Towards a complete genome characterization of all African indigenous cattle

*An initiative of the dairy genomics program of CTLGH
*A strategic alliance of ILRI, Roslin Institute, SRUC and African research partners
*Aims to facilitate the generation of a collated set of sequences and genotype information on African cattle
*For use by African and international research and breeding communities in cattle genomics for the ultimate benefit of African livestock keepers
*Facilitate the capacity building of African researchers in the field of genomics
*More partners especially from North and South of Africa are welcome
*Signed MTA and country ABS permit are required

**Project Objectives**

We aim to develop a genomic reference resource for African cattle through a consortium of African partners. Our current objectives include:

- Identification of most informative SNPs for designing African reference SNP genotyping arrays
- Identification of selection signatures underpinning adaptation and productivity traits
- Pan-genome analyses of African cattle including de novo sequencing and transcriptomic analyses
- Facilitate bioinformatics capacity building among African Scientists

**Expected outcome**

- Design of tailored African SNP array(s)
- Define and characterize important cattle adaptability, resilient and productivity traits
- Project consortium, database and website
- Bioinformatics trainings targeted at African partners

**Project update**

- 13 African partners, 40 African cattle breeds and about 1500 samples (Figure A)
- Whole genome sequences of up to 380 samples is already in our database and the generation of new sequences is on-going
- Sequences are being mapped to the latest reference genome assembly (ARS-UCD1.2) for variants discovery and further analyses
- About 38 million SNPs identified in 346 samples and PCA of these samples shown in Figure B