

Guyana Expedition 2017

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For the first time in over 20 years, the University of Glasgow Exploration Society (ExSoc) launched an expedition to Guyana. From its initial stages, the Guyana Expedition worked in tight collaboration with the Protected Areas Commission (PAC), the main conservation authority in Guyana, aiming to provide research which was of interest to them, and to set up a potential long-term collaboration. This 2017 Expedition was seen partially as a pilot study to assess the feasibility of UoG students working alongside Guyanese conservationists, for the benefit of both parties.

The site chosen for the Expedition was the Kanuku Mountains Protected Area (KMPA), located in the Rupununi area in the south-west of Guyana. This Protected Area was established in 2011, and is home to 70% of mammal species and 53% of bird species found in Guyana (Montambault & Missa, 2002). Despite the high diversity, the KMPA has received little scientific attention to date, perhaps due to its remoteness and difficulty of access. The Expedition consisted of 4 weeks in the field, split into two periods: one longer period of 3 weeks spent at a stationary base camp near Nappi village, and one shorter period of 1 week spent travelling south to north up the Rupununi River.

The research programme for the Guyana Expedition was determined based on the priorities identified by the PAC, the specific interests of the UoG team members, and logistical considerations. The programme consisted of four projects: a baseline survey of amphibian diversity, a parallel study to determine the presence of Chytrid fungus in amphibians, a baseline survey of bat diversity, and a survey of mammals using camera traps.





1) A baseline survey of amphibian diversity in the Kanuku Mountains Protected Area

Guyana is particularly rich in amphibians due to its unique geographic location, and yet it is still a relatively data-deficient area of study (Cole *et al.*, 2013). The study carried out by Cole *et al.* (2013) is the first modern account of amphibian fauna in Guyana, with 27% of the species sampled being endemic. In the above report, C. Cole and colleagues describe 324 species of amphibians and reptiles from voucher specimens, and estimate that the number will rise to 350 within the next decades. No detailed account of amphibian diversity has been carried out in the KMPA, and was therefore considered a priority for the PAC, and adopted as an aim for the Guyana Expedition 2017.

Amphibians were surveyed on 22 days between 15-July and 8-August 2017, both diurnally and nocturnally. A total of 250 anuran amphibians were surveyed, 238 of which are identified at least to family level. 16 species of anuran amphibians were positively identified. 67 individuals were only identified to family or genus levels, and 12 individuals remain fully unidentified.

The results from our survey illustrate clearly the lack of data on amphibians in Guyana. For instance, during our survey we encountered 6 *Anomaloglossus kaiei* individuals. This species, which is currently under investigation by the IUCN due to the lack of data on its distribution and conservation status (R. Downie, personal communication, Sept-2017), has only been recorded in Kaieteur National Park and the Pakaraima Mountains in Guyana (Kok, 2008). Yet despite our relatively low sample size, we encountered this species in the KMPA. Other

species such as *Rhinella martyi* and *Allobates spumaponens*, encountered relatively frequently during the KMPA amphibian surveys are also not recorded for this area. The discovery of these three species outside their known range is a great success for the Expedition, demonstrating that our survey provides valuable data on biodiversity. We hope our findings encourage the PAC to put forward further research into amphibian diversity in the Protected Areas of Guyana. It is our intention to share our data with the PAC and the IUCN, in order to broaden the knowledge of the amphibian fauna of Guyana.

	
<p><i>Hypsiboas boans</i>, one of the few arboreal anurans we captured in the KMPA</p>	<p><i>Rhinella martyi</i>, currently not reported for the KMPA</p>
	
<p><i>Leptodactylus mystaceus</i>, the most frequently encountered anuran species in the KMPA</p>	<p>A specimen identified as <i>Leptodactylus sp.</i>, unable to assign to a species</p>

2) The first assessment of *Batrachochytrium dendrobatidis* in amphibians in the Kanuku Mountains Protected Area of Guyana

The fungus *Batrachochytrium dendrobatidis* (*Bd*) is known to cause the disease chytridiomycosis in all orders of amphibians: anura, caudata and gymnophiona. Chytridiomycosis causes high morbidity and mortality in susceptible species and individuals. The fungus infects the sensitive, permeable skin of amphibians, proliferating intracellularly in the superficial layers of the epidermis and causing hyperkeratosis (Van Rooij *et al.*, 2015). Hyperkeratosis disrupts respiration, osmoregulation and electrolyte exchange across the skin, resulting in water and electrolyte disturbances which ultimately lead to cardiac arrest (Campbell *et al.*, 2012). This fungal pathogen can be spread by direct contact between individuals or contact with water sources infected with waterborne fungal zoospores (Van Rooij *et al.*, 2015). Chytridiomycosis has contributed to the extinction of species such as the

Golden Toad, both species of Gastric Brooding Frogs (IUCN, 2016) and Rabb's Fringe-limbed Tree Frog (Emerson, 2016). Many more amphibian populations across the globe are experiencing huge declines and are seriously threatened by chytrid fungus (Lips *et al.*, 2006). Guyana is data deficient for the presence/absence of *Bd*. To our knowledge, there is only one *Bd* survey including data from Guyana, comprising a sample of 22 caecilians from the Iwokrama area, all of which were negative (Gower *et al.*, 2013). With reports in the neighbouring countries of Venezuela (Sánchez *et al.*, 2008) and Brazil (Valencia-Aguilar *et al.*, 2015; Jenkinson *et al.*, 2016), it is important that surveillance is conducted in Guyana to add to the epidemiological knowledge of this disease.

A total of 250 anurans were swabbed successfully, and DNA was successfully extracted from 247 of 250 swabs, and analysed via PCR for the presence of *Batrachochytrium dendrobatidis* DNA. All samples of anurans from the KMPA were found to be negative for *Bd* DNA, as seen in Figure 8 by the absence of *Bd*-specific amplicon in all gels.





The combination of high diversity and endemism of amphibians in Southern Guyana make this area a priority for conservation. Our survey showing the absence of evidence for *Bd* in the KMPA gives a hopeful view for amphibians in the pristine rainforest of Southern Guyana, but it remains true that an outbreak of chytridiomycosis in this area would be catastrophic. Through our close work with the KMPA rangers, local field guides and the PAC, this project has led to a new awareness of chytridiomycosis amongst conservation stakeholders in Guyana. We hope that this survey serves as a first step towards continued monitoring and surveillance, as well as implementation of pre-emptive measures which could help prevent such an outbreak. It is our firm belief that the prevention of chytridiomycosis should be paramount in the conservation agenda of Guyana's Protected Areas Commission.

3) A baseline survey of bat diversity in the KMPA

There are 107 recorded species of bats in Guyana, making it a country with one of the highest bat diversity levels in Latin America (Lim *et al.*, 1999). Bats account for roughly 50% of the mammal diversity in Guyana (Lim, 2013) and play important roles in seed dispersal, pollination and insect population control, making them a vital part of Neotropical ecosystems. The KMPA is a national hotspot for bats, with 89 species recorded so far (Montambault & Missa, 2002). The KMPA provides an ideal habitat for bats, due to its pristine forest and extensive river system.

Bat surveying occurred in the KMPA between 14th July and 8th August. Bats were surveyed by mist-netting, using two ground nets and one triple-high. Bats were surveyed on 22 nights, and the nets were opened as soon after dusk as possible.

A total of 432 bat captures occurred in the 22 nights of surveying. 359 individuals were positively identified to species level; 31 individuals were either recaptures, or escaped from the net or hand before identification was possible; and 42 individuals are not identified to species level.

	
<p>(a) The greater bulldog bat or fisherman bat (<i>Noctilio leporinus</i>), the only piscivorous bat caught in the KMPA.</p>	<p>(b) The common vampire bat (<i>Desmodus rotundus</i>) feeds on mammalian blood.</p>
	
<p>(c) Parnell's mustached bat (<i>Pteronotus parnellii</i>) is a gleaning insectivore, meaning feeds by capturing insects sitting on leaves.</p>	<p>(d) Pallas's long-tongued bat (<i>Glossophaga soricina</i>) is a nectarivore.</p>

4) An understory community survey of the KMPA using camera traps

To obtain a synopsis of the mammal and understory community of the KMPA, the Expedition used nine Bushnell HD Trophy camera traps to capture footage of the animals present. The aim was to create a baseline inventory for the Nappi area of the KMPA. Four camera traps were also brought and set up for single nights along the river trip. The KMPA region has a rich mammal community, including 11 of the 12 red-listed mammal species of Guyana (PAC, 2015).

283 trigger events of animals were recorded. A total of 19 species (Figure 12) have been confirmed from across 16 families. Six species were birds, one species of reptile, and the remaining 12 are mammals. The majority of mammal trigger events were by *Myoprocta acouchy* (red acouchi, 14.8%) and *Dasyprocta leporina* (Red-rumped agouti, 12.7%) both in the family *Dasyproctidae*. The most common bird species was *Psophia crepitans* (Grey-winged trumpeter, 13.7%).



Leopardus pardalis (Ocelot)



Agouti paca (Paca)



Tapirus terrestris (Brazilian Tapir)





Cerdocyon thous (Savanna / Crab-eating Fox)



Dasypus novemcinctus (Nine-banded Armadillo)



Eira barbara (Tayra)

	
<p><i>Lontra longicaudis</i> (Neotropical otter)</p>	<p><i>Puma concolor</i> (Puma)</p>

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