



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.

Aim of the research: Identify the rate of admixture in Ugandan Cattle using 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 \leq 0.01, genotype call rate (SNPs) \leq 0.95, genotype call rate (Animals) \leq 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).

Tab.1: Number of Animals sampled per Breed and relative acronym.

Species	Acronym	Origin	Subgroups	Sample size
<i>Bos indicus</i>	EAZ	Uganda	East African Shorthorn Zebu	133
<i>Bos indicus</i>	SEZ	Uganda	Small East African Zebu	64
<i>Bos indicus</i>	SHZ	Uganda	Shorthorn Zebu	210
Cross	NGA	Uganda	Nganda	37
Cross	AZC	Uganda	Ankole Zebu cross	10
<i>Bos taurus</i>	NKI	Uganda	Nkiga	27
<i>Bos taurus</i>	NSO	Uganda	Nsongora	10
<i>Bos taurus</i>	NTO	Uganda	Ntoro	10
<i>Bos taurus</i>	ANK	Uganda	Ankole	287
<i>Bos taurus</i>	FRI	Italy	Italian Holstein	400

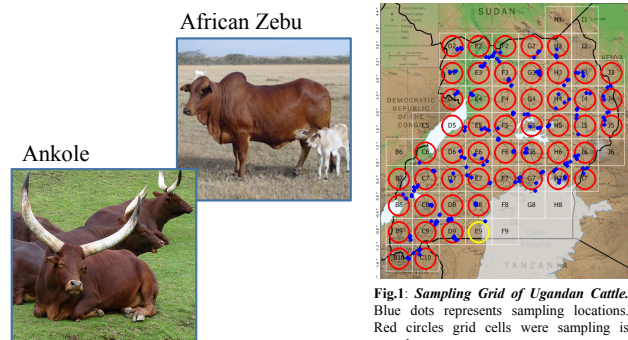


Fig.1: Sampling Grid of Ugandan Cattle. Blue dots represents sampling locations. Red circles grid cells were sampling is complete.

Results

The software Admixture identified four ancestral genomic components. Three of them likely correspond to European taurine, African indicine and African taurine components (Figure 2). The fourth has a still unidentified origin (Yellow, Figure 2d). Most Ugandan individuals investigated have a remarkable level of admixture. Overall, about 20% of the Zebu genome is of African taurine origin, confirming previous data on the foundation of African Zebu. The European taurine (Blue, Figure 2) is a minor component of African genomes, rare in Zebu and evenly distributed in Ankole, other taurine subgroups and Ankole-Zebu crosses. Indicine and taurine components show a clear geographical structure, the former being predominant in north-eastern Uganda, and the latter in the south-west. Holstein Friesian introgression is spread mostly in south-western Uganda, while the fourth component is located in restricted geographical area in the East (Figure 3).

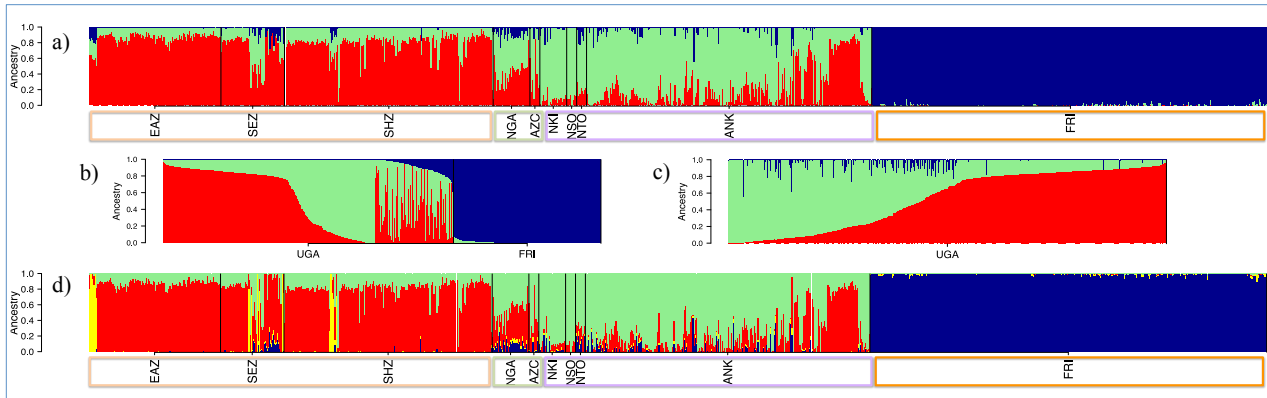


Fig.2: Bayesian assignment test (Admixture software). The picture shows the results of the assignment test obtained by hypothesizing the existence of 3 (a, K=3) and 4 groups (d, K=4) of individuals under the assumption of Hardy-Weinberg equilibrium. Panel b highlights the contribution of the genomic component of European origin (in blue) in Ugandan cattle sampled. Panel c highlights the contribution of the indicine component (in red).

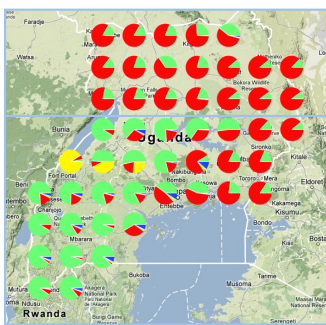


Fig.3: Geographical representation of individual Q score values obtained with Admixture software (4 pseudo populations hypothesized; Figure 2d) and averaged per sampling cell.

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.

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