

THE UTILITY OF GENETIC AND MORPHOLOGICAL DATA IN UNDERSTANDING TAXONOMY IN VERVET MONKEYS

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Over the past seven years we have trapped, sampled and released nearly 500 vervet monkeys (*Chlorocebus aethiops*) from five African countries and St. Kitts in the Caribbean. The animals sampled represent all commonly recognized subspecies of vervets. Samples of blood and tissue were used for genetic analysis. In addition, thirty morphometric measures were obtained for each animal. An analysis of the morphometric measures reveals substantial differences in size between different subspecies of vervets living in northern and southern Africa. Within South Africa, where the majority of our samples were obtained, and where all the animals are members of the same subspecies, significant size differences (as evidenced by bivariate correlation) between animals living in varying habitats reflect local climatic conditions as opposed to taxonomic differences or access to human food. While these size differences are significant, genetic differences between local populations in South Africa, confirmed by AMOVA and STRUCTURE analysis utilizing ten microsatellite loci, 158 SNP loci and the mtDNA cox 1 locus do not reveal genetic structuring of the populations. Whole genome sequencing of representatives of each subspecies is currently in process. In order to clarify vervet taxonomy the International Vervet Genome/Phenome Research Group plans to collect additional samples for sequencing, RNA analysis and tissue storage from nearly 1000 more animals over the next two years. When our project is complete and genome wide polymorphisms have been characterized, these samples will be available to the larger primatology community.

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