Avian Communities and their pathogens in the lake Chivero-Manyame ecosystem

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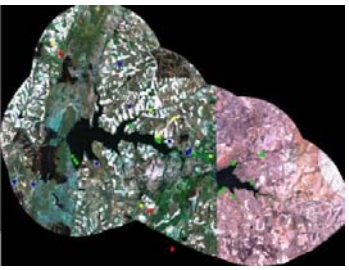


In the framework of the GRIPAVI project, an observatoire has been implemented in 2007 in Zimbabwe. Four avian compartment are studied: waterfowl population, ostrich farms, intensive poultry and backyard poultry. The objectives are:
1) to explore the dynamics of the waterfowl community and their drivers in relation to viral circulation,
2) to understand the role of juveniles in the epidemiology of AI in the waterfowl compartment,
3) to understand the linkages between the different compartments and the time of highest risk of pathogen transmission,
4) to compare the dynamics of Avian Influenza , Newcastle Disease Virus and West Nile Virus in the same ecosystem.

Community description

- **Waterfowl Counting:**

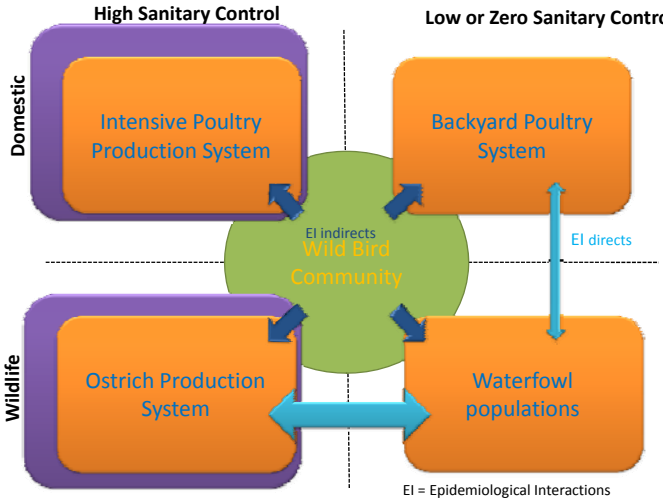
Since May 07 to Mars 09, resulting in 360hrs of counting and more than 100,000 birds observed.

- **Domestic compartment (*3):**

From June 08 to April 09; Domestic and wild birds species were recorded.

- **Mixed counting:**

Since mid-2009, mixed counting session protocols (domestic and wild)



EI = Epidemiological Interactions

Sampling birds

- **Waterfowl sampling:**

From May 07 to Mars 09, more than 2000 wild birds sampled

- **Domestic sampling:**

More than 3000 ostriches, backyard chicken and intensive poultry chicken were sampled regularly since 2007

- **Bridge species sampling:**

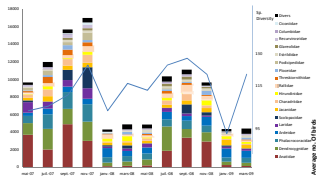
Since November 2009, specific protocols target identified bridge species

- **Juvenile sampling:**

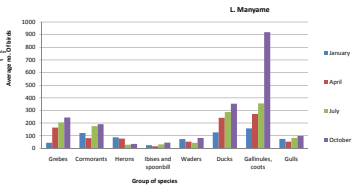
In 2010, specific protocols will target juvenile duck

Observed bird communities

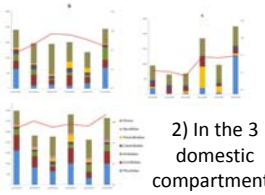
Community composition & Species diversity per mission



1) In waterfowl

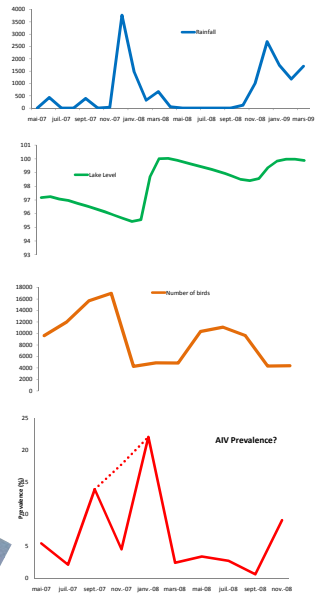


3) 10 years database in waterfowl



2) In the 3 domestic compartments

Virus profil in relation to potential drivers



1. Rainfall from year 1 can predict the lake level at year 2
2. Lake level drives the resource availability for birds and can predict their numbers
3. Main Hypothesis: Bird ecology can predict pathogen dynamics in the community (preliminary results)

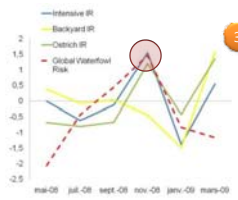
Bridge Species identification

- **Risk Factor Model** for the 255 wild species observed

1
- **Dynamic Risk Factors:** Abundance, Gregariousness, Mixing, Immigration, proportion of Juveniles
- **Non-Dynamic Risk Factors:** migration patterns and feeding habit

- **Epidemiological Interaction Model**

2
- **Overlap of communities** observed at the same time in different compartment
- Each species in the overlap is weighted by its **risk value**



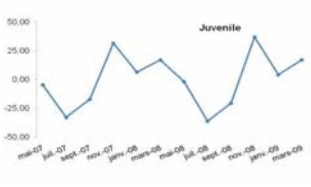
3
- **Interaction Risk (IR)** for each domestic compartment and global waterfowl risk

Intensive Poultry	November Peak	Representative Species
Ploceidae	30,30%	Red-billed quelea (77%)
Estrilidae	21,80%	Bronze mannikin (50%)
Hirundidae	8,50%	Barn swallow (90%)
Ardeidae	0,00%	Cattle egret (85%)

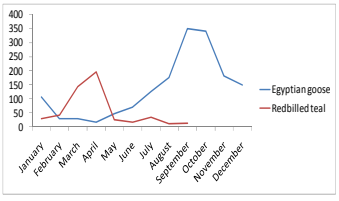
4
- **Identification of bridge species**
  - The most represented species of the observed interaction

Role of Juvenile in AIV circulation

Juveniles constitute naive individuals to pathogens and arrive in the population in vast numbers. In Africa, the timing of reproduction of different key species is spread over the year (1) and the epidemiological role of juvenile is unknown.



Juvenile Risk curve in the waterfowl community based on bird count and a simple population dynamic model



Juvenile dynamics in 2 duck speciess based on nest cards collected by ornithologists

The objective is to test the juvenile hypothesis by using 10-years strong ornithological databases and to investigate the viral profil in the juvenile population of the key duck species in the system