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ABSTRACTS

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01-35 Poster

ABSENCE OF INBREEDING DEPRESSION DESPITE UNPRECEDENTED SCALE OF DEMOGRAPHIC BOTTLENECK IN WHITE RHINOCEROS (*CERATOTHERIUM SIMUM SIMUM*)

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The southern white rhinoceros (*Ceratotherium simum simum*) was at the brink of extinction as a result of uncontrolled hunting and habitat destruction throughout its historical range with ~100 animals surviving in South Africa. Here conservation efforts resulted in the species' protection and recovery with 90% of the remaining ~11000 rhinos resident in South Africa. New populations have been established in reserves across southern Africa, all sourced from the original surviving population. In this study we test the hypotheses that (i) extant populations of white rhinoceros will exhibit genetic evidence of their demographic bottleneck, and (ii) founder events will result in reduced genetic diversity and levels of differentiation among seeded. We analysed data from ten microsatellite loci for 176 animals that represent both the South African population (Umfolozzi-Hluhluwe Complex) and three seeded populations in southern Africa (Waterberg Reserve in Namibia, Welgevonden Reserve in South Africa and Matobo National Park in Zimbabwe). Despite the extraordinary decline of the species no evidence of a genetic bottleneck was detected. It is noteworthy that the diversity in the white rhinoceros is lower than that seen in any other rhinoceros species. All seeded populations had reduced levels of heterozygosity relative to the source population. With the exception of Waterberg, all populations showed a positive F_{IS} suggestive of inbreeding within populations but this has not led to decreased fecundity. Both pairwise F_{ST} and R_{ST} were similar were found to be highest among the seeded populations. This study provides baseline genetic information about this important species as well as insight into the genetic outcomes associated with demographic recovery after a bottleneck.

01-36 Poster

LONG-TERM PERSISTENCE OF ORIBATID MITES IN HETEROGENEOUS SOIL ENVIRONMENTS

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The fossil record reflects the origin, diversification and extinction of major groups of organisms. Oribatid mites, a diverse group of soil-living arthropods, have persisted throughout geological and paleontological changes. We applied a molecular clock approach to estimate the origin of oribatid mites and the age of large parthenogenetic clusters, which probably radiated while being parthenogenetic. Using fossil dates and 18S rDNA sequences, our study revealed that oribatid mites originated in the late Precambrian and that the major splits in this group are several hundred million years old, and therefore evolved and diversified over a very long period. Our molecular data confirm the fossil-based opinion that all major lineages of oribatid mites were established before the Jurassic. Survival and radiation combined with only moderate morphological changes of these lineages suggests that the basic structure of their niches remained constant throughout their evolutionary history. Presumably, niches in decomposing plant material changed little despite major turnover of the types of vegetation covering the earth's surface. The consistency of niches of oribatid mites likely also explains why they consist of a number of parthenogenetic lineages which radiated and formed several clades of "ancient asexual scandals".