ENVIRONMENTAL CHANGE AND THE RISK POSED BY NEW HOST-VECTOR-PATHOGEN INTERACTIONS

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Evolving Promises of the Life Sciences
Emerging vector-borne diseases – what are we up against?

- Increasing emergence of vector-borne pathogens worldwide with huge impacts on livelihoods and economies

- Multi-host, multi-vector systems

- Multiple drivers govern arrival, establishment, spread
  - Trade and travel
  - Climate and land use change
  - Human behaviour and social context

- Involve novel host-vector-pathogen interactions (ecological or evolutionary)

E.g. Bluetongue virus serotype 8 and Schmallenberg virus in Northern Europe
European midge species ‘latently competent’ to bluetongue and Schmallenberg virus

- Biting hosts?
- Reproductive behaviour?
- Breeding sites?
- Susceptibility to infection?

C. obsoletus complex

C. pulicaris complex

Culicoides imicola

Areas affected by BTV

- Areas affected by BTV before 1998
- Southern areas affected by BTV 1998-2006
- Areas affected by BTV-8 in 2007
- Areas affected by BTV-8 in 2006

Purse et al. 2008 OIE review
Challenges and weapons in our battle against emerging diseases

1. How can we better understand and predict disease emergence?

- **New diagnostic tools**
- **Molecular basis of**
  - infectivity
  - susceptibility
  - insecticide resistance
- **Statistical and biological models of vectors and disease**
  - intrinsic and extrinsic drivers
  - Key species interactions and networks
  - Test out theoretical paradigms e.g. Does biodiversity protects us against disease?

2. How can we integrate this improved understanding into frameworks for risk communication and disease management?

- **Trait-based models of disease**
- **Ecosystem approaches to disease management**
- **Multi-scale, spatial datasets** of social, climate, land use drivers
- **Policy relevant early warning systems and risk frameworks**
- **Pressure-state-response frameworks**
Is emergence convincingly linked to climate change?: Tick-borne encephalitis virus in eastern Europe

- Geographic variation in timing of upsurge
- Not explained by:
  - variation in warming
  - changes in health care systems

Sumilo et al. 2009, PLoS ONE 2(6)
Sumilo et al. 2008, Vaccine 26, 2580-2588
Higher TBE incidence

Socio-economic factors determine human exposure to disease: Tick-borne encephalitis virus in eastern Europe

Intrinsic processes govern spread of orbiviruses across landscapes following arrival in new land masses

- Traditional view: midges are passengers on the wind
- BTV-8 spread across Northern Europe, analysed role of random and upwind active midge movements versus ‘passive’ downwind spread

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\text{Ghent} \\
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\text{Maastricht}
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- largely local scale (2km a day), disease moves in short hops, few downwind or long distance movements
- 70% farms transmission “dead ends”
- Implications for scale of control and surveillance

How does exposure to infection depend on how individuals use ecosystems? Malaria in Camargue

- *Anopheles* mosquitoes historically transmitted *Plasmodium* malaria
- Patch work landscape, different uses by mosquitoes and people determine exposure and re-emergence

- Who is most at risk and where?
  Socio-economic surveys + agent-based modelling

Linard et al. 2009 Ecological Modelling
How does exposure to infection depend on how individuals use ecosystems? Malaria in Camargue

Agent based model

People vary in movements and protective behaviours

Groups of people using the landscape

Mosquitoes – abundance and movements

• Contact rates highest in highly populated areas close to rice fields
• Hunters most exposed agents – sunset activity

Linard et al. 2009 Ecological Modelling
Integrating ecological understanding into frameworks for risk communication and disease management.

![Diagram showing the integration of ecological understanding into risk communication and disease management frameworks.](image-url)
Horizon-scanning for new pathogens: promise of trait-based risk assessment

How can we predict latent suitability of host and vector communities for emergence of different pathogens?

• Lab assessments of susceptibility/infectivity, costly and time consuming – “Needle in a haystack”

• Trait-based models useful for establishing general patterns in invasion biology

• Can we link ecological traits of hosts and vectors to susceptibility (under different environmental conditions)?

• Can we link functional traits of pathogens to their virulence, infectivity and propensity for emergence and spread?

  • e.g. Woolhouse et al. TREE 2005. Directly transmitted RNA viruses most likely to jump between host species
  • 2011 ESA Annual Meeting : Toward Trait-based Disease Ecology: Integrating Theory and Data Across Kingdoms
- Horizon-scanning for new pathogens: promise of trait-based risk assessment

Slide provided by Mark Fife, Pirbright Institute

- This provides opportunity for comparative genomics
- Common transmission mechanisms between all vector species?
- Specific genes common to the vector competent Culicoides species
Improving the weapons in our battle against emerging diseases

1. Understanding disease emergence
   - New diagnostic tools
   - Molecular basis of Vector-host-pathogen interactions
   - Statistical and biological models of vectors and disease
   - Multi-scale, spatial datasets of social, climate, land use drivers

2. Frameworks for risk communication and disease management
   - Links to strengthen
   - Geo-referenced, genotype-specific surveillance data
   - Prevalence in wild animals?
   - Human decisions and exposure
   - Human decisions and environmental change
   - Trade offs between ecosystem services

- Trait-based models of disease
- Policy relevant early warning systems and risk frameworks
- Pressure-state-response frameworks
- Ecosystem approaches to disease management
- Links to strengthen