

Balancing Conservation and Production: A Molecular Genetic Approach in Aid of Buffalo Ranching

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ABSTRACT: In order to ensure sustainability the commercial ranching of Cape buffalo in South Africa requires strategies aimed at addressing both conservation and production priorities. Breeding and management practices are generally characterised by anthropological interventions, which may affect the population dynamics and subsequently vital genetic parameters such as level of genetic variation and effective population size, both of which are vital when devising management strategies for ranched populations. The ranching industry is also moving towards increasing production efficiency by improving traits of economic and biological importance. This requires scientifically sound practices for the recording of performance traits. Currently, however the industry lacks phenotypic, genotypic and pedigree data which form the basis for estimating the genetic merit of an animal regarding a particular trait. The suitability of DNA markers for complementing existing strategies associated with ranching of wild African buffalo is collated in this review.

Keywords: Buffalo; Genetics; ranching

Introduction

South Africa has more than 20 million hectares of commercial wildlife ranches, contributing significantly to the economy of the country (Dry, 2012). Ranching with Cape buffalo (*Syncerus caffer caffer*), one of the focal species of the industry, is accompanied by certain challenges, including the fact that they are host to diseases such as bovine tuberculosis (Disease Risk Management Directive 2002) and the fact that baseline information regarding population genetic parameters is lacking (Greyling, 2013). Breeding on ranches is to a certain extent also mediated through management, often focusing on market desired phenotypes of economic importance. More recently, buffalo ranchers have expressed their interest in using performance testing to identify genetically superior animals, similar to what has become an established practice among cattle breeders worldwide. In this regard the application of DNA-based technologies exhibit enormous potential. The impact that the incorporation of different types of information has on breeding strategies is shown in Figure 1.

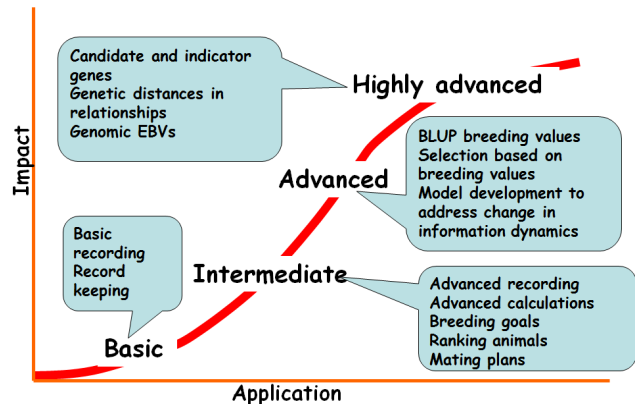


Figure 1. A graphical illustration of the impact that different types of information have on the advancement of breeding strategies.

While basic recording builds the foundation for genetic improvement, the impact of incorporating additional information from different sources elevates the impact on genetic improvement. The aim of this paper is to highlight the application of DNA technology in studies pertaining to the African buffalo and to propose an approach for using the technology to address the needs and challenges experienced by the buffalo ranching industry.

Materials and Methods

A range of DNA markers, including microsatellites, mitochondrial DNA sequences and more recently single nucleotide polymorphisms (SNP's), have been used for assessing the following genetic aspects within and among buffalo populations:

- Levels of genetic variation and inbreeding
- Degree of population differentiation and gene flow between populations
- Effective population size
- Admixture and hybridization
- Heterozygosity-fitness correlations
- Gene regulation and expression in response to environment
- Random match probability for traceability and forensic purposes

Table 1. Markers and their primary application in genetic studies of the African buffalo

Marker type	Primary application	Reference	Main outcome
MHC complex	Genetic variation	2	High genetic variation
Autosomal Microsatellites	Genetic variation population differentiation Traceability Forensics Individual relatedness Heterozygote fitness correlations	3, 4, 5, 6, 7, 8	Little variation in small selected populations; significant variation but little differentiation among large populations; male biased gene flow, heterozygosity correlated with body condition
Y-chromosomal microsatellites	Phylogeography Gene regulation in response to environment	9, 10.	Origin and expansion of subspecies; sex ratio distortion correlated with body condition; selection on Y-chromosome in response to rainfall
mtDNA sequences	Phylogenetics Phylogeography Herd level differentiation Gene flow	6, 11	Little differentiation between herds; male biased gene flow; West and Central African population differentiated from East and Southern African population
SNP's	BTB association studies	12, 13	SNP's identified for African buffalo; SNP's associated with Bovine Tuberculosis infection

²Wenink et al, 1998, ³O'Ryan et al, 1998, ⁴Simonsen et al, 1998, ⁵Greyling et al, 2008, ⁶van Hooft et al, 2003, ⁷van Hooft et al, 2000, ⁸van Hooft et al, 2014 (submitted), ⁹van Hooft et al, 2007, ¹⁰van Hooft et al, 2010, ¹¹Smitz et al, 2013, ¹²le Roex et al, 2013, ¹³le Roex et al, 2012.

- Levels of relatedness between individuals, including paternity verification
- Genetic variants associated with phenotypic traits

While most studies focused on population differentiation and genetic variation (Table 1), more recent developments include the identification of single nucleotide polymorphisms (le Roex et al., 2012) for buffalo that are associated with resistance to bovine tuberculosis (le Roex et al., 2013).

Results and Discussion

Studies using DNA markers have contributed immensely to our understanding of the factors that affect the dynamics of population genetics of the African buffalo (Table 1). Recent trends in the ranching industry however created a drive for selection based on improved production, which necessitates the development of technologies and models, similar to that used by the cattle breeding industry. SNP data has now emerged that enables potential target breeding, e.g. BTB (bovine tuberculosis) resistance. Marker assisted selection can fast track targeted genetic improvement and has been shown to be a viable option for the genetic improvement of domesticated livestock. Except for BTB resistance, no studies have yet investigated or identified genetic variants associated with quantitative traits of economic importance. Full genome sequencing is however already underway for Cape buffalo and will lay the foundation for the identification of markers associated with traits of importance. In view of the developments over the past few years, a number of ranchers have initiated basic recording practises (including pedigrees) aimed at developing a

system for the quantification of the genetic merit of their breeding stock.

Conclusions

Insights gained through large scale population genetic studies of Cape buffalo have potential beneficial applications for improved conservation- and production management of ranched populations. However, prior to embarking on genetic improvement strategies, basic recording of phenotypes and pedigrees needs to be available. The latter will also be a prerequisite when genome-wide association studies are attempted in future.

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