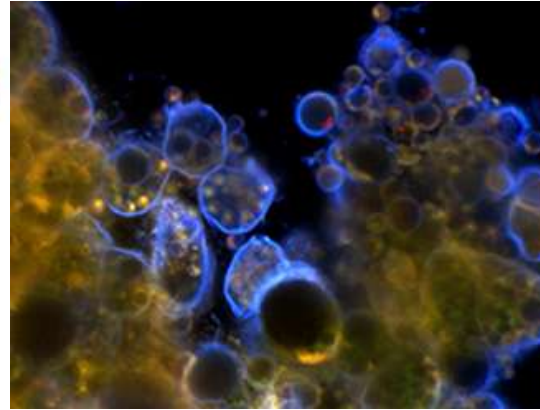


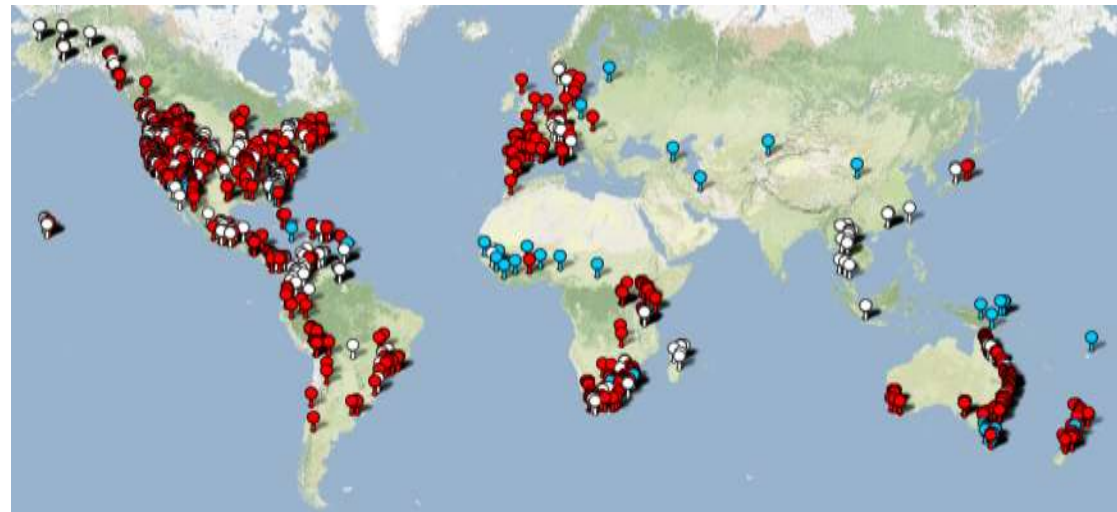
**Imperial College  
London**



# Emerging fungal threats to animal, plant and ecosystem health

**Matthew Fisher**

**Dpt Infectious Disease  
Epidemiology**



# Emerging infectious fungi, and oomycetes, present an escalating threat to animal and plant health

*Batrachochytrium dendrobatidis* (Bd)  
Amphibian chytridiomycosis worldwide



*Geomyces destructans*  
Bat white-nose syndrome, USA

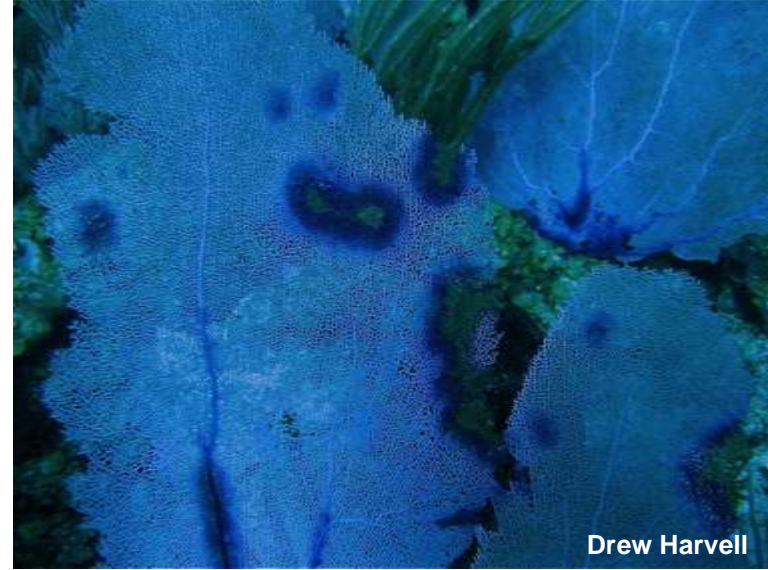


# This threat appears to be widespread

*Fusarium solani* & turtles



*Aspergillus sydowii* & coral



*Nosema* & honeybee CCD



*Aphanomyces astaci* & Crayfish plague



# This threat appears to be widespread

*Chalara fraxinea* (*Hymenoscyphus pseudoalbidus*). Ash dieback



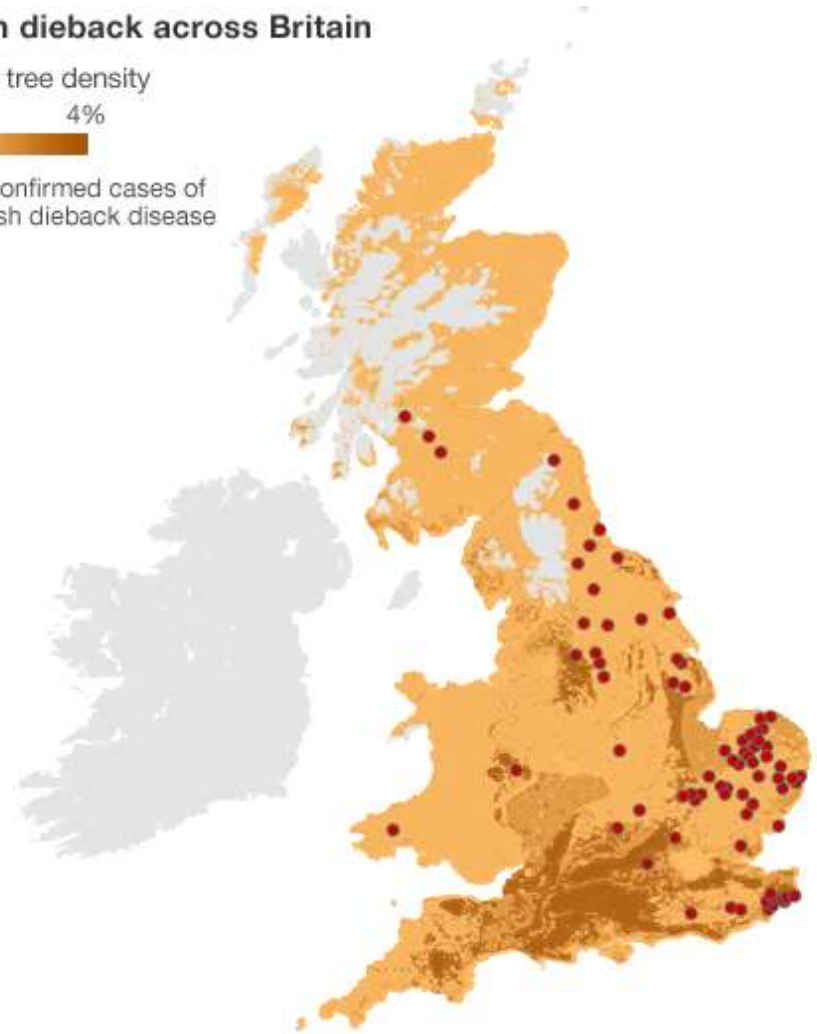
## Ash dieback across Britain

Ash tree density

0% 4%



● Confirmed cases of ash dieback disease



Information correct at 1400 on 7 Nov 2012. No data for Northern Ireland. No nursery cases included.

Source: Countryside Survey, Forestry Commission

Are we seeing ↑ incidence of fungal pathogens?



**MEDICAL RESEARCH**  
**CHILDREN OF THE NINETIES**  
*Pioneering birth cohort study comes of age*  
**PAGE 155**



**FICTION**  
**TO GREECE VIA COPENHAGEN**  
*Michael Frayn on science, farce and uncertainty*  
**PAGE 102**

**INNOVATION**  
**SCIENCE MEANS BUSINESS**  
*Getting to grips with technology transfer*  
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9 770028 083095

April 484: 2012

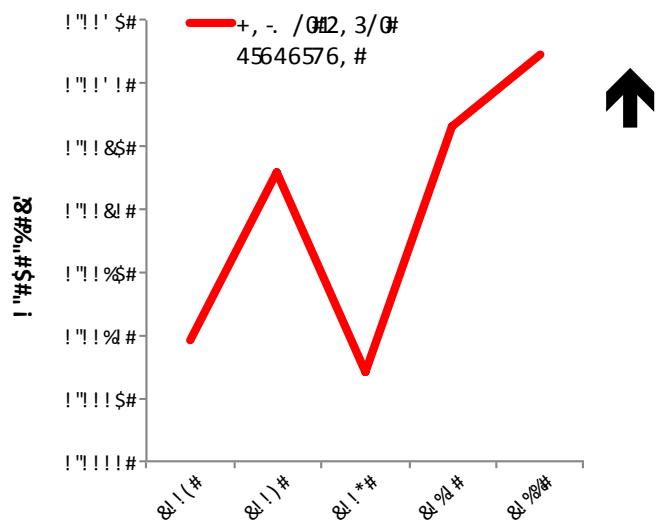
## Global disease alerts captured by



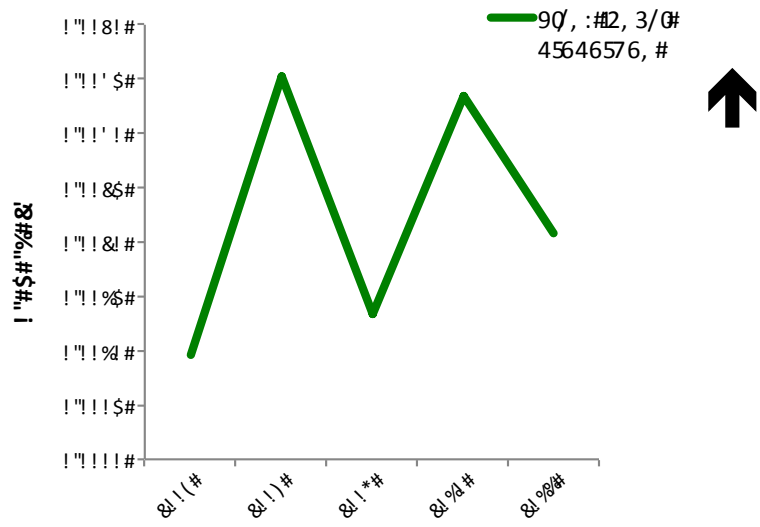
- **ProMED (Active reporting, 1994 – 2010; 38,000 records)**
- **HealthMAP (Captures online datasources, 2006 – 2010; 43,000 records)**
- **Species extinction catalogued by *Web of Science* literature searches**

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

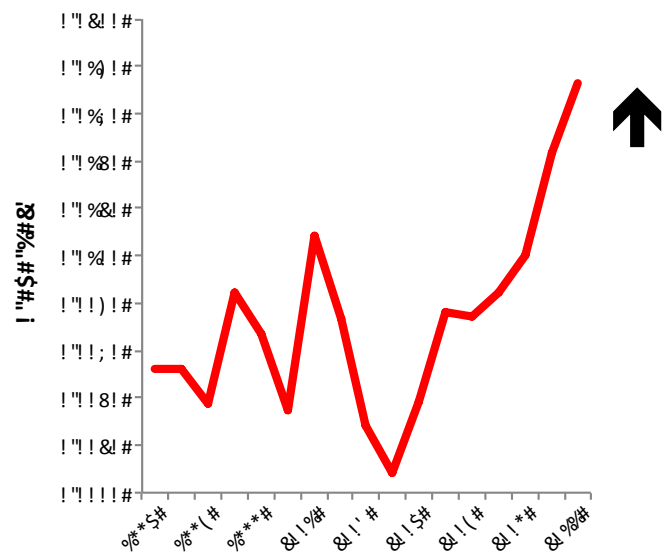
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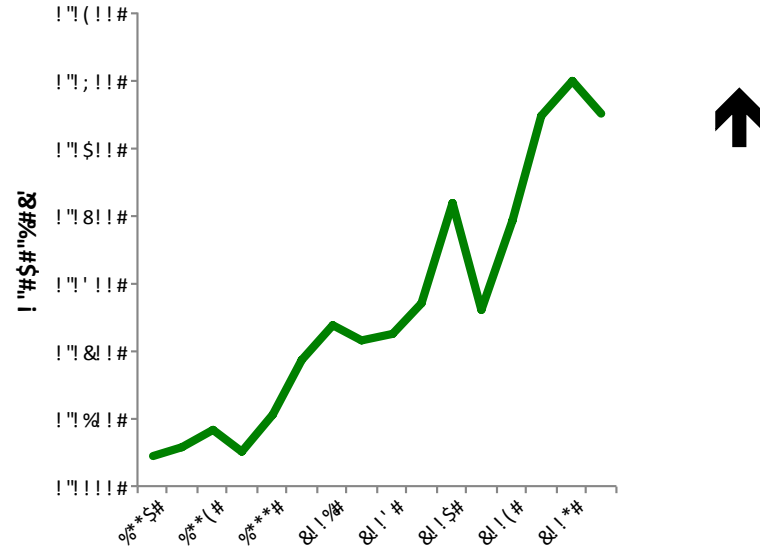
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!"#. 56 '\*&/0 \*+12&3\*+\*+) ",4'

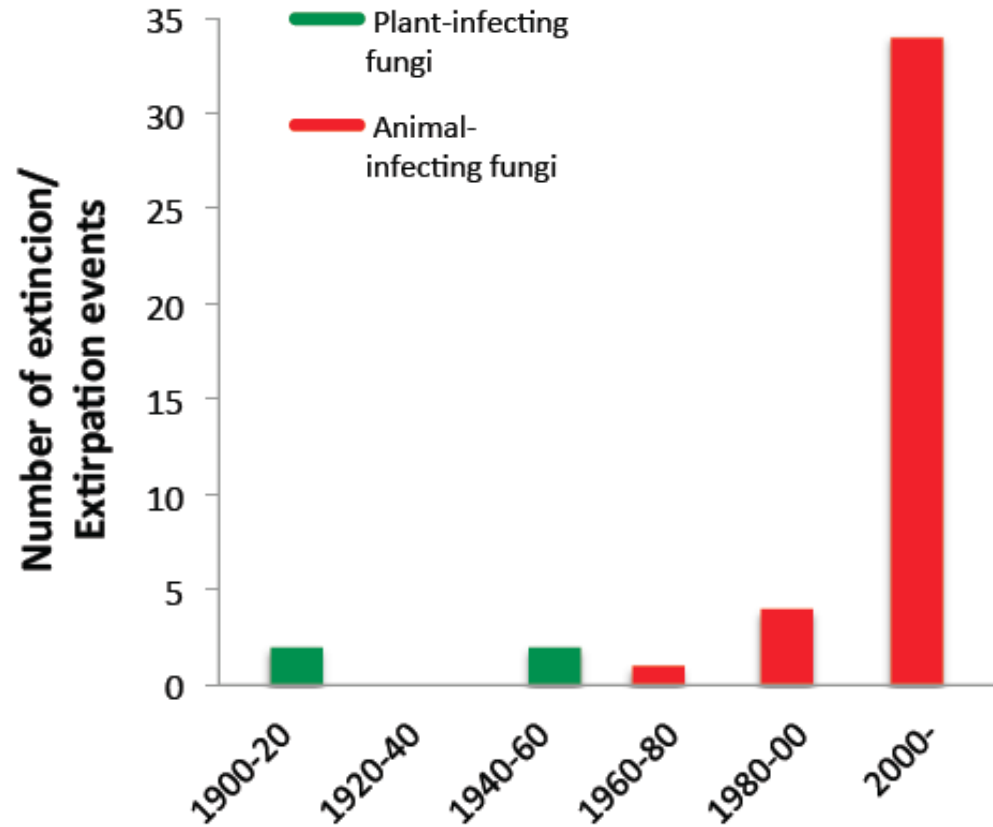
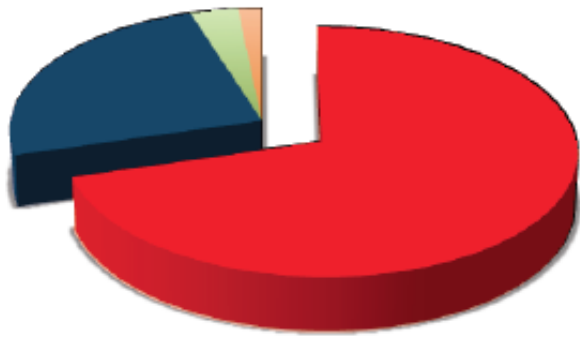


!"#. ) 7! '+\*&'12&3\*+\*+) ",4'



**Fungi comprise the highest threat for both animal (72% of extinctions) and plants (64% of extinctions) and this threat is increasing**

■ Fungi  
■ Protist  
■ Viruses  
■ Bacteria  
■ Helminth  
■ other





# Why? Fungal disease dynamics predispose them to emergence and drive extinction processes

- **High virulence.** Associated with high intra-host growth rates leading to rapid inter-host transmission, spread, and avoidance of density dependence.
- **Long lived environmental stages.** Sapronotic potential or long term persistence of inocula decouples growth rate from host density. Allows spread.
- **Highly generalist pathogens.** Community superspreaders lead to extirpation of susceptible host species.
- **Recombination.** Accelerates evolution and allows the potential for macroevolutionary change; '*Hopeful monsters*'

# *Batrachochytrium dendrobatidis* is the cause celebré for mycotic outbreaks

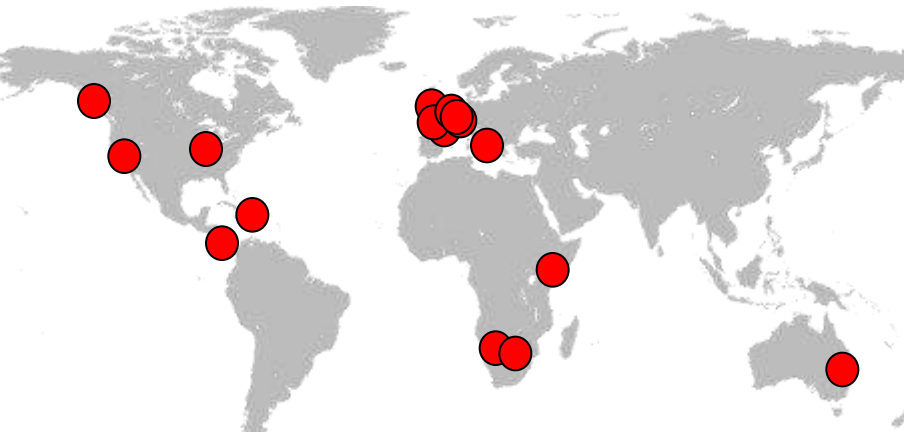
[www.bd-maps.net](http://www.bd-maps.net) & [www.bd-maps.eu](http://www.bd-maps.eu)



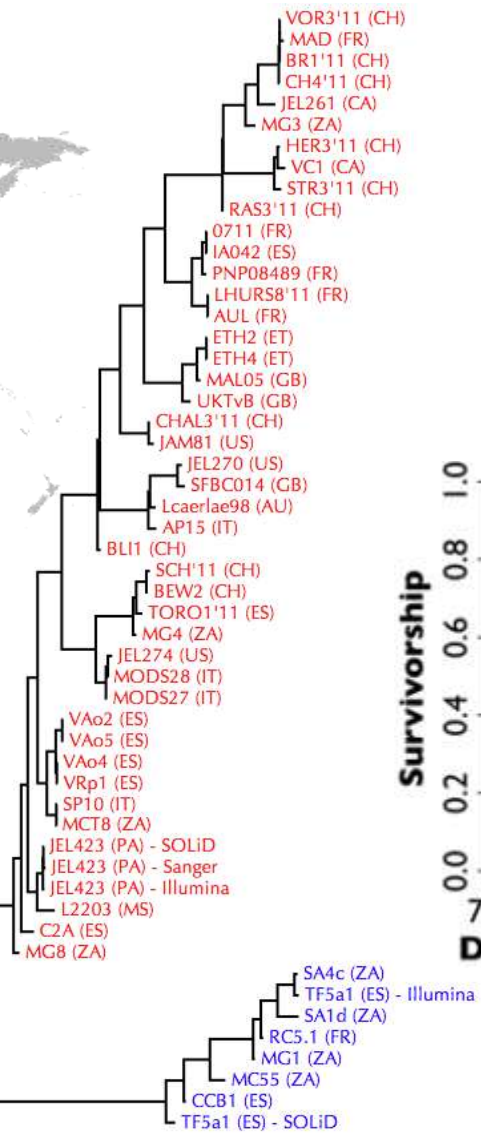
<b>Total Samples</b>	7167 positive from 34792
<b>Total Locations</b>	1613 positive from 3653
<b>Total Countries</b>	53 positive from 80
<b>Total Species</b>	489 positive from 1106



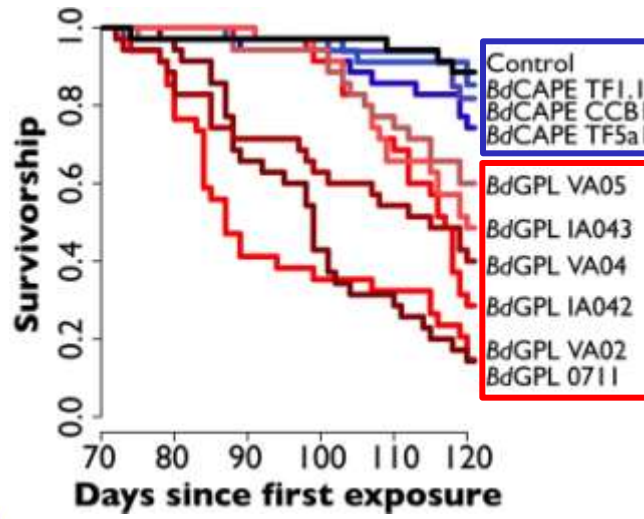
# Panzootic chytridiomycosis is caused by a single hypervirulent 'outbreak' lineage **BdGPL**, 20<sup>th</sup> Century spread (Farrer et al *PNAS* '11)



- **Bd CAPE**
- **Bd CH**
- **Bd GPL**



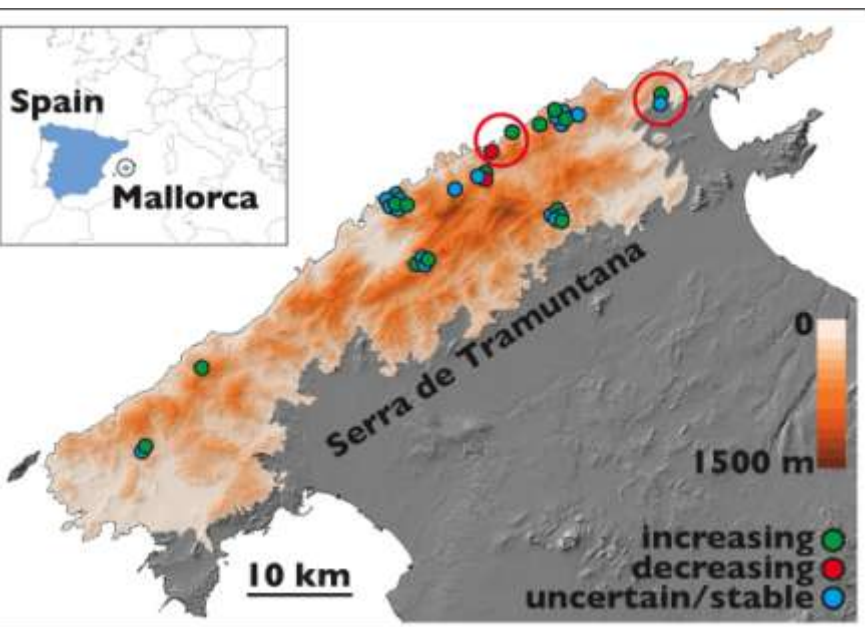
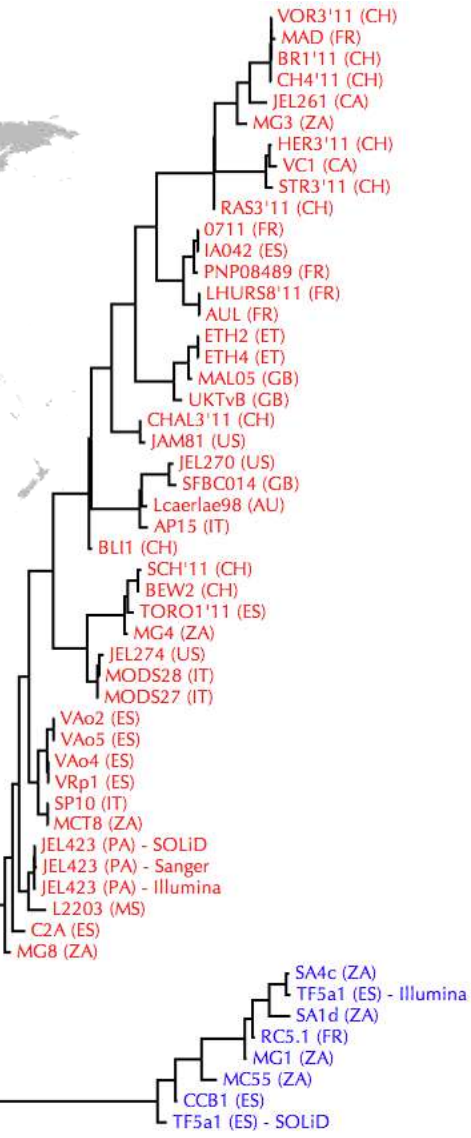
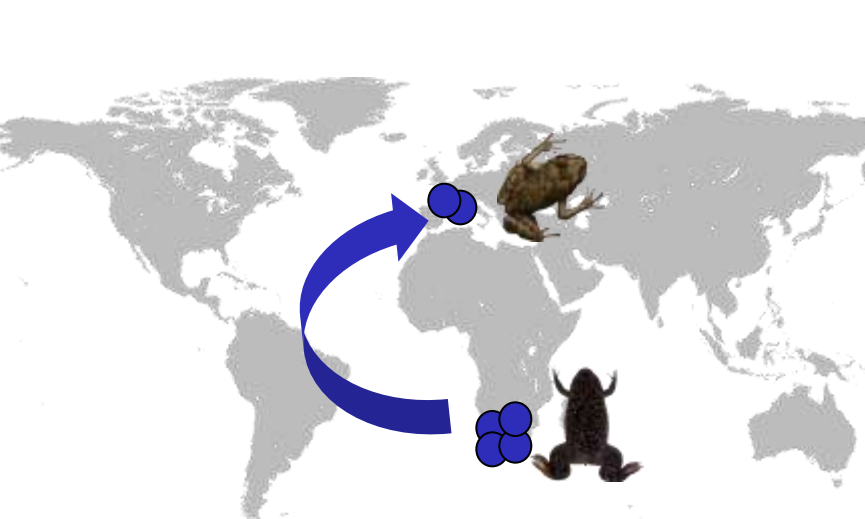
- 57 genomes sequenced
- ~22k SNPs
- hypervirulence of *BdGPL* in a toad model



A Control (CH)  
A Peptide 42 (CH)  
Control 2A Frozen (CH)

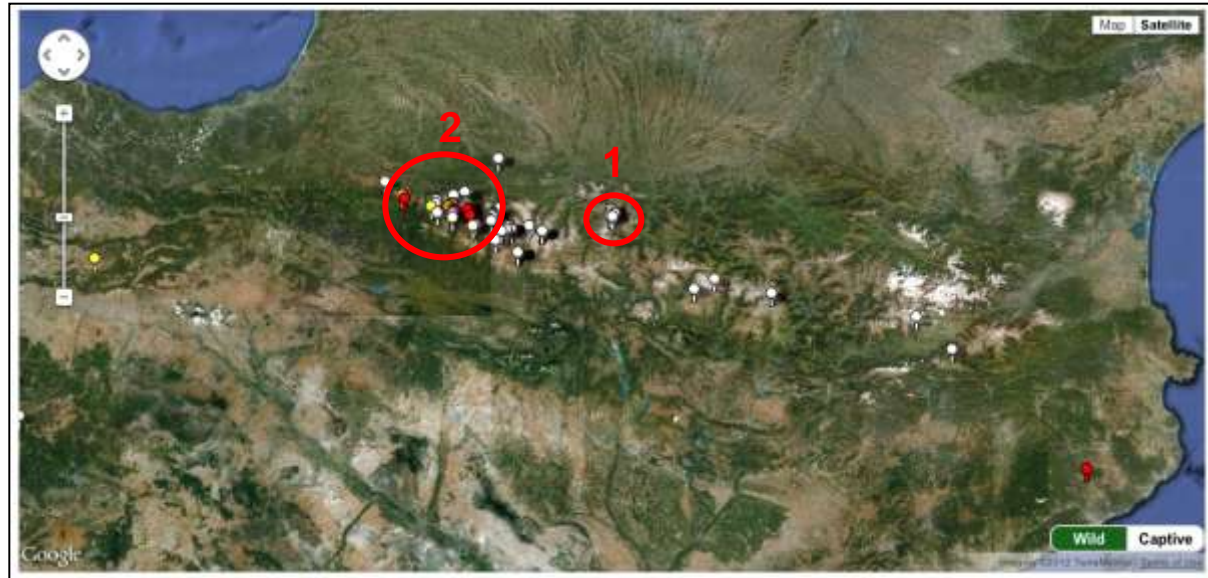
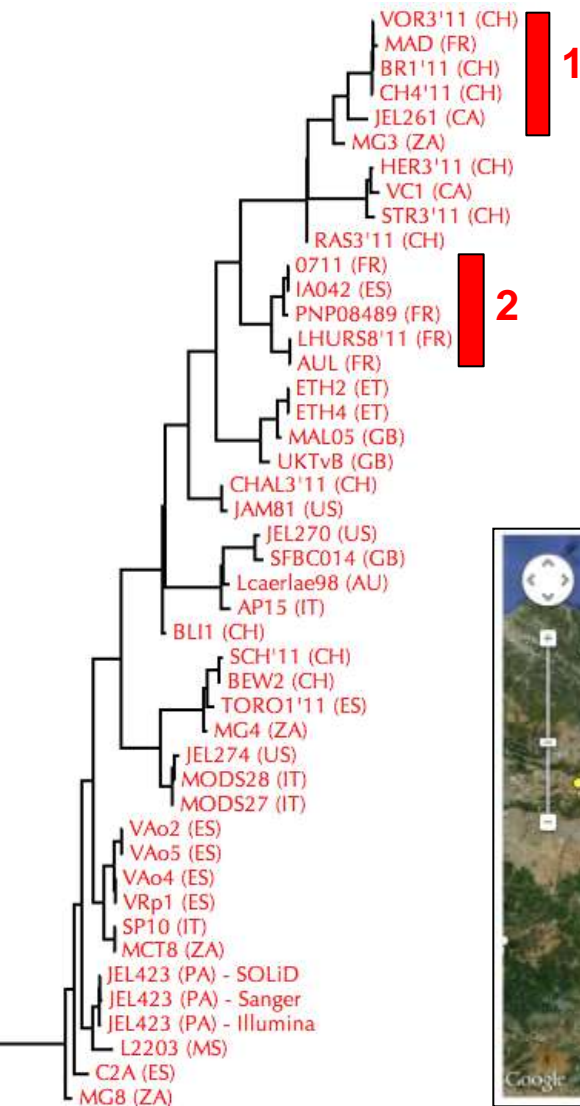
1000.0

# 'BdCAPE' is also being spread worldwide in the amphibian trade, but doesn't kill

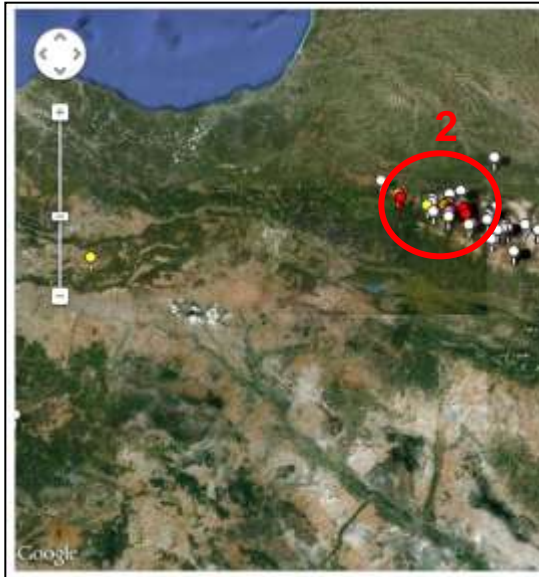
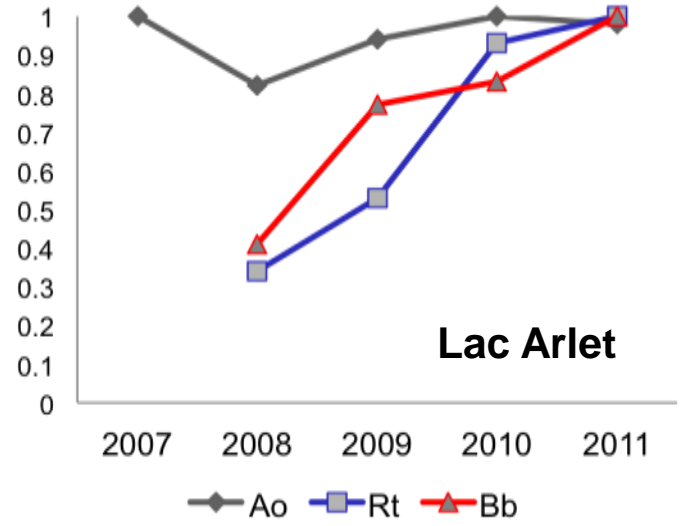
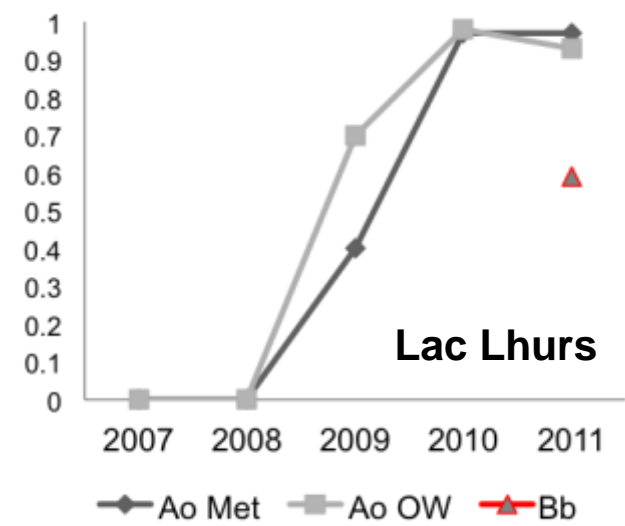
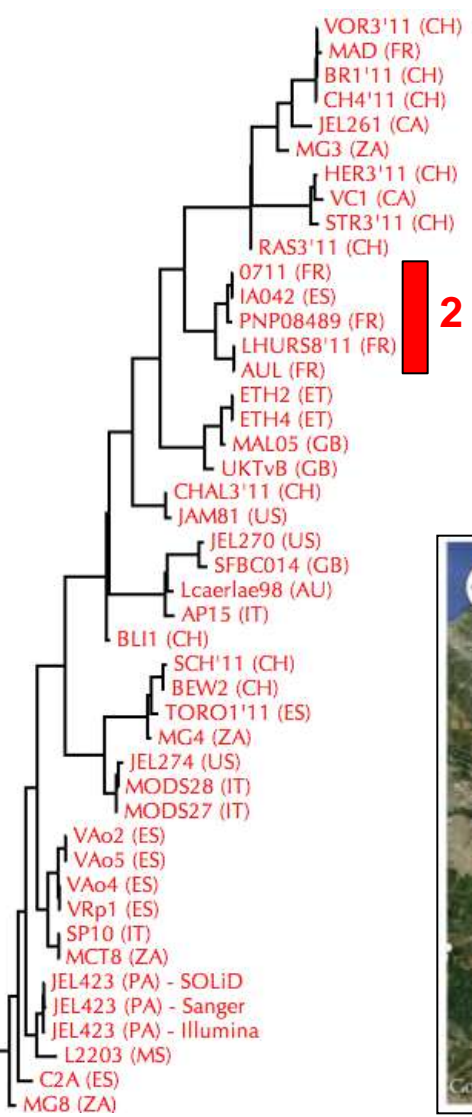


# The Pyrennees clearly show two unlinked introductions of *BdGPL* causing hotspots of chytridiomycosis

- Local spread documented in both sites 1 (Neovieille) & 2 (Aspe) post 2006
- Vector unknown. Fish stocking? Birds?

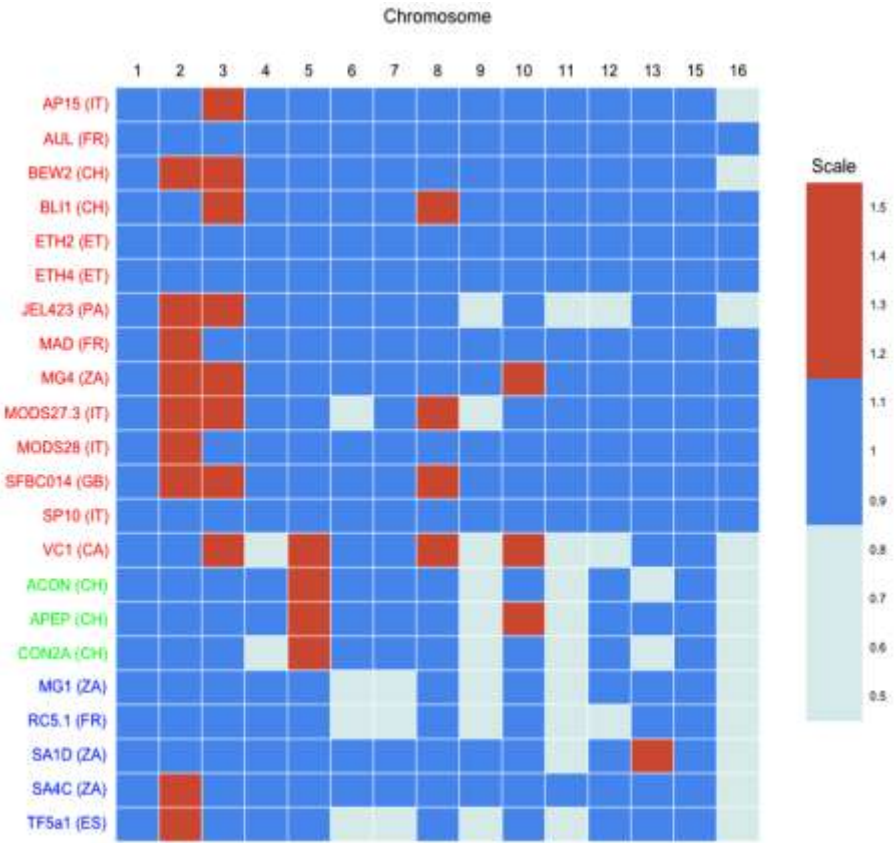
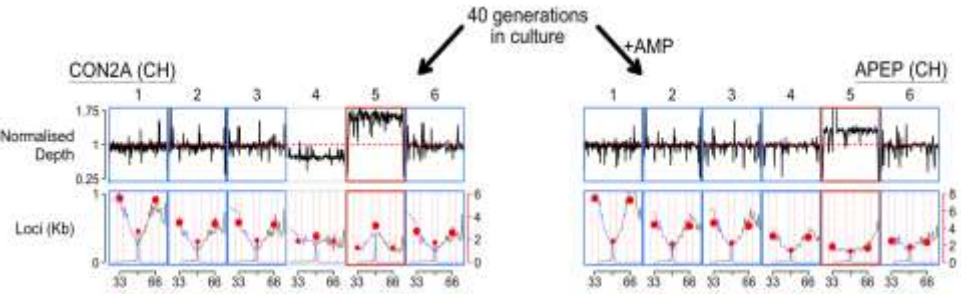
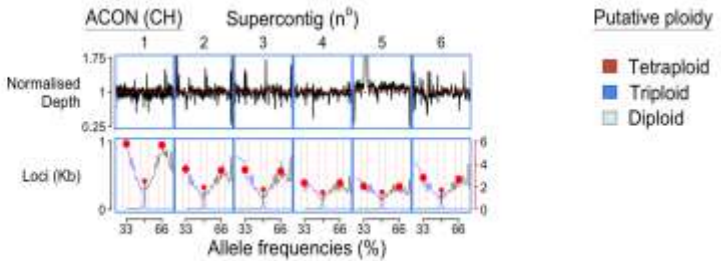


# All infected valleys in the Pyrenees show clear increases in the force of infection, transpecific infection and mortality



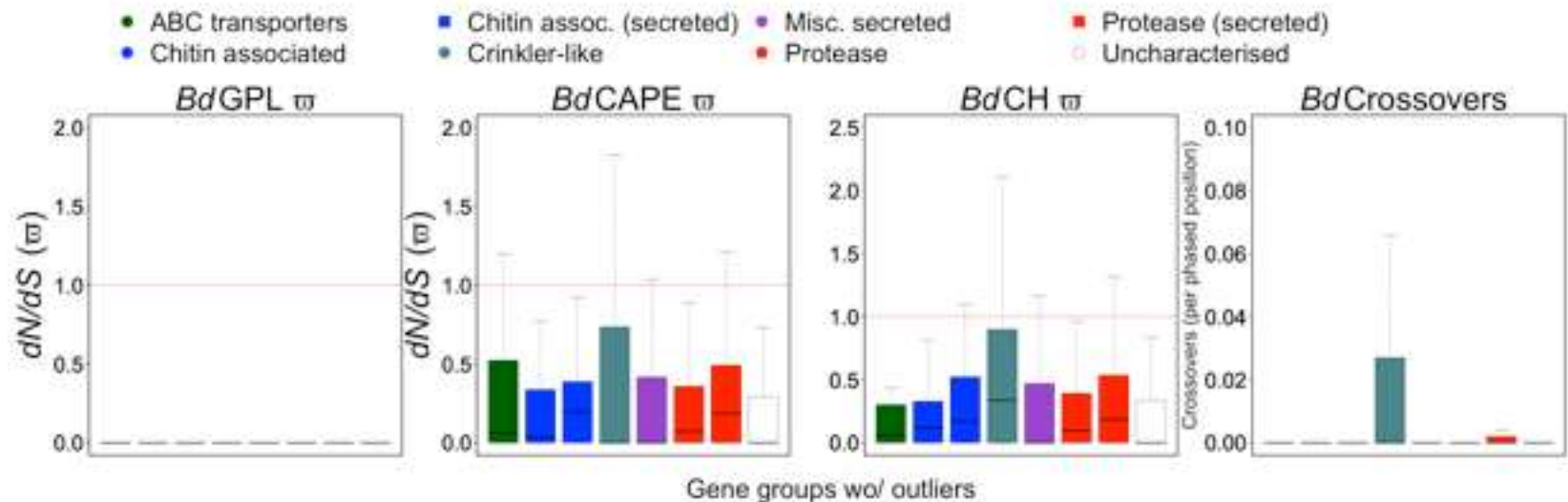
# *Bd's* genome is highly dynamic...

At the level of the chromosome (chromosomal copy number variation)



# *Bd*'s genome is highly dynamic...

Directional selection and recombination are highest at genes with a putative role in virulence; the crinkler-like genes



We now need to understand how the evolution of virulence in *Bd* is linked to these dynamic-genome processes, and what make *BdGPL* different

...and how widely these processes are predictive across other pathogenic fungi



- *Lessons from Bd, Geomyces, and many others, clearly demonstrate the increasing risk that fungi pose to biodiversity*
- *The wider ecosystem-level impact of these ‘environmental mycoses’ have not been adequately assessed*
- *The vectors, and routes of introduction, of pathogenic fungi are little understood*
- *...as are the evolutionary dynamics following non-endemic ‘genetic pollution’*

*but....*

- *We know that our borders are wide open to these invading lineages*

*bioINsecurity!!*

- *Do we have the political will to initiate the levels of quarantine that are necessary to prevent further invasions? (no!)*
- *Do we have the rapid diagnostics to test for fungal EIDs at borders? (no!)*
- *Do we know the full economic cost of emerging fungi? (no!)*

**Daniel Henk, Rhys Farrer, Sarah Gurr (Oxford), Larry Madoff (ProMED), John Brownstein (HealthMAP), Cherie Briggs (UCSB), Benedict Schmidt (U of Zurich), Claude Miaud (Montpellier), Trent Garner (IoZ)**

Jon Bielby, Dirk Schmeller, Francois Balloux, Dede Olson, Jaime Bosch, Kathryn Ronnenberg, Gerardo Garcia, Joyce Longcore, Benedict Schmidt, Dirk Schmeller, Andrew Cunningham, Hui Ng, David Aanensen, Chris Powell



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