A novel approach to studying the Endangered Riverine Rabbit population, using scent-detection dogs and non-invasive genetic sampling

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The Critically Endangered Riverine Rabbit is regarded as one of Africa's most endangered mammals, threatened predominantly by transformation across its Karoo habitat. The species is known from three populations: one in the Nama Karoo, where it was first discovered near Richmond in 1902, one near Touwsriver in the Succulent Karoo, where it was discovered in 2003, and a third, discovered in 2018, just west of Baviaanskloof. It is essential to understand connectivity between these fragmented populations, to assess their potential resilience and thereby inform conservation priorities.

Our team collected data to further investigate the species' geographic distribution and assess genetic connectivity between the populations. With the assistance of our trained scent-detection dog, Delta, we collected over 130 rabbit scats (droppings) from across the known distribution and beyond, confirming species identity using DNA barcode analysis. We identified 7 837 genome-wide SNP markers for Riverine Rabbits using Next Generation ddRAD sequencing. These can be used to study many aspects, including the species' evolutionary history, gene flow (dispersal), population size, and genetic diversity.

Our preliminary analyses suggest that the southern population is the youngest, or most derived population of Riverine Rabbits, with the lowest genetic diversity and lowest number of private alleles. The northern- and eastern populations appear to be older. The insights gained from these analyses will help inform and guide the conservation management of the species. Furthermore, a new population size estimate has resulted in the imminent downlisting of the species from Critically Endangered to Endangered. We trust that this is a result, whether direct or indirect, of the ongoing conservation work, research, monitoring, and habitat protection that the EWT has contributed to over the past two decades.