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	325	Rice Blast	212 to 742
Oryza sativa	476* milled for food	1 for	Magnaporthe oryzae 10-35%	
Wheat	679 harvest	341	Stem Rust	202 to 1,413
Triticum aestivum	but 432* for food		Puccinia graminis 10-70%	
Maize	820 harvest but	355	Corn Smut	26 to 262
Zea mays	271* for food		Ustilago maydis 2-20%	
Potato	333* harvest but	357	Late Blight	81 to 1,270
Solanum tuberosum	ior iood		Phytophthora infestans 5-78%	
Soybean	232 harvest but	372	Soybean Rust	75 to 600
Glycine max	148* for food		Phakospora pachyrhizi 10-80%	
				TOTAL: Could feed 596 – 4,287 million mouths per annum**

Table S1: Food security and crop losses due to fungal/oomycete diseases: Five major crops that feed the world's population are challenged by the fungal/oomycete diseases shown. All global harvests are from 2009/2010 (www.fao.org or FAOSTAT1). \*Figures are estimates and are based on 100% of milled rice and 100% of potato harvest being used for human consumption. However, 34% of the global wheat harvest is produced in developing countries, of which 100% is assumed to be used for human food, but only 45% of the total wheat harvest produced from developed countries is used for human food (the rest is used as animal feed and biofuel). Of the global maize harvest, 32% is produced in developing countries and 100% is assumed to be used for food and in the US 2.5% of their total harvest of 333m tonnes of maize (41% of global harvest) is used directly as food. Of the global soybean harvest, 36% is from US and Canada (10% of this is used as food, the rest goes into processed food and animal feed) and 64% is produced in developing nations, where 100% is assumed to be used as food. These figures do not take into account post-harvest storage losses.

<sup>\*\*</sup>This is 8.5% - 61.2% of the world's population, based on the 2011 population estimate of 7 billion people.

Database	Year	Animal fungal alerts	Plant fungal alerts	Total fungal alerts	Total EID alerts
HealthMap	2007	9	9	18	9369
-	2007	13	20	33	5659
HealthMap					
HealthMap	2009	8	15	23	11284
HealthMap	2010	23	29	52	8672
HealthMap	2011	28	18	46	8674
Total		81	91	172	43658
ProMED	1995	6	5	11	1153
ProMED	1996	10	11	21	1923
ProMED	1997	9	20	29	2384
ProMED	1998	20	12	32	2357
ProMED	1999	14	22	36	2079
ProMED	2000	7	37	44	2002
ProMED	2001	21	46	67	1930
ProMED	2002	14	41	55	1894
ProMED	2003	6	47	53	2092
ProMED	2004	2	64	66	2382
ProMED	2005	10	108	118	2582
ProMED	2006	18	62	80	2374
ProMED	2007	21	111	132	2829
ProMED	2008	19	123	142	2251
ProMED	2009	24	144	167	2399
ProMED	2010	37	142	179	2586
ProMED	2011	40	66	106	2307
Total		278	1061	1338	37524

**Table S2.** Summary of HealthMap (2006-2011) and ProMed (1994-2011) alerts for mycoses with the first year of data collection excluded. For our analyses we downloaded the complete ProMED and HealthMap databases from the start of data collection through to the last year of complete data collection (2010). We then used Boolean searches of the database using generic fungal search terms (fung\*, mycosis) and refined this with the following specific search terms (rust, blast, blight, wilt, sigatoka, bunt, smut, light leaf spot, jarrah, oak death, blue stain, aspergillosis, blastomycosis, cryptococcosis, foot fungus, histoplasmosis, mucormycosis, paracoccidioidomycosis, sporotrichosis, thrush, valley fever, white nose syndrome, fusarium keratitis, dermatophytosis, zygomycosis, basidiobolomycosis, chromoblastomycosis, lobomycosis, mycetoma). Records were subsequently curated to remove false positives.

Table S3

Published infectious disease-driven extinction and regional extirpation events across animal and plant taxa. Data was acquired from the following review sources [1-9] and from Web of Science literature searches.

Host species <sup>§</sup>	Pathogen	Kingdom	Factors driving	Year of	Reference
	species	(Phylum)	emergence	occurrence	
Tropical central American	Batrachochytrium	Fungi	Pathogen	late 1980's -	[7, 10]
amphibian spp. (30 species	dendrobatidis	(Chytridiomycota)	invasion/endemic	present	
and 4 families)			host populations		
EXTINCTION/EXTIRPATION					
Australian amphibian spp.	B. dendrobatidis	Fungi	Pathogen	early 1980's	[11, 12]
$(n \sim 4; 2 \text{ families})$		(Chytridiomycota)	invasion/endemic		
EXTINCTION			host population		
Alytes obstetricans	B. dendrobatidis	Fungi	Pathogen	1997	[13]
(Common midwife toad)		(Chytridiomycota)	invasion/endemic		
EXTIRPATION			host population		
Nextophrynoides asperginis	B. dendrobatidis	Fungi	Pathogen /	2003	[14]
(Kihansi spray toad)		(Chytridiomycota)	habitat		
EXTINCTION			modification		
Leptodactylus fallax	B. dendrobatidis	Fungi	Pathogen	2000	[15, 16]
(Dominica and Montserrat		(Chytridiomycota)	invasion/endemic	(Dominica)	
Mountain Chicken Frog)			host population	2009	
EXTIRPATION				(Montserrat)	
Myotis lucifugus (little	Geomyces	Fungi	Pathogen	~2006	[17, 18]
brown bat)	destructans	(Ascomycota)	invasion?		
EXTIRPATION*					
Partula turgida (Hawaiian	Steinhausia sp.	Fungi	Pathogen	1996	[19]
tree snail)		(Microsporidia)	invasion/endemic		
EXTINCTION			host population		
Native European Crayfish	Aphanomyces	Protoctista	Pathogen	~1970's	[20, 21]
(eg. white clawed crayfish	astaci	(Oomycota)	invasion/spill-		
Austropotamobius pallipes)			over		
EXTIRPATION*					
Lottia alveus	Labyrinthula	Protoctista	Knock-on effect of	~1930	[22]
(Eelgrass limpet)	zosterae	(Slime molds;	pathogen-driven		
EXTINCTION		Heterokontophyta)	food loss		

Avian malaria?		_		[23]
			2002	
	Plasmodium sp.)	habitat loss		
Tasmanian devil	Mammalian	Frequency-	1996	[24]
facial tumour	infectious cancer	dependent		
disease		contact; low host		
		genetic		
		diversity(?)		
Canine distemper	ssRNA Virus	Pathogen spill-	1985	[25]
_	(genus			
(== .)				
	Morbilityirus	dikilowii vector		
Canine distemper	ssRNA Virus	Pathogen spill-	~1960 -	[26, 27]
virus (CDV)	(genus	over from	present	
	Morbillivirus	domesticated		
		dogs		
Trypanosoma	Protoctista	Pathogen spill-	~1905	[28]
lewisii ?	(Euglenozoa)	over following		
		introduction of R.		
		rattus?		
	9	_		[29]
parasitica	(Ascomycota)	invasion	~1930	
Ophiostoma ulmi	Fungi	Pathogen	~1910	[30]
	(Ascomycota)	invasion,		
		recombination		
Phytophthora	Protoctista	Pathogen	1935	[31]
	(Oaata)	_		=
cinnamomi	(Oomycota)	mvasion		
cinnamomi	(Oomycota)	mvasion		
cinnamomi	(Oomycota)	invasion		
cinnamomi	(Oomycota)	invasion		
cinnamomi	(Oomycota)			
cinnamomi Fusarium	Fungi	Pathogen	1946	[32]
			1946	[32]
Fusarium	Fungi	Pathogen	1946	[32]
Fusarium	Fungi	Pathogen	1946 ~1995	[32]
Fusarium circinatum	Fungi (Ascomycota)	Pathogen invasion		
	facial tumour disease  Canine distemper virus (CDV)  Canine distemper virus (CDV)  Trypanosoma lewisii?  Cryphonectria parasitica  Ophiostoma ulmi  Phytophthora	Tasmanian devil facial tumour disease  Canine distemper virus (CDV)  Canine distemper virus (CDV)  Canine distemper virus (CDV)  Canine distemper virus (CDV)  Canine distemper virus (Genus Morbillivirus  Morbillivirus  Trypanosoma Protoctista  lewisii?  Phytophthora Fungi (Ascomycota)  Phytophthora Protoctista	Tasmanian devil facial tumour infectious cancer dependent contact; low host genetic diversity(?)  Canine distemper virus (CDV) (genus over from Morbillivirus unknown vector  Canine distemper virus (CDV) (genus over from Morbillivirus domesticated dogs  Trypanosoma Protoctista Pathogen spillover following introduction of R. rattus?  Cryphonectria parasitica (Ascomycota) invasion  Phytophthora Protoctista Pathogen invasion, recombination  Phytophthora Protoctista Pathogen invasion, recombination	Tasmanian devil Mammalian infectious cancer dependent contact; low host genetic diversity(?)  Canine distemper virus (CDV) (genus over from Morbillivirus unknown vector  Canine distemper virus (CDV) (genus over from Morbillivirus domesticated dogs  Trypanosoma Protoctista Pathogen spill- over following introduction of R. rattus?  Cryphonectria Fungi Pathogen 71930  Ophiostoma ulmi Fungi Pathogen 71930  Ophiostoma ulmi Fungi Pathogen 71910  (Ascomycota) invasion, recombination  Phytophthora Protoctista Pathogen 1935

[34]	~1950	Unknown.	Fungi	Pestalotiopsis	Torreya taxifolia (Florida
			(Ascomycota)	microspora?	torreya)
					EXTINCTION* (~99%
					decline)
[35]	~1930	Unknown	Protoctista	Labyrinthula	Zostera marina and Zostera
			(Slime mold;	zosterae	caulescens (Eelgrass)
			Heterokontophyta)		EXTIRPATION
			Heterokontophyta)		EXTIRPATION

Note: We only include species where there is published evidence of extinction/extirpation, or published evidence of declines with a high likelihood of future loss. Many EIDs did not meet these strict criteria despite causing high levels of population decline (e. g. bird West Nile Virus, Red squirrel parapox virus, Prairie dog plague). \* indicates species where extirpation or extinction is predicted based on projections of future population viability. (?) indicates that data is persuasive but deficient

**Table S4.1**Data for Fig. 1. Summary of major taxonomic groups of pathogens that cause animal species extinctions/extirpations from Table S1

Taxonomic	Disease-driven	Corrected for
groups of	extinction/ extirpation	community-level
pathogens	events (% of total)	extinctions (% of total)
Fungi	39 (72.0)	11 (64.7)
Protist	12 (22.0)	3 (17.6)
Viruses	2 (3.7)	2 (11.7)
Bacteria	0 (0)	0 (0)
	- (-)	- (-)
Helminths	0 (0)	0 (0)
others*	1 (1.9)	1 (5.88)

<sup>\*</sup>Note: 'Others' includes mammalian carcinogenic cell lines and prions

**Table S4.2**Data for Fig. 1. Summary of major taxanomic groups of pathogens that cause plant species extinctions/extirpations from Table S1

Taxonomic	Disease-driven	Corrected for
groups of	extinction/ extirpation	community-level
pathogens	events	extinctions
Fungi	4 (57.1)	4 (57.1)
Protist	3 (42.8)	3 (42.8)
Viruses	0 (0)	0 (0)
Bacteria	0 (0)	0 (0)
Helminths	0 (0)	0 (0)
others*	n/a	n/a

Disease	Pathogen	Host range	Regional losses <sup>1</sup>	Regional losses of absorbed CO <sub>2</sub> (megatonnes) <sup>2,3</sup>
Dutch Elm	Ophiostoma ulmi	Elm	25 million elms (UK, 1990's)	0.395 <sup>2</sup> to 1 <sup>3</sup>
			77 million elms (USA, by 2001)	
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	0.012 to 0.05
ramorum bilgili			Pre-emptive cull of 4 million larches (UK 2011)	0.012 00 0.00
'Jarrah' dieback	Phytophthora cinnamomi	2,000 of 9,000 native <i>spp</i> . in Western Australia	1 million hectares of western Australia (by 2009)	9 to 23
Discriberable /	Consequence	I a dan a ala ada a	16.3 million	
Pine beetle / blue stain	Grossmania clavigera	Lodge pole pine	hectares of western Canada (by 2011)	207 - 520
				TOTAL: ~ 230 to 580 megatonnes

## Table S5. Tree carbon sequestration losses caused by fungal/oomycete diseases

Regional losses¹ are given as trees felled/succumb to disease and resulting losses in  $CO_2$  absorption for 5 different fungal/oomycete pathogens. Such regional losses determined for total number of lost trees estimated over period stated, with minimum² and maximum³ estimates based on either ² carbon sequestration data-base at Office of Sustainability, Tufts University US (with 25 -120 year old trees is 2.52 lbs to 5.58 lbs  $CO_2$  per year per tree: 25 - 120 year old pines is 15 - 11.7 lbs  $CO_2$  per year: crude mean of values is 3.95 Kg  $CO_2$  per tree per year) or on the assumption³ that one broad-leaved tree will absorb around 0.01 tonne of  $CO_2$  per annum [36]. Estimates for losses due to *Phytophthora cinnamomi* are based on a eucalyptus planting density of 2300 trees per hectare [37]. Pine beetle/blue stain losses are based on a pine planting density of 1400 trees per hectare. We note that we have not evaluated losses owing to timber decay as a result of tree death. Atmospheric  $CO_2$  levels (December 2011, http://co2now.org/) were recorded at 391.80 ppm or 834.5 Gigatonnes; maximum regional losses recorded herein equate with 0.069% global  $CO_2$ 

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