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 streams of Plasmodium spp. are entirely host specific; they infect one species of passerine bird, but not another in the same family (Chauvet et al., 2009). Liouvel et al. (2010). Other streams infect many species of birds and are considered generalists (Bonneaud et al., 2009, Liouvel 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-parasite 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 standardized for rapid deforestation in favour of a palm plantation.

METHODOLOGY

1. Site selection and characterization

2. Field methods

Before and after control-impact pairs (BACP) experimental design (Possee 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 in the 3rd and 4th year. Blood samples were also recorded using HOBIO data loggers.

2.1. Bird Sampling

2.2. Mosquito Sampling

3. PRELIMINARY RESULTS

3.1. Species diversity

3.2. Diversity and abundance of mosquitoes captured following two years of sampling in Talangaye rain forest

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

3.4. Abundance of mosquitoes with respect to season and temperature in Talangaye rain forest

3.5. Habitat type and distribution of mosquito species collected in 2 years in Talangaye rain forest

3.6. Seasonal abundance of mosquito species collected in 2 years in Talangaye rain forest

4. DISCUSSION AND CONCLUSIONS

Our current preliminary data indicates that we can in real time track the effects of molluscan deforestation on the transmission of malaria in birds.

A significant decrease in the distribution of mosquitoes in pristine compared to disturbed/fragments 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/phylgenetic 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 compare sequences from the palm plantations on completion of fieldwork. Several new leucocytozoon species has been described along with other existing mosquitoes not previously identified in Cameroon. The role of these vectors in disease transmission remain 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 uprisings in the North West and South West Regions of the country has temporally forced field work in the third year to take in data from the palm plantations opened on deforested areas cannot be collected to assess before and after impact and do modeling using geospatial tools.

REFERENCES


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RESULTS CONTINUED

VECTORS

Over 8,941 mosquitoes belonging to 12 genera captured in both pristine and fragmented forests and identified using morphological keys.


SIX (6) NEW SPECIES OF CULEX

CULEX lactuor, Culex notius, Culex padoi adnatus, Culex lineariz, Culex quantitii var talanganyae; Culex borealis and

EIGHT (8) NEW SPECIES OF ERATMAPODITES

ERATMAPODITES veronae, Eretmapodites simplex, Eretmapodites productivus; Eretmapodites intervesfaciens; Eretmapodites brunonis, Eretmapodites aerodromi; Eretmapodites pilosus.