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

Can we anticipate emerging infectious diseases in their hotspots?

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How to follow pathogen emergence?

- Pathogens are dependent on the mobility of their hosts or their vectors for survival and spread
- We cannot « see » most of pathogens
- To track pathogen mobility:
  - Use host movements & contacts as an "a priori" estimator of pathogen movements
  - Use pathogen data in multiple host populations as an "a posteriori" estimator of movements

→ **We present a framework to investigate and predict pathogen movements in a given ecosystem based on their known pathogens**

Theoritical

Problematic

Applied

Emerging Infectious diseases (EID) and their hotspots

- Identified hotspots for emerging infectious diseases are often characterised by an extensive wildlife/domestic/human interface in tropical ecosystems (Jones et al., 2008, Woolhouse , 2008)
- This interface is a complex multi-hosts / ~~/~~multi-pathogens systems.

→ **How do we anticipate emerging events in these hotspots, when they have not yet occurred?**

Necessity of a new concept: Epidemiological Interaction (EI)

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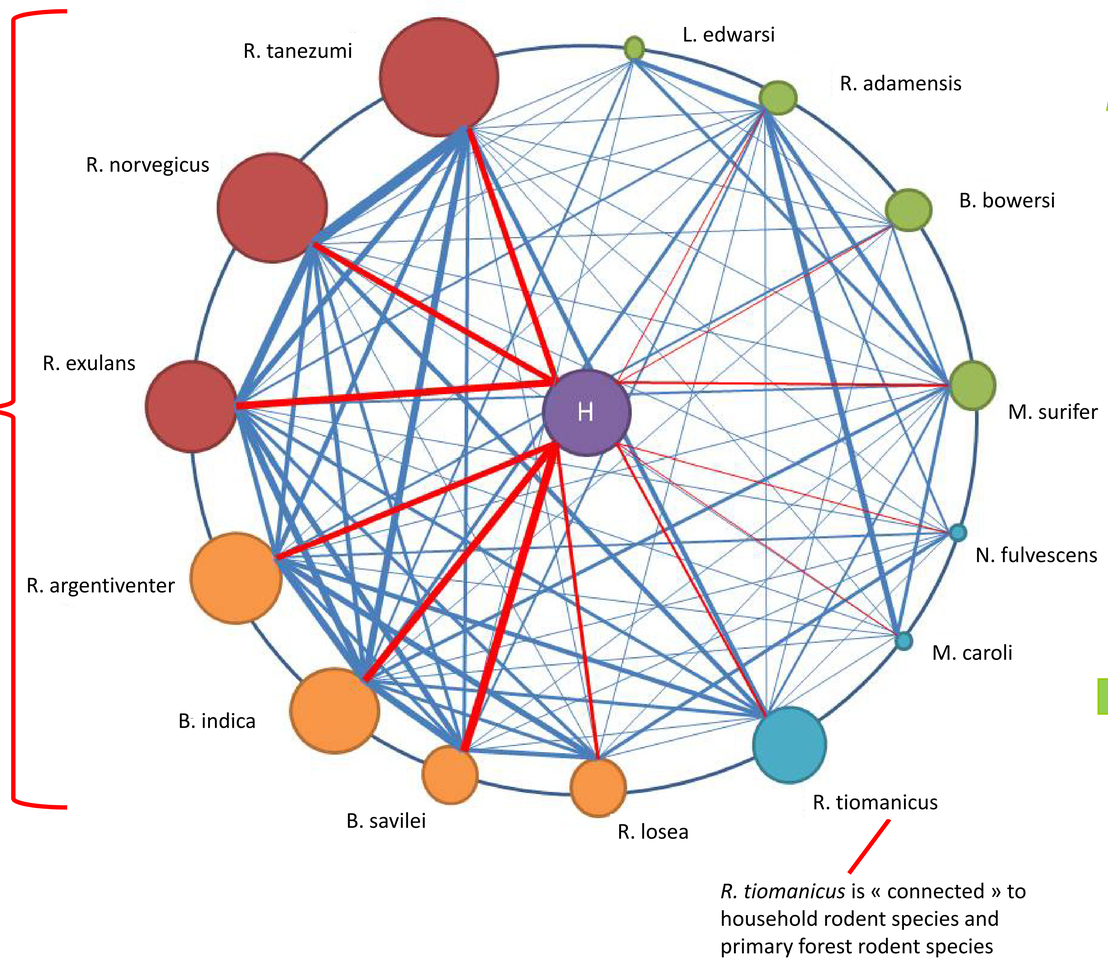
« Any ecological interaction resulting in the transfer of one or more pathogens between two host species »

This concept focus on the **transmission process** instead of a focusing on an individual host or a pathogen

Theoritical example: parasite of rodents and human in South-East Asia

Epidemiological Interaction Network *based on the Jaccard index calculated for each pair of host. Each node represents a host species, the size of the node is proportional to the number of parasite species harbored by the host and the color of the circle represents the environment in which the host species is mostly found (except for human): red=in human settlements; orange=in rice fields; blue=in modified forest; green=in primary forest. Each edge between two nodes represents the shared parasite community and its width is proportional to the Jaccard index.*



Based on field and literature data; study site is South-East Asia for macroparasite and Thailand for microparasites; presence/absence data on the following species of hosts and pathogens

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

Preliminary analysis

This EI network gives only indications on the intensity of EIs.

EIs can also be characterised in addition to their 'intensity', by their 'direction' and their 'frequency' (molecular data and time series dataset can help estimate these properties)

If the question is the probability of EID in the target human species from a rodent host in this ecosystem, this network can orientate surveillance protocols towards the most relevant rodent host species (e.g., species living in the human settlements or key species between the primary forest and human settlement – *R. tiomanicus*).

Specific discussion

However, exhaustive pathogen data is difficult to access

- For macroparasite data, you need to kill the host to have a total count
- For microparasite data, you cannot « see » the pathogen and need to look for it with specific diagnostic tools
- Advances in molecular tools can overcome these problems (e.g., "blind" RNA or DNA detection in faeces)

Once the EI network is built, you can target nodes (host populations) or edges (EI) for surveillance and control. By prioritizing key transmission pathways in the network, the future pathogen emergences can be more efficiently detected and prevented.

GENERAL CONCLUSIONS

Can we combine in EIs, information from different pathogens?

2 hypotheses:

1. EI network needs to be separately built for pathogens with different modes of transmission (e.g., directly transmitted, vector-borne)
2. There are common properties in transmission processes that can determine EI to a certain extent independently µfrom the parasite species.

This framework could help to develop the new field of transmission ecology

References

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This work has been implemented in the framework of the RP-PCP (Research Platform « Production and Conservation in Partnership »)

This work was co-funded by the ANR/CERoPath propject

and by the French Ministry of Foreign Affairs