A lack of genetic variation in commercially bred Nile crocodiles (*Crocodylus niloticus*) in the North-West Province of South Africa

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Abstract

Although much is known about the genetic variation of crocodilians, very little is known about the levels of variation in Nile crocodiles. The purpose of this study was to compare the low levels of genetic variation reported for wild crocodile species with levels in 50 sub-adult crocodiles bred for commercial utilisation. Gene products of 52 protein-coding loci in *Crocodylus niloticus* were examined by horizontal starch gel electrophoresis. No detectable genetic variation was observed at any of these loci, which possibly indicates captive inbreeding or represents the natural state of the wild population where the breeding stock was captured. Possible explanations for this unexpected result are discussed.

Introduction

The Nile crocodile is endemic to Africa and has been classified as vulnerable in the *South African Red Data Book* for reptiles and amphibians (Branch, 1988). Populations of crocodiles have been severely depleted in recent years due primarily to the reduction of riverine habitat induced by the construction of dams, weirs and irrigation schemes (Jacobsen, 1988). This, along with the flooding of nesting banks, pollution of water sources and competition with man due to incompatibility with livestock farming has led to the fragmentation of breeding populations and a subsequent decrease in hatchling numbers (Jacobsen, 1988). Although poaching is no longer considered a threat (Blake and Jacobsen, 1992), some crocodiles are still poached from reserves either for their skins or for traditional medicine (Leslie, 1997). In 1992, there were only an estimated 8 000 Nile crocodiles remaining in the wild in South Africa.

The Nile crocodile is of considerable economic importance as its hide is in great demand in the leather trade (Patterson, 1987). More recently, the flesh of the crocodile has become a gourmet dish, highly valued both in South Africa and abroad. In 1992, the Convention on International Trade in Endangered Species of the World Fauna and Flora (CITES) downlisted South Africa to Appendix II (Mulder, 1992). This made trade in captive-bred crocodile products legal. The increasing demand for crocodile products and the corresponding decrease in numbers led to the establishment of crocodile farms. They protect wild populations from hunting by supplying an easily accessible source of crocodiles for the market, create job opportunities, are usually tourist attractions and play an educational role. The abundance of crocodiles on farms has also been identified as a reservoir for the re-establishment of crocodiles in suitable habitats (Jacobsen, 1988; Mulder, 1992) if the environmental causal factors of decline could be removed or reduced. Although conservation authorities would support such measures should they become necessary, the genetic implications of such a strategy must first be assessed. For example, there is concern that the breeding practices employed at crocodile farms may change the genetic variation in captive crocodiles. Due to the possible negative effects of inbreeding or other changes in a population's genetic structure, an estimate of the genetic variability within reserve populations and populations intended for supplementation of protected populations may help in formulating management strategies and prevent deleterious consequences. The aim of this study was to determine if crocodiles bred for commercial purposes had different levels of genetic variation when compared to values previously reported for wild crocodiles.

Materials and methods

Nile crocodiles were sampled from a captive-bred population at the Kwena Gardens crocodile farm near Sun City in the North West Province, South Africa (25º30'S; 27º04'E). The original breeding stock was collected in the Okavango Delta, Botswana. Tissue samples from the heart, kidney and liver were collected from 50 offspring during a routine slaughter of one-and-a-half to two year old crocodiles (size: 1.0 to 1.75 m) of the F_1 generation. Muscle samples were obtained from the flesh remaining on the hide when it was removed. As the muscle did not always adhere to the skin, muscle samples were only obtained from 30 of the 50 individuals. Blood samples were collected from 10 individuals when the spinal column was severed for comparison with other tissue samples as blood is a non-invasive sampling technique. Following electrophoretic analysis it was determined that blood did not provide sufficient loci for the purposes of this investigation. All the samples were frozen and transported to the laboratory for analysis by horizontal starch gel electrophoresis.

The following buffer systems were used to separate the enzymes investigated: **MF**- a continuous Tris (0.18 M), boric acid (0.1 M) and EDTA (0.004 M) buffer system (pH 8.6) (Markert and Faulhaber, 1965); **TC**- a continuous Tris (0.3 M) and citric acid (0.1 M) buffer system (pH 6.9) (Whitt, 1970) and **A**- a continuous Tris (900 mM), boric acid (500 mM), EDTA (20 mM) and magnesium chloride (40 mM) buffer system (pH 8.6) (Gonchurenko et al., 1992). Two tissue extracts for each individual were prepared from

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