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Project Update:

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Report by:

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The response to the Covid-19 pandemic in the form of a National Lockdown in South Africa severely affected the ability of many researchers to conduct in-field research. In addition, the laboratories at Rhodes University were shut down and did not allow any students / researchers to utilise the laboratories facilities, without express permission from the University (i.e. production of sanitizer). Thus, from the end of March 2020 up until August 2020 I was unable to conduct fieldwork or genetic analyses. In August 2020, the Zoology and Entomology Department opened up following strict Covid-19 protocols. As such I re and I was one of the first users back.

Camera trap surveys:

To date, 90-day camera trap surveys have been successfully completed in Kariega Game Reserve (October 2019 to January 2021), Lalibela Game Reserve (January to May 2020) and Amakhala Game Reserve (August to November 2020). Brown hyaenas were captured at all three reserves, but due their low population densities, recaptures are low which means that density estimates may not be reliably estimated. Despite the low captures and recaptures, occupancy analyses can still be run to determine spatial dynamics (i.e. habitat use). Over the next couple of weeks camera trap photographs will be tagged and analysed in CameraBase. Thereafter, statistical analyses will be carried out in R.

Figure 1: Photographs of carnivores captured on the camera trap surveys (black-backed jackal (top left), brown hyaena (top right), lion (bottom left), caracal (bottom right)).

Genetic analyses:

Currently, 79 brown hyaena paste markings (Figure 2) have been collected from six game reserves (i.e. Amakhala Game Reserve, Kariega Game Reserve, Lalibela Game Reserve, Shamwari Game Reserve, Mountain Zebra National Park and Addo Elephant National Park. Genetic analyses of these collected past markings began in August 2020, as soon as the Molecular Laboratory was opened. DNA has been extracted from 65 of the 79 samples collected thus far. By November 2020, I had successfully sequenced the cytochrome-b gene for 29 samples, but unfortunately the genetic diversity amongst individuals for this gene is exceptionally low (practically non-existent) and so individuals could not be distinguished.

Our new approach for 2021 is to sequence three microsatellite loci (i.e. the most diverse loci within brown hyaenas) and use these loci as a fingerprinting tool in order to pick up on slight differences between samples (i.e. number of repeat motifs for each microsatellite) in order to determine individuals. We will also be using SRY primers to determine the sex of samples collected and if the microsatellite fingerprinting works we will be able to determine the sex of individuals sampled and determine a rough sex ratio for brown hyaenas in the Eastern Cape of South Africa.

Figure 2: An example of a brown hyaena paste markings found on a grass stalk alongside the road in Amakhala Game Reserve.