Project Update: January 2017

I have established 18 transects in forest, forest edge, plantations and plantation edge along Lots 5, 6 and 7 of the Lower Kinabatangan Wildlife Sanctuary. A total of 15 frog species belonging to four different families were identified (*Rhacophoridae*, *Ranidae, Dicroglossidae* and *Microhylidae*) (Table 1). Beside the current persistent dry season we were able to collect 308 buccal swabs of 15 species of frogs. 134 from *Rhacophorus appendiculatus* (forest specialist), 48 of *Hylarana glandulosa* (plantation specialist), 58 of *Hylarana megalonesa* (generalist) and the rest of the 68 samples are from the other 12 species collected. Data collection for this project is still in progress and will be ongoing from March to October of 2017.

Table 1. List of species found in LKWS. Habitat types Forest (F), Edge forest (EF), plantation (P) and edge plantation (EP).

Species	***F***	***EF***	***P***	***EP***	***Endemic***	***Pop. Trend***	***Threat***
Dicroglossidae							
F. limnocharis	0	1	0	0		Stable	LC
L. finchi	3	0	0	0	Y	Decreasing	LC
O. laevis	1	0	0	0		Stable	LC
Microhylidae							
K. baleata	2	0	0	0		Stable	LC
M. borneensis	3	0	0	1	Y	Decreasing	LC
M. perpava	12	7	1	0	Y	Decreasing	LC
Ranidae							
H. erythraea	0	3	0	0		Stable	LC
H. glandulosa	1	2	45	4		Decreasing	LC
H. raniceps	53	69	54	16		Stable	LC
Rhacophoridae							
P. leucomystax	1	0	0	0		Stable	LC
P. macrotis	2	4	0	0		Unknown	LC
R. appendiculatus	61	32	0	0		Decreasing	LC
R. dulitensis	0	2	0	0	Y	Decreasing	NT
R. harrissoni	2	2	0	0	Y	Decreasing	NT
R. pardalis	7	2	0	0		Decreasing	LC

I used Biodiversity Pro 2.0 software to assess richness (rarefaction plot) and abundance in four main habitats types, using Shannon Index to assess diversity of species (Fig 1 and 2). Preliminary results show that species richness and abundance are higher in forest habitats than in plantation. Forest had the higher Shannon index (SI=0.525) meaning that it holds more diversity than the others habitats, in the other hand plantation holds the lowest diversity with SI=0.299. While these results are comparable with those found by other authors (Scriven 2011; Barnett J et al. 2013; Gillespie et al. 2012) these are preliminary results and there is the need for more surveys.

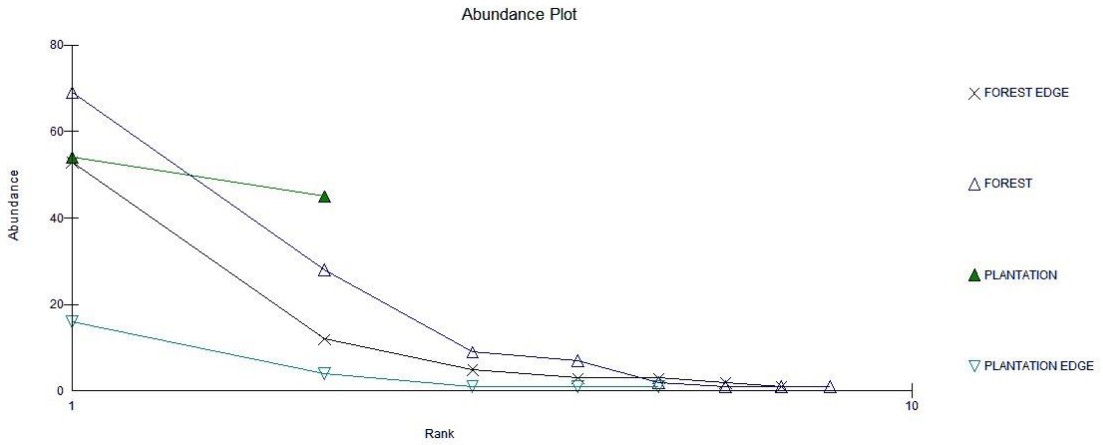

Fig 1. Abundance plot showing different habitat types. The X axis shows the number of species found in each habitat. Only two species were found in plantation.

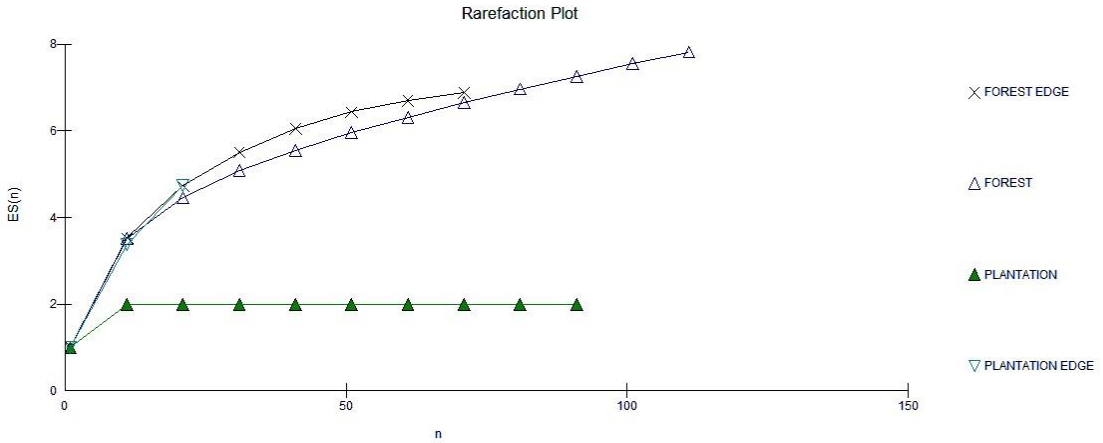

Fig 2. Species richness plot showing different habitat types.

DNA extractions have been done for 150 samples. We test the markers Cytochrome Oxidase subunit (CO1) and a fragment from the 16S gene and results show that DNA from buccal swabs are a good source for DNA Barcoding. Microsatellite analysis will be carried out to measure genetic diversity from the three target species, as well as gene flow and genetic structure. Molecular analysis should be straightforward but will require new markers to be developed from sequence reads produced from a whole genome low coverage genomic library produced with Cardiff University's Illumina NextSeq 500. Next generation sequence (NGS) will be used to develop microsatellite. , a minimum of 20 microsatellites will be developed between field seasons at Cardiff University. The data analysis will be performed using Arlequin (v3.5.1.3), Structure (v2.3.4) and approximate computation (Beaumont 2001).