. taurus*. The data were filtered with the following exclusion criteria: MAF < 0.01, genotype call rate (Animals) < 0.95, genotype call rate (SNPs) < 0.95. The resulting working dataset were composed of 43494 SNPs and 1188 animals. Hidden genetic structures were investigated by a Bayesian clustering approach with the ADMIXTURE software (Novembre et al. 2010).

Results

The software Admixture identified four ancestral genomic components. Three of them likely correspond to European *B. taurus* (in blue) in Ugandan cattle sampled. Panel K=3) and 4 groups (Fig.2) of individuals under the assumption of Hardy-Weinberg equilibrium. Panel b) highlights the contribution of the average geographical area in the East (Fig.3).

Conclusions

The Ugandan cattle population is a complex admixture of African taurine (green in Figure 2) and zebuine (red) genomes, with a minor component of European origin (blue) and a rare but relevant contribution (yellow) from a still unidentified source. This complexity is to be accounted for in the following GWAS and selection signatures analyses planned within the NextGen project.