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# The invasive bank vole (Myodes glareolus): A model system for studying parasites and ecoimmunology during a biological invasion

Andrew McManus (MTU); Prof. Celia Holland (TCD); Dr. Peter Stuart (MTU).

### Background

- 60% of Emerging Infectious Diseases (EIDs) originated from wildlife (Jones et al., 2008).
- From 1,415 pathogenic species infecting humans; 61% zoonotic and 32% helminth species (Taylor, Latham & Woolhouse, 2001).
- Parasites impact fecundity and mortality rates of rodents (Scott & Lewis, 1987; Pedersen & Greives, 2008).
- Need for wildlife models to understand EIDs; rodents present informative model species (Pedersen & Babayan, 2011).

# The Irish bank vole invasion

- Depauperate small mammal community in Ireland.
- Myodes glareolus suspected arrival in 1920s, with a single introduction point (Stuart et al., 2007).
- Invasion gradient 2.23-2.63km/year (White et al., 2012)
- No eradication attempts.
- Baseline parasite data for *M. glareolus and Apodemus* sylvaticus (native wood mouse) (Loxton et al., 2016, Loxton *et al.*, 2017, Stuart *et al.*,2020).

**Table 1.** Helminth species recorded in *A. sylvaticus* and *M.* glareolus (see Loxton et al., 2016; 2017 and Stuart et al., 2020). Names in brackets are previous species names.

A. sylvaticus						
Taxon	Loxton et al. (2016; 2017)	Stuart et al. (2020)				
Nematoda	Syphacia stroma	Syphacia stroma				
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# **Bio-invasion Disease dynamics**



(C) Dilution & Spillback Non-native species infected with native parasites and can cause (i) spillback or (ii) dilution of infection

Figure 1. Disease dynamics of a biological invasion. Parasites introduced with the non-native species are indicated by red circles, while parasites from the native host are indicated by yellow diamonds. Adapted from Loxton (2015) and Hatcher and Dunn (2011).

# Dynamics in the Irish rodent model

- Enemy Release: only 3 species recovered in Irish bank vole population compared to their native range, which carry between 3-14 species.
- **Dilution:** Overall lower Brillouin's Index of Diversity in A. sylvaticus at core invaded sites compared to expansion front and uninvaded sites.
- Spillback: increased prevalence of Aonchotheca

			Aonchotheca murissylvatici	Aonchotheca murissylvatici	
			Trichuris muris	Trichuris muris	
			Heligmosomoides polygyrus	Heligmosomoides polygyrus	
		Cestoda	Hymenolepis hibernia	Hymenolepis hibernia	
			Skrjabinotaenia lobata	Hymenolepis sp.	
			Taenia martis	Skrjabinotaenia lobata	
			Hydatigera taeniaeformis	Taenia martis	
			(Taenia taeniaeformis)	Taenia polyacantha	
				Hydatigera taeniaeformis	
		Trematoda	Brachylaemus recurvum	Brachylaemus recurvum	
			Corrigia vitta	Corrigia vitta	
		Total Sp.	10	12	
M. glareolus					
		Taxon	Loxton et al. (2016; 2017)	Stuart et al. (2020)	
		Nematoda	Aonchotheca murissylvatici	Aonchotheca murissylvatici	
			Aspiculuris tianjinensis	Aspiculuris tianjinensis	
		Cestoda	Taenia martis	Taenia martis	
				Taenia polyacantha	
		Total Sp.	3	4	
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*murissylvatici* in *A. sylvaticus* at core sites invaded by *M.* glareolus.

**Amplification:** both Syphacia stroma and Skrjabinotaenia lobata show higher abundances in A. sylvaticus at core sites compared to expansion front and uninvaded sites.

(Loxton et al., 2016, Loxton et al., 2017, Stuart et al., 2020)

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