

# Using geospatial tools to investigate how deforestation affects the transmission of malaria in birds

<sup>1</sup>Anong Damian Nota, <sup>2</sup>Ndukum Julius Awah, <sup>3,4</sup>Njabo Kevin Yana, <sup>5</sup>Anton Cornel, <sup>6</sup>Ravinder Sehgal

<sup>1</sup>University of Buea, Cameroon, <sup>2</sup>University of Dschang, Cameroon, <sup>3</sup>Higher Institute of Environmental Sciences, Cameroon, <sup>4</sup>The University of California, Los Angeles, <sup>5</sup>The University of California, <sup>6</sup>San Francisco State University, USA.

## INTRODUCTION

Global climate change, and increasing human population growth have been implicated as major factors contributing to the emergence of infectious diseases (Patz and Hahn, 2013). Perhaps even more immediate, however, is the impact that large-scale deforestation may have on disease emergence.

What are the proximal effects of large-scale deforestation on the transmission of vector-borne infectious diseases? We have approached this problem by studying malaria in natural populations of rainforest birds threatened by rapid environmental degradation in Cameroon. Previous data from our US supported partner's research in Africa have shown that certain strains of *Plasmodium* spp. are entirely host specific; they infect one species of passerine bird, but not another in the same family (Chasar *et al.*, 2009, Loiseau *et al.*, 2010). Other strains infect many species of birds and are considered generalists (Bonneaud *et al.*, 2009, Loiseau *et al.*, 2012). Little is known about how vector ecology can affect host switching. To address this gap in knowledge, we propose to determine how vector species communities change with deforestation in real time, and identify the natural vectors of both specialist and generalist parasites in Talangaye forest of SW Cameroon, An African ecosystem scheduled for rapid deforestation in favour of a palm plantation.

## METHODOLOGY

### 1. Site selection and characterization



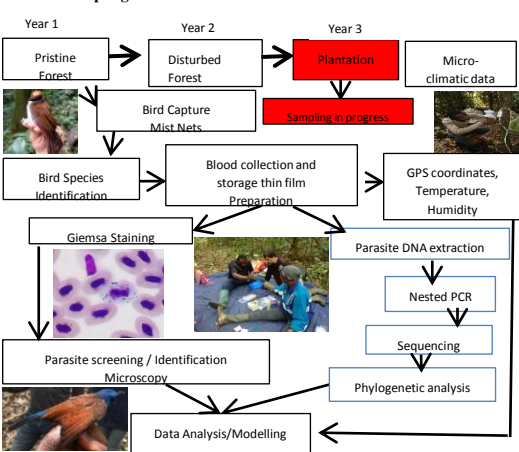
Figure 1. Pristine rainforest areas slated to be clear-cut for palm plantation development by SG-SOC (Herakles Farms) in Cameroon. Figure shows Cameroon (bottom left) with the Southwest Region shaded in green. The plantation sites are detailed in the larger map. Our work commenced in January 2016 at Ntugi Block 2 (pink). The Banyang-Mbo Wildlife Sanctuary Preserve is adjacent to Ntugi Block 2.

### 2. Field methods

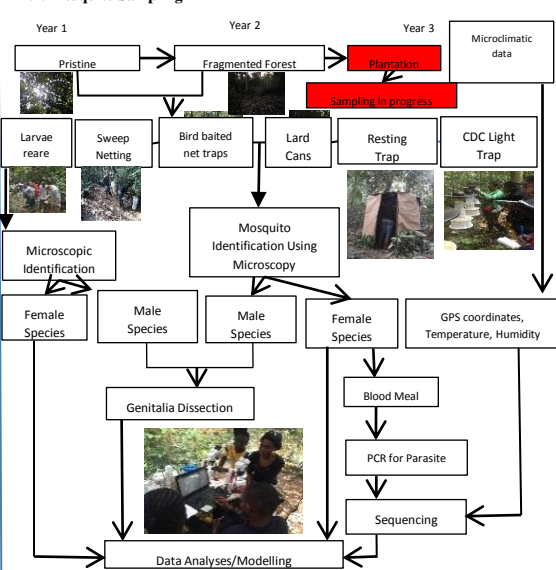
#### Before - after control- impact pairs (BACIP) experimental design (Popescu *et al.*; 2012)

Birds and mosquitoes were sampled from January 2016 to November 2017, sampling being done 3 times a year for a duration of three weeks. For better sampling at each site, traps were set at least 200 m apart and GPS coordinates of each trap taken. Microclimatic conditions of temperature and relative humidity were also recorded using HOBO® data loggers.

#### 2.1. Bird Sampling



#### 2.2. Mosquito Sampling



## 3. PRELIMINARY RESULTS

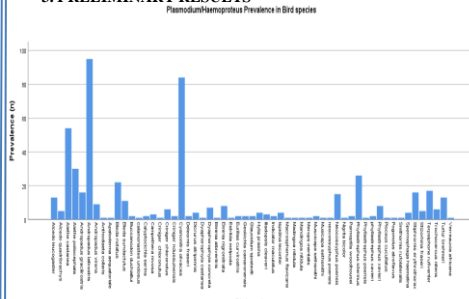


Fig. 3.1: Bird species of Talangaye rainforest and prevalence of *Plasmodium/Haemoproteus* sp

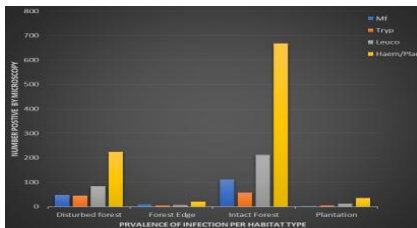


Fig. 3.2: Prevalence of avian blood borne parasites per habitat type following 2 years of sampling in Talangaye rainforest



Fig. 3.3: Diversity and abundance of mosquitoes captured following two years of sampling in Talangaye rain forest

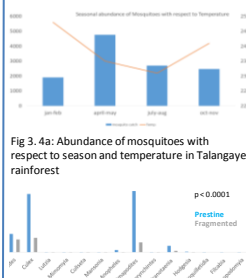


Fig. 3.4a: Abundance of mosquitoes with respect to season and temperature in Talangaye rainforest

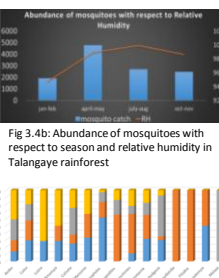


Fig. 3.4b: Abundance of mosquitoes with respect to season and relative humidity in Talangaye rainforest

Fig. 3.5a: Habitat type and distribution of mosquitoes in Talangaye rainforest

Fig. 3.5b: Seasonal abundance of mosquito species collected in 2 years in Talangaye rainforest

### Evolutionary relationships of *Leucocytozoon* isolates

The evolutionary history was inferred using the Neighbor-Joining method. The optimal tree with the sum of branch length = 0.24188677 is shown. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown above the branches. The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The evolutionary distances were computed using the Jukes-Cantor method and are in the units of the number of base substitutions per site. The rate variation among sites was modeled with a gamma distribution (shape parameter = 1). The analysis involved 43 *Leucocytozoon* sequences with those obtained from the GenBank shown in bold. Codon positions included were 1st+2nd+3rd+Noncoding. All ambiguous positions were removed for each sequence pair. There were a total of 535 positions in the final dataset. Evolutionary analyses were conducted in MEGA6. The vertical lines indicate the major clades.

### Acknowledgements

This research was funded by the USAID PEER project 4-360 awarded to Anong Damian Nota (PhD), Principal Investigator, of the Department of Microbiology and Parasitology of the University of Buea. We thank all the students, laboratory and field workers who are currently taking part in this study and The management of the Global-Sustainable Oils Cameroon (SG-SOC) a subsidiary of Herakles Farms for granting us the permit to collect samples from the sites.

## RESULTS CONTINUED

### VECTORS

- Over 8,941 mosquitoes belonging to 12 genera captured in 2 years in both pristine and fragmented forests and identified using morphological keys.
- Over 20 new species of mosquitoes, described before have been described and named

These include 5 new species of *Aedes*: **Genus *Aedes***  
*Aedes stenostylus*; *Aedes pseudostenostylus*; *Aedes latofium*; *Aedes pseudomullitii*; *Aedes intermedus*;  
*Aedes spinisudanicus*

### SIX (6) NEW SPECIES OF CULEX:GENUS CULEX

*Culex lanzoni*; *Culex natego*; *Culex pseudo subaequalis*; *Culex hirtusyle*; *Culex quintetti* var *talangaensis*; *Culex bicolor* and  
**EIGHT (8) NEW SPECIES OF ERATMOPODITES MOSQUITOES: GENUS ERATMOPODITES**  
*Eratmopodites veronica*; *Eratmopodites simplex*; *Eratmopodites productus*; *Eratmopodites intercavernosus*; *Eratmopodites brycensis*; *Eratmopodites aedesimilis*; *Eratmopodites plioleucus capillus*

### IDENTIFIED BLOOD FED VECTORS FOR AVIAN MALARIA INCLUDED:

*Culex nebulosus*, *Culex albiventris*, *Culex wigglesworthi*

## 4. DISCUSSION AND CONCLUSIONS

Our present preliminary data indicates that we can in real time demonstrate the effects of large scale deforestation on the transmission of malaria in birds. The high diversity of bird species in Talangaye rainforest with infections of *Plasmodium/Haemoproteus* indicates that several parasite lineages that belong to either generalists or specialist parasites may be present in the area. The presence of diverse mosquito species, especially known vectors of avian malaria such as *Culex* also increases the dynamics of transmission of several parasite lineages among birds which is good to test the effects of deforestation on the transmission of malaria.

A significant decrease in the distribution of mosquitoes in pristine compared to disturbed/fragmented forest supports our hypothesis that after disturbance from logging, the diversity of vectors will decrease. A decrease in avian *Plasmodium* across a gradient from pristine to degraded forest and forest edge, is good indication that only a limited and particular parasite lineages will predominate and with sequence data and phylogenetic analysis which are ongoing may confirm the hypothesis that after deforestation, although mosquito vectors will decrease, the remaining vectors will harbor more generalists malaria parasites.

Our preliminary sequencing/phylogenetic analysis reveal several novel *Leucocytozoon* parasite lineages. *Plasmodium* and *Haemoproteus* lineages are still to be analyzed and may reveal further novel lineages that may become significant when we analyze sequences from the palm plantations on completion of fieldwork. Several new mosquito species have been described along with other existing mosquitoes not previously identified in Cameroon. The role of these vectors in disease transmission still remains to be elucidated.

### Further Information

Field work for this project has been suspended in its third year because of the current Anglophone crisis in Cameroon. The uprising in the North West and South West Regions of the country has temporarily forced field work in the third year to stop and so data from the palm plantations opened on deforested areas cannot be collected to assess before and after impact and do modelling using geospatial tools.

### REFERENCES

- Bonneaud C, Sepil I, Mila B, Buermann W, Pollinger J, Sehgal RNM, Valkiunas G, Iezhova T, Saatchi S, and Smith TB. 2009. The prevalence of avian *Plasmodium* is higher in undisturbed tropical forests of Cameroon. *Journal of Tropical Ecology*, 25, 439-447.
- Chasar A, Loiseau C, Valkiunas G, Iezhova T, Smith TB, Sehgal RNM. 2009. Prevalence and diversity patterns of avian blood parasites in degraded African rainforest habitats. *Molecular Ecology*, 18, 4121-4133.
- Loiseau C, Harrigan RJ, Robert A, Bowie RCK, Thomassen A, Smith TB, Sehgal RNM. 2012. Host and habitat specialization of avian malaria in Africa. *Molecular Ecology*, 21, 431-441.
- Loiseau C, Iezhova T, Valkiunas G, Chasar A, Hutchinson A, Buermann W, Smith TB, Sehgal RNM. 2010. Spatial variation of haemosporidian parasite infection in African rainforest bird species. *Journal of Parasitology*, 96, 21-29
- Patz JA, Hahn MB. 2013. Climate change and human
- Popescu VD, Valpine P, Tempel D and Peery ZM. (2012) Estimating Population Impacts via dynamic occupancy analysis of Before-After Control-Impact studies. *Ecological Application*, 22,1389-1404

