Population genomics of the Cape buffalo subspecies (*Syncerus caffer caffer*) of the Southern African region based on SNP markers

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Recent phylogeographical and population genetic studies on the African buffalo (*Syncerus caffer*) have revealed a complex population structure both at continental and regional scales. These studies were mainly focused on the analysis of the genetic variations of mtDNA amplicons and microsatellites molecular markers. With the advances 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) technology was applied on 450 samples of African buffaloes spread all over its distribution range (sub-Sahara), including a more intensive sampling in Southern African regions (Mozambique, South Africa, Zimbabwe, Zambia and Botswana). The African buffalo being a non-model organism, the use of a closely related species genome (*Bos taurus*) to map the reads (64bp) and identify nucleotide variations was the most reliable approach. Population structure analyses and demographic parameters estimations were based on 42,643 identified SNPs. Clustering analyses revealed a structuring into 8 populations at the continental scale, with low levels of genetic differentiation, indicative of high historical gene flow. Population fragmentation impact in the Southern African region was evaluated using different indices. The confinement within protected areas, obstructing natural migrations, was shown to have impacted some of these populations. Those results are particularly of conservation concern, as the management of genetically distinct populations can increase species-wide resilience. The resolution of the results obtained with SNPs and microsatellites will be also discussed, based on datasets obtained from the same set of samples.