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Aspects of the sociality, ecology, reproductive biology and genetic relatedness of colonies of the highveld mole-rat, *Cryptomys hottenetotus pretoriae.*

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genetic variation more explicable in terms of social structure, effective population size and stochastic processes like genetic drift.

Summary

Although relatedness estimates are slightly higher than expected for outbred first-order relatives, it can be stated with reasonable confidence that colonies of the highveld mole-rat consist of first-order relatives (mother-offspring/full siblings). Colonies are composed of highly related individuals, although it is unlikely that they are simply monogamous family groups, it is more likely that colonies are composed of extended family groups.

The higher than expected estimates of relatedness can be explained by low sample size (in terms of the number of individuals, colonies and loci used in the study), limited gene flow or a hypothesised mating system where close relatives breed.

The identification of a reproductive female in colonies by morphological characteristics is reliable in this species, while the identification of the breeding male is unreliable when using morphological characteristics. The breeding male(s) do not appear to be resident in the colonies; when and where mating takes place is unknown at this time.

Offspring of the reproductive female appear, in most cases to be full siblings, although multiple paternity was identified in a number of colonies. Whether multiple paternity is within or between litters is unknown at this time. Individuals which were identified as not being the offspring of the reproductive female generally are thought to be her offspring or full siblings but were mistyped or had a null allele or had genotypes that differed from the expected alleles by a single base pair (evidence of mutation).