

## Parasite community ecology and epidemiological interactions at the wildlife/domestic/human interface

Can we anticipate emerging infectious diseases in their hotspots?



## « One Health » at the wildlife/domestic Interface

- 70% of emerging diseases with a link with wildlife, a lot are zoonosis
- Sanitary issue where wildlife & domestic systems are in interaction

### Hot spots of Emergence in tropical and sub-tropical ecosystems

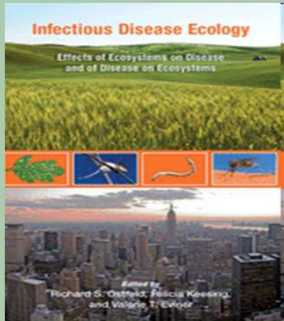
- Complex multi-host systems
- How do we anticipate the next emergence? How do we survey something not yet there?

### Ecology of disease transmission in multi-host systems

# Describe and anticipate the emergence at this interface

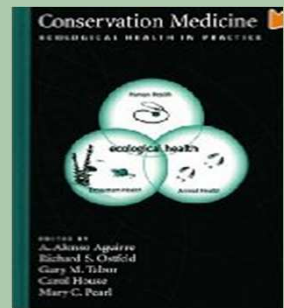
- Needs expertise from:
  - **Epidemiology** (classical, risk analysis, molecular epidemiology, etc.)
  - **Ecology** (evolutionary biology, community ecology, landscape ecology, etc.)
  - **Social sciences**
- Already multidisciplinary work exists





**Infectious Disease Ecology:  
Effects of Ecosystems on Disease and of Disease on  
Ecosystems**

Ostfeld R.S. et al. (2008)



**Conservation Medicine:  
Ecological Health in Practice**

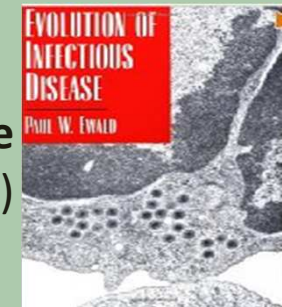
Aguirre A.A. et al. (2002)



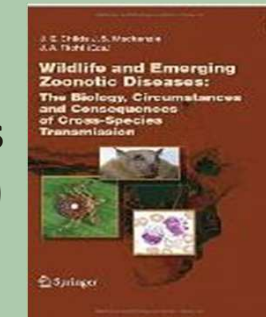
**Disease Ecology:  
Community structure and pathogen dynamics**

Collinge S.K. (2006)

**Evolution of Infectious Disease**  
Ewald, P.W. (1994)



**Wildlife and Emerging Zoonotic Diseases**  
Childs J.E. et al. (2007)



Necessity to develop  
new operational framework  
for early detection and surveillance adapted to  
multi-host systems  
at the wildlife/domestic/human interface



New concepts

# Which host do we survey?

- Usually empirical decision-making
- Define concept of:

- Epidemiological Functional Groups (EFGs)



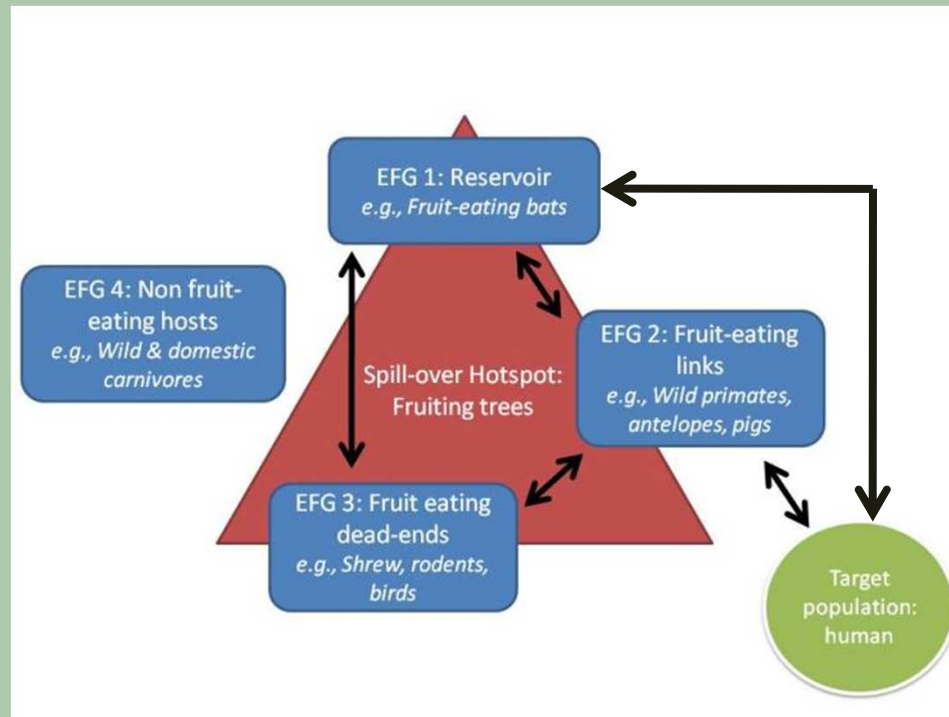
“allocate the species coexisting in a given ecosystem into EFGs according to their specific life-history traits and the role they play in the transmission of a parasite, or a group of parasites, in this ecosystem”

- Based on the concept of ecological functional groups (borrowed from community ecology)
- After defining target species (according to definition by Haydon et al. 2002)



Selection process for host populations

## e.g. Ebola in Central Africa



Arrows in the figure represent epidemiological interactions between host populations.

Based on Leroy et al. 2005, Gonzales et al. 2007 :

**EFG1:** fruit-eating bats reservoir but not in direct contact with the target species, human populations;

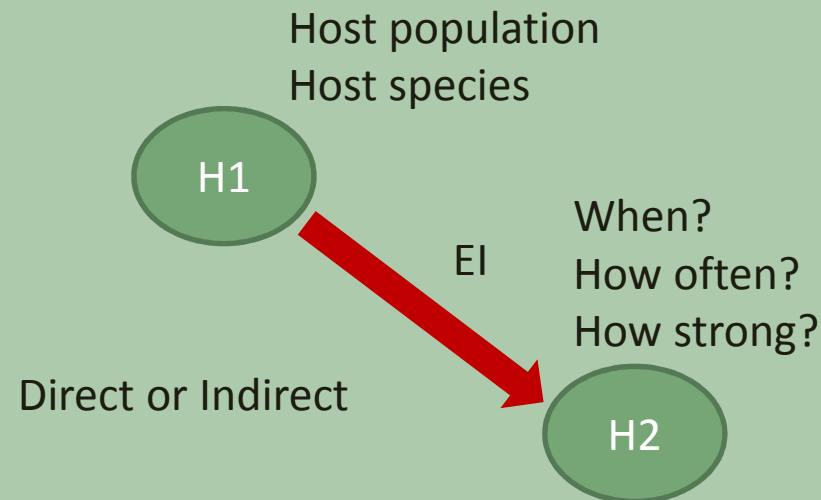
**EFG2:** fruit-eating links in contact with humans; (e.g., wild primates, some antelopes and livestock such as pigs)

**EFG3:** fruit-eating dead-ends not in contact with the target species; (e.g., shrew, rodents or birds which are not hunted and consumed by human)

**EFG4:** non fruit-eating animals with no role in the epidemiology of the virus. (e.g., wild and domestic carnivores)

# Concept of Epidemiological Interactions (EIs)

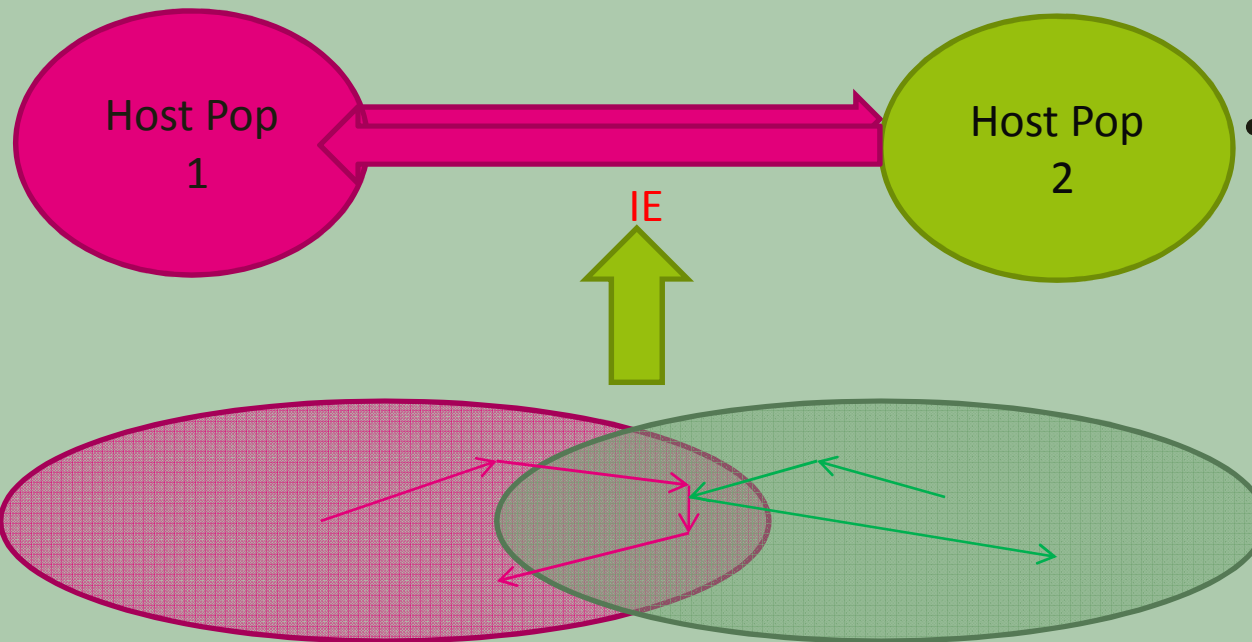
- « Any ecological interaction between 2 hosts which may result in the transmission of one or more pathogens »



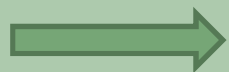
Two approaches

## Host Approach

## Principle

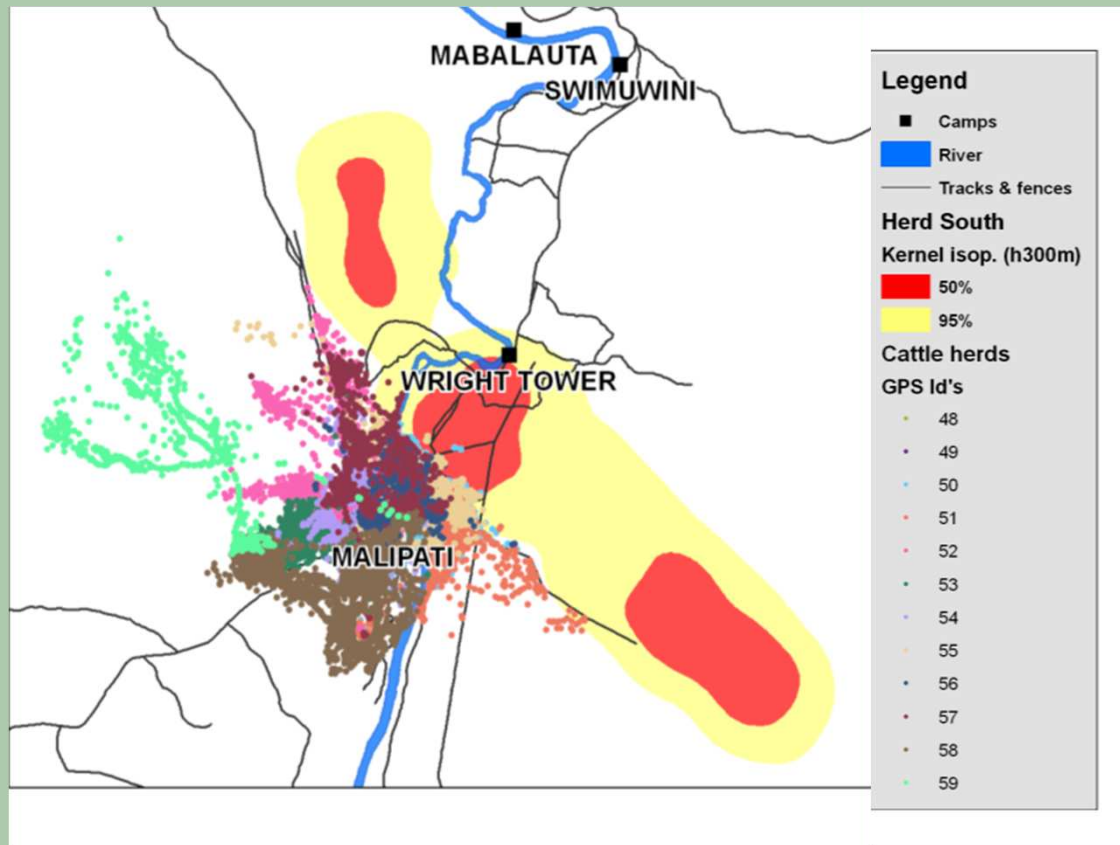


- **Host approach: *A priori***
  - Movements of hosts
  - Contacts of hosts



Determine the potential for pathogen transmission

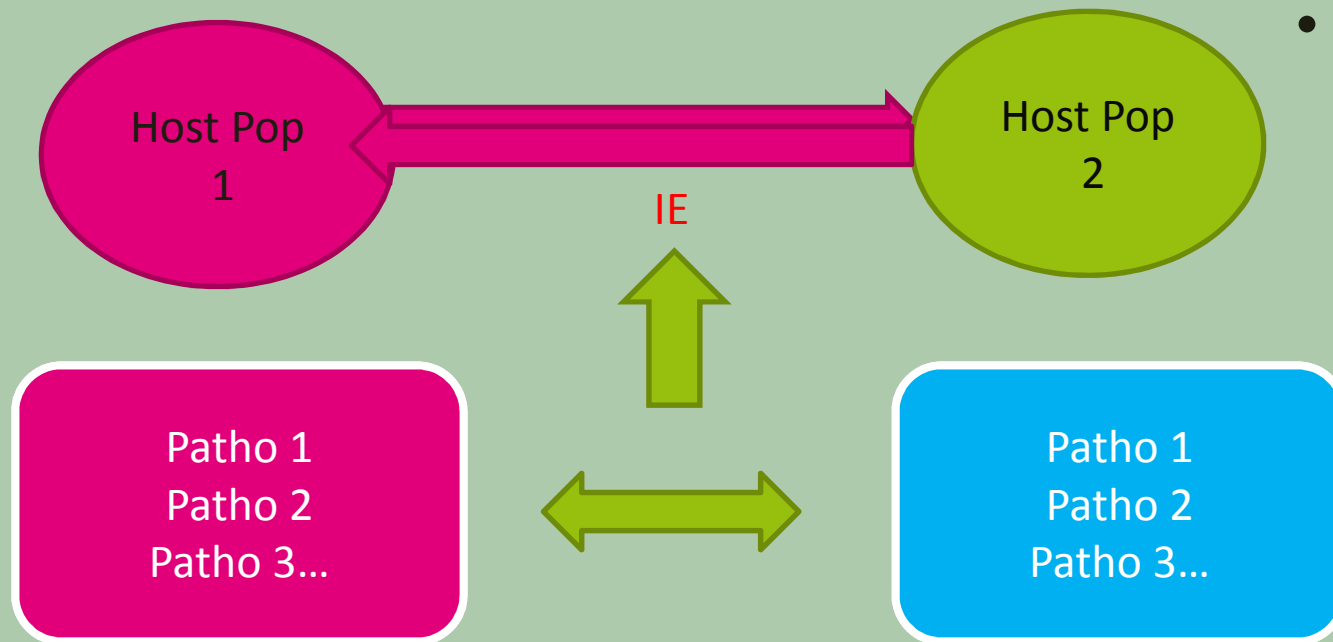
# Buffalo/cattle Interaction using telemetry in Zimbabwe



*Southern buf herd kernel map + 12 cattle herd locations*

## Pathogen Approach

# Principle



- **Pathogen approach: A *posteriori***
  - Observed pathogens in hosts
  - Shared community of pathogens

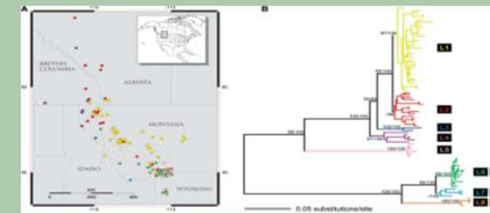


➡ Identify most probable transmission pathways in the ecosystems

## Recent Advances in:

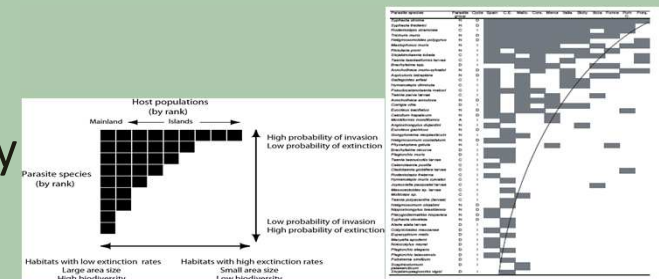
- Molecular epidemiology

- *A Virus Reveals Population Structure and Recent Demographic History of Its Carnivore Host*, Biek et al., Science, 2006



- Community ecology

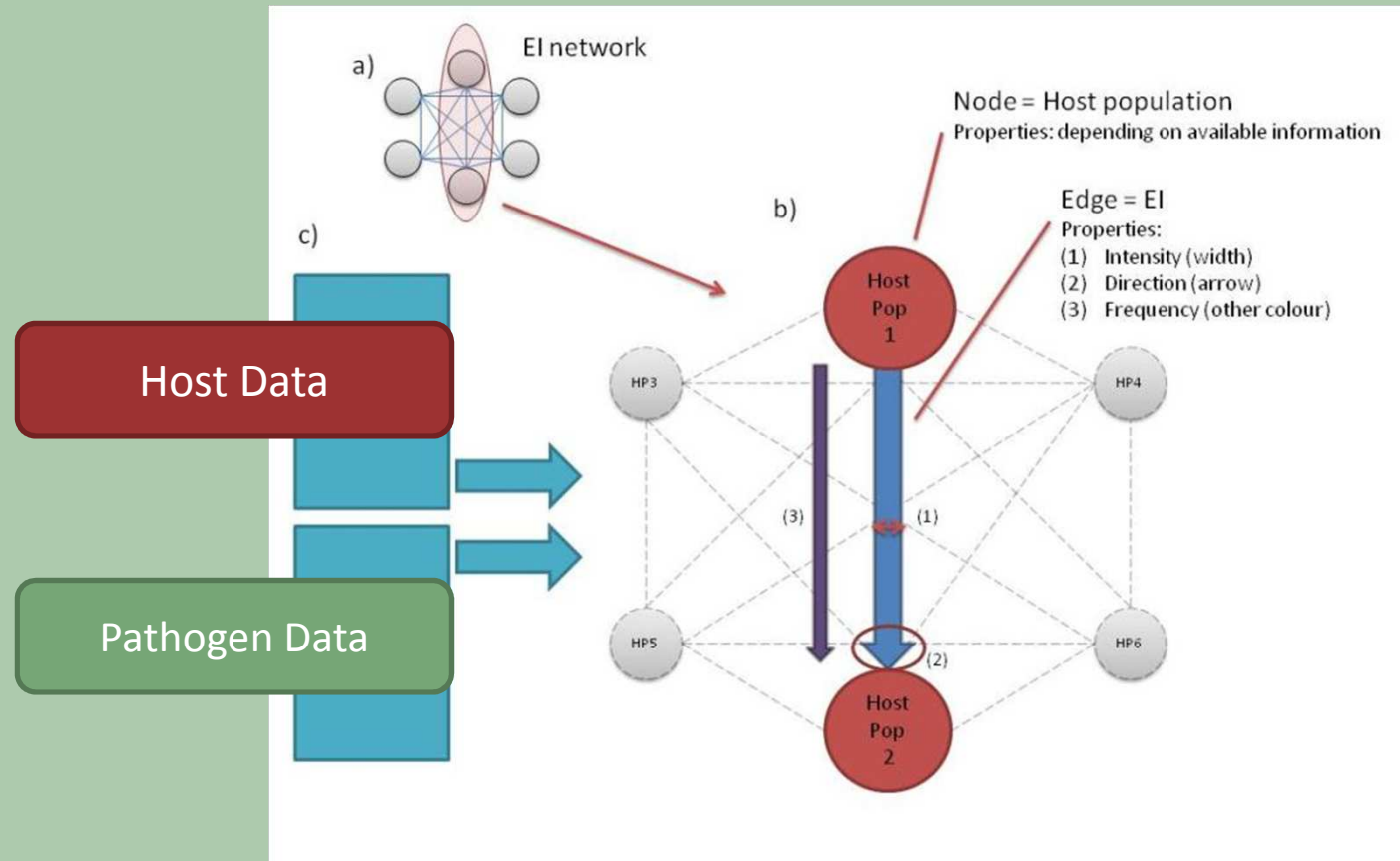
- Presence/absence – Prevalence – Molecular data
- Statistical tools e.g., controlling for host phylogeny



Information on: *Intensity & Direction of Els*

Integrating tool

# Network analysis as an integrative tool



Health et al. 2008  
Bansal et al. 2007  
Luke et al. 2007

Example

## e.g., Rodent community and their pathogens in SE Asia

- Theoretical example based on collected and literature data
- Ecosystems of South East Asia (Laos, Cambodia, Thailand)
- Target species: Human species
- Host populations: rodent community in SouthEast Asia
  - Presence-Absence data for:
    - Rodents in particular ecosystems
    - 34 macroparasites of rodents, pres/abs in humans from literature
    - 8 microparasites of rodents, , pres/abs in humans from literature

(Chasiri et al. 2010, Herbreteau et al. Unpublished)



## Pathogen Approach

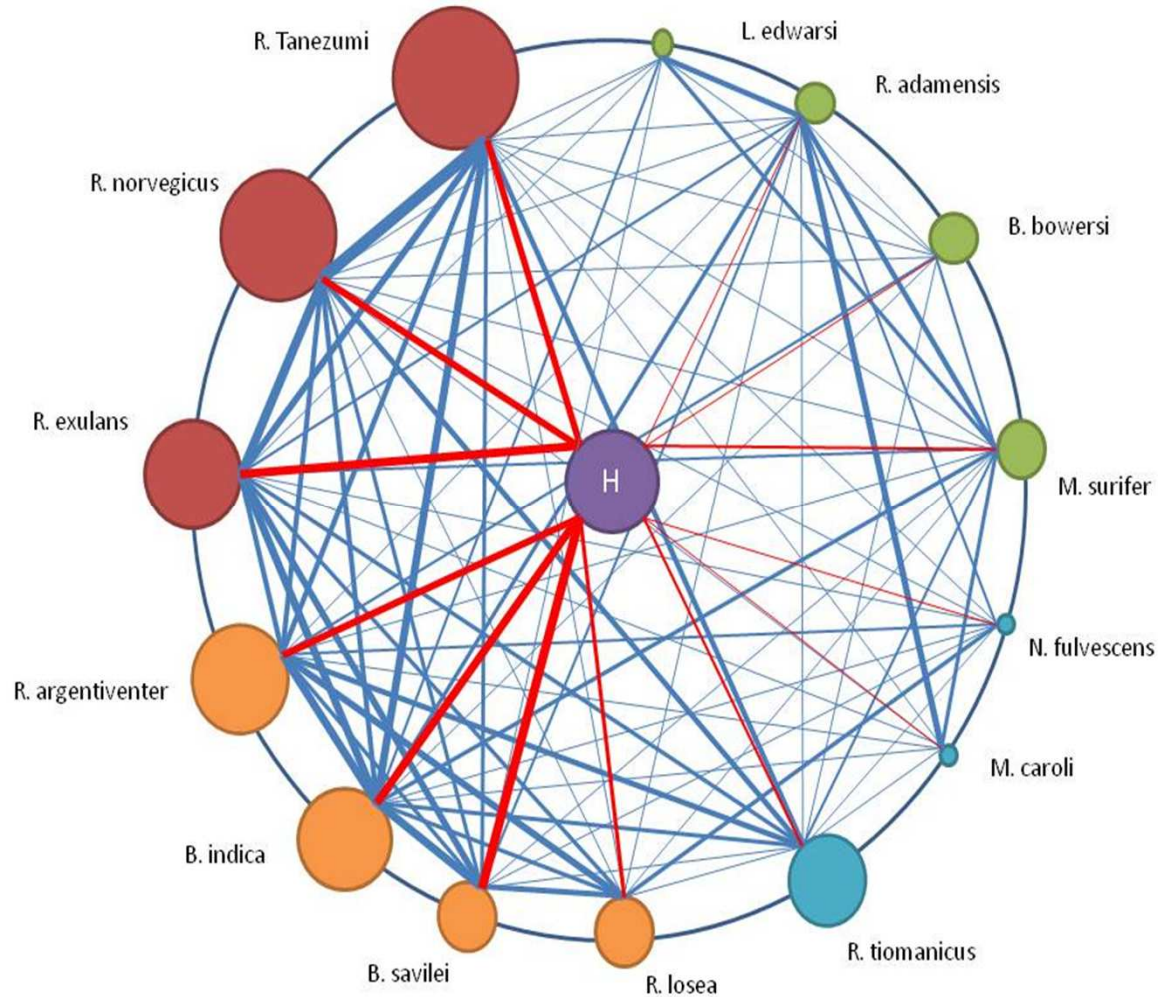
# Matrix of EIs

Target sp.	<i>Homo sapiens</i>
Rodent sp.	<i>Bandicota indicata (Bi)</i> , <i>Bandicota savilei (Bs)</i> , <i>Verylmys bowersi (Bb)</i> , <i>Leopoldamys edwardsi (Le)</i> , <i>Maxomys surifer (Ms)</i> , <i>Mus caroli (Mc)</i> , <i>Niviventer fulvescens (Nf)</i> , <i>Rattus andamanensis (Ran)</i> , <i>Rattus argentiventer (Rar)</i> , <i>Rattus exulans (Re)</i> , <i>Rattus losea (RI)</i> , <i>Rattus norvegicus (Rn)</i> , <i>Rattus tanezumi (Rta)</i> , <i>Rattus tiomanicus (Rti)</i>
Macroparasite sp.	<i>Hymenolepis nana</i> , <i>Rodentolepis sp.</i> , <i>Taenia sp.</i> , <i>Taenia taeniaeformis</i> , <i>Ascaris sp.</i> , <i>Gnathostoma malaysiae</i> , <i>Ganguleterakis spumosa</i> , <i>Citellina levini</i> , <i>Syphacia muris</i> , <i>Physaloptera sp.</i> , <i>Rictularia sp.</i> , <i>Rictularia tani</i> , <i>Gongylonema neoplasticum</i> , <i>Mastophorus muris</i> , <i>Protospiura-Mastophorus sp.</i> , <i>Cyclodontostomum purvisi</i> , <i>Strongyloides ratti</i> , <i>Strongyloides sp.</i> , <i>Nippostrongylus brasillensis</i> , <i>Nippostrongylus sp.</i> , <i>Orientostrongylus tenorai</i> , <i>Echinostoma ilocanum</i> , <i>Echinostoma malayanum</i> , <i>Notocotylus sp.</i> , <i>Quinqueserialis quinqueserialis</i> , <i>Gastrodiscoides hominis</i> , <i>Centrocestus sp.</i>
Microparasite sp.	<i>Leptospira</i> , scrub typhus, <i>Bartonella</i> , hanta virus, herpes virus, LCM virus, Trypanosoma, rabies virus.

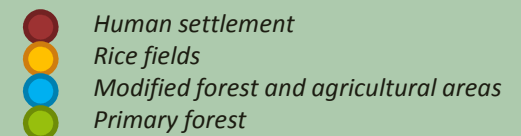
	Nb Para	Bi	Bs	Bb	Le	Ms	Mc	Nf	Ran	Rar	Re	RI	Rn	Rta	Rti	Hs
<b>Bi</b>	16															
<b>Bs</b>	9	0,47														
<b>Bb</b>	7	0,15	0,00													
<b>Le</b>	3	0,12	0,09	0,11												
<b>Ms</b>	8	0,20	0,06	0,15	0,22											
<b>Mc</b>	2	0,06	0,00	0,00	0,00	0,25										
<b>Nf</b>	2	0,06	0,10	0,00	0,00	0,00	0,00									
<b>Ran</b>	5	0,24	0,17	0,09	0,33	0,30	0,40	0,17								
<b>Rar</b>	17	0,43	0,24	0,14	0,00	0,09	0,06	0,12	0,10							
<b>Re</b>	18	0,48	0,35	0,00	0,11	0,13	0,05	0,05	0,15	0,30						
<b>RI</b>	9	0,19	0,29	0,00	0,00	0,06	0,00	0,22	0,08	0,37	0,23					
<b>Rn</b>	23	0,34	0,23	0,03	0,04	0,07	0,04	0,09	0,08	0,33	0,52	0,19				
<b>Rta</b>	32	0,45	0,24	0,11	0,06	0,14	0,03	0,06	0,09	0,32	0,47	0,17	0,72			
<b>Rti</b>	13	0,26	0,05	0,05	0,00	0,17	0,07	0,07	0,06	0,36	0,24	0,10	0,33	0,36		
<b>Hs</b>	15	0,48	0,50	0,05	0,06	0,21	0,06	0,06	0,18	0,28	0,43	0,20	0,41	0,42	0,17	

Matrix of shared community of pathogens between pairs of hosts  
(Jaccard Index =  $N_{\text{common}} / N_{\text{total}}$ )

## Epidemiological Interaction Network



- EIN skewed on the left
- Rodent Sp with the highest EI have the highest EI with humans
- Other species can be identified as potential link between environments:
  - *R. tiomanicus* could be a bridge species between forest environment and human settlements
- Provide more information than a separate analysis





# Conclusions



- Perspective:
  - New concepts and approaches open new perspective for exploring disease transmission ecology
  - Are there common properties for EIs → across ecosystems  
→ across pathogens
  - To which extent can we assume that transmission pathways used by some pathogens will be used by emerging pathogens?
  - How can social sciences be incorporated in this framework?
- From a practical point of view, this operational framework can be used:
  - to select host populations to survey for EIDs (EFG concept)
  - to develop an early detection surveillance based on available knowledge (in resource limited environment) targeting the most probable transmission pathways

## Conclusions

We believe that this operational framework could be an integrative tool for “One Health” studies exploring complex processes and systems at the Human/Livestock/Wildlife interface



# Acknowledgements



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- EU – PARSEL project



## Gripavi

Ecologie et épidémiologie  
de la grippe aviaire dans les pays du Sud

<http://gripavi.cirad.fr/>



Merci de votre attention