Genetic structure of the African Buffalo, based on SNP markers

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Over the last decades, phylogeography and population genetic studies were mainly based on the study of the variation between nucleotide sequence(s) or in the number of nucleotide repeats. Within the African buffalo (*Syncerus caffer*), both mtDNA fragment and microsatellites were used to resolve population structure and to investigate the evolutionary history of the species at different spatio-temporal scale (i.e., continental and regional).

With the advent of Next-Generation Sequencing technologies, large-scale sequencing and identification of large sets of single nucleotide polymorphism from library-construction became possible. In the present study, the ‘Genotyping-by-Sequencing’ (GBS) technic was applied on 450 samples of African buffalo spread all over its distribution range (sub-Sahara). The African buffalo being a non-model species, the use of a closely related species genome (*Bos taurus*) to map the reads (64bp) and identify nucleotide variations was the best approach.

Population structure analyses and demographic parameters estimations were based on 42,643 SNPs. Clustering analyses revealed a structuring of 8 populations at the continental scale, with low levels of genetic differentiation, indicative of high historical gene flow. Population fragmentation impact was evaluated using different indices. The confinement within protected areas, obstructing natural migrations, was shown to have impacted the African buffalo genetic health. Those results are particularly of conservation concern, as the management of genetically distinct populations can increase species-wide resilience. The resolution of SNPs and microsatellites will be also discussed in light of the recent results obtained with both datasets on the same set of samples.