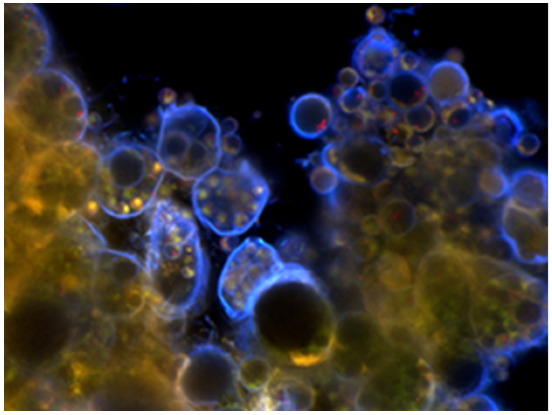
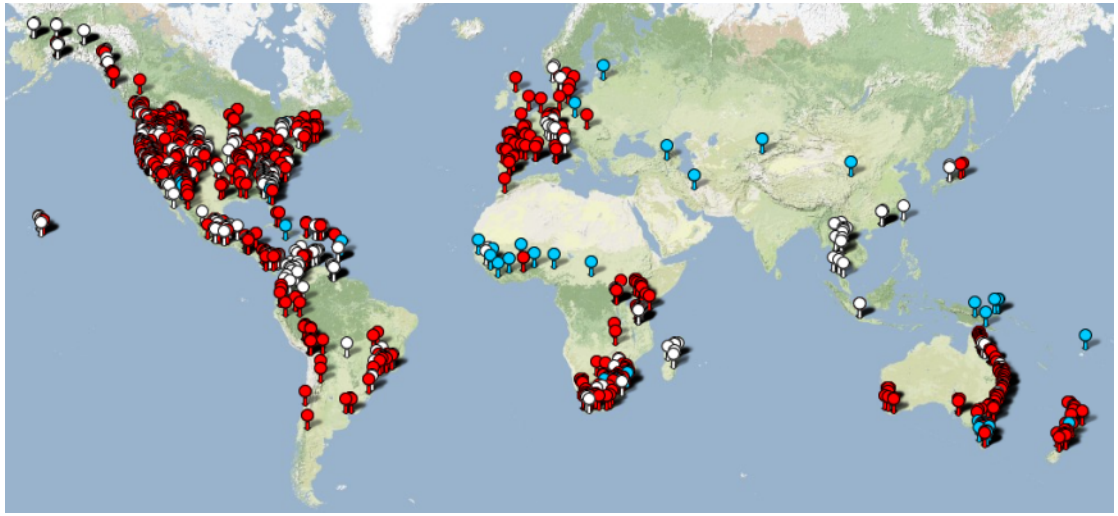
Imperial College London



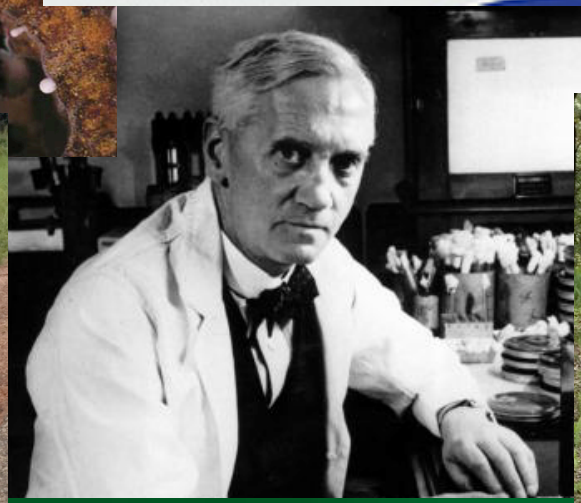
Emerging fungal threats to animal, plant and ecosystem health

Matthew Fisher

Dpt Infectious Disease Epidemiology



The Kingdom fungi are dazzlingly diverse, ~150,000 described species but 1~5 million estimated (>5% described)



‘Planetary disasters: It could happen one night’ *Nature* 8 Jan’13

‘Planetary disasters: It could happen one night’ *Nature* 8 Jan’13

- Death by volcano
- Death by solar flares
- Death by tsunami
- **Death by fungal epidemics**

Are emerging infectious fungi, and ‘fungal-like’ oomycetes, a real or imagined threat?

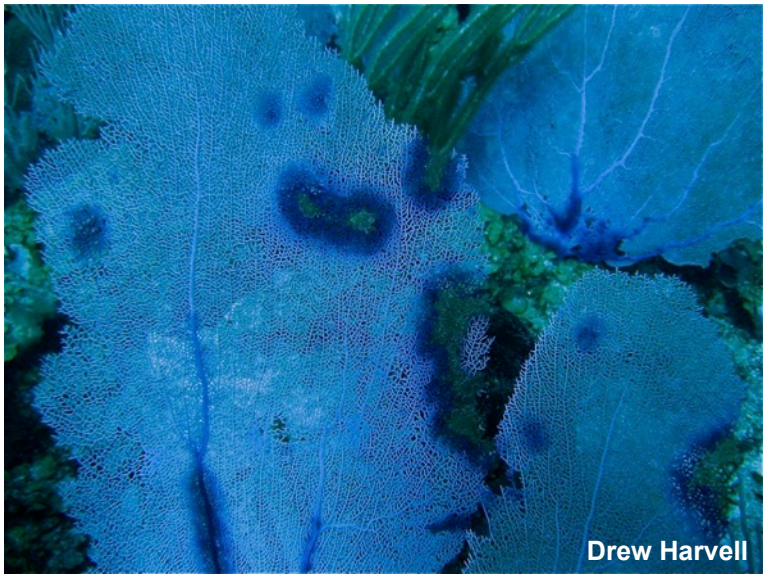
Batrachochytrium dendrobatidis (*Bd*)
Amphibian chytridiomycosis worldwide

Pseudogymnoascus destructans
Bat white-nose syndrome, USA

The fungal threat appears widespread across ‘animal’ species

Fusarium solani & turtles

Aspergillus sydowii & coral



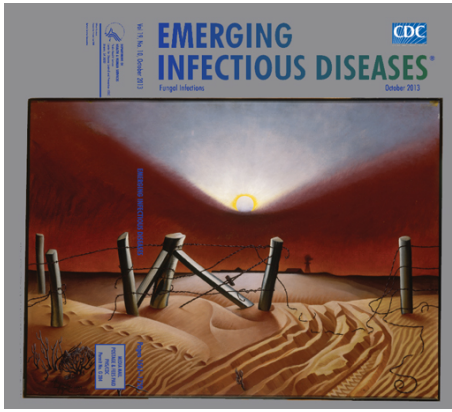
Nosema & honeybee CCD

Ophidiomyces and Snake Fungal Disease

The fungal threat appears widespread across ‘animal’ species

Humans are animals

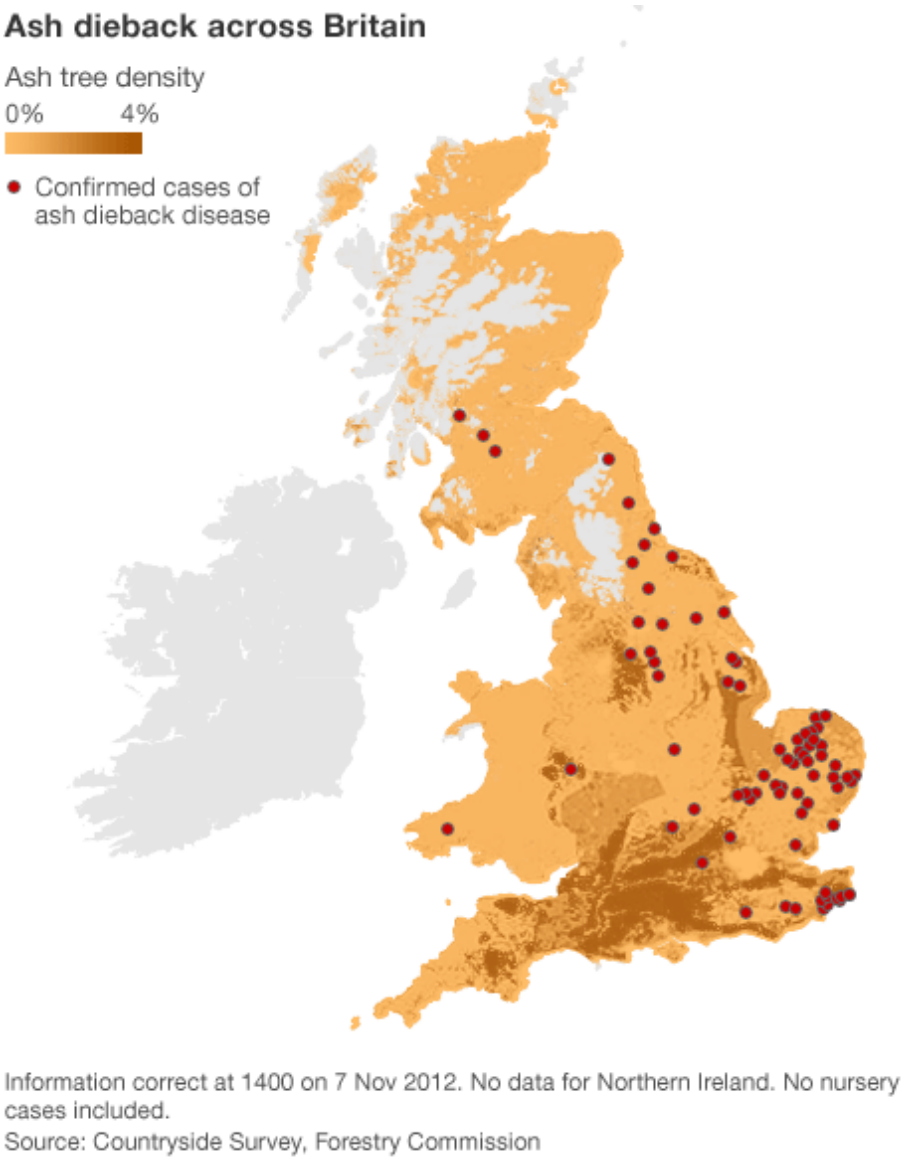
Latest edition of *Emerging Infectious Diseases*



- ↑ **Coccidioidomycosis–associated hospitalisations** (Sondermeyer *et al*)
- ↑ **in *Cryptococcus gattii* in the Pacific Northwest USA** (Harris *et al*)
- ↑ **Incidence of invasive fusarosis, Brazil** (Nucci *et al*)

And lets not forget the Plants either…

Chalara fraxinea (*Hymenoscyphus pseudoalbidus*). Ash dieback invades UK, first described in Poland in the ’90’s



Emerging fungal disease threatens ecosystem services

Disease	Pathogen	Host range	Regional losses[1]	Regional losses of absorbed CO_2 (megatonnes)
Dutch Elm	***Ophiostoma ulmi***	Elm	25 million elms (UK, 1990's) 77 million elms (USA, by 2001)	0.395 to 1
Chestnut blight	***Cryphonectria parasitica***	Chestnut	3.5 billion US chestnuts (USA, by 1940's)	13.8 to 35
Sudden oak death / ramorum blight	***Phytophthora ramorum***	Oak, larch *etc.*	1.4 million oaks in California Pre-emptive cull of 4 million larches (UK 2011)	0.012 to 0.05
'Jarrah' dieback	***Phytophthora cinnamomi***	2,000 of 9,000 native *spp.* in Western Australia	1 million hectares of western Australia (by 2009)	9 to 23
Pine beetle / blue stain	***Grossmania clavigera***	Lodge pole pine	16.3 million hectares of western Canada (by 2011)	207 - 520

Total: 230 – 580 megatonnes of CO_2 (0.07%) of the global total

Emerging fungal disease threaten food security

Crop *Host species*	2009/2010 harvest (million tonnes)	Calories per 100g flour (un-cooked)	Disease/Pathogen and variation in % losses	Loss of food* for *x* million over 1 year, given diet of 2,000 calories per day
Rice	701 harvest but 476* milled for food	325	***Magnaporthe oryzae*** 10-35%	212 to 742
Wheat	679 harvest but 432* for food	341	***Puccinia graminis*** 10-70%	202 to 1,413
Maize	820 harvest but 271* for food	355	***Ustilago maydis*** 2-20%	26 to 262
Potato	333* harvest but for food	357	***Phytophthora infestans*** 5-78%	81 to 1,270
Soybean	232 harvest but 148* for food	372	***Phakospora pachyrhizi*** 10-80%	75 to 600

Total: Could feed 596 (9%) - 4,287 (61%) million mouths *per annum*

Are we seeing ↑ incidence of fungal pathogens?

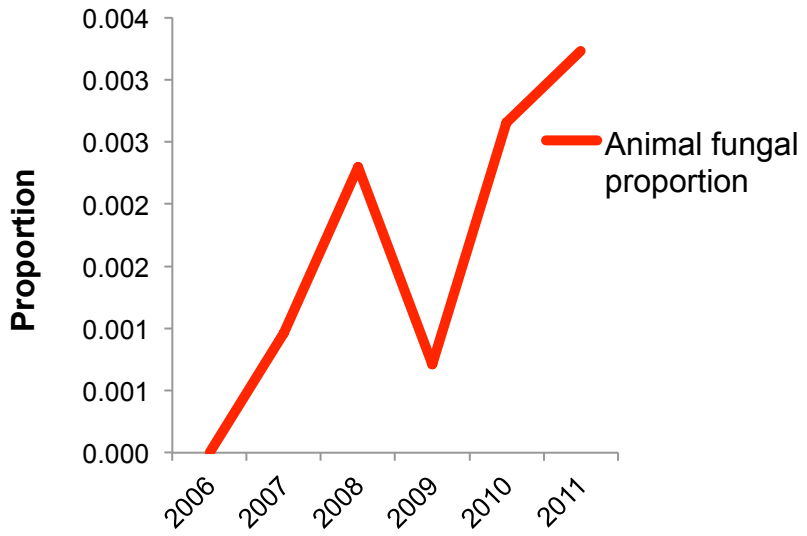
April 484: 2012

Global disease alerts captured by

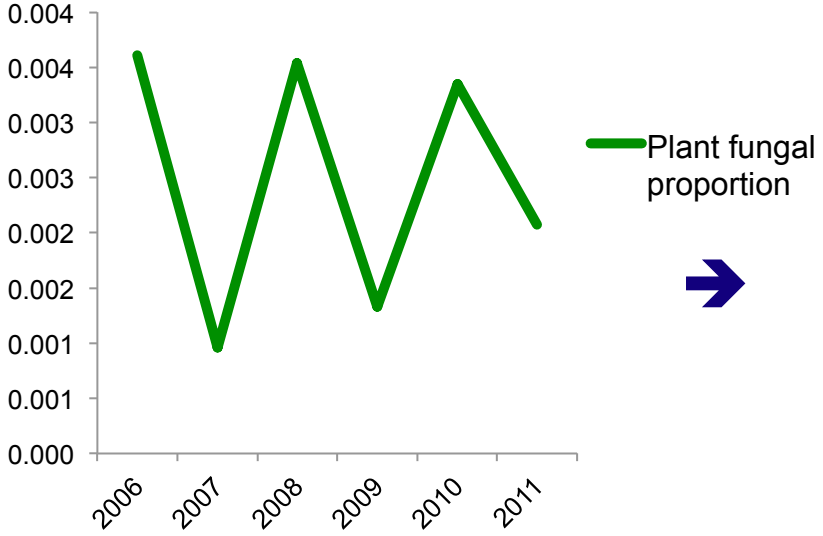
- **ProMED (Active reporting, 1994 – 2010; 38,000 records)**
- **HealthMAP (Captures online datasources, 2006 – 2010; 43,000 records)**
- **Species extinction catalogued by *Web of Science* literature searches**

Fungal alerts are generally increasing in relation to other pathogen taxa in both databases

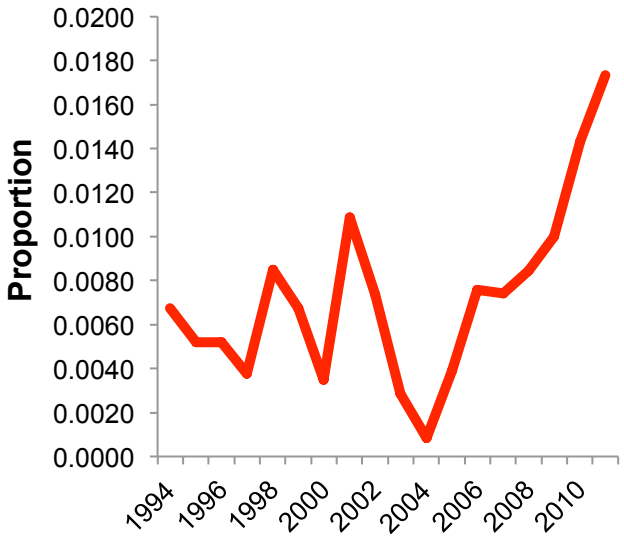
HealthMap **animal fungal alerts**



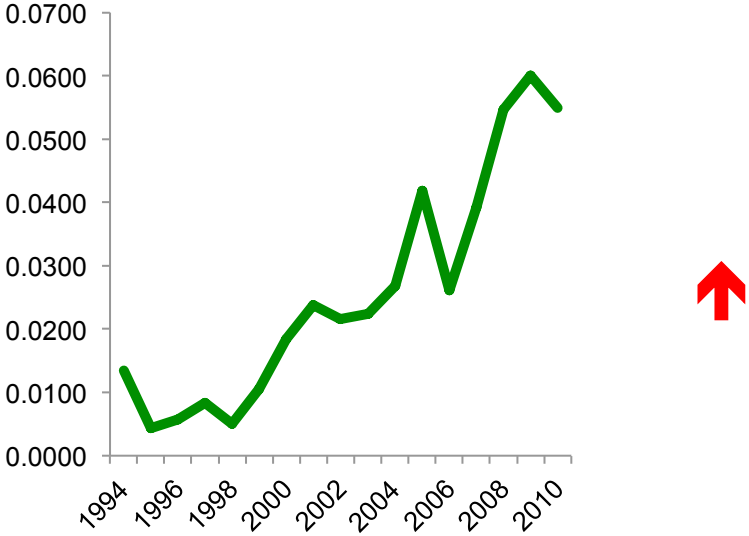
HealthMap **plant fungal alerts**

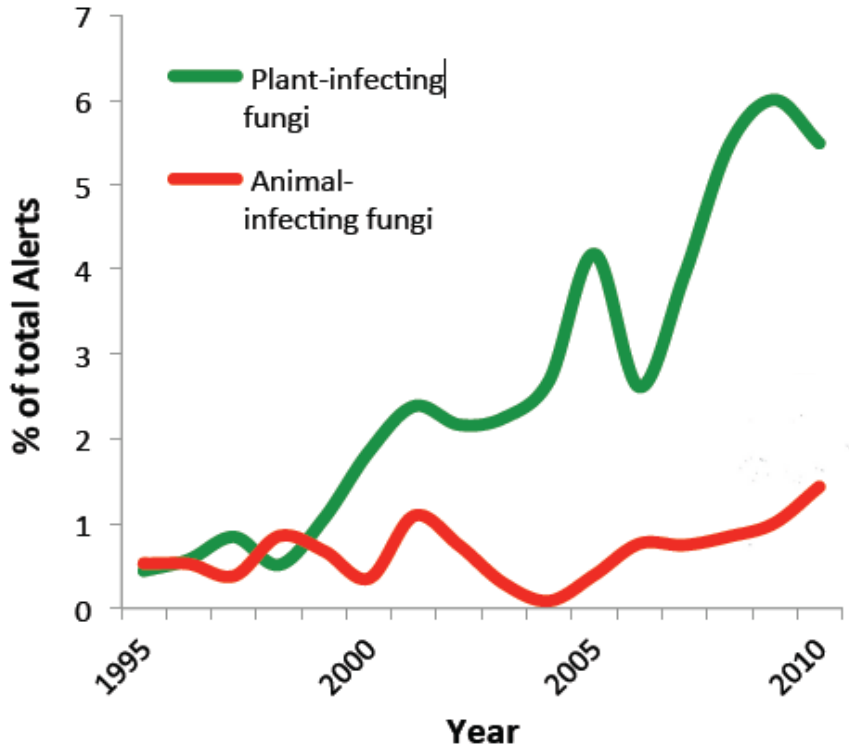


ProMED mail **animal fungal alerts**



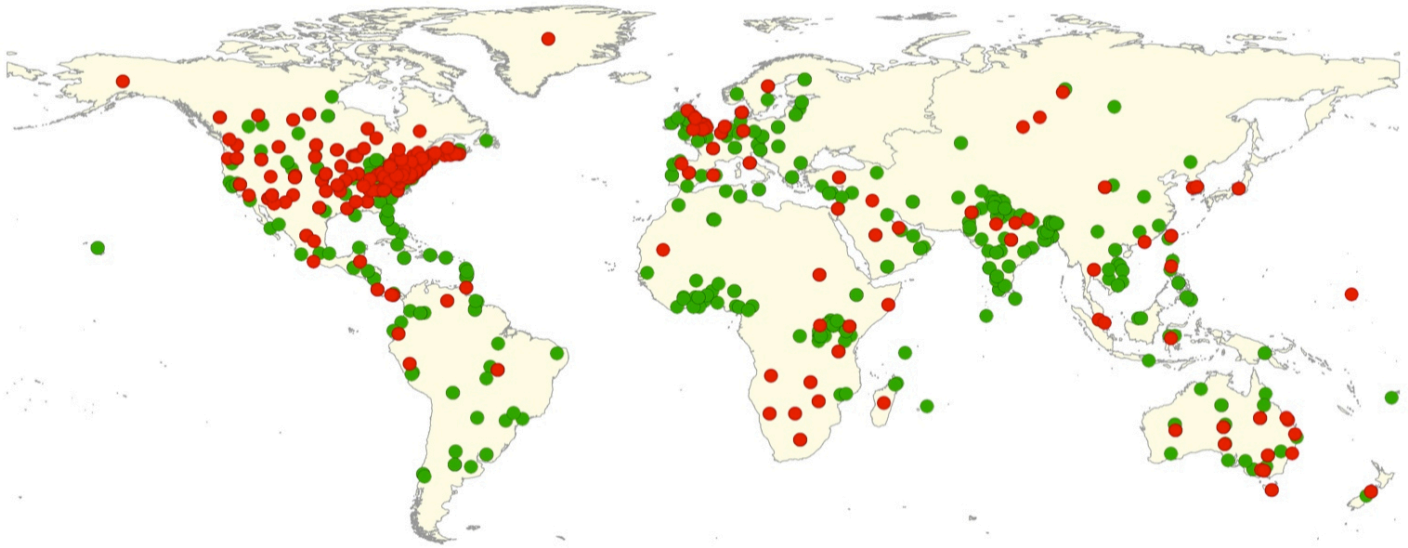
ProMED mail **plant fungal alerts**



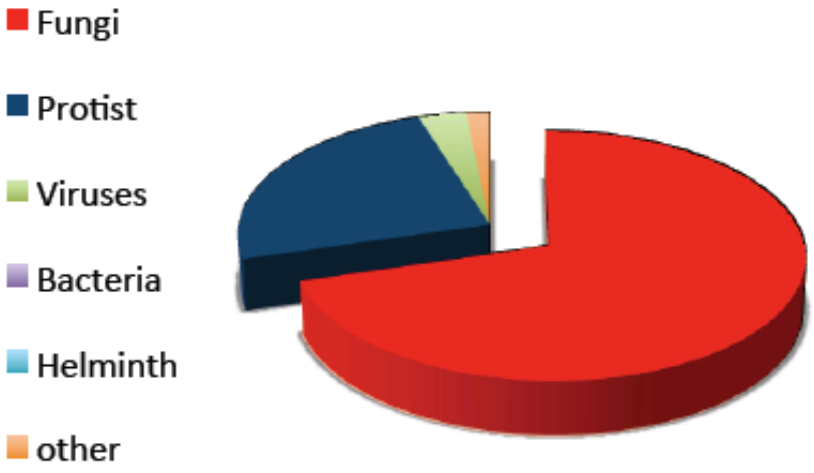


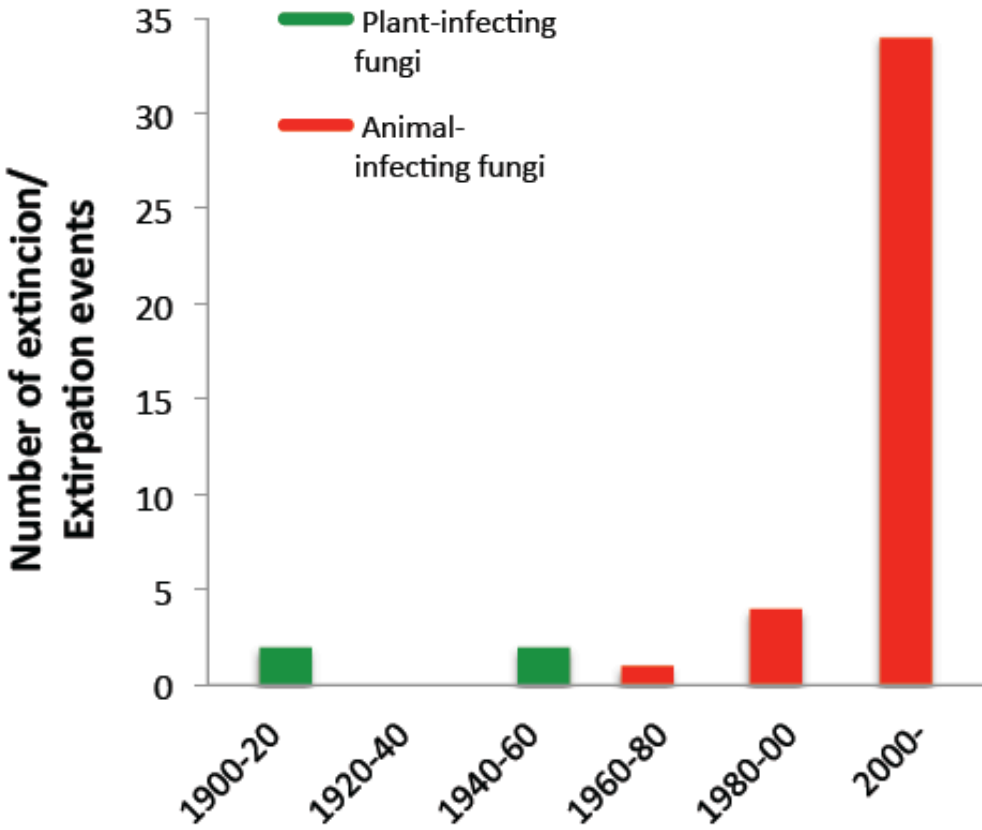
ProMED mail

Alerts are globally distributed

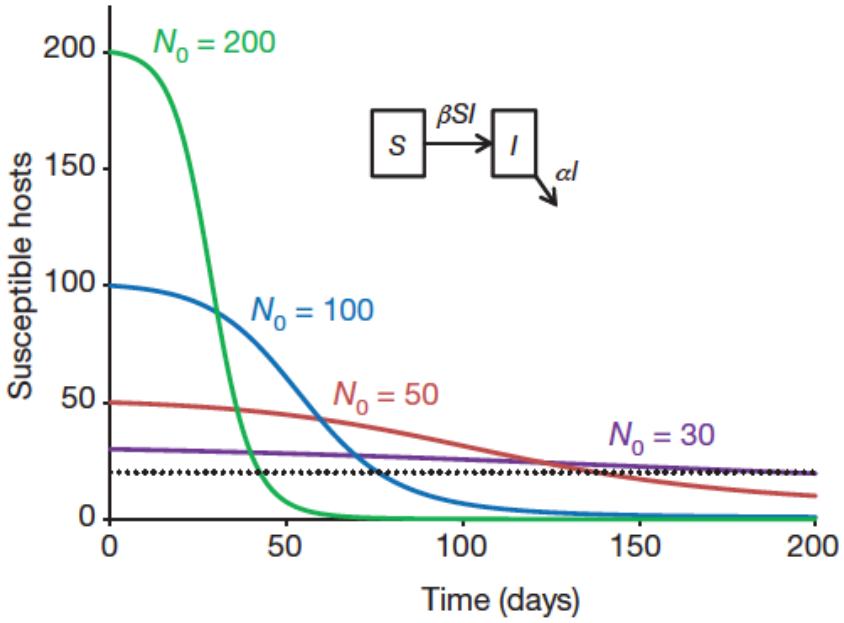


Fungi comprise the highest threat of extinction owing to infection for both animal (72% of extinctions) and plants (64% of extinctions), and this threat appears to be increasing



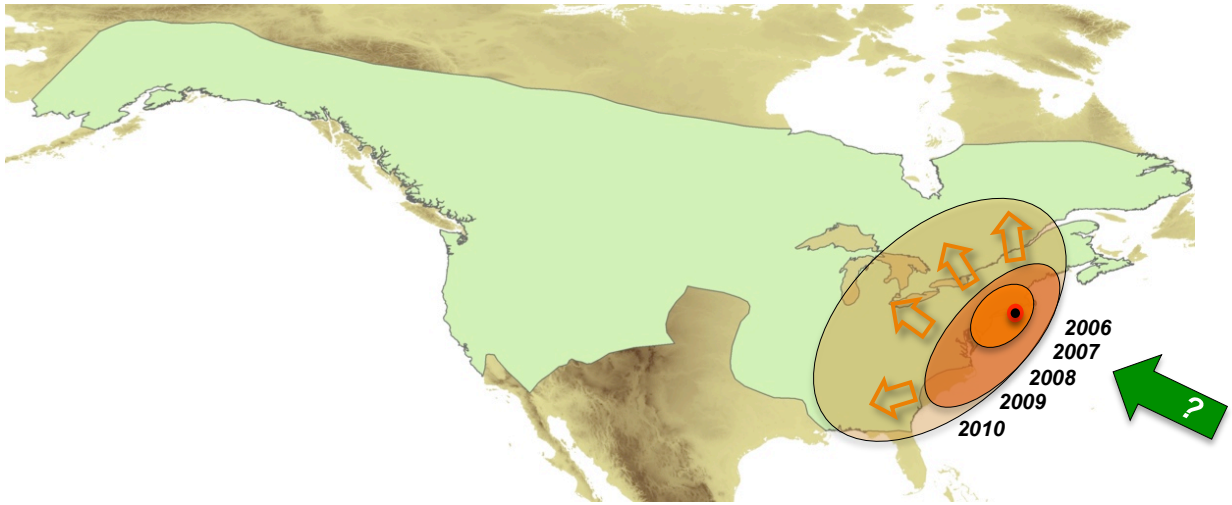


Fungal disease dynamics predispose them to emergence and drive extinction processes. *In combination….*



High virulence

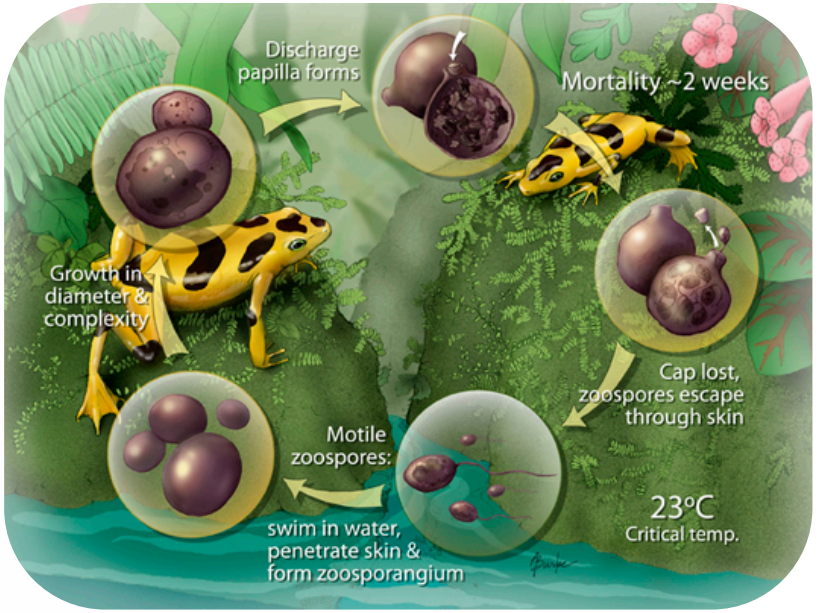
99% probability of *Myotis* bat regional extinction in the next 16 years as the invading clonal genotype of *Pseudogymnoascus* spreads (Frick *Science* 2010)

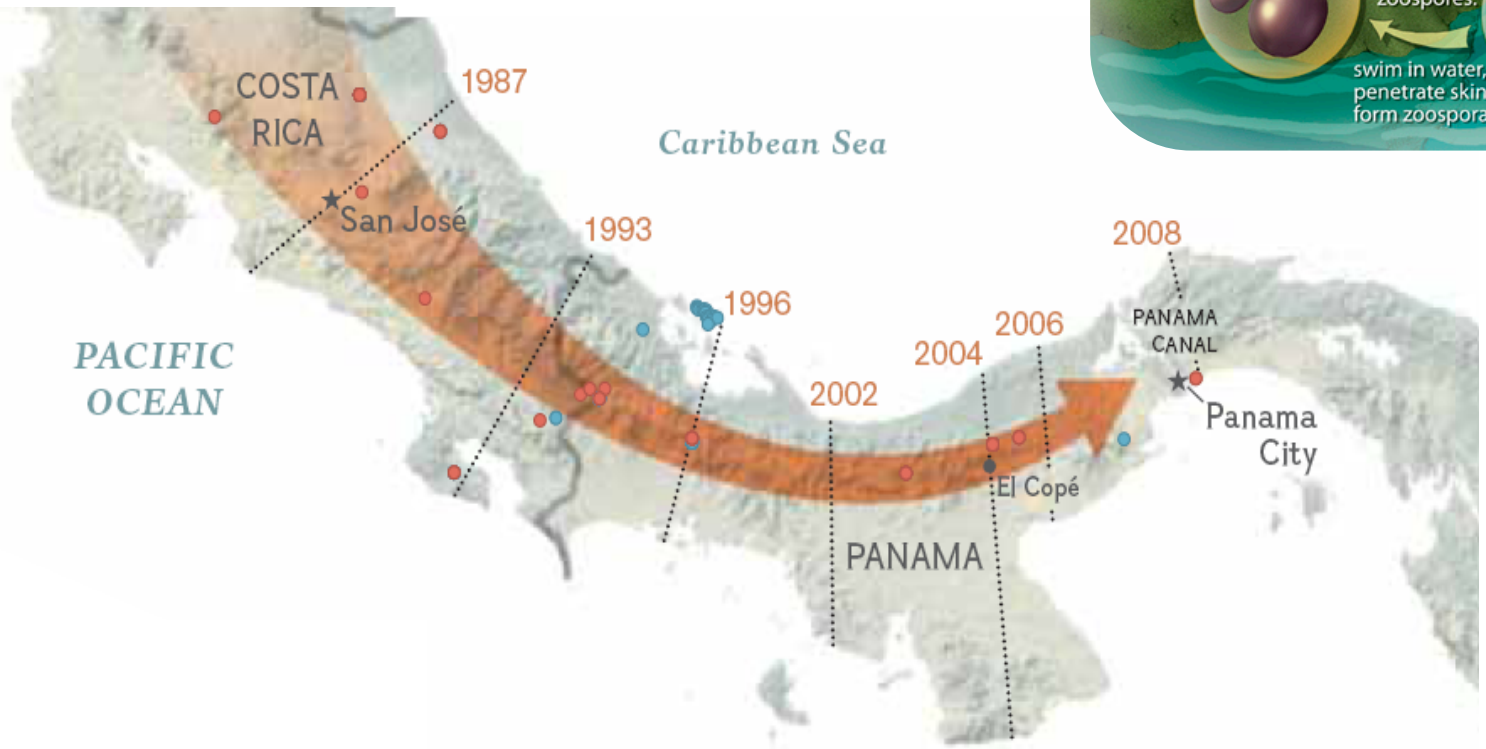


Equates to a loss of $3.7 billion pa. in pest-control services

Batrachochytrium dendrobatidis is the cause celebré for mycotic outbreaks

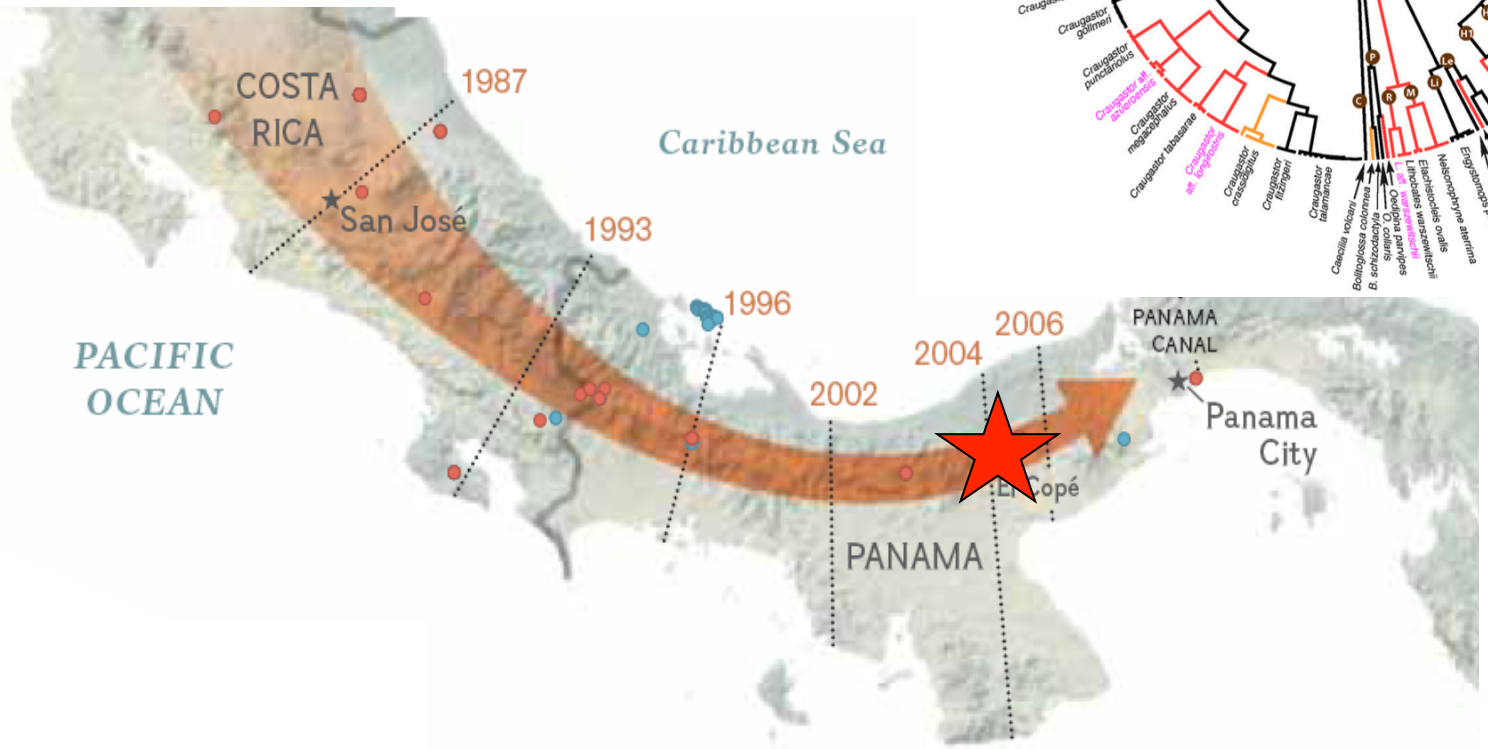
'The worst infectious disease ever recorded amongst vertebrates in terms of the numbers of species impacted and its propensity to drive them to extinction..'
ACAP 2007

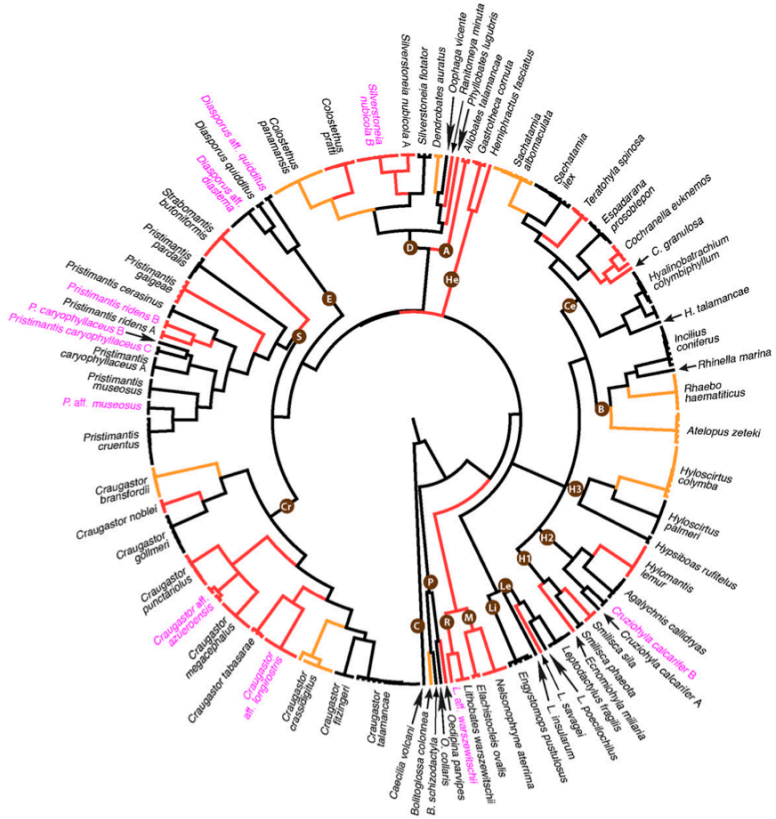




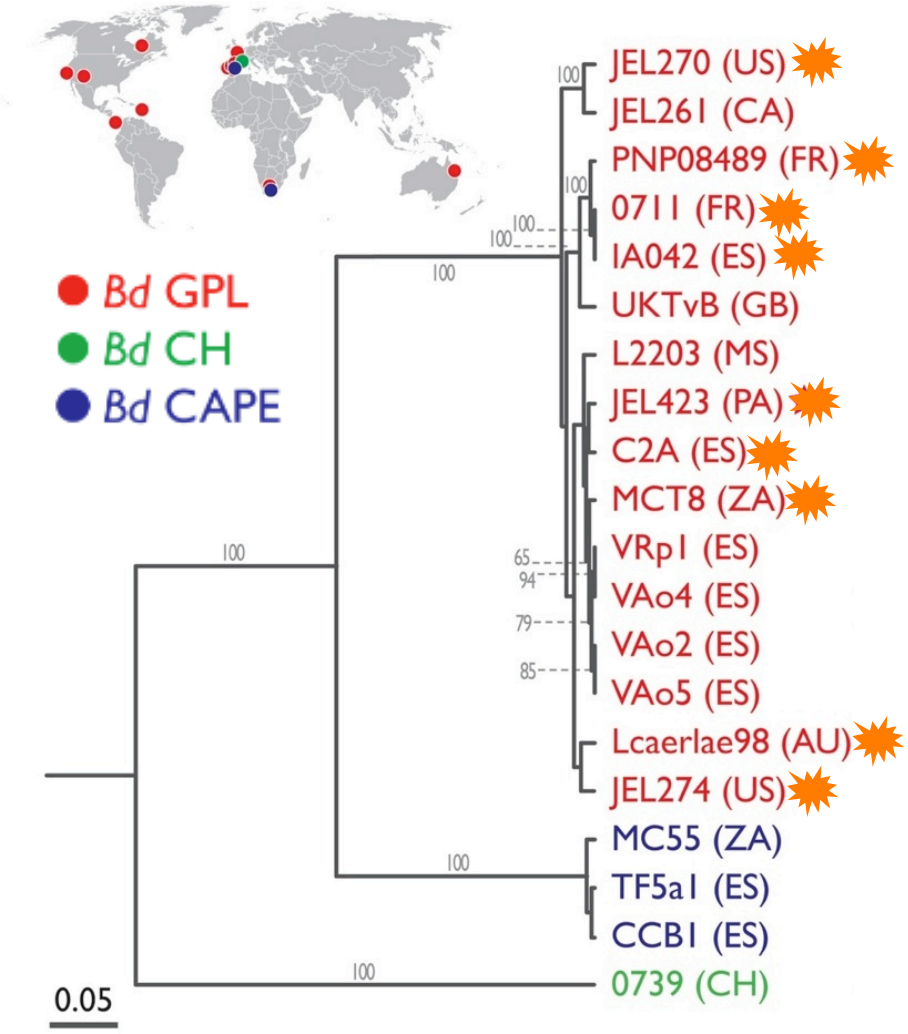
41% of amphibian lineage diversity in El Cope extirpated by the infection

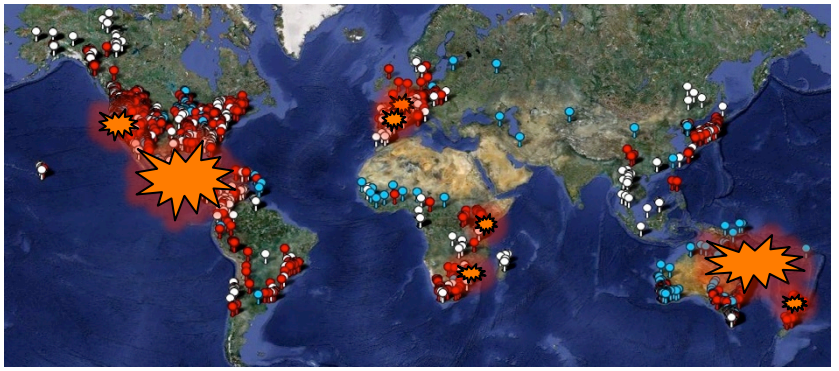
Crawford et al PNAS 2010

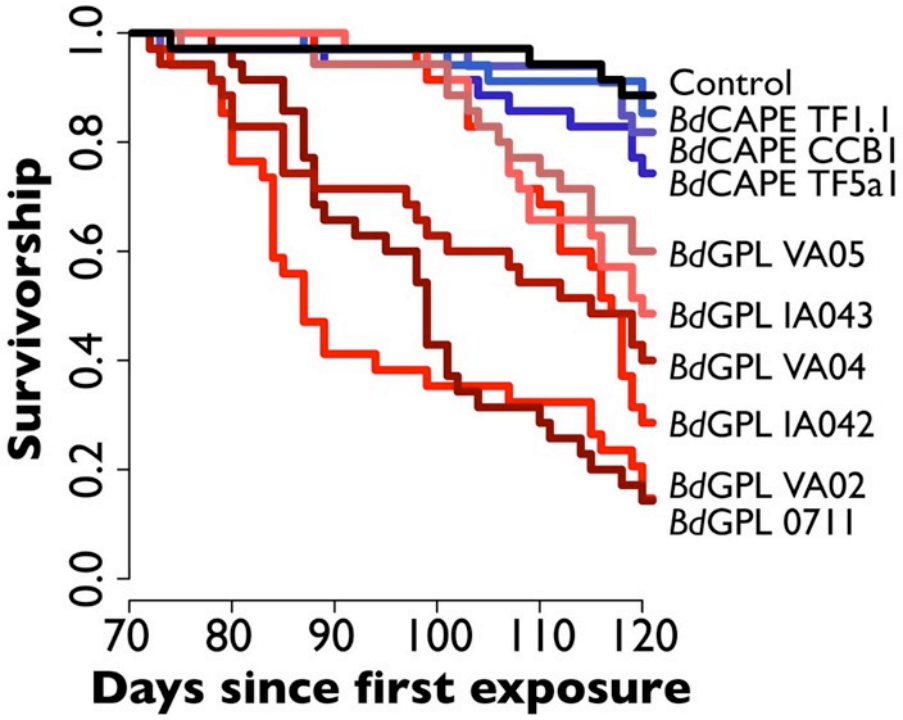




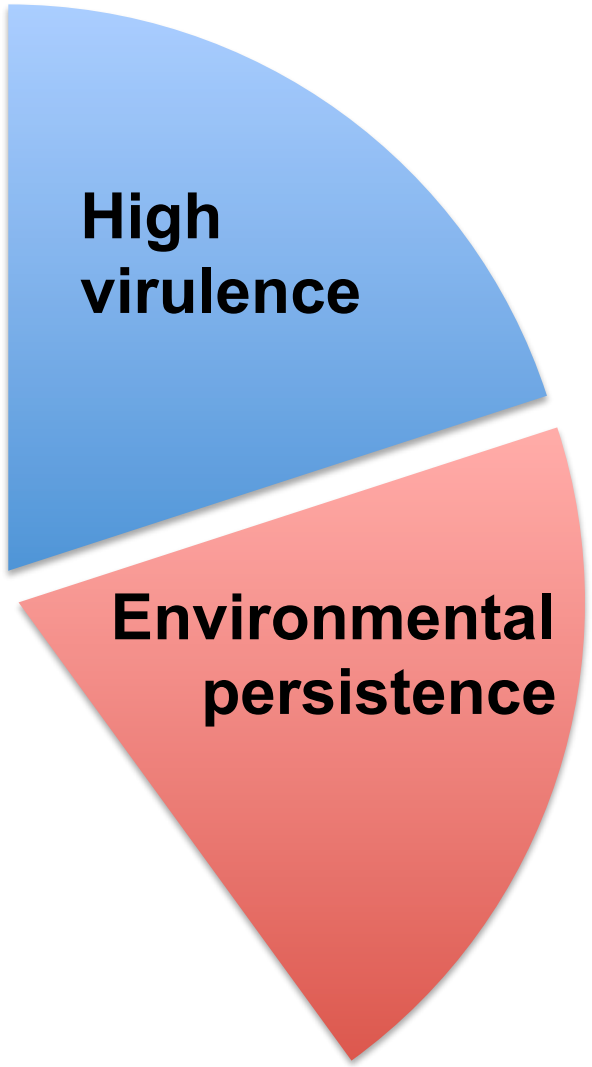
One lineage, the *Bd* Global Panzootic Lineage *Bd*GPL,shows high virulence and is associated with the emergence of 20th Century epizootics worldwide (Farrer et al *PNAS* 2010)



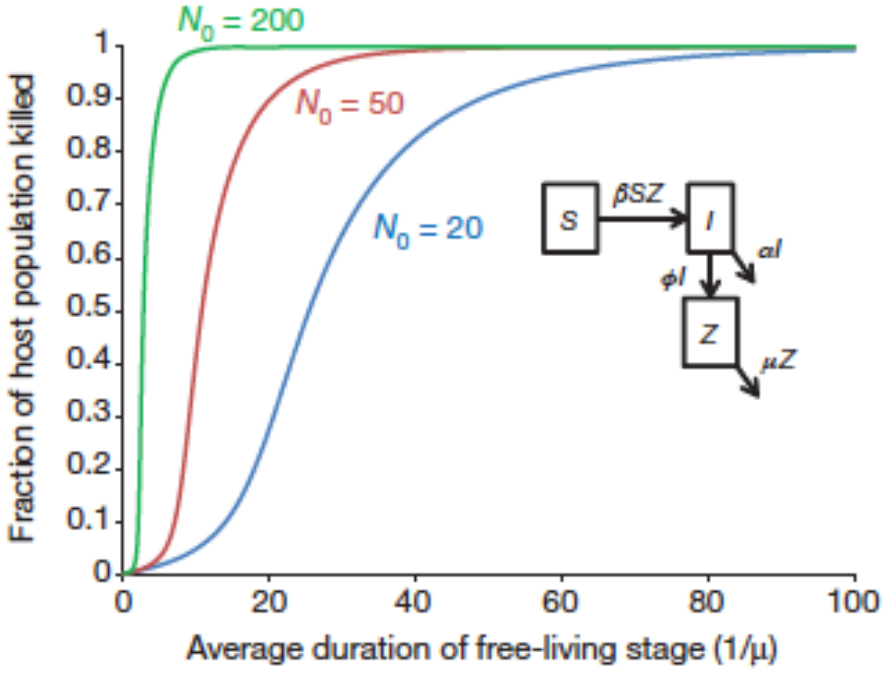


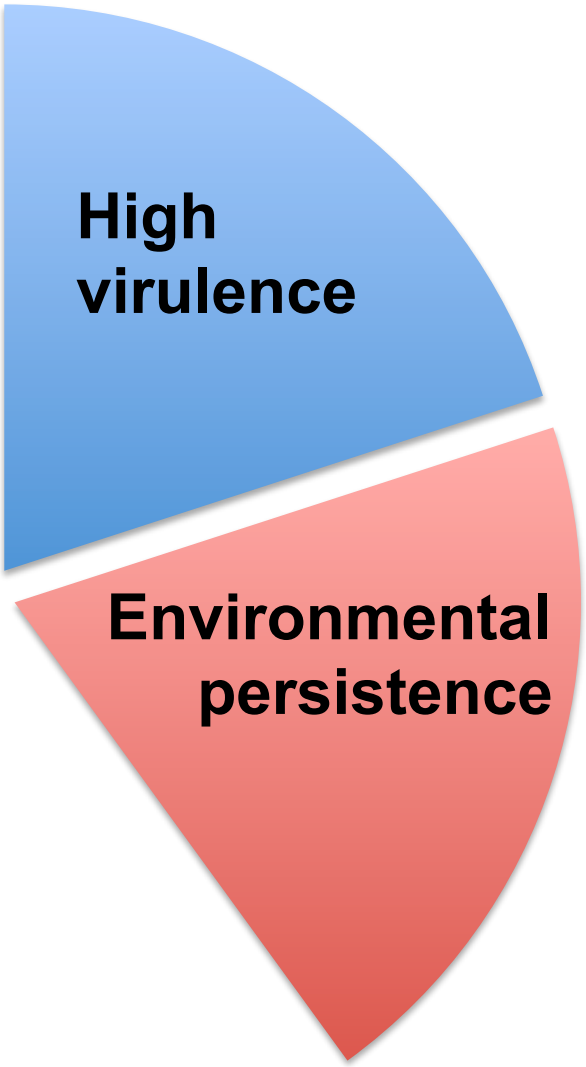


Disease dynamics 2.



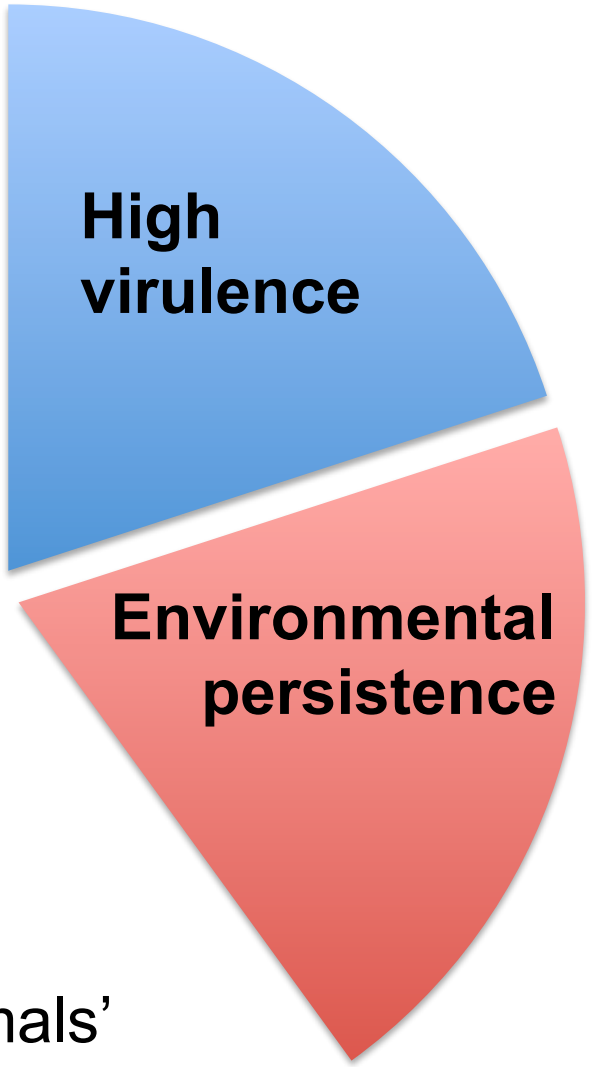
Disease dynamics 2.





Sapronotic potential or long term persistence of inocula decouples growth rate from host density. Allows spread and avoidance of density dependence

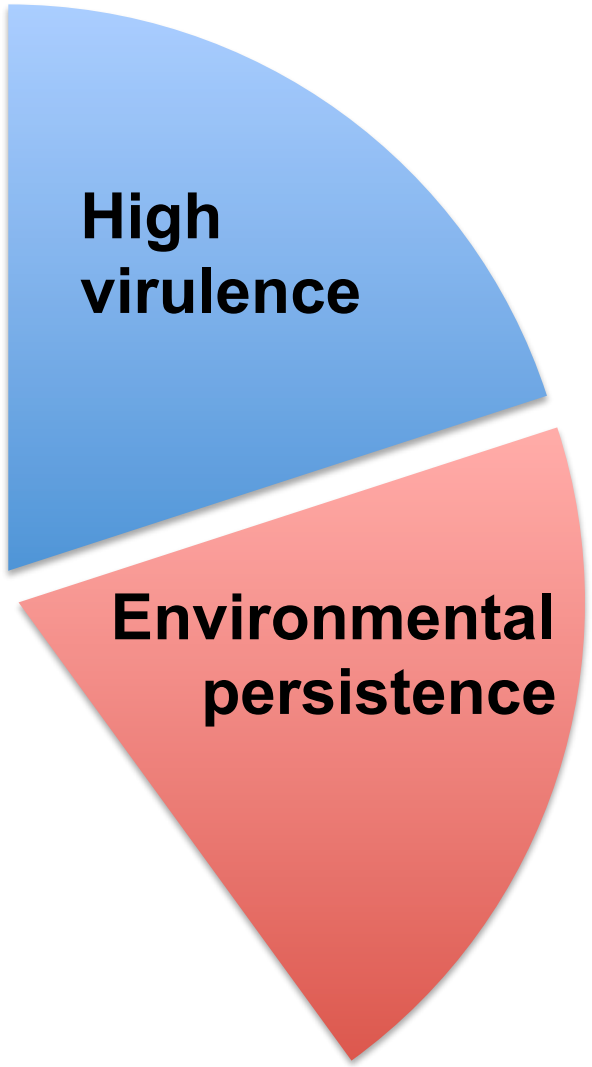
Disease dynamics 2.



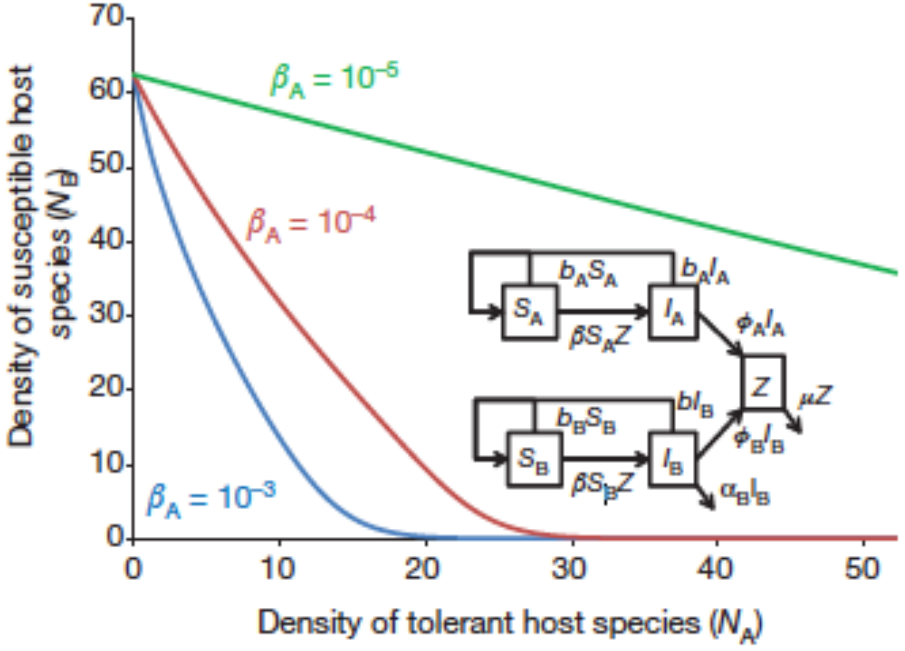
‘Fungi and the rise of mammals’
Casadevall PLoS Path. 2012

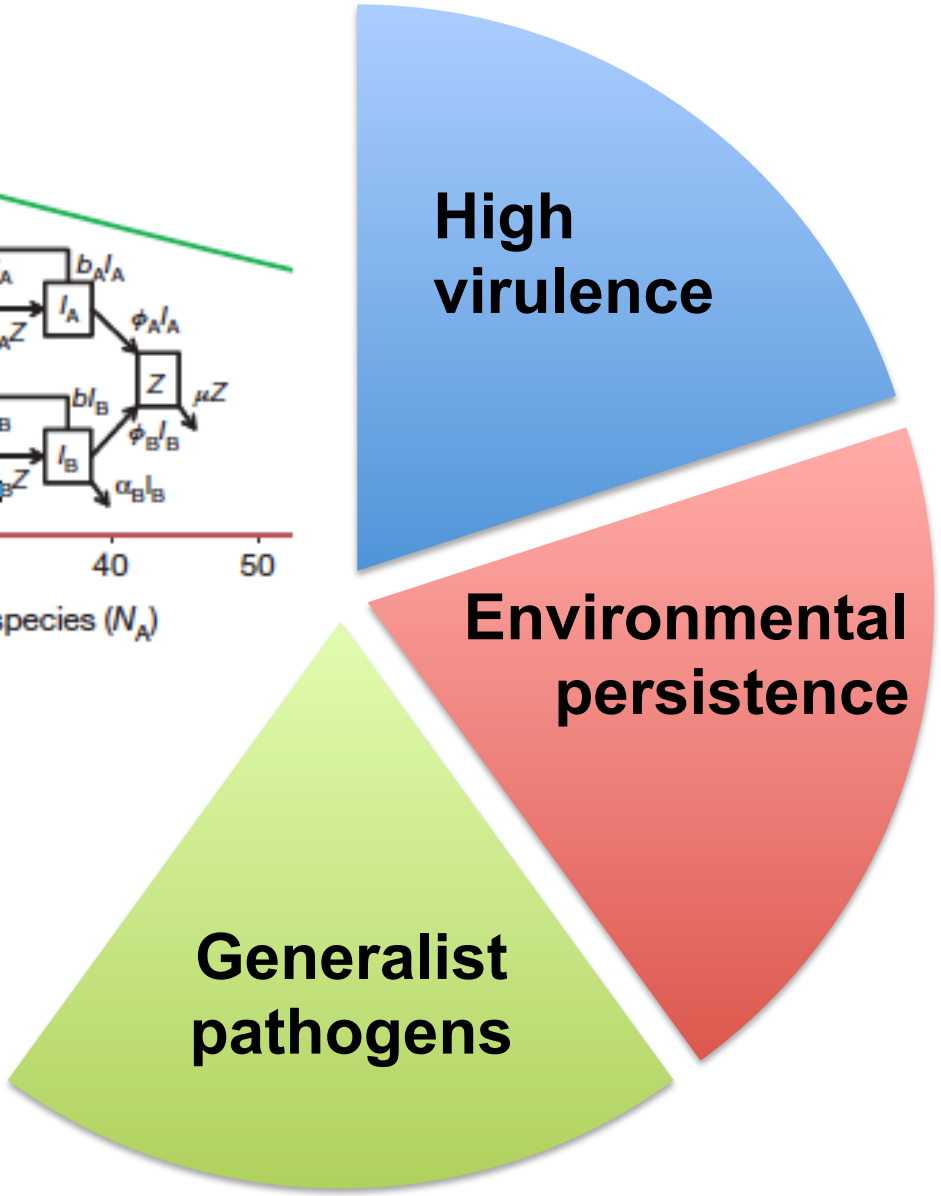
Disease dynamics 2.

- *Aspergillus fumigatus*
- *Coccidioides* sp.
- *Penicillium marneffei*
- *P. destructans*

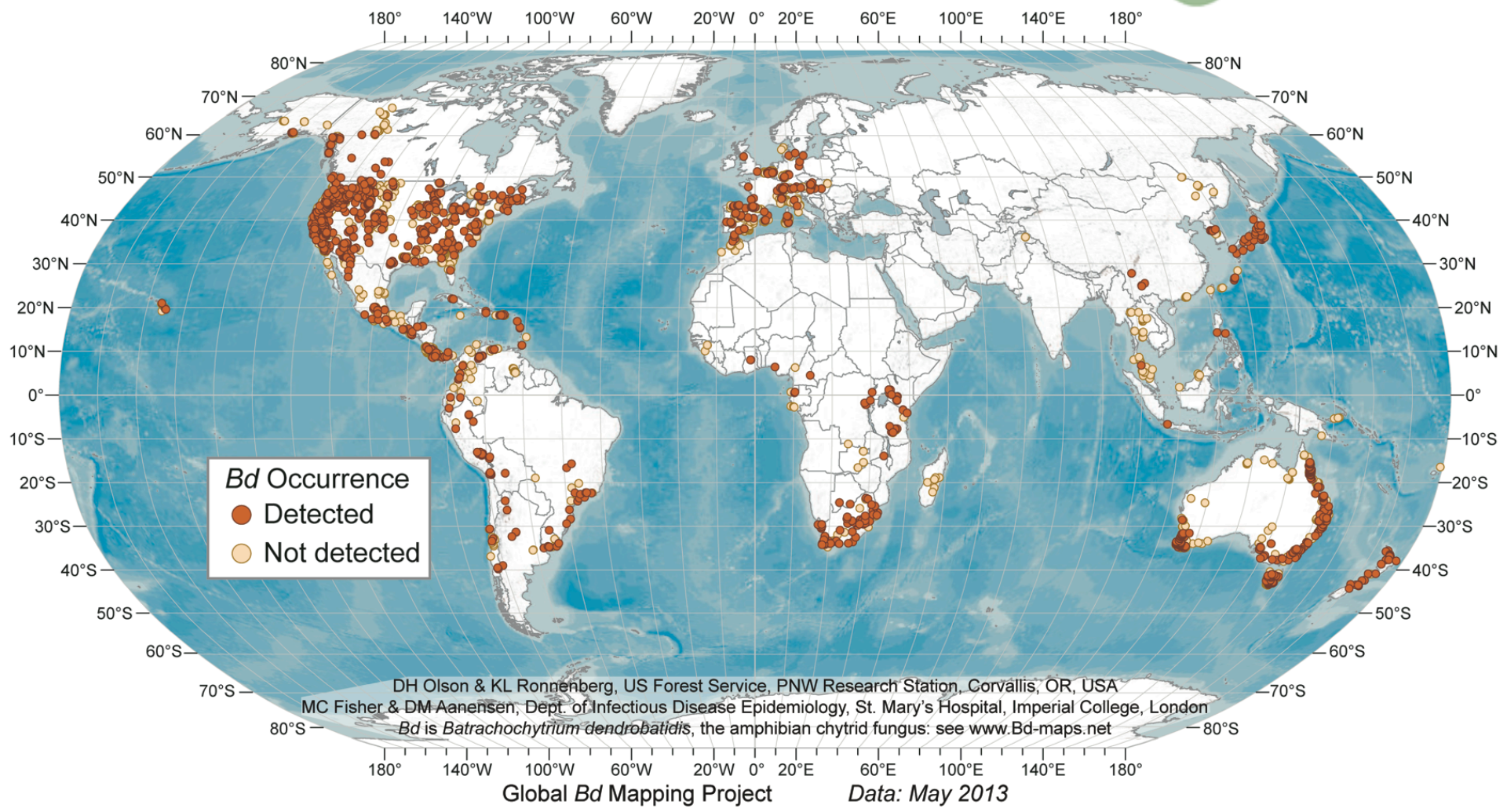


Disease dynamics 3.



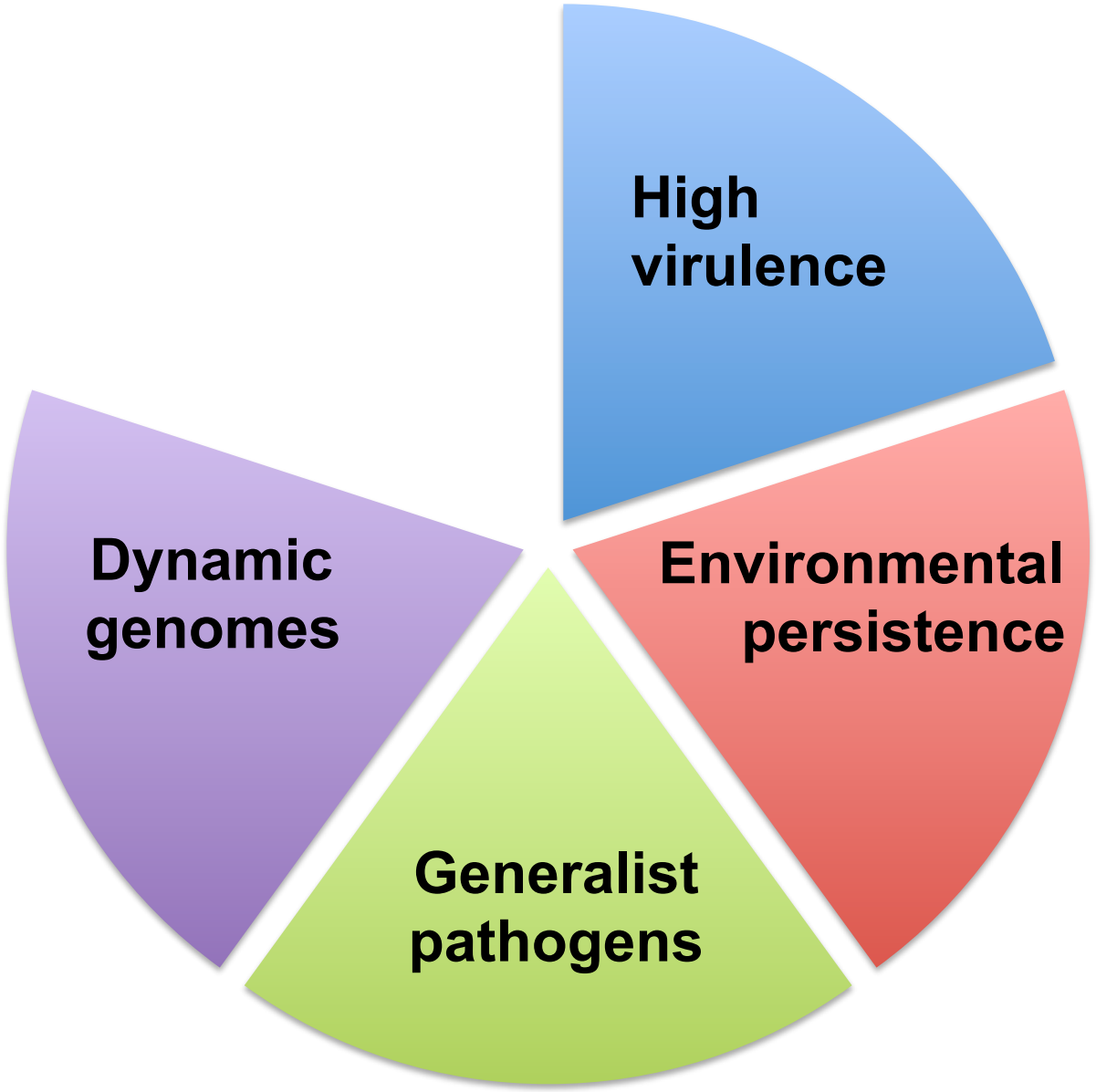


Mapping *Bd*: Global data capture from surveillance shows extremely broad host-range



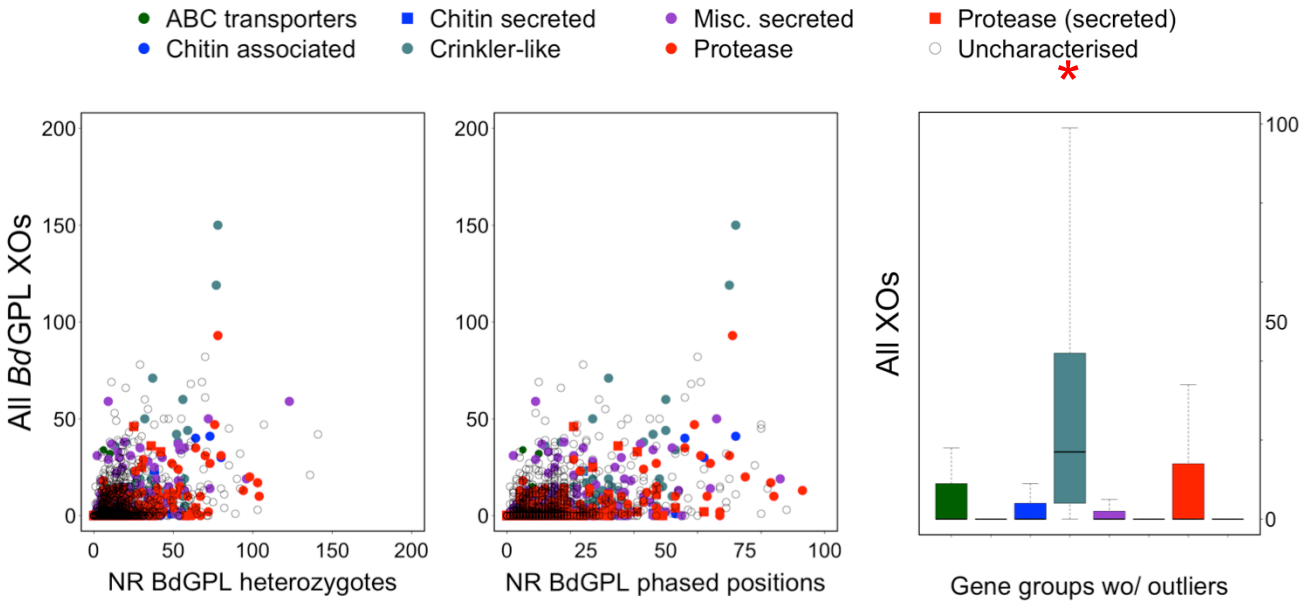
Total number of animals	**7425 positive out of 40380**
Total number sample sites	**1651 positive out of 3926**
Total number countries	**56 positive out of 82**
Number of Species	**520 positive out of 1252**

Disease dynamics 4.

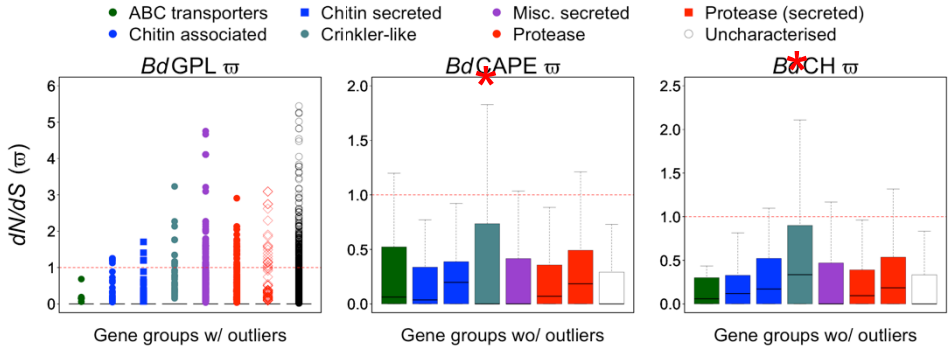


In *Batrachochytrium dendrobatidis,* crossovers are associated with specific motifs involved in pathogenicity, specifically crinkler-like effectors (Farrer *PLoS Genetics* 2013)

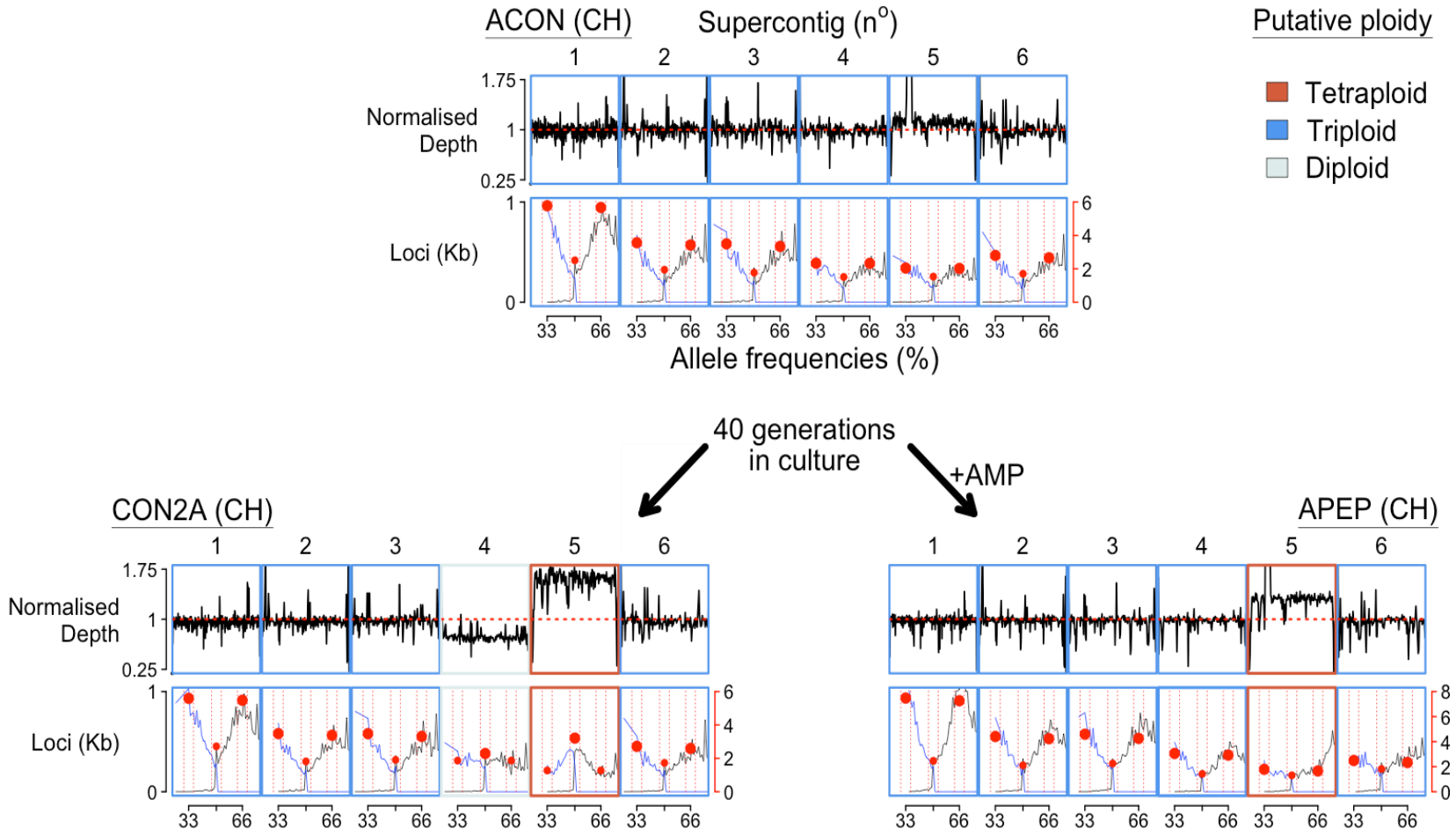
Crossovers (XO's)



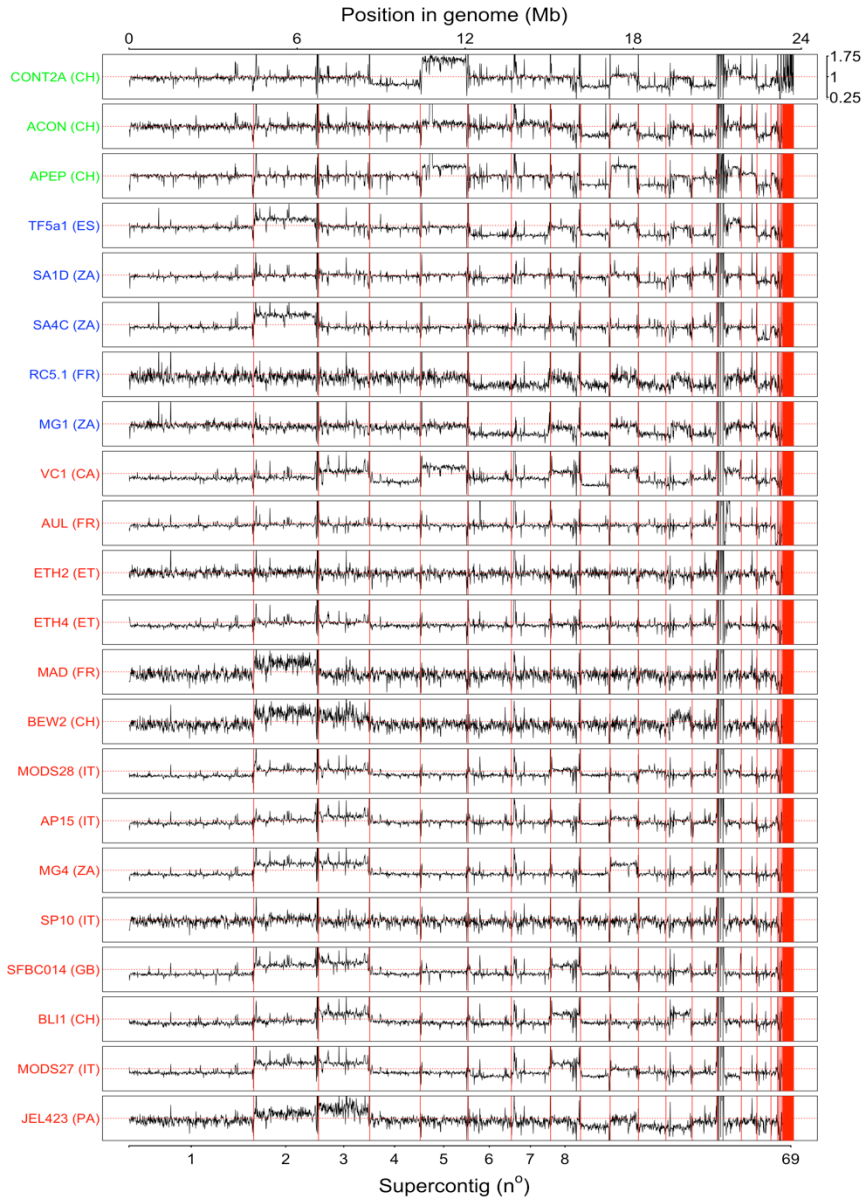
dN/dS



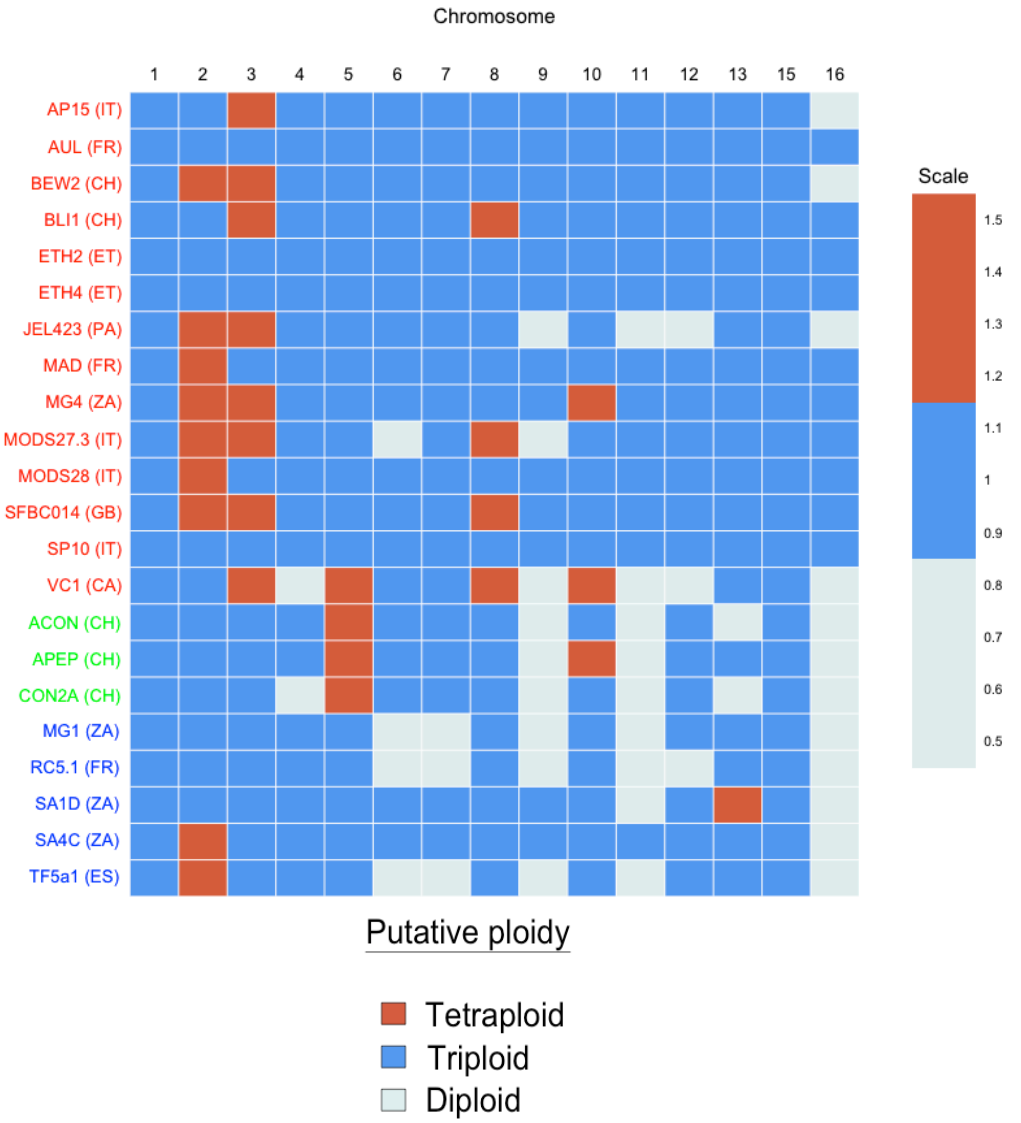
Experimental evolution of *Bd* shows that macromutations, such as chromosomal copy number variation (CNV) occur very rapidly (under 40 generations)



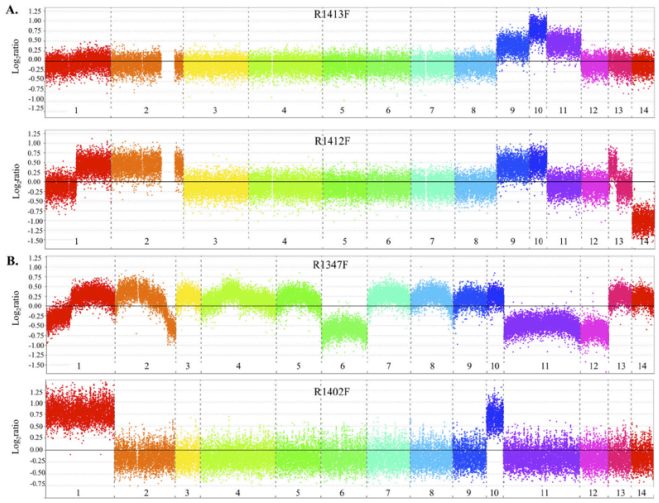
CNV is very common in natural populations of *B. dendrobatidis* (22% of chromosomes)



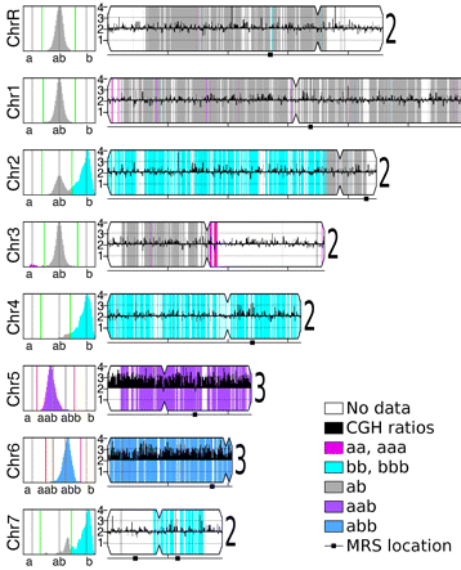
Basal ploidy is triploid, dropping to diploid and including tetraploid



Widely, chromosomal CNV appears to be common across pathogenic fungi

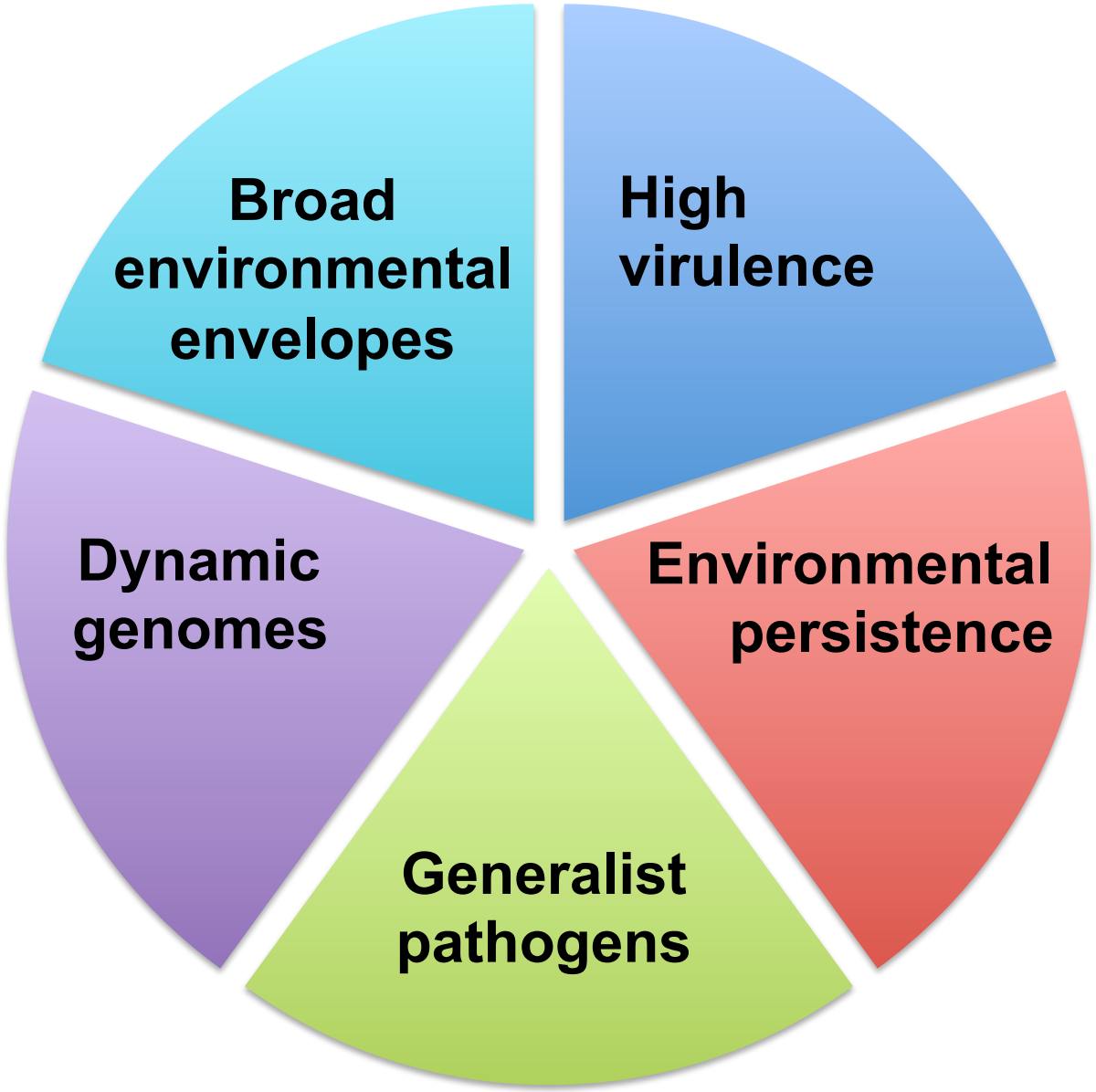


Comparative genome hybridisation shows that CNV is common in *Cryptococcus gattii* (deSouza *mBio* 2011)



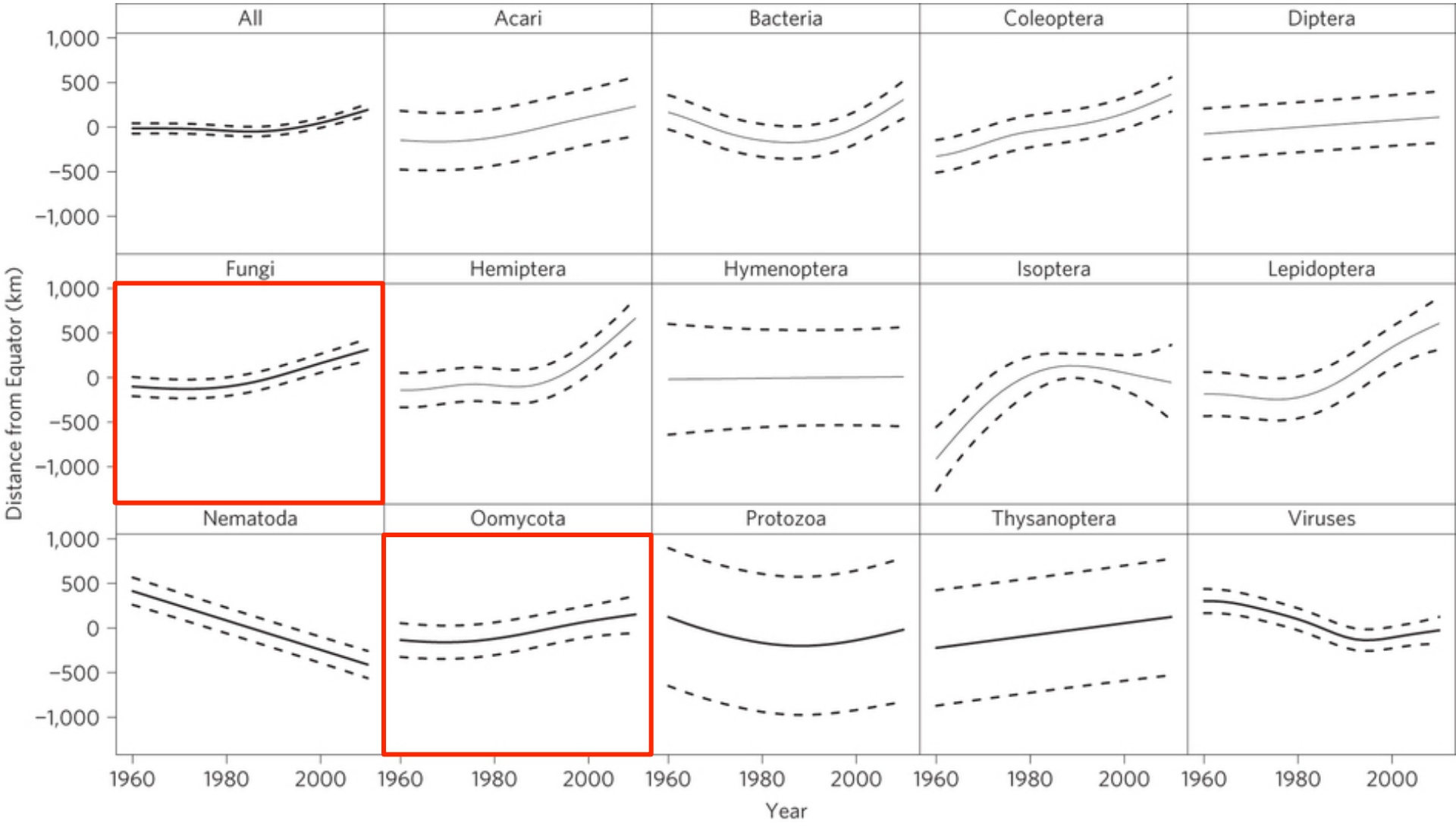
…and *Candida*…(Abbey mBio'11)…

Disease dynamics 5.

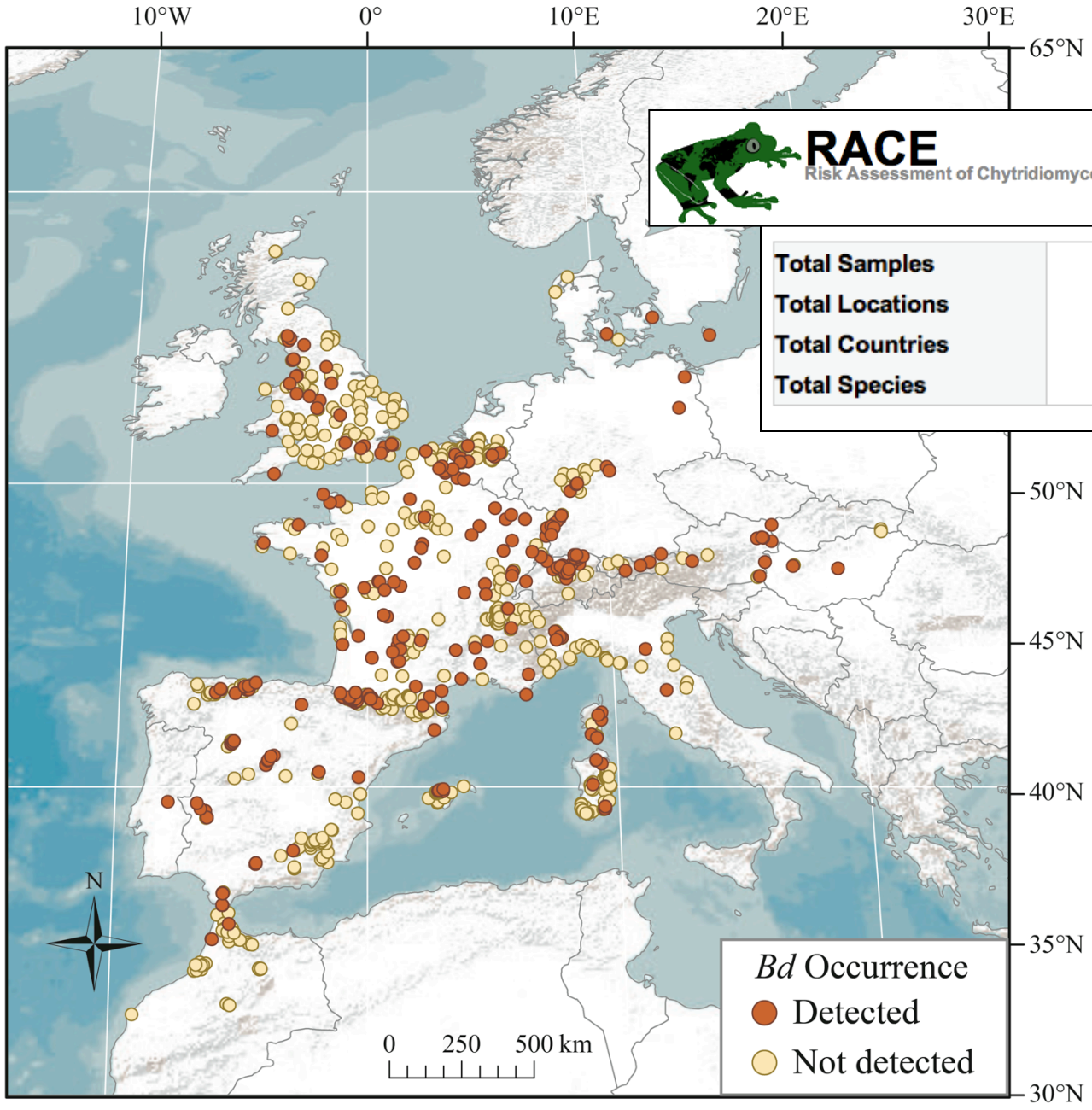


Fungi track global warming by moving polewards

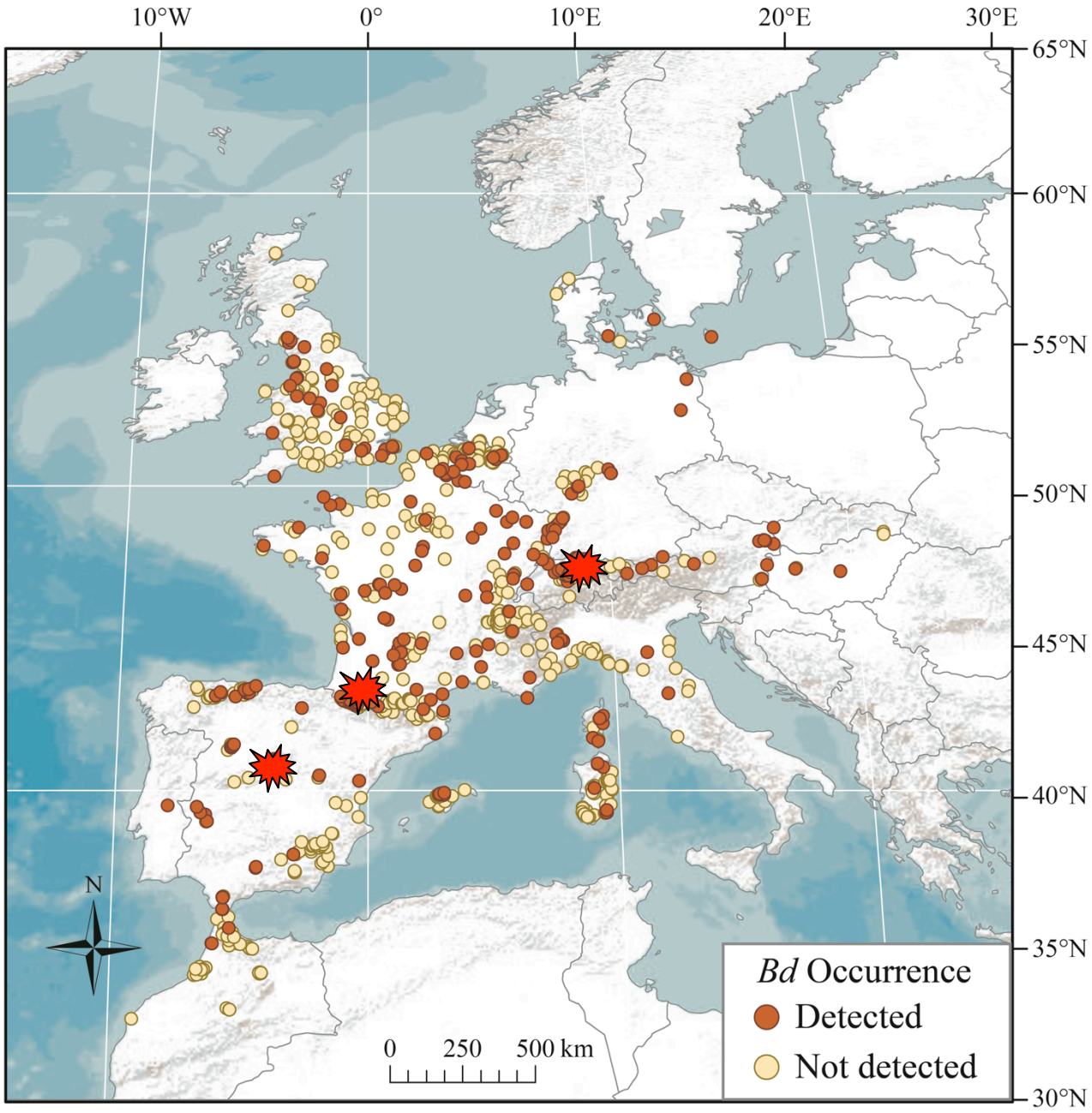
(Bebber *et al* Nature Climate Change '13)



There is no environmental envelope for *Bd* in Europe



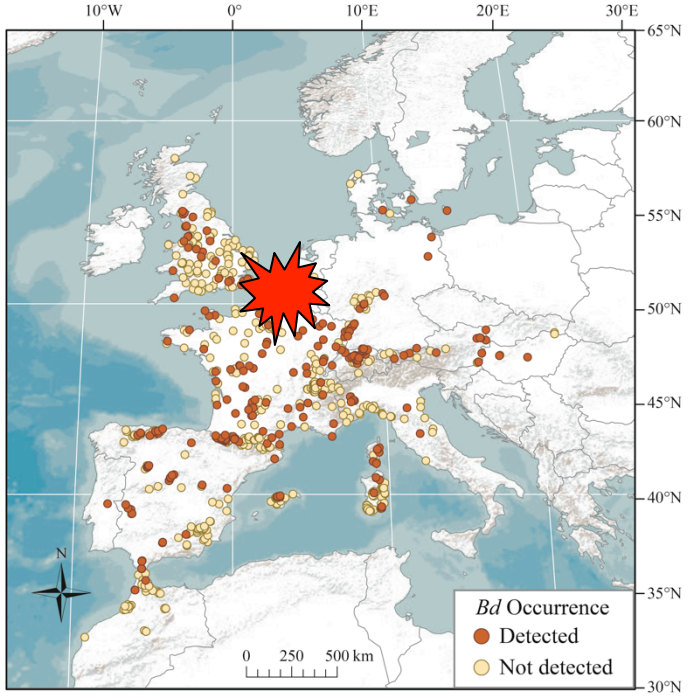
But there is for chytridiomycosis. All epizootics are above >1000 m absl

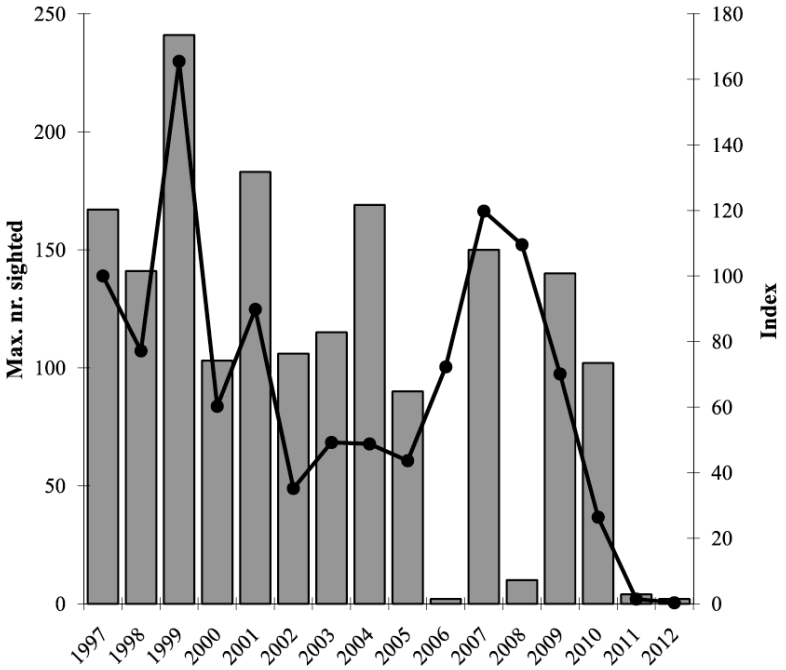


The Über-driver: *Homo sapiens* has been spreading fungi around at ever increasing rates

Generalist pathogens

Chytrid 2.0! Recent dieoffs of fire salamanders in the Netherlands (Martel *PNAS* 2013)

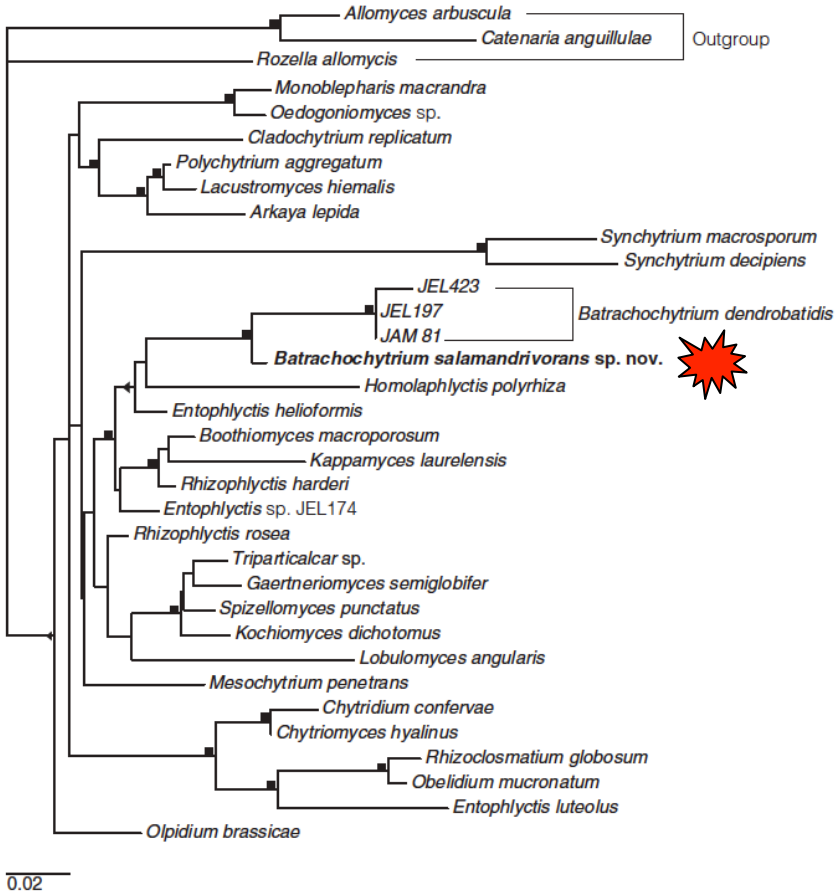




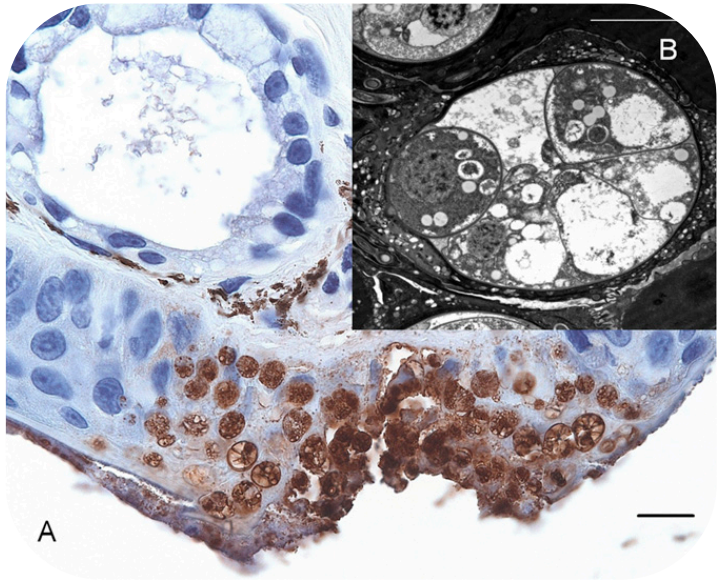
Spitzen *Amphibian Reptilia*'13

- 96% decline 2010-2013 (10 known survivors)
- 19/39 *ex situ* animals died in captivity
- Negative for all known pathogens, **including *Bd***

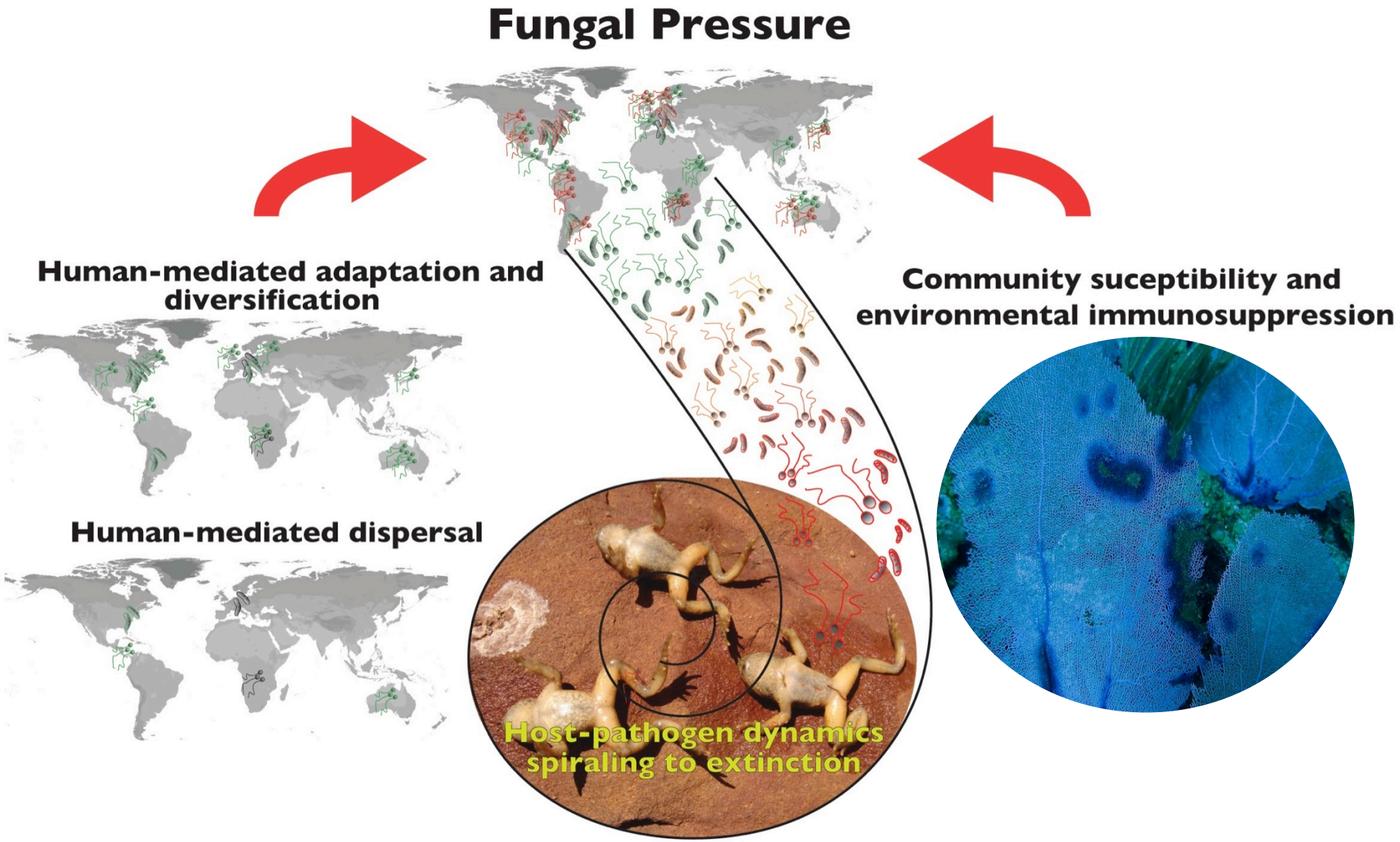
Chytrid 2.0! *Batrachochytrium salamandrivorans* sp. nov.



- A chytrid was isolated from the skin of one dead salamander
- 18S+28S shows ~4% sequence divergence from *Bd*
- MiSeq reads are unmappable to the JEL423 *Bd* reference genome
- Produces motile zoospores
- Forms ulcerative lesions rather than hyperkeratosis



Humans are ratcheting up ‘fungal pressure’ in natural systems



Imperial

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