Review

A Synoptic Review of Plant Disease Epidemics and Outbreaks Published in 2021

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ABSTRACT: A synoptic review of plant disease epidemics and outbreaks was made using two complementary approaches. The first approach involved reviewing scientific literature published in 2021, in which quantitative data related to new plant disease epidemics or outbreaks had been obtained via surveys or similar methodologies. The second approach involved retrieving new pest presence records added to the CABI Distribution Database in 2021. The literature review for the first approach had two stages. Stage 1 aimed to identify publications on plant diseases caused by pathogen taxonomic groups and led to retrieval of 99 core articles describing studies in 62 categories (pathogen species or species complexes) across more than 40 host species in 6 continents. In Stage 2, the core articles were augmented with further articles providing more context and information for the pathogen species identified in Stage 1. When both sets of articles were combined, the pathogen species with more than 5 articles were: *Bursephalenchus xylophilus*, *Candidatus* Liberibacter asiaticus, cassava mosaic viruses, citrus tristeza virus, *Erwinia amylovora*, *Fusarium* spp. complexes, *Fusarium oxysporum* f.sp *cubense*, *Magnaporthe oryzae*, maize lethal necrosis co-infecting viruses, *Meloidogyne* spp. complexes, *Pseudomonas syringae* pvs, *Puccinia striiformis* f.sp *tritici*, *Xylella fastidiosa*, and *Zymoseptoria tritici*. The automated search of the CABI Distribution Database led to 617 new distribution records from 283 plant pathogens in 2021 and was followed by manual review of all pathogens with more than 4 new records, to identify confirmed first reports in a new location. A total of 15 pathogens was identified: apple hammerhead viroid, apple rubbery wood viruses, *Aphelenchoides besseyi*, *Biscogniauxia mediterranea*, *Ca.* Liberibacter asiaticus, citrus tristeza virus, *Colletotrichum siamense*, cucurbit chlorotic yellows virus, *Erwinia rhapontici*, *Erysiphe corylacearum*, *Fusarium oxysporum* f.sp. *cubense* Tropical Race 4, *Globodera rostochiensis*, *Nothophoma quercina*, potato spindle tuber viroid, and tomato brown rugose fruit virus. Although 3 very important pathogens – *Ca.* Liberibacter asiaticus, citrus tristeza virus and *Fusarium oxysporum* f.sp *cubense* – were represented in the results of both approaches, in general the two approaches revealed distinct sets of plant disease outbreaks and new records, with little overlap in the results.

Keywords: Plant disease epidemics

INTRODUCTION

Plant diseases pose a continuing threat to food security, plant health, and ecosystem health globally (Jeger et al. 2021; Ristaino et al. 2021; Rizzo et al. 2021).

Historically, plant disease epidemics and outbreaks have been associated with increased interconnectedness of the landscape, climate change, human movement, and increased intensification of crop production practices such as irrigation. Crop losses attributed to disease have been estimated mainly for globally important food crops (Savary et al. 2019, 2022). Much less is known for minor crops, for those of regional importance only, for non-food crops or concerning the provision of ecosystem services from native wild plant populations and communities (Gougherty and Davies 2021, Jeger 2021). It is reasonable to assume that reported losses are probably a consequence of epidemics or major outbreaks of disease but what is often missing from reports is quantitative information on the disease dynamics that led to the losses observed. This knowledge gap should be filled recognising the different perspectives of plant health regulation, epidemiological analysis, and crop loss assessment.

This review fills this gap and has two main objectives. The first objective of this review is to provide a synoptic view of plant disease outbreaks across all hosts as reported in peer-reviewed scientific articles published in 2021. The second objective of the review is to summarise information from comprehensive data bases on new reports of pathogens spreading or emerging in new geographical regions – or on new host species – in 2021. Our working hypothesis was that there would be little overlap in the results obtained from meeting the first objective of the study with those with meeting the second objective, largely because it is reasonable to assume that new reports of a pathogen species will normally precede epidemics or major outbreaks of that species that might subsequently occur. By accessing information from these two complementary approaches, we anticipate that this will fill the knowledge gap and moreover identify limitations in current approaches in identifying emerging and re-emerging plant diseases.

Objective 1. A literature search was made to identify articles in which the objectives of the study and the underlying methodology, particularly the use of surveys and other surveillance methods, are well-described. As we describe below, the key importance of such studies lies in providing information that goes beyond that obtained in reports of the presence or absence of a given disease. We accept that restricting the review to publications from just a single year, 2021, may be considered a limitation, but – as will be shown – the periods referred to often span multiple years. However, difficulties in obtaining up-to-date information on epidemics/outbreaks may affect decision-making in disease management (Thompson et al., 2018; Severns & Mundt, 2021). A wider problem is how to correct for inevitable time lags between data collection, analysis, and reporting (Bastos et al., 2019).

The breadth of our ambition makes it impractical to use expert-based assessment methods (Savary et al. 2019), important though these may be for estimating global crop losses. We do not limit the review to major food crops, or indeed any plant host category, or to pathogens experts consider important. Instead, we use methods accounting for disease outbreaks reported in the scientific literature irrespective of geographical regions, hosts, or causal organisms. In the latter case, comprehensive reviews have been published for pathogen taxonomic groupings, for example viruses and viroids (Jones, 2021), fungi and oomycetes (Fones et al., 2020), bacteria and mollicutes (Agrios 2005), nematodes (Bernard et al., 2017) and parasitic plants (Erdogan, 2021). The methods used were based on principles of a systematic review that recognise the need to: (i) avoid as much bias as possible in the choice of pathogens or hosts; (ii) identify pathogen species in the search and not specify them *a priori* because of their perceived importance; and (iii) avoid giving undue emphasis to pathogens or plants which are used as model systems or for presenting novel scientific interest.

We note that in searching the scientific literature, it is important to recognise the different terminologies used. For example, 'harmful organisms' (a term used in plant health and pest risk analysis, Devorshak, 2012) is a generic term, including pests and weeds. Pests could also be used to refer to both invertebrate organisms that cause damage due to, for example, herbivory, and pathogens causing disease. The term parasite can be used to describe a wide range of symbiotic associations, from mutualistic to pathogenic (Jiang et al., 2020). The term pathogen is used to describe a parasite that causes disease, although there can be some fluidity depending on the biotic and abiotic environment (Méthot and Alizon, 2014). Disease itself often requires both a pathogen and a vector for it to manifest. A vector may itself be a pest in the absence of the pathogen. For this reason, it is important that the results of automated searches are scrutinised to confirm their relevance to the search strings used. Plant pathology is also still influenced – and arguably over-influenced – by the 'one pathogen-one host' paradigm (Lamichhane and Venturi, 2015). However, disease complexes, mixed infections, the co-occurrence of closely related species (a major problem with plant viruses), subspecies, and other intraspecific designations of variety, biovar, pathovar and forma specialis, are all known to occur. These factors complicate disease assessments, risk assessments and indeed systematic reviews. For this reason, we have tried to reflect these complexities in our methodology and interpretation of results.

Objective 2. The second objective of the review reflects the distinction between outbreaks of long-established and well-characterised pathogens, and new reports of pathogens, sometimes poorly or newly characterised, spreading or emerging in new geographical regions or hosts (Bebber et al. 2013, 2014). Such reports often arise from the requirements of national and regional plant health regulations for official surveys to determine the presence or absence of a named harmful organism, usually at the species level. For new reports across all hosts, pathogens, and geographical regions, the use of a comprehensive database is essential to assess patterns that emerge in any given year, in our case 2021.

The comprehensive database we use here is the CABI Distribution Database (DDB). This database holds over 1.2 million geographic records of organisms and their locations, with a focus on species which are important to agriculture and the environment. Over 55,000 species are represented, across key areas such as crop pests, crop and animal diseases, invasive species, and natural enemies. Most of the data has been sourced from peer reviewed published literature and other authoritative third parties such as plant protection organisations. Whenever available, information is stored on the origin, extent of distribution and the invasive status. The DDB was used for this review as it has the most comprehensive global coverage of plant pests and diseases relevant to agriculture, and since it is regularly updated to reflect changing species distributions.

METHODS

Objective 1. Published articles on disease outbreaks and epidemics

A systematic review was made on Web of Science of journal articles published in 2021 (including online access of copy-edited but not necessarily typeset articles prior to full publication, aka 'Early View' or 'First Look' or other synonyms) following a systematic map protocol and search criteria based on thematic blocks and search strings (Vilvert et al., 2021). This was done in two stages (Figure 1). A scoping, proof-of-concept study used three thematic blocks and the preliminary search strings "Plant disease" AND "survey" AND ("epidemic" OR "outbreak"). The intention was to identify pathogen species for further study and to assess the extent of coverage in the set of recovered articles. This resulted in 45 articles which were checked manually for relevance. Of these, 8 articles were excluded, since they reported on food-borne diseases, plant-based vaccines, pharmacological and therapeutic activity of plants, mosquitoes/malaria, or animal/human diseases, leaving 37 articles remaining. This was considered an inadequate coverage and hence the search was extended to four thematic blocks with search strings “plant disease” AND (“survey” OR “surveillance” OR “monitoring”) AND (“pathogen” OR “vector”) AND (“epidemic” OR “outbreak” OR “impact” OR “damage”). We term this the ‘Stage 1’ search.

Stage 1 resulted in a larger set of 141 articles which again were checked for relevance. Given the larger number of articles recovered, criteria were set for excluding articles, recognising that in some cases this is a matter of judgement rather than the result of any absolute criterion. In the main, excluded were articles on: inoculative weed control with pathogens; non-refereed literature reviews or routine listings of pathogens; soil surveys of microbial communities; development of detection sensors; and primer design and genomic approaches. Unless linked directly to new field observations of disease, also excluded were articles reporting analysis of seed samples; small scale experimental plots using artificial inoculation; analysis of historical culture collections; aerobiological studies; and mathematical models. However, articles that dealt with functional aspects of microbial communities associated with the natural occurrence of disease in the field were retained. Also retained were grower surveys and citizen science that referred to or were combined with field observations of disease. This selection process resulted in 92 articles that were retained for further analysis.

A separate search was done in Stage 1 for plant parasitic nematodes by substituting the term “plant nematode” for “plant disease” in the search string. This was done because nematodes are often referred to as parasites associated with pest damage rather than pathogens causing disease. Following the same exclusion procedures as above, 7 further articles were retained. Hereafter, we exclusively refer to plant parasitic nematodes as pathogens.

The 99 (= 92 + 7) articles recovered in Stage 1 were allocated to categories corresponding to: 1) a single named pathogen species, but also including a recognised disease complex with co-infecting often related species (65 categories); and 2) multiple pathogens in a crop, cropping/production system, forest trees, or in wild plant populations (6 categories). These articles are termed the “Core articles”.

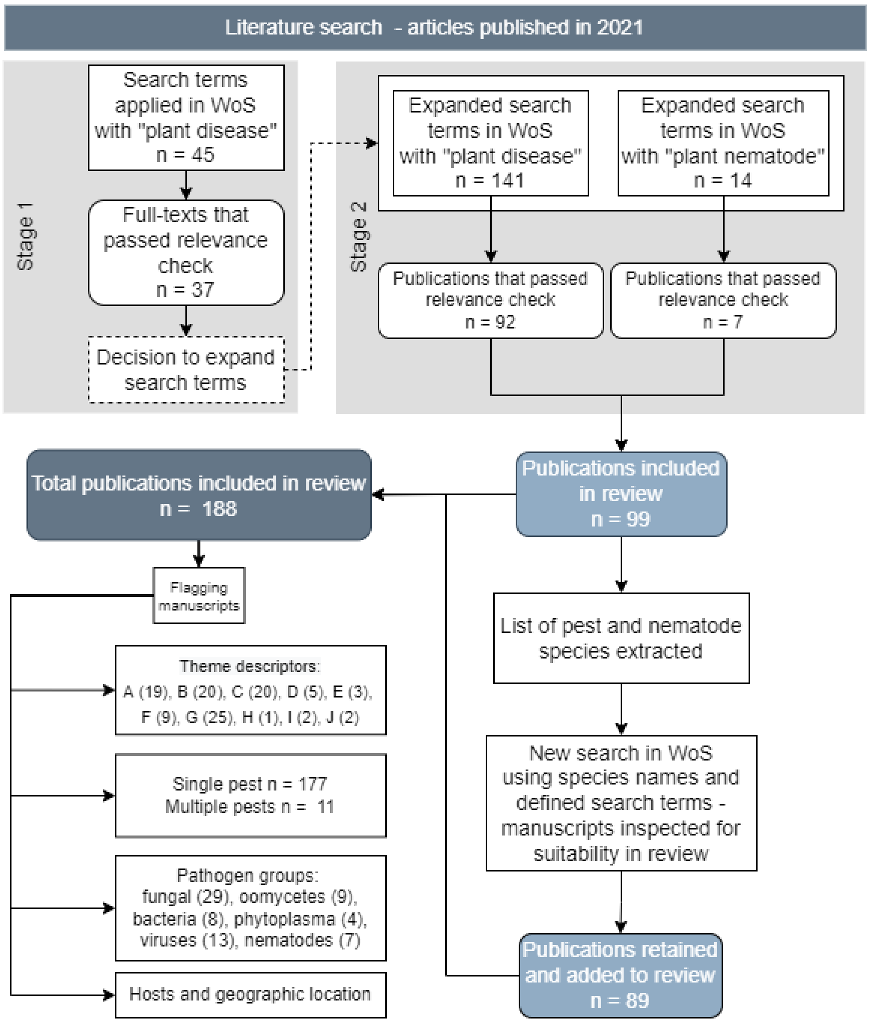

Figure 1. Methodology for the survey of published articles on disease outbreaks and epidemics. The workflow and number of results after each stage of filtering for the review of the scientific literature published in 2021. Numbers represent the number of identified articles at each stage: the final review after all exclusions were applied summarises n = 89 articles.

Each core article was flagged by host (crop, cropping/production system, or wild plant), pathogen group (fungus, oomycete, bacterium, phytoplasma, virus, nematode) and geographical origin (regions, country, continent, global), and one of 10 descriptor types for the main motivation of the study, recognising that many articles were motivated by more than one of these descriptors. These descriptors were as follows.

detection, discrimination, and analysis
surveillance, including growers and citizen science
emergence of new pathogens, strains, and vectors
wild hosts and weeds as inoculum reservoirs
wild relatives, land races, and genetic resources
wild plant populations and communities
disease management, including varietal resistance
biological control
climate change and variability
yield loss estimation

The purpose of the Stage 1 search was to identify pathogen species for which disease epidemics or outbreaks had been identified through surveys or other systematic approaches. To provide additional context and information on the pathogen species identified, an augmented Stage 2 search was done with two thematic blocks and the search strings: "<pathogen name>" AND ("survey" OR "epidemic" OR "outbreak"), again restricted to 2021 publications. In Stage 2, the "survey" and the "epidemic or outbreak" thematic blocks were combined in a single thematic block. Hence, the search was intended to recover articles reporting on an epidemic or outbreak of a given pathogen but without reporting a survey, and *vice-versa*. The search strings used in Stage 2 for the pathogen species identified did not include "surveillance", "monitoring", "impact", or "damage" as used in Stage 1. A similar approach was followed for the multiple pathogen categories identified, but with an appropriate thematic block defined for the cropping/production system rather than the single pathogen name. Articles recovered with these modified search criteria were allocated to the defined categories from Stage 1, giving a total of 188 retained articles across all categories after the results of both Stages were included.

Objective 2. Records in the CABI Distribution Database

Automated identification of potential new pathogen records

The DDB attempts to maintain up-to-date presence/absence status records across 507 geographic areas. These can be national or sub-national (e.g., state, province), administrative areas and other regions, islands, or sea areas of biogeographic importance. To perform the following analysis, data were initially extracted from the MS SQL Server database and subsequently analysed in MS Excel and QGIS.

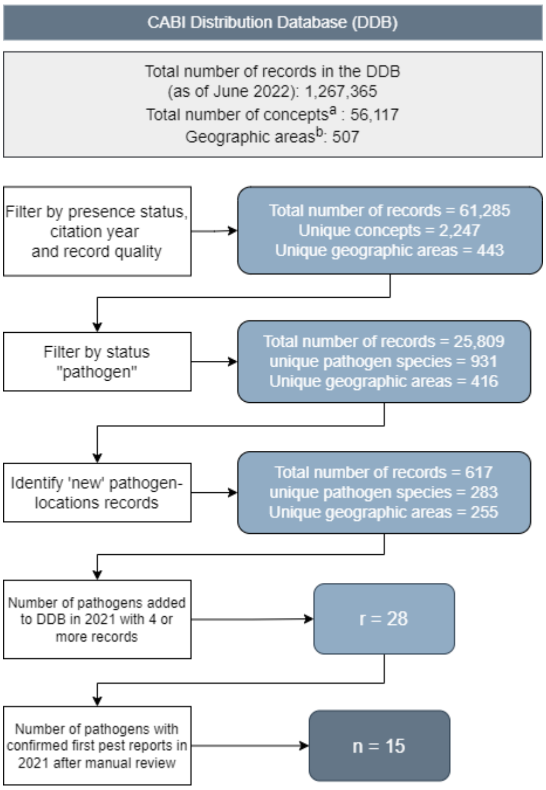

Figure 2. Review of records in the CABI Distribution Database (DDB). The workflow and number of results from the exploration of the DDB for new species occurrence records added to the database in 2021. Numbers represent the number of identified records which consist of a concept and the related geographic area. Totals are also shown for the number

of unique geographic areas and concepts at each stage of the process. A total of 28 pathogens had four or more new occurrence records in 2021 according to DDB. It was followed by manual review of all pathogens with more than 4 new records (r = 28), to identify confirmed first reports in a new location (n=15).

Firstly, all distribution records with a 'Present' status and a source reference citation year of 2021 were extracted from the database (Figure 2). If no citation year was published, we only considered records added to the database between 01/01/2021-31/12/2021. Records with a poor "Data Quality" flag were excluded.

The next step was to filter to consider only plant pathogens. To classify organisms, the GBIF taxonomic library (GBIF Secretariat, 2021) was used to exclude organisms which are not pathogenic, e.g., Plantae and the Animalia phyla: Chordata, Arthropoda, and Mollusca. The classification was also cross-referenced with the CABI Crop Protection Compendium (www.cabi.org/cpc). If an organism had datasheet type 'Pest' it was considered a plant pathogen. Any remaining unclassified organisms were manually checked against EPPO Global Database (EPPO, 2021) and/or search of scientific literature for evidence that they cause plant disease. This resulted in a set of 25,809 distribution records from 931 organisms in 416 geographic areas identified as plant pathogens.

To establish which of the 2021 records represented a first record of a pathogen in a location, a check was made against the rest of the DDB for any pre-2021 records of the organism in the geographic location. Where no previous 'Present' status records were held in the location in question, the record was considered a 'new' occurrence record.

The data were then summarised for each pathogen to count the number of geographic locations with at least one new record. A list ordered by the number of locations was used to select pathogens for manual review. Pathogens which had new 2021 records for at least four locations were selected for further investigation. The threshold of four records was chosen because the number of pathogens returned with three records or fewer was much larger, to the extent a manual review would have been overwhelming.

Manual review

To test the efficacy of the automated process, and to assess the proportion of records which represented pathogen spread to a new location or presence on a new host, for each of the pathogens with four or more new 2021 records, the individual distribution records and their sources were reviewed in detail. Records were categorised as either:

1. A confirmed first report in a location or on a new host
2. Not a confirmed first report

Records were considered first reports if the cited reference confirmed that a pathogen had been recorded in a new geographic location (of the 507 used in the DDB), where it had not previously been recorded. A record was also considered to be a first report if the cited reference confirmed that the pathogen had been identified on a host plant on which it had not previously been recorded. Records that failed to meet these criteria were considered not to be confirmed first reports.

The date of each confirmed first report was identified as the year that symptoms were first observed or the year that samples of the pathogen or affected host plant/s were collected, not the year the report itself was published.

Details of the confirmed first reports for each pathogen were then described, summarising the recent changes in distribution of the pathogen, the host plants with which it was associated and any other information from the reports that was considered relevant.

RESULTS

Overview of results

Objective 1. Published articles on disease outbreaks and epidemics

Core articles from Stage 1 (single pathogen species or species complexes allocated to categories, hereafter 'named species') are summarised in Table 1 for fungi, oomycetes, bacteria, phytoplasmas, viruses, and nematodes, respectively. The greatest number of categories was for fungal pathogens (29), followed by plant viruses (11) (see also Figure 3). Together these groups accounted for 60% of all categories. No core articles were identified for viroids. Table 2 shows core articles relevant for multiple pathogens affecting a crop or cropping system, including crop-associated weeds, production system (including tree and forest systems), or wild plants.

Table 1. Core articles on single named species identified in Stage 1 of the review of published articles on disease outbreaks and epidemics. Results from Stage 1, categorised by the class of named species agent: fungi, oomycetes, bacteria, phytoplasmas, viruses/viroid and nematodes. "Type" is relative to our categorisation: A = detection, discrimination & analysis; B = surveillance, including growers and citizen science; C = emergence of new pathogens, strains, and vectors; D = wild hosts and weeds as inoculum reservoirs; E = wild relatives, land races, and genetic resources; F = wild plant populations and communities; G = disease management, including varietal resistance; H = biological control; I = climate change and variability; and J = yield loss estimation. Rows with "Species" starting Ca. designate the relevant Candidatus.

FUNGI

Species	Host/disease	Source	Location	Type
Alternaria brassicola	*Cakile maritima*	Papaix 2021	Australia	F
Athelia rolfsii	*Vincetoxicum* spp./southern blight	Pethybridge et al. 2021	USA	D
Austropuccinia psidii	Myrtaceae/myrtle rust	Fensham & Radford-Smith, 2021	Australia	F
Bretziella fagacearum	Oak spp./oak wilt	Pellegrini et al. 2021	USA	F
Ceratocystis ficicola	Fig/vascular wilt	Tsopelas et al. 2021	Greece	C
Ciboria caunculoides *Ciboria shiraiana* *Scleromitrula shiraiana*	Mulberry/mulberry sclerotial disease	Lv et al. 2022	China	A
Colletotrichum siamense	Rubber trees/leaf disease	Du et al. 2021	China	A
Colletotrichum spp.	Apple/bitter rot	Martin et al. 2021	USA	G
Cronatium ribicola	White pines/blister rust	Dudney et al. 2021	USA	I
Diaporthe spp	Tree species/dieback	Lopes et al. 2021	Portugal	C
Diplodia corticola *Diplodia quercivora*	Oak spp./canker	Fereira et al. 2021	USA	A
Fusarium graminearum	Cereals and legumes/head blight, seedling disease and root rot	Breunig and Chilvers 2021	USA	G
Fusarium oxysporum f.sp *cubensis*	Banana/Fusarium wilt	Heck et al. 2021	Brazil	G
Fusarium species complex	Sugarcane/pokkah boeng disease	Shan et al. 2021	China	G
	Tomato/Fusarium disease	Nawaz et al. 2021	Pakistan	G
	Chickpea/Fusarium wilt	Bekele et al. 2021	Ethiopia	G
Magnaporthe oryzae	Rice/ leaf and panicle blast	Wang et al. 2021b	Italy	I
Neonectria neomacrospora	Abies/shoot necrosis and cankers	González et al. 2021	UK	C
Phyllachora maydis	Maize/tar spot	Oh et al. 2021	USA	B
Physoderma sp.	Faba bean/gall disease	Bitew et al. 2021	Ethiopia	C
Plenodomas lingam *Plenodomus biglobosus* *Pyrenopeziza brassicae*	Brassicaceae crops and weeds/black leg and chlorotic leaf spot	Claasen et al. 2021	USA	D
Podosphaeria plantaginis	Ribwort plantain/powdery mildew	Eck et al. 2021	Finland	F
Pseudocercospora fijiensis	Banana/black leaf streak	Carlier et al. 2021	Central America & Caribbean	B

Puccinia polysora	Maize/southern corn rust	Halvorsun et al. 2021	USA	A
Puccinia striiformis f.sp *tritici*	Wheat/ yellow rust	Perronne et al. 2021 Esmail et al. 2021 Sandhu et al. 2021	France Egypt Australia	C C G
Pyrenophora semeniperda	Barley/ring spot	Dokhanchi et al. 2022	Iran	C
Raffaelea quercus-mongolicae	Oak/systemic wilt	Lee et al. 2021	South Korea	C
Septophoma terrestris	Onion/pink root rot	Yoshida 2022	Japan	G
Sporisorium scitamineum	Sugarcane/sugarcane smut	Tegene et al. 2021	Ethiopia	G
Tilletia indica	Wheat/Karnal bunt	Arif et al. 2021	Pakistan	G
Zymoseptoria tritici	Wheat/Septoria tritici leaf blotch	Garnault et al. 2021	France	C
OOMYCETES				
Phytophthora austrocedri	Juniper mortality	Donald et al. 2021	UK	C
Phytophthora capsici	Vegetable crops/Phytophthora blight	Hudson et al. 2021	USA	G
Phytophthora cinnamomi	Many hosts	Shayka et al. 2021	Global	-
	Holm oak/oak decline	Hornero et al. 2021	Spain	B
Phytophthora infestans	Potato/late blight	Monteros-Altamirano & Delgado, 2021 Kanetis et al., 2021	Ecuador Cyprus	E C
Phytophthora megakarya	Cacao/black pod	Djeumekop et al. 2021	Cameroon	G
Phytophthora ramorum	Tree & horticultural hosts/sudden death oak & larch, leaf & shoot blights	Jung et al. 2021	East Asia	F
	Tree hosts/sudden oak death	Rosenthal et al. 2021	USA	F
BACTERIA				
Ca. Liberibacter asiatica/africanus	Citrus/Huanglongbing	Bibi et al. 2021 Espinosa-Zaragoza et al. 2021 Garcia-Figuera et al. 2021	Pakistan Mexico USA	G C G
Dickeya and *Pectobacterium* spp.	Potato/black leg and soft rot.	Curland et al. 2021	USA	A
Erwinia amylovora	Pear/fire blight	Trad & Tauoeb 2021	Tunisia	E
	Wild walnut-fruit forests/fire blight	Doolotkeldieva et al. 2021	Kyrgyzstan	E
	Rosaceae plants/fire blight	Song et al. 2021	Korea	C
	Strawberry/bacterial blight	Ozturk & Soylu 2021	Turkey	C
Pseudomonas syringae pathovars	Pea/bacterial blight	Kant et al. 2021	Australia	A
Ralstonia solanacearum	Potato/bacterial blight	Tafesse et al. 2021 Marković et al. 2021	Ethiopia Serbia	G A
	Tobacco/wilt disease	Tan et al. 2021	China	H
Xanthomonas citri pv. *citri*	Citrus/Asiatic citrus canker	Pruvost et al. 2021	South-west Indian Ocean islands	C

Xylella fastidiosa and vectors	Almond/leaf scorch	Lazaro et al. 2021	Spain	B
	Spittlebug vectors on grapevine	Bodino et al. 2021 Gargani et al. 2021	Italy Italy	B B
	Olive/olive quick decline	Beal et al. 2021 Poblete et al. 2021	USA Spain	B A
	Almond/almond scorch disease Grapevine/Pierce's disease	Olmo et al. 2021	Balearic Islands (Spain)	C
	Olive/olive quick decline Almond/almond scorch disease	Zarco-Tejada et al. 2021	Italy/Spain	B
PHYTOPLASMAS				
Ca. Phytoplasma dypsidis	Ornamental palms/lethal wilt disease	Jones et al. 2021	Australia	**C**
Ca. Phytoplasma solani	Multiple hosts and weeds/"bois noir" & "stolbur" diseases	Contaldo et al. 2021	European countries	A
Ca. Phytoplasma vitis	Grapevine/flavescence doree	Rizzoli et al. 2021	Switzerland	D
Unassigned phytoplasma/virus associations	Areca palm/yellow leaf disease	Lei et al. 2021	China	B
VIRUSES & VIROIDS				
Cassava viruses and vectors	Cassava/African cassava mosaic disease and cassava brown streak disease	Munguti et al. 2021	Kenya	C
	Cassava/Sri Lankan cassava mosaic disease	Saokham et al. 2021	Thailand	A
Cereal/barley yellow dwarf viruses	Cereals and grasses	Somera et al.	Estonia	A
Citrus tristeza virus	Citrus	Pais da Cunha et al. 2021	Angola	C
	Wild citrus	Liu et al. 2021	China	A
Groundnut bud necrosis orthotospovirus	Tomato Groundnut N. benthamiana	Chaudhary et al. 2021	India	A
Maize chlorotic mottle virus/Sugarcane mosaic virus	Maize/maize lethal necrosis	De Groote et al. 2021	Kenya	B
Maize rayado fino virus Corn stunt spiroplasma Maize bushy stunt phytoplasma and vectors	Maize/corn stunt	Rossini et al. 2021	Argentina	G
Rice stripe mosaic virus	Rice/rice stripe mosaic disease	Wang et al. 2021c	China	G
Rice yellow mottle virus	Rice	Issaka et al. 2021	Niger	B
Plantago viruses	*Plantago lanceolata*	Susi & Laine 2021	Finland	F
Tomato brown rugose fruit virus	Tomato	González-Concha et al. 2021	Mexico	G
Tomato chlorosis virus	Multiple hosts	Esquivel-Fariña et al. 2021	Brazil	G

			USA	
NEMATODES				
Bursephalenchus xyophilus and vectors	*Pinus*/pine wood nematode	Atkins et al. 2021 Zhang et al. 2021 Yu et al. 2021	USA China China	B B B
Globodera rostochiensis	Potato/cyst nematode	Borzykh et al. 2021	Ukraine	B
Heterodera glycines	Soybean/cyst nematode	Bradley et al. 2021	USA/Canada	J
Meloidogyne spp complexes	Tomato	Teston et al. 2021	USA	G
Pratylenchus hippeastri	Strawberry	Brenes-Campos et al. 2021	Costa Rica	A

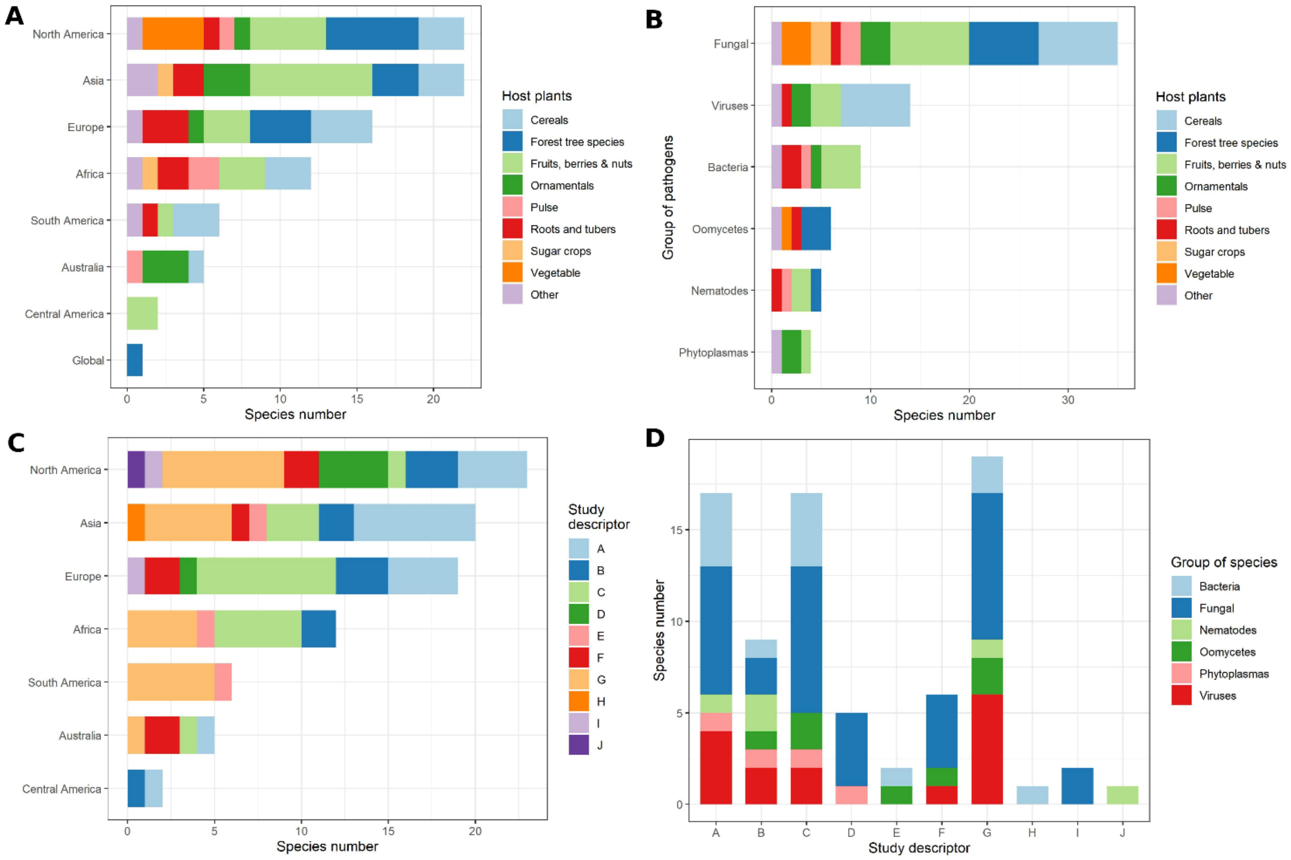

Figure 1. Categorisation of core articles on single named species identified in Stage 1 of the review of published articles on disease outbreaks and epidemics. A – Number of host plants per continent where retrieved pathogen species were observed. B – Number of pathogen species per group of pathogens and host plants on which they were observed. C – Number of pathogen species per continent and study descriptor. D – Number of reported species grouped by study descriptors and pathogen group.

Table 2. Core articles on multiple pathogens affecting a crop or cropping system identified in Stage 1 of the review of published articles on disease outbreaks and epidemics.

System	Hosts	Source	Location
Aquaculture	Seaweed	Mateo et al. 2021	Philippines
Cropping systems	Maize/soybean	Hampf et al. 2021	Brazil
Crop-associated weeds	Annual and perennial species, many *Asteraeae* /Tobacco	Korbecka-Glinka et al. 2021	Poland
	Capsella bursa-pastoris/annual crops	Ahmed et al. 2021	Canada
	Many species, including wild basil and legumes/Phaeolus	Mwaipopo et al. 2021	Tanzania
Forest/tree pathogens	Native and exotic trees, bamboo	Thu et al. 2021	Vietnam
	General: trees, forests, & plantations	Panzavolta et al. 2021	Global
	Forest tree seedlings	Spear & Broders 2021	Panama
Nursery production systems	Avocado	Ramírez-Gill & Osorio, 2021	Colombia
	Major nursery crops	Weiland et al. 2021	USA
Wild plants	Plant communities in meadows	Halliday et al. 2021	Switzerland

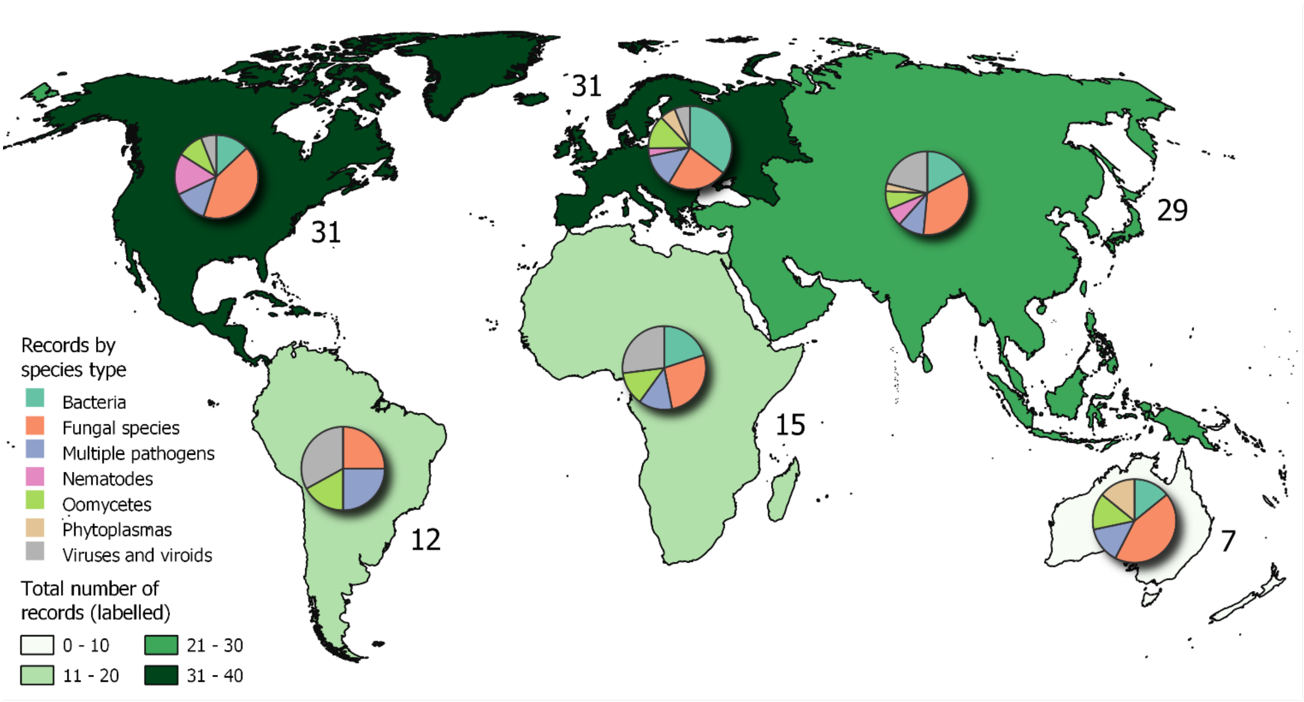

Figure 2. Map showing number of pathogen-location pair records retrieved from core articles on single named species and multiple pathogens identified in Stage 1 of the review of published articles on disease outbreaks and epidemics. The number of records by continent and species type of pathogen. Two studies had global remit, therefore n=2 was added to each continent's totals. Country by country data is available in Electronic Supporting Information, S1 - Additional visualisations.

Table 3. Combined results following Stage 1 and 2 from the review of published articles on disease outbreaks and epidemics. Summaries of the results for each of these categories are given in the main text.

NAMED SPECIES OR SPECIES COMPLEX	**Number of articles**
Candidatus Liberibacter asiaticus and vectors	10
Cassava mosaic viruses	10
Xylella fastidiosa and vectors	10
Erwinia amylovora	7
Puccinia striiformis f.sp *tritici*	7
Zymoseptoria tritici	7
Bursephalenchus xylophilus	7
Meloidogyne spp. complexes	6
Magnaporthe oryzae	6
Citrus tristeza virus	6
Fusarium spp. complexes	6
Fusarium oxysporum f.sp *cubense*	5
Pseudomonas syringae pvs	5
Maize lethal necrosis co-infecting viruses	5

MULTIPLE PATHOGENS/CROPPING PRODUCTION PRACTICE	**Number of articles**

Aquaculture	5
Crop-associated weeds	5
Cropping systems	5
Forest tree pathogens	5
Wild plants	5

Figure 3. **Symptoms caused by the diseases identified in the review of published articles on disease outbreaks and epidemics.** A) Fusarium oxysporum f.sp. cubense (Panama disease of banana); symptoms on a banana plant (Public Domain - Released by Scot Nelson/via flickr - CC0); B) Meloidogyne enterolobii (Pacara earpod tree root-knot nematode); rootknot symptoms on an ornamental Petunia species (©Jeffrey W. Lotz/Florida Department of Agriculture & Consumer Services/Bugwood.org - CC BY 3.0 US); C) Cassava mosaic disease (African cassava mosaic); symptoms on cassava leaf. (©Phil Taylor, CABI); D) Citrus tristeza virus

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(©Tim Gottwald); E) Erwinia amylovora (fireblight) on pear (©Phil Taylor, CABI); F) Candidatus Liberibacter asiaticus (Asian greening); HLB symptoms. April 2016 (©Nian Wang (Citrus Research and Education Center)); G) Pseudomonas syringae pv. syringae (bacterial canker) symptoms on peach (Prunus persica), bark peeled to show discoloration beneath (©University of Georgia Plant Pathology/University of Georgia/Bugwood.org - CC BY 3.0 US); H) Fusarium on wheat (©Phil Taylor, CABI); I) Magnaporthe oryzae (rice blast) in Myanmar (©Phil Taylor, CABI); J) Puccinia striiformis f.sp. tritici; symptoms of yellow rust on triticale leaf (©Rasbak/via Wikimedia Commons - CC BY-SA 4.0); K) Zymoseptoria tritici, septoria on wheat (©Phil Taylor, CABI); L) Symptoms of maize lethal necrosis disease (©Joseph Mulema, CABI); M) Bursaphelenchus xylophilus (pine wilt nematode); pine wilt symptoms, one year after death of tree (©USDA Forest Service/Region 2- Rocky Mountain Region/USDA Forest Service/Bugwood.org - CC BY 3.0 US); N) Symptoms of Xyella fastidiosa on olive in Apulia, Italy, 2015 (©Dr Stephen Parnell).

Of 45 host species covered in the core articles, only pathogens of maize (6), wheat (4), rice (4), tomato (4), citrus (3) and potato (3) were reported at least twice (Figure 3). Geographically, the core articles reported studies in 42 countries. Most articles described studies done in the United States (20), followed by China (9). At the continental scale, the comparable numbers of articles were Europe (25), North America (23, including Canada and Mexico), Asia (23 across Central, South, East and South-east Asia), Africa (13), South America (9, including Central America and the Caribbean) and Australasia (5, only Australia). Accounting for articles which reported multiple pathogen-location pairs, as well as for two articles which took a worldwide focus and so were relevant to every continent, allowed us to project a graphical summary of the results of Objective 1 onto a global map showing counts of pathogen-pair locations (Figure 4).

Five article types were dominant (Figure 3): disease management, including deployment of resistant cultivars (20), emergence of new pathogens, strains, and vectors (18); disease surveillance, either remote or ground-based (15); detection, discrimination, and analysis of pathogens (14); and across all articles for wild plant populations, weeds, and wild relatives (14).

Combining the results of Stage 1 and Stage 2 resulted in 14 categories for named species or species complexes with five or more articles (Table 3; Figure 5). These named species are discussed individually in the extended part of the review, below. For the remaining categories with fewer than five articles, the additional articles retrieved in Stage 2 are listed in Electronic Supporting Information, S2 - Additional source material, with reference to the categories in Table 1, but with no further commentary. Where articles were grouped into multiple pathogen categories or by cropping/production practices, combining the Stage 1 and Stage 2 searches resulted in five categories with five or more articles.

Objective 2. Records in the CABI Distribution Database

The automated process to identify new 2021 records from the DDB resulted in 617 distribution records from 283 pathogen designations (Figure 6). Of these, 180 plant pathogens returned a single new 2021 record. A total of 255 geographic locations recorded at least one new 2021 record. The majority of new 2021 records were for occurrences of pathogens in Asia (226), the fewest records were from Oceania (20), with a high proportion of records for fungi and viruses for all continents.

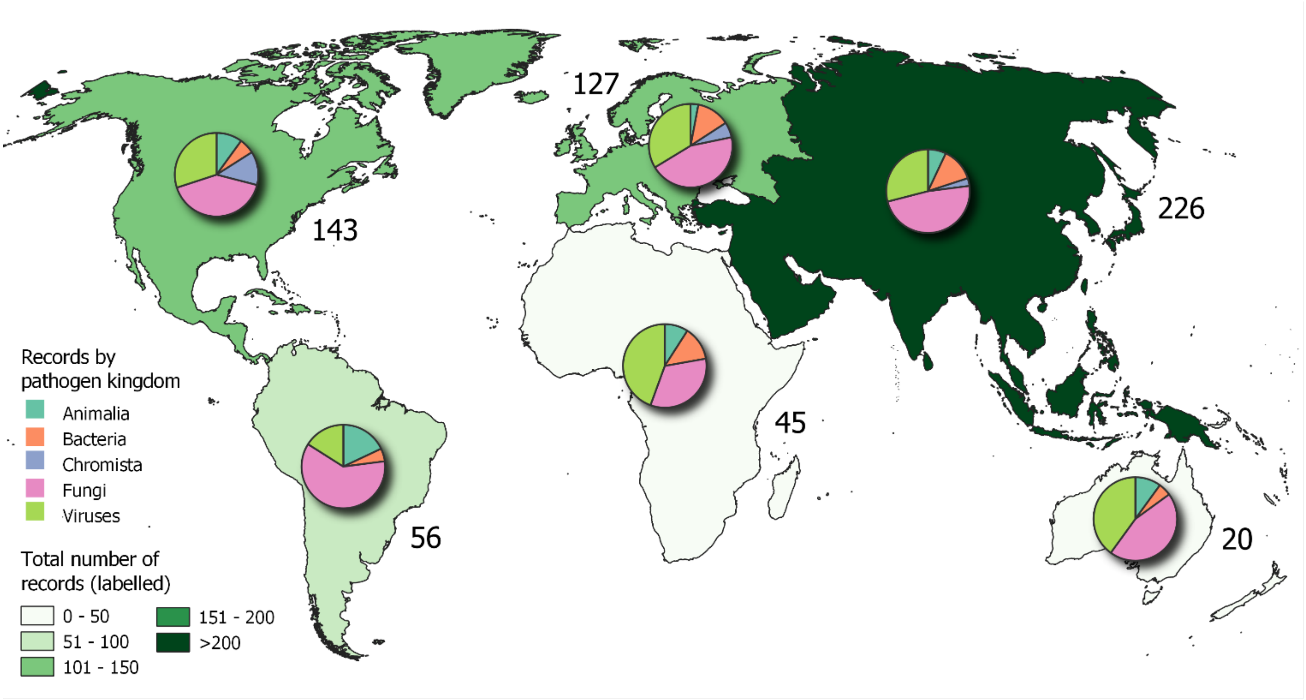

Figure 4. Map showing locations of new pathogen records reported in 2021 in the CABI Distribution Database (DBB) based on the automated process. Counts at a DBB geolocation level are summarised by continent, with a breakdown of pathogen type by kingdom. Country by country data is available in Electronic Supporting Information, S1 - Additional visualisations.

Of these, 28 pathogens met the threshold for manual review, i.e., four or more new 2021 records (Figures 7 & 8). The manual review determined whether the records were confirmed first reports in a new geographic location or on a new host plant. Fifty-nine records were classified as such, covering 15 plant pathogens (Table 4); again, a more detailed description of these pathogens is provided in the extended part of the review below.

Records for the remaining 13 plant pathogens that were manually reviewed were not considered to be first reports for various reasons, including taxonomic revisions, external databases referenced by the date the information was accessed, and when it was determined surveys focused on a pathogen in a region it was already known to occur.

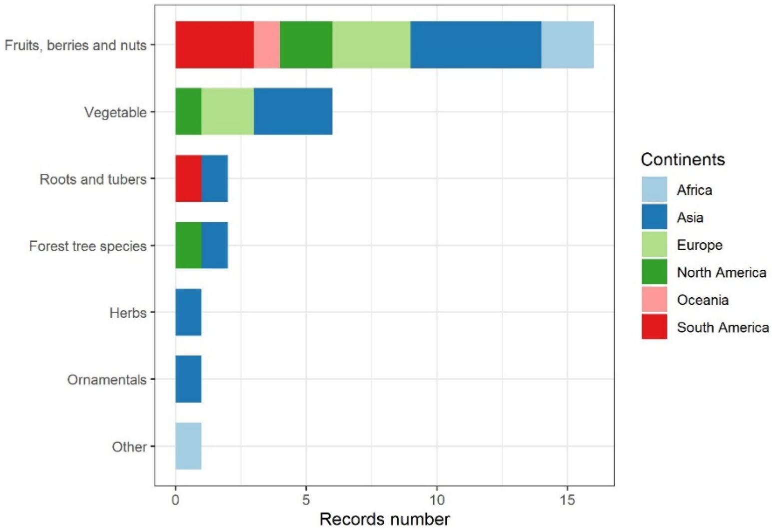

Figure 5. Unique pathogen-host pairs in new pathogen records reported in 2021 in the CABI Distribution Database (DDB). Host species were identified in each location where new pathogen records were added to DDB in 2021 and were reported in four or more geolocations defined in DDB. One or more host species could be identified in each geolocation. Host species were classified in groups, and locations by continent.

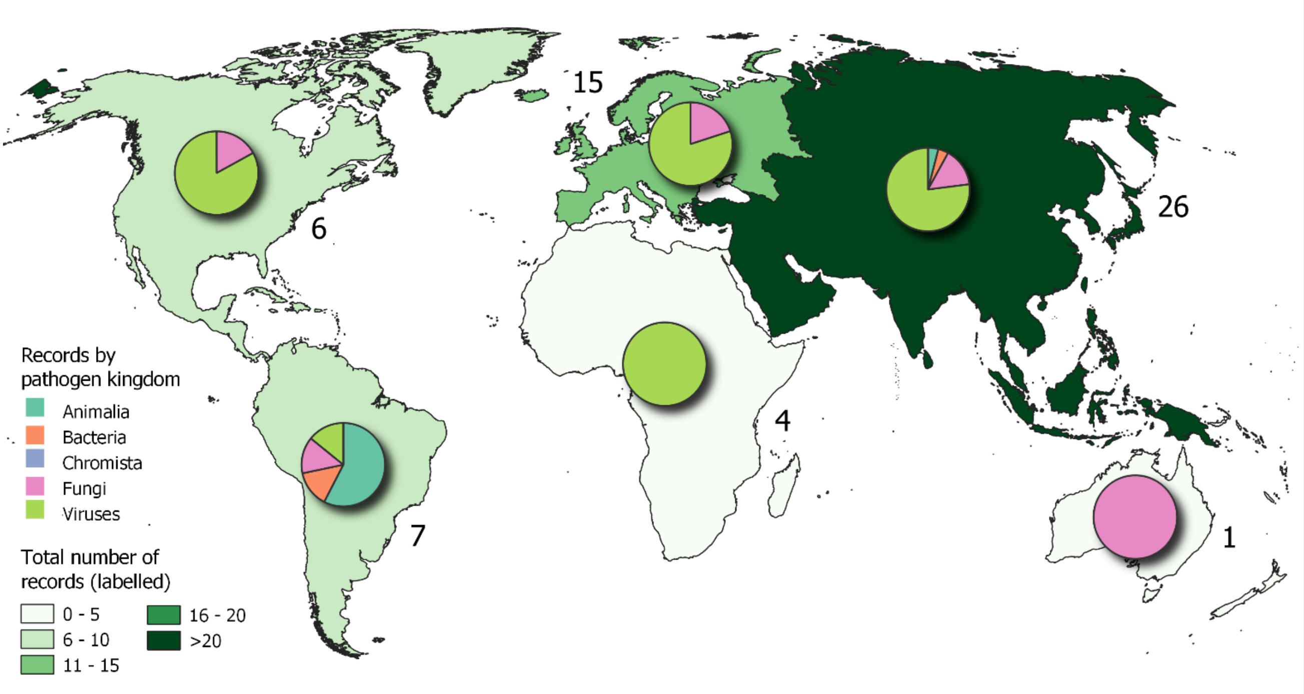

Figure 6. Map showing locations of new pathogen records reported in 2021 in the CABI Distribution Database (DDB) following manual review. Counts at DDB geolocation level are summarised by continent, with a breakdown of pathogen type by kingdom. Country by country data is available in Electronic Supporting Information, S1 - Additional visualisations.

Comparing results obtained for Objective 1 and Objective 2

Six named pathogens were identified by both of our two approaches. In alphabetical order, these were: *Candidatus* Liberibacter asiaticus, *Citrus tristeza virus*, *Colletotrichum siamense*, *Fusarium oxysporum* f.sp. *cubense* Tropical race 4, *Globodera rostochiensis* and *Tomato brown rugose fruit virus.* Of these, three were reported in at least 5 publications in Objective

1 (Table 3). These were *Ca.* Liberibacter asiaticus, *Citrus tristeza virus* and *Fusarium oxysporum* f.sp. *cubense.*

Thirteen additional pathogens identified by the automated review of DDB records overlap with pathogens identified by the literature review, but these were not reviewed manually as they did not reach the threshold of four new 2021 records. In some cases, the literature review identified pathogens at the level of genus or as species complexes or groups of pathovars. There is some overlap in DDB with these groupings, e.g., *Colletotrichum* spp. (13 species identified in DDB results), *Pseudomonas syringae* pathovars (2 pathovars identified in DDB results).

Table 4. New pathogen records reported in 2021 in the CABI Distribution Database. Of the 28 pathogens which met the threshold for manual review – i.e., had at least four new records – a total of 15 were confirmed as constituting new reports of a named pathogen in a new location (the rows highlighted in light green). These 15 plant pathogens are described in the main text of the review.

PATHOGEN	NUMBER OF DDB RECORDS		
	Pre-2021	New in 2021	After manual review
Tomato brown rugose fruit virus	18	16	15
Cucurbit chlorotic yellows virus	24	12	11
apple rubbery wood viruses	27	8	8
Aphelenchoides besseyi	130	8	4
Apple hammerhead viroid	1	5	4
Colletotrichum siamense	0	4	4
Potato spindle tuber viroid	56	5	3
Erysiphe corylacearum	16	4	3
Erwinia rhapontici	10	8	1
Citrus tristeza virus	160	7	1
Globodera rostochiensis	99	7	1
Biscogniauxia mediterranea	3	5	1
Fusarium oxysporum f.sp. *cubense* Tropical race 4	31	5	1
Candidatus Liberibacter asiaticus	105	4	1
Nothophoma quercina	2	4	1
Urocystis colchici	0	62	0
Cerotelium fici	9	21	0
Phytophthora ramorum	46	16	0
Calonectria pseudonaviculata	47	13	0
Gibberella indica	20	11	0
Xiphinema rivesi	45	7	0
Diaporthe destruens	4	6	0
Peronospora aquilegiicola	0	6	0
Apple fruit crinkle viroid	1	5	0
Potato latent virus	2	5	0
Acidovorax citrulli	59	4	0

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Cucumber mosaic virus	250	4	0
Ralstonia pseudosolanacearum	12	4	0
225 pathogens with <4 2021 records	5006	351	N/A

A map showing the combined counts of locations from both the literature review and the CABI Distribution Database is Figure 9.

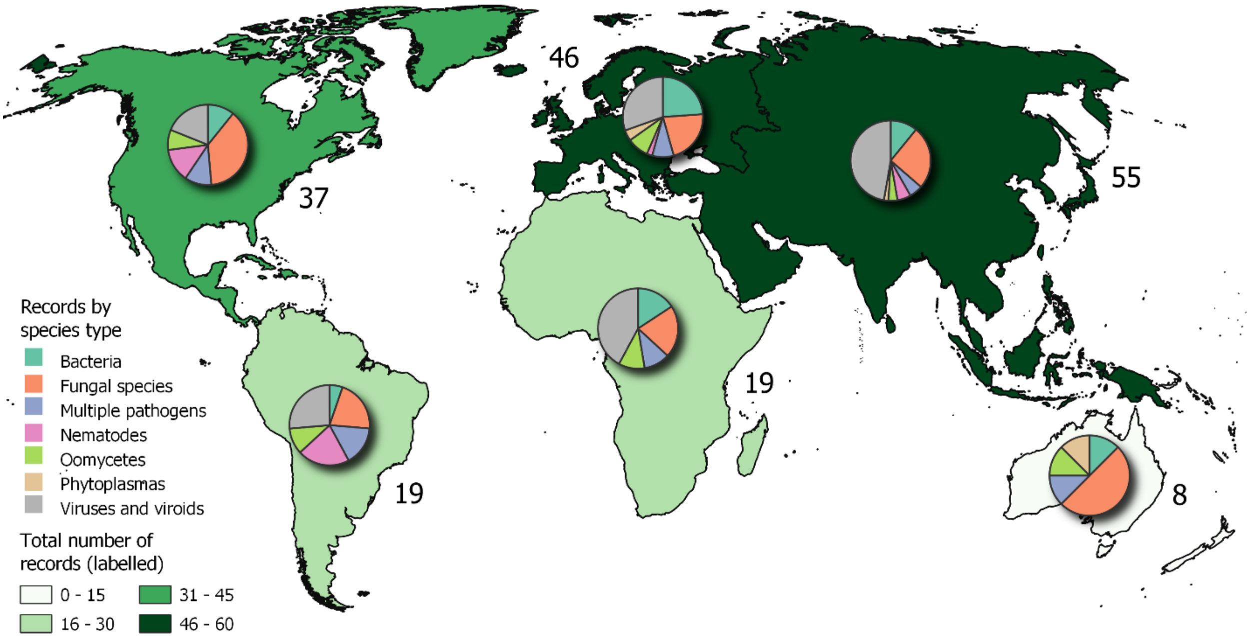

Figure 7. Map showing combined locations of new pathogen records reported in 2021 from both the literature review and from the CABI Distribution Database (CDD) (following manual review). Counts at CDD geolocation level are summarised by continent, with a breakdown of pathogen type by kingdom. Country by country data is available in Electronic Supporting Information, S1 - Additional visualisations.

Detailed results

Summary

Below, three distinct sets of information are reported, taking pathogens (or multiple pathogens/cropping systems/production systems) in alphabetical order. The first two sets correspond to the results for Objective 1 and concentrate on what the literature review of published articles determined to be the most important named single pathogens (Table 3; top section), and multiple pathogens/cropping systems/production systems (Table 3; bottom section), respectively. The final set of information corresponds the results for Objective 2 and concentrate on pathogens identified in the search of the DDB that were confirmed following manual review (Table 4; green highlighted rows). As described above, for three pathogens there is overlap between the first and third sets of results; such cases are denoted by an asterisk (*).

Objective 1. Literature review of published articles on disease outbreaks and epidemics (single named pathogens)

The following sections summarise the results for named pathogens identified by the literature review (see Table 3; top section), reporting pathogens in alphabetical order.

Bursephalenchus xylophilus

Bursephalenchus xylophilus, the pine wood nematode (PWN) affects *Pinus*, causing pine wilt disease. The organism is native to North America and has spread to Asia and more recently to Europe.

Core articles: Atkins et al. (2021), Yu et al. (2021), Zhang et al. (2021).

A survey was made to determine the occurrence of PWN and its beetle vectors (*Monochamus* spp.) on the native *Pinus ponderosa* in Colorado, USA, over two years and in forests (32 sites) and urban settings (12 settings) (Atkins et al., 2021). There was much variation in the incidence of PWN with many host trees not displaying symptoms; overall, the incidence of the nematode in sampled pines and beetles was about 4%. The nematode was found to be associated with *Monochamus clamator* for the first time in the USA. The results indicated that natural forests are natural reservoirs of PWN, especially with previous wildfires, with beetles moving to urban areas late in the growing season.

Detection of PWN was conducted using UAV (unmanned aerial vehicle) based hyperspectral imaging, light detection and ranging (LiDAR) techniques. PWN was reported in a forested area of approximately 55700 ha, in Zhejiang province of China (Yu et al. 2021). The predominant tree species was *P. massoniana*. Field observations on individual trees were made in October 2020 with five infection classes recorded based on needle coloration, growth vigour, and secretion of resin. The combination of UAV and LiDAR gave an overall accuracy of about 74% in predicting the infection class.

Airborne imagery and ground surveys were used to characterise the spatial pattern of PWN outbreaks in Hubei province of China (Zhang et al. 2021). The forested area of almost 70000 ha is covered predominantly by *P. massoniana* and P. *elliottii*. Sentinel-2 L2A level image data was used to derive vegetation indices. Georeferenced information on topographical and forest type variables was assembled from the local forestry administration and the US Geological survey. The number of dead PWN trees sampled was about 19000 with an equivalent number of randomly selected points where PWN was absent. A range of machine learning models was used to predict the probability of PWN occurrence in the region based on constructed explanatory variables. The best fitting model had a detection rate of 96% but with a high “false alarm rate” (27%) when correcting for omission errors caused by the PWN-absent points. Explanatory variables based on elevation and vegetation indices were most important in predicting PWN but also important were variables describing human activity.

Some 180 strains of *B. xylophilus*, each consisting of about 40 individual nematodes from a single chopped tree, were collected from infected trees in 16 Provinces across China (Ding et al. 2021). Strains were cultured to obtain a sufficient sample size and used for sequencing and SNP genotyping, with a geographical location prediction model used to analyse genomic variation. It was found that the *B.xylophilus* population in China can be divided into distinct subpopulations with some interchange through migrations, suggesting that the nematode has been adapting to different temperature zones and that survival may be greater at lower temperatures than previously anticipated.

The spatiotemporal pattern of pine wilt disease in the Yangtze River Basin has been analysed based on statistical data obtained from the State Forestry and Grassland Administration of China covering the years 2000 to 2018 (Hao et al. 2021). Pine wilt in this area showed an “increase-decrease-increase” trend with a massive increase in 2018. Spatial trends showed a sequence of jumps to multiple outbreak locations moving west along the river, with large clusters of pine wilt disease forming across four regions of the river basin. This form of analysis was repeated across China and showed strong concentrations and spatial correlations of the disease in south-eastern part of the country (Hao et al. 2022). The direction of spread was from south to north and from coastal to inland areas, with clusters forming following the pattern “spread-stabilization-outbreak-major outbreak” at this larger spatial scale.

The community diversity of xylophagous beetles at different stages of PWN infections was studied in *P. massaniana* and *P. thunbergia* forests in Fujian and Shandong provinces of China respectively (Chu et al. 2021). A total of 27 PWN-infected trees were cut to the ground at each site and all beetles present in the whole tree were collected and identified to species. Beetle diversity was significantly higher on *P. massaniana* than on *P. thunbergia* and varied with infection class (initial, dying, and terminal). *M. alternatus*, an important vector of PWN, occupied a large niche with different aggregation patterns at the three infection classes. It was concluded that diversity and competitive interactions among xylophagous beetles may be involved in regulating their population dynamics.

Candidatus Liberibacter asiaticus and vectors (: see also results of Objective 2)*

Ca. Liberibacter asiaticus is the causal agent of huanglongbing disease of citrus, also known as citrus greening disease. The bacterium is vector-borne by psyllid species *Diaphorina citri* and *Trioza erytreae.*

Core articles: Bibi et al. (2021), Espiniosa-Zaragoza et al. (2021), Garcia-Figuera et al. (2021).

The Asian citrus psyllid *Diaphorina citri* is a vector of the phloem-limited bacterium *Ca.* Liberibacter asiaticus (CLas), the pathogen causing Huanglongbing disease of citrus. Population dynamics of the psyllid were monitored in two study locations at the University of Faisalabad (UAF), Pakistan (Bibi et al. 2021). At each location, 15 trees each of *Citrus sinensis sensu lato* and *C. reticulata* were selected randomly for population monitoring population numbers at weekly intervals from March 2011 to 2013. Daily standard meteorological data were recorded at the meteorological observatory at UAF. Three models were used to predict the population dynamics of the psyllid based on multiple linear regression, classification with decision trees, and neural networks. The neural network-based model gave the best predictions of eggs, nymphs, and adults over the monitoring period.

The African citrus psyllid *Trioza erytreae* vectors *Ca.* Liberibacter africanus (CLaf) and can also vector CLas, also causing Huanglongbing disease, and has spread to parts of Asia and Europe. To determine whether the environment in Mexico would be suitable, an ecological niche modelling approach was used based on distribution points for the vector in Africa obtained from the scientific literature and the Global Biodiversity Information Facility, Natural History Museum, London, databases (Espinoza-Zaragoza et al., 2021). A total of 122 data points was obtained, split for training the model and subsequent evaluation. The same data base was used to map the distribution of white sapote crops (*Casimiroa edulis*) on which the vector can feed. The citrus-growing areas of Mexico were found to have environmental suitability for *T. erytreae*, matched by the distribution of *C. edulis*, and with connectivity to ports, potential pathways of entry for the psyllid.

Huanglongbing (CLas) was detected in California in 2012, and to prevent the spread of the bacterium to commercial citrus groves, growers have formed a voluntary code of best management practice (Garcia-Figuera et al. 2021). This study evaluated the take-up of these practices by the citrus industry, based on grower surveys and a novel approach using multivariate ordinal regression. Part of the grower surveys referred to monitoring practices, with most respondents favouring scouting for the psyllid and surveys, but not making use of early detection methods that could precede the statutory qPCR tests. Participatory citrus grower surveys of HLB aimed at diagnosis have also taken place in Bahia, Brazil, where *D. citri* is present but the disease is currently absent and phytosanitary preparedness is considered possible only through grower participation (Oliveira et al. 2021).

Population fluctuations of *D. citri* and its natural enemies were monitored from March to December 2019 at two separated sites in Florida (Shrestha et al. 2022). Twenty trees were selected randomly from four pairs of organic and intermittently managed groves. Sentinel psyllids were placed on caged branches and counts of all beneficial arthropods were made for 2 mins at each sampling period. Adult psyllids were in stem-tap samples taken every 3 weeks from May to September. The study was mainly motivated by the need to look at different management practices, including pesticide spraying. Intermittent spraying did affect the activity of natural enemies but did not eliminate their populations. Importantly for Europe, *D. citri* was found in Israel for the first time in July 2021.

Early decline of fruit-bearing Mandarin (*C. reticulata*) and low productivity have proved to be a major concern in Bhutan, despite favourable conditions for citrus cultivation (Ghosh et a., 2021). Surveys were made of the incidence of HLB and citrus tristeza virus in four main citrus growing regions by taking leaf samples from healthy and declining trees showing symptoms of greening- and tristeza-like symptoms from different orchards of southern Bhutan. From a total of 51 samples, 36 were positive for CTV and 14 for HLB, using PCR-based diagnosis and genetic markers. There was a high level of mixed infections, all but one of the positives for HLB tested positive for CTV. The relationship between the natural occurrence of HLB, vectors and environmental conditions in Bhutan showed that the presence of *D. citri* was the most important factor, moderated by unfavourable environmental conditions and altitude (Om et al. 2021).

In many cases, the detection of plant pathogenic bacteria is made from samples of different environmental origin: soils and plant debris, living plants, and insects. Diagnosis of HLB using standardised RT-PCR methods was attempted from samples taken from plants, psyllid vectors, and parasitoids of the psyllid (Morán et al., 2021), a total of 4915 samples. A total of 2783 samples were taken from asymptomatic plants collected in surveys made between 2009 and 2018 in Spain. A total of 1052 samples of *T. erytreae* specimens came from colonies established on citrus plants in the greenhouse, and 1081 samples were of the parasitoid *Tamarixia dryi* introduced as a classical biological agent against *T. erytreae* and maintained in colonies at a Research Institute in the Canary Islands. The results showed that about 9% were amplified using a first rapid screening test, reduced to 0.03% using more specific tests. Most amplifications were associated with parasitic wasps. New primers external to target regions of the RT-PCR protocols were designed and showed that all amplifications came from other procaryotic organisms in the samples, not from *Ca.* Liberibacter spp.

Feral citrus trees are found as understory plants in forested areas in Florida. A survey was made of feral grapefruit (*Citrus x paradisi*) in wooded areas, mostly hardwood trees, elevated above surrounding wetlands and close to three commercial citrus groves, heavily infested with HLB (Vincent et al., 2021). Measurements of overstory shading above the grapefruit trees and understory daily incident radiation, *D. citri* detections using sticky traps, and CLas detections using RT-PCR, were all made. In addition, some phytochemical and physiological measurements were made. The main conclusion from the study was that the naturally shaded understory environment greatly inhibits HLB by deterring the arrival of the vector and enhances the survival of feral citrus by improving the photosystem-II performance. Given these results, further work is required to investigate the potential of shade in horticultural systems to reduce disease transmission by vectors and enhance plant growth. A review of potential control methods against HLB (Li and Nangong, 2022) covers genetic improvement, thermotherapy and tissue culture for propagating material, eradication of infected trees, vector control, physical methods including mobile thermotherapy of trees, and biological control of the vector. Precision trunk injection technology to deliver antibiotics or pesticides is proposed as a promising method to control HLB.

Cassava mosaic viruses and vectors

Cassava mosaic virus is the common name of 11 different virus species pathogenic on cassava belonging to the genus *Begomovirus*. The virus is transmitted by the *Bemisia tabaci* species complex.

Core articles: Munguti et al. (2021), Saokham et al. (2021).

The whitefly *Bemisia tabaci* is the vector for many important crop viruses globally. It is a species complex with more than 40 species that are indistinguishable by morphology and that attack a wide range of plant hosts. More than 300 plant viruses are transmitted by *B. tabaci*, including the two most important viruses of cassava in sub-Saharan Africa, cassava mosaic virus(es) and cassava brown streak virus. A specific 'cassava-type' of the whitefly is unique to cassava. A survey was made between July 2018 and July 2020 to determine the whitefly species present at sites in coastal, eastern, central, and western regions of Kenya (Munguti et al. 2021). The number of sampled sites depended on the number of cassava fields found in each region. At each sampled site, 5-10 adults were collected from 10 randomly selected cassava plants (a total of 76 specimens) and kept for molecular analysis, genotyping, and phylogenetic analysis. Three *B. tabaci* groups were found, two previously classified as sub-Saharan groups of putative species, and one Indian Ocean group not thought previously to colonise cassava.

A greater understanding is required of the diversity of the *B. tabaci* species complex, the prevalence and host range of cryptic species, and the consequences for transmission of viruses. Some weeds are known to harbour cassava *B. tabaci*. Whitefly adults were collected on crops and weeds in fields from July to August 2013 in Uganda (Mugerwa et al., 2021). Sites were selected based on observations of whiteflies on crops and wild weeds along the main and rural roads at intervals of 10-20 km, with digital photographs taken of weeds to aid subsequent identification. A total of 59 plant species were identified with 25 unidentified weeds. Three individual whiteflies from the stored samples were selected for DNA extraction, PCR amplification, identification of artefacts in the sequences obtained, phylogenetic analysis, and a hierarchical cluster analysis to infer host range profiles. Sixteen *B. tabaci* putative species were identified, three of which are proposed as novel. The most prevalent whiteflies were classified as *B. tabaci* MED-ASL (non-cassava type), sub-Saharan Africa 1 (the cassava type), and Bemisia Uganda1 (associated with sweet potato) and these whiteflies were the most polyphaghous. Multiple species occurred on some crop plants and weeds, and these plants may have the potential to be reservoirs for mixed virus infections.

The *B. tabaci* species complex also causes direct pest damage to cassava when present in large numbers. Field studies were made in 2016 and 2017 at two or three sites, respectively, with contrasting rainfall patterns (unimodal or bimodal) and different historical levels of whitefly abundance (Katono et al., 2021). The aim was to understand better how environment, cassava genotype and their interactions give rise to the increased abundance of *B. tabaci*. The overall conclusion across these factors was that temperatures of 28-30 C, rainfall in the range 30-15-mm, RH of 55-70%, and deployment of cassava genotypes with low height and large leaf area and lobe width significantly increases population growth of *B. tabaci*.

In Africa, at least nine species of cassava mosaic virus have been recognised. In India only two are known. Indian cassava mosaic virus (ICMV) and Sri Lankan casava mosaic virus (SLCMV), with the latter emerging in Southeast Asia in 2015 (Saokham et al. 2021). In this study, a survey was made for cassava mosaic disease caused by SLCMV in five cassava-producing provinces of Thailand adjoining the Cambodian border from October 2018 to July 2019. Some 201 cassava fields in plantations covering an area of 458 ha were sampled across the five provinces. Thirty cassava plants were sampled from a 1-ha area with leaves collected for PCR detection. A comprehensive set of disease assessment scores was compiled: prevalence, based on percentage of fields infested; incidence, based on percentage of leaves with symptoms; severity, calculated from five defined severity class; and a ‘latent’ infection score, based on percentage of asymptomatic plants. An attempt was made to differentiate symptoms arising from cutting transmission (whole plant symptoms) from vector transmission (top leaves only). The number of whiteflies on the five topmost leaves of each sampled plant was also counted. Cassava mosaic disease (CMD) prevalence ranged from 19 to 80% of fields across the five provinces, incidence ranged from about 1 to 43% of leaves with average severities per plant ranging from mild chlorosis to moderate mosaic. Asymptomatic plants ranged from 0 to 12% following PCR analysis. Phylogenetic analysis showed a close similarity of the virus isolates with SLCMV isolates from Vietnam and Cambodia. About 95% of infection was estimated as due to whitefly transmission rather than through infected stem cuttings, the original source of infection. A TAS-ELISA for SLCMV detection in southeast Asia has been developed in

Thailand and was shown to have 99.6% accuracy and 100% when tested with stem cuttings derived from 490 field samples collected between 2018 and 2019 (Charoenvilaisiri et al. 2021). The status of cassava mosaic disease caused by SLCMV in Southeast Asia has been reviewed (Om, et al. 2021). Following outbreaks in several countries, systems of healthy seed and distribution networks have been developed, combined with CMD-resistant planting material, although no information was given on the spatial coverage.

Field surveys were made in 2015 (184 farms) and 2017 (328 farms) to determine the incidence of African cassava mosaic virus (ACMV) and East African cassava mosaic virus (EACMV) across 12 Nigerian States and the Federal Capital Territory (Eni et al. 2021). Cassava farms were surveyed at about 10 km distances depending on their scattered distributions. At each farm, 30 cassava plants were assessed visually for foliar symptoms, whiteflies were counted on the topmost five leaves, and an average of four leaves was collected at each farm for ACMV and EACMV detection using PCR analysis. In total, more than 1300 cassava leaf samples were taken and analysed. In both years, the estimated proportion of cutting transmission was high, about 75% across the surveyed regions. ACMV in single infections was present in 74% of samples in 2015, in 50% of samples in 2017. EACMW in single infections was less than 1% in both years but the incidence of mixed infections was close to 5% in both years. Data were also aggregated according to north-west (lower overall incidence) and south-west (higher overall incidence) regions of Nigeria.

Surveys were carried out in 2016 and 2017 in multiple sites across eight cassava growing regions of Burkina Faso to ascertain the status of CMD in the country and the cassava mosaic viruses involved using field observations of symptoms and phylogenetic analysis (Soro et al., 2021). Disease incidence and severity varied across locations with CMD incidences ranging from 6-52% and symptom severities based on a score scale from mild to moderate. In all but one of the regions, cutting-borne infections were higher than whitefly-vectored infection. PCR and sequencing analysis of 687 samples across both years (452 with symptoms, 235 without) showed almost 80% of symptomatic samples to be ACMV-like and 1% to be EACMV-like in single infections, with almost 20% to be co-infected. Most of the EACMV-like positives were found to be East African cassava mosaic Cameroon virus, one of several EACMV-like viruses.

A survey was made of 96 smallholder cassava growers across five provinces of Zambia between 2015 and 2017 where cassava mosaic viruses had previously been reported (Szyniszewska et al. 2021). Accessible roadside fields along main roads at 10-15 km distances were used for the field-owner surveys which consisted of questionnaires and structured interviews. Participants were questioned on their awareness of CMD, symptom recognition, presence in their fields, and how the disease spread. Fields were separately assessed for the incidence and severity of disease, and 208 leaf samples were taken from the 96 fields for virus detection. Symptoms of CMD were observed in more than 80% of fields with an average incidence of about 50% within fields. No symptoms of cassava brown streak disease were observed. Most growers used planting material from their own (94%) fields or from adjacent fields. Only 48% of growers received information on or access to the use of certified clean planting material.

The historical genome of a 90-yr-old ACMV was reconstructed from small RNA sequences in an herbarium specimen (Rieux et al., 2021). Evolutionary divergence times estimated with the historical genome were significantly higher than those estimated without and are more in accord with historical disease records.

Citrus tristeza virus (: see also results of Objective 2)*

Citrus tristeza virus is a virus species of the genus *Closteroviridae*, causing economic damage to host plants of *Citrus* and related genera. The virus is transmitted by a range of aphid vectors, the most efficient being *Toxoptera citricida*.

Core articles: Pais da Cunha et al. (2021), Liu et al. (2021).

Citrus plants from eleven sources located in nurseries and an orchard in Angola were surveyed for the presence of citrus tristeza virus (CTV) using random-primed RNA-seq and multiple molecular marker amplification for the main CTV strains (Pais da Cunha et al., 2021). A wide range of strains was found to be present in the surveyed citrus locations, including some close to known severe strains as well as emerging strains in California and Uruguay. Much of the knowledge of the diversity of CTV strains comes from work on commercial citrus, with little known of virus diversity in wild citrus (Liu et al. 2021). Analysis was made of RNA libraries from wild citrus samples from the Ailao mountains of central Yunnan province, China. Some 44 virus isolates were found including CTV and other putative virus species within the *Closteroviridae*, with the frequent occurrence of recombination across members of the family. Novel viruses within the family may emerge from wild citrus as pathogens and stresses the need for surveillance of their pathological and epidemiological characteristics.

Citrus is affected by many viruses and viroids, some of which are widespread throughout citrus-growing countries, with some restricted to individual countries and regions. Virus isolates and source plants originating from China and Sicily and previously testing positive for CTV were used to generate small RNA libraries and sequenced using high throughput sequencing to assemble virus genomes, followed by bio-indexing (Licciardello et al., 2021). The HTS procedures were able to detect mixed CTV variants from plant samples but not non-EU variants, a key requirement for quarantine surveillance in the EU.

Local varieties of Mandarin orange (*C. reticulata*) in remote areas of Arunachel Pradesh, India, have been found in surveys to be in severe decline associated with aphid infestations (Datta et al. 2021). Four orchards showing poor health and symptoms of citrus tristeza virus infection were surveyed by taking 40 leaf samples in a stratified design and aphid samples (50-60 specimens per orchard). Leaf samples were subjected to RT-PCR methods for CTV detection, with genetic regions subsequently amplified and clonally sequenced. Phylogenetic analysis showed close affinity and clustering with ‘western lineages’, distinct from sequences found elsewhere in India and neighbouring countries. The evidence suggested that the ancestral western strain originated in the north-eastern region of India, part of the Indo-Burma biodiversity hot spot, with a relatively recent introduction to Europe, Africa, and the Americas (400-500 years ago). The ancestral stain diversified and spread to south-eastern Asia and elsewhere in India to form the Asian and Indian lineages.

CTV-positive leaf samples were collected from symptomatic trees during surveys in the upper Gulf Coast area of Texas from Corpus Christi to the Louisiana border from 2013 to 2018 (Park et al., 2021) with 36 samples analysed by strain-specific RT-PCR and then by amplicon sequencing of genomic regions. Variability in strain diversity observed over this 6-year period confirmed the presence of multiple strains in the samples, albeit with some inconsistent genotypic data. CTV was first reported in Texas in the mid-1950s, and the authors suggest that the current strain diversity has resulted from multiple introductions of CTV-infected propagation material since that time.

Disease caused by CTV can also be affected by changes in citrus management following outbreaks of other diseases. In Cuba the detection of huanglongbing led to the production of budwood in protected nurseries, eradication of infected plants and affected orchards, and chemical control of the psyllid vector (Llanes-Alvarez et al. 2021). The authors conducted a study to investigate the impact of these management changes on the incidence of CTV-infection and changes in the virus population. Although only a small number of isolates was obtained (27), the results showed a decrease in CTV incidence and a wider spread of mild CTV strains, which according to the authors, could be partially explained by the changed management practices.

Erwinia amylovora

Erwinia amylovora is a gram-negative bacterium and the causal agent of the economically damaging disease fire blight in apples and pears, and other members of the family *Rosaceae*.

Core articles: Doolotkeldieva et al. (2021), Song et al. (2021), Trad and Taoueb (2021).

Fire blight was first reported in Kyrgyzstan in 2008 and has reached the unique wild walnut-fruit forests in South Kyrgyzstan, a site of internationally important global biodiversity and genetic resources for species of *Juglans*, *Malus*, *Prunus*, *Acer*, *Pyrus* and *Crataegus*. Surveys were made for fire blight during 2018-2019 in private gardens, orchards, and wild trees across the forest, at a total of 29 sites with about 150 samples taken from representative plants of these species (Doolotkeldieva et al. 2021). GPS coordinates of sampled sites, positive and negative samples by plant species, and *E. amylovora* genotypes, were combined with the occurrence locations of endangered species of *Malus* and *Pyrus*. Fire blight was found in 12 of the sites in or close to the forest, but mostly on domesticated varieties. No infection was found on the endangered species but their proximity to infected sites raises concern and calls for preventative measures to be put in place. The genotypic analyses of previously collected isolates from North Kyrgyzstan indicated that natural disease spread had occurred.

A fire blight outbreak caused an unprecedented loss of pear trees in Tunisia in 2013. Five years of field surveys were made from 2015 – 2019 in parts of the country comprising 95% of the pear growing areas (Trad and Taoueb 2021). The purpose of the surveys was to inventory the impact on pear genetic resources in the country. The area of pear production harvested had declined from 8500 ha prior to the outbreak to 3000 ha in 2018, with the tonnage harvested reducing from more than 60000 tons to less than 13000 over the same period. Of 16 cultivars inventoried, 10 were of European origin, all of which were sensitive to fire blight. The six local cultivars which tended to shorter blooming periods, although sensitive, were more resilient to the disease and ex-situ conservation of these genetic resources was recommended as a means of sustaining future production.

A naturally occurring fire blight epidemic occurred in 2020 in the USDA *Malus* germplasm collection held at Geneva, New York State in the USA (Dougherty et al., 2021). Some 1142 trees of 41 *Malus* species were assessed for shoot severity (no. infected shoots/total no. shoots) with 2525 trees of 48 species also assessed for cut severity (amount of tree removed with fire blight). A subset of 667 trees was assessed for disease progression in June and July, with on average shoot severity increasing by about 12% from June to July, although there was considerable variation across *Malus* spp. representing the range in fire blight resistance and susceptibility in the collection.

Two lateral-flow diagnostic kits were compared with DNA-based methods and tested for their in-field use in fire blight diagnosis (Singh et al., 2021). Unusually for such studies, grower surveys and cost-benefit analyses were done, indicting the suitability of immunoassay test kits for their use in fire blight management. For other studies such as the recent emergence of fire blight in East Asia, the use of genomic studies has been essential both to characterise *E. amylovora* strains and to infer their origin and potential introduction pathways (Song et al. 2021). In the case of the emergence in Korea, genomic analysis of isolated strains indicated an ancestral lineage with North American strains.

Biological control of the fire blight pathogen has been proposed as an environmentally benign alternative to antibiotics such as streptomycin, now banned in Switzerland (Gschwend et al., 2021), with the increased availability of DNA sequencing in plant microbiome studies opening-up new areas of research. Blossom samples were taken in a low-input apple orchard and subjected to standard DNA-based methods to estimate microbial diversity. It was concluded that an abundance of natural fungal and bacterial antagonists counteracted the establishment of *E. amylovora* in the low-input orchard. However, no direct comparison with fire blight incidence on individual trees was made in this study.

Erwinia amylovora also infects other members of the Rosaceae. A natural outbreak of bacterial blight of strawberry in Turkey caused by *E. amylovora* was recorded following surveys made in 2018 and 2019 (Ozturk and Soylu 2021). Some 38 diseased plant samples taken from 22 fields in 14 production areas in two provinces. Isolations were confirmed as *E. amylovora* rather than other known *Erwinia* species, confirming the record as a new disease in Turkey. Previously its occurrence on strawberry had only been reported in Bulgaria. The significance of the finding for strawberry growers lies in the transmission of the bacterium by bees and the need for control measures where there is proximity to pome fruit and other susceptible ornamental plant species.

Fusarium spp. complexes

The genus Fusarium is a ubiquitous group of fungi, some species of which are pathogenic on plants and can be airborne as well as soilborne. They are often found in species complexes with some cryptic species. The presence of disease-causing complexes makes risk assessment, epidemiology, and disease management difficult.

Core articles: Shan et al. (2021), Bekele et al. (2021), Nawaz et al. (2021).

Pokkah boeng disease of sugar cane is caused by a *Fusarium* species complex, including *Fusarium verticillioides* and to a lesser extent *F. proliferatum*. Epidemics occur following outbreaks of the disease in large areas of susceptible crops. Sugarcane varieties bred in China for pokkah boeng disease resistance were screened in regional field experiments in areas where incidence of the disease has been high (Shan et al. 2021). A total of 60 new elite varieties and 31 established varieties were tested in the study. A greater proportion of the new elite varieties were moderately-resistant to resistant (59%) compared with the established varieties (41%). The results suggested that in areas conducive to the disease, new elite varieties should replace established varieties to obtain an appropriate distribution of varieties, control outbreaks of the disease, and improve the development of the sugarcane industry in China.

In Sri Lanka, pokkah boeng disease has recently emerged since 2019. Leaf samples were taken from three diseased plants showing typical symptoms in each of two farms, followed by pathogen isolation and pathogenicity testing, morphological and DNA sequencing, and phylogenetic tree construction (Srimali et al. 2021). Two isolates were confirmed as *F. proliferatum* and *F. incarnatum,* which when inoculated onto healthy plants appeared to induce different phases of symptom development.

In sugar cane co-infections of *Colletotrichum falcatum* (a member of the *C. gramimicola* complex causing red rot disease symptoms) and *Fusarium* spp. can occur. Twenty-two samples of stalks and leaves from plants with red rot symptoms were collected (two stalks per sample) from five locations in Minas Gerais and Paraná, Brazil, to understand better the aetiology of the disease (Costa et al. 2021). A total of 30 isolates were obtained and identified within the genera *Colletotrichum* (two species) and *Fusarium* (three species belong to the *F. fujikuri* complex). The Fusarium species also induced symptoms of pokkah boeng disease.

The joint effect and compatibility of phosphite and *Trichoderma* in controlling the Fusarium spp. involved in pokkah boeng disease was tested in planta (in the greenhouse not in the field) (Solic-Palacios et al. 2021). The *Fusarium* spp. complex used in the study had been isolated from the rhizosphere of cultivar with pokkah boeng symptoms in a sugar cane plantation in Mexico. In each of 80 pots a single sugarcane cutting bud was planted with phosphite (six levels) and *Trichoderma* (two isolates) and *Fusarium* treatments were applied in a full factorial design. The best treatment was found to be a combination of an intermediate level of phosphite and one of the *Trichoderma* isolates, improving plant height, culm length, and leaf dry weight. It was concluded that phosphite and Trichoderma could act synergistically in reducing infection while at the same time stimulating plant growth.

The Fusarium wilt and root rot complex is a major constraint to chickpea cultivation in Ethiopia. In 2015 and 2016, GPS-referenced field surveys were done covering 51 districts representing 17 chickpea growing areas (Bekele et al. 2021). Fields were selected at 5-10 km intervals and quadrat samples were taken using a diagonal transect design with 23-32 plants per quadrat, depending on plant density. Across all sites *Fusarium oxysporum* f.sp. *ciceri* was the predominant species (almost 70% of total isolates) but with *F. solani*, *Rhizoctonia bataticola*, *R. solani*, *Sclerotium rolfsii*, and other unidentified fungi represented among the isolates. The incidence of the disease was significantly associated with clay soils, with the highest incidence of about 45% found in the Amhara region where heavy clay soils (vertisols) predominate.

In Pakistan, tomato wilt is one of several diseases of tomato that reduce crop yield on an annual basis. The disease is associated with a complex of soil-borne pathogens including *F. solani*, *F. oxysporum*, and Verticillium spp. A survey was made in five districts of Punjab province over two consecutive years (Nawaz et al., 2021). Five locations were selected in each area with five sites at each location. Samples were taken at the nursey, flowering and fruit stages, disease was assessed, and isolations made. Across all sites, *F. oxysporum* was found with severe attacks at the flowering stage – subsequently confirmed as f.sp. l*ycopersici*. As well as *Fusarium* wilt, *Verticillium dahlia*, *Alternia solani*, *Pythium* spp., parasitic nematodes, and tobacco mosaic virus were found at different growth stages indicating the difficulties in tomato cultivation in Punjab province.

Fusarium oxysporum f.sp cubense (: see also results of Objective 2)*

Fusarium oxysporum f.sp *cubense* is a fungal plant pathogen that causes Panama disease of *Musa* spp., also known as fusarium wilt of banana. Tropical race 4 has been of particular concern on commercial banana cultivars, and the species designation *F. odoratissimum* has been proposed, but not fully accepted.

Core article: Heck et al. (2021).

The spatial and temporal dynamics of Fusarium wilt of banana caused by *Fusarium oxysporum* f.sp *cubense* (*Foc*) was assessed in surveys of 30 banana fields ranging in size from 0.85-6.67 ha covering 95 ha across different states of Brazil, and including three commercial banana subgroups (Silk, Pome, Cavendish) (Heck et al. 2021). Disease incidence, spatial aggregation and yield in the surveyed fields were assessed. For every 1% increase in disease incidence there was an increase in the estimated economic loss of about US$ 110 ha^{-1} year^{-1}. Evidence was found for the secondary spread of disease to neighbouring and distant plants. The key to managing the disease is to understand how the pathogen arrives in the field and the mechanisms of dispersal.

A major concern in banana production is the differential pathogenicity of races of *Foc* on banana cultivars/types and the implications for future development and deployment of resistance; in particular, the tropical and sub-tropical forms of Race 4 affecting the Cavendish Group. Surveys in India have shown the presence of Race 1 and both forms of Race 4, with typical incidences of up to 45% from Foc leading to the abandonment of banana production in some areas. A total of 61 Foc isolates were collected from widely separated banana-producing States in India, race-typed and virulence tested, and subjected to genome analysis (Thangavelu et al., 2021). Molecular markers were developed that differentiated between all three races present in India that could be used for both quarantine and disease management purposes.

Understanding the dispersal of *Foc* is key to the development of control strategies, both the initial introduction with planting material, and the subsequent spread in farmers' fields, with the latter aspect being particularly poorly understood. A range of mechanisms has been proposed for within field spread, including the possibility of insect root feeding and subsequent movement of soil-borne pathogens. The banana weevil *Cosmopolites sorditus* is a major pest in banana cultivation with larvae feeding mainly on the rhizome of banana plants. Laboratory experiments were done in which inoculum of *Foc* was acquired externally or internally in the digestive tracts of the weevil from Gros Michel bananas (Sánchez et al. 2021). Although viable external and internal inoculum (through faeces) declined, weevils remained infective for 2-3 days, considered sufficient for dispersal. Pathogenicity of isolates was confirmed on Gros Michel, i.e., race 1 of *Foc*, not the destructive race 4 on Cavendish bananas.

Soil properties, nutrition, and production system affect disease progression within fields as well as cultivar resistance. A comparison was made of chemical-physical plant nutritional status effects in *Foc* infected and healthy plots in two banana production systems and climates in Brazil (Teixeira et al., 2021): five farms in a lowland tropical monsoon area (average area 10-20 ha, altitude ≤ 150 masl, intensive inputs), and four farms in a dry winter subtropical highland area (average area < 5 ha, altitude ≥ 900 masl, low inputs). In the intensive input lowland area, *Foc* was associated with higher soil acidity and lower levels of P, Ca, and Mn but showed no association with physical attributes. In the low-input highland area, soil chemical/physical attributes were not associated with wilt incidence, except that boron was lower in *Foc*-infested plots and bulk density and penetration resistance were higher. Wilt also affects the plants' nutritional status with Ca, K and their N ratios lower in *Foc*-infected plants. Although soil management practices are shown to have an impact on *Foc*, the question arises as to whether these are relevant for banana production in sub-optimal areas.

The destructive nature of *Foc* Race 4 means that novel methods of disease control are urgently needed. The use of endophytic bacteria has been proposed as one such measure (Tian et al. 2021). A strain of *Bacillus amyloliquefasciens* isolated from banana roots was found to be antagonistic to Race 4 and a full genomic and transcriptomic analysis was made, which showed an enhanced production of anti-fungal metabolites contributing to the inhibition observed.

Magnaporthe oryzae

Magnaporthe oryzae is a member of the *Magnaporthe grisea* species complex and causes rice blast, a serious disease of rice. The pathogen can also affect other members of the *Poaceae*, including wheat, rye, barley and pearl millet.

Core article: Wang et al. (2021).

Rice cultivation in Italy is seriously affected by rice blast with most cultivars grown either moderately or highly susceptible to the disease, leading to a high reliance on fungicides. A process-based simulation model was developed to forecast the incidence and severity of leaf and panicle blast in northern Italy and future trends under climate change scenarios (Wang et al., 2021b). The data set for initial model testing was a 3-year experimental trial (2013-2015) at three locations where leaf and panicle blast were assessed on four rice cultivars of differing susceptibilities, agrometeorological records of temperature, relative humidity, and rainfall at these sites, and historical records of the disease in different municipalities. Spatial simulations based on a 2 km x 2 km resolution were run for time horizons up to 2030 or 2070. The climate change scenarios considered predicted little change in current levels of the disease by 2030, with a slight decline by 2070. The key factor in modulating trend in disease was the level of cultivar resistance, which highlighted the need for continuing investment in breeding for improved resistance.

Multiple constraints affect rice yields in West Africa. Rice blast can cause losses estimated at about 4% in sub-Saharan Africa. Pairs of sites in three geographical zones of Burkina Faso, each with an irrigated area and a rainfed area, were surveyed over four consecutive years 2016-2019 (Barro et al. 2022). Within the six sites, fields were selected, based on aerial photographs, that were accessible and evenly distributed spatially within site. Fields were about 625 m^2 in area and numbered between 5 and 11 at each site per year. A total of 2864 plants in 179 fields were observed over the four years, with corresponding farmer interviews held at 81% of the surveyed fields. Four main diseases were found: rice yellow mottle disease, bacterial leaf blight, blast, and brown spot. The average incidence of blast across the whole data set was just under 10%, considerably less than the 30% for brown spot (*Bipolaris* spp). Blast symptoms were more common in irrigated areas, but there was no interaction with geographical zone. Co-occurrence of blast with other diseases ranged from about 10 to 40% across the whole data set with a higher frequency in irrigated areas. The highest level of co-infected plants found, considering only two of the main pathogens including *Magnaporthe oryzae*, was 20% of sampled plants at one field in an irrigated area.

Rice blast occurs on commercial rice in northern Australia and is also found on wild rice (*Oryzae australiensis*). An investigation of the host range of *Magnaporthe oryzae* in Australia was made on commercial and wild rice, and a range of other *Poaceae* hosts both cultivated and wild, using four isolates from commercial rice (Pak et al., 2021). Inoculations, plant growth and disease assessments were made under glasshouse and controlled environment conditions. Pathogenicity on the *Poaceae* species was made by extracting fungal DNA from infected plants to confirm fungal identity. There was variation in pathogenicity across the four isolates, however pathogenicity was confirmed across all *Poaceae* hosts under these conditions indicating that they could serve as reservoirs of *M. oryzae* strains and spread these to commercial rice, and potentially enable the development of more host-specific strains of the pathogen.

The *Triticum* pathotype of *Magnaporthe oryzae* causes wheat blast and is endemic in some South American countries (Mills et al., 2021). The first report and epidemic of wheat blast in Bangladesh in 2016 represents a food security risk to South Asia (He et al. 2021). The evolutionary history of *M. oryzae* from the grass genus *Setaria* to rice and from *Lolium* spp to wheat, and the recent emergence of blast on maize in Iran since 2012, with a suggested host jump from *Echinochloa* spp to maize (Pordel et al. 2021), demonstrates the potential for range expansion of this pathogen.

Maize lethal necrosis

Maize lethal necrosis is a disease of maize caused by coinfection with maize chlorotic mottle virus (MCMV) and one of several potyviruses, including sugarcane mosaic virus (SCMV).

Core article: de Groote et al. (2021).

Maize lethal necrosis disease (MLN) first appeared in Kenya in 2011 (de Groote et al. 2021). The first survey of 121 communities in 2013 using a hierarchical two-stage approach across the agroecological zones for maize cultivation estimated the proportion of households affected at 76% and a yield loss estimated overall at 22%, but in western Kenya (highland tropical and moist transitional zones) at 94%. In the second survey in 2018, the same communities were revisited, repeating the same questions. The results showed that the overall proportion of households affected by MLN had declined to 26%, but remained high in western Kenya at 60%, with an annual loss of 8.5%, but with western Kenya again disproportionately affected (yield loss of 79%). The reasons for these declines were unclear but may have involved the use of insecticides to control the fall armyworm *Spodoptera frugiperda*, disease-free seed, and unfavourable weather, but not the use of resistant varieties or adoption of new management practices.

Multispectral high-resolution techniques combined with field-based data have been evaluated in a semi-humid climatic zone of Kenya to estimate MLN severity and to map this onto three severity levels (mild, moderate, high) (Richard et al., 2021). However, the results suggested spectral confusion in the mildly and moderately affected fields due to the onset of early MLN symptoms, rather than other biotic or abiotic stressors.

The seed production system for maize was assessed for the status of MLN with both small- and large-scale seed producers in Kenya (Eunice et al. 2021). A survey was made over four years (2015, and 2017-2019) in five agroecological zones based on rainfall and altitude. Surveyed fields in the seed production areas were selected at 10-20 km intervals for assessment of MLN incidence and severity, noting the variety, growth stage, and environmental conditions. Overall, some 2550 ha were surveyed. Immuno-strip kits were used for in-field detection of MCMV, and leaf samples were taken for qRT-PCR analysis. The results showed an overall incidence of MLN at 21% with no significant differences among varieties, agroecological zones, or growth stages, although elevated levels were found in sub-humid counties known to be crop production hotspots for MLN. Of the leaf samples analysed by qRT-PCR analysis, 38% had MCMV alone, 14% SCMV alone, and

18% with both MCMV and SCMV. The results highlighted the need for phytosanitary inspections to be included in seed legislation as a legal requirement.

A field survey was made in Ethiopia where MLN had been reported to determine whether infection by MCMV was present in alternate hosts (Regassa et al., 2021). Field assessments were made in two contrasting regions of Ethiopia during the cropping systems of 2016 and 2017. Maize fields were quadrat sampled alongside accessible roads at 5-10 km intervals with the number of leaf samples collected varying with the level of MLN assessed. A range of weed species with and without virus-like symptoms were assessed with herbarium specimens taken for species identification where possible. A total of 434 samples belonging to 28 species and 11 families were collected, with 113 displaying virus-like symptoms. DAS-ELISA was used to detect MCMC and SCMV and back-inoculations were made onto healthy susceptible maize plants using sap preparations from positive-tested leaves. MCMV was detected in 23 and SCMV in 4 of 113 symptomatic plants collected from the maize fields, with 11 being coinfected. The *Poaceae* family had the highest number of grass species with natural infection of MCMV with *Cyperus rotundus*, sugarcane and sorghum having coinfections of MCMV and SCMV.

The spread of MLN in East Africa presents a potential threat to maize production in all south African countries as it has already reached Tanzania. In 2019, a survey was made in South Africa along the main grain transport route from Gauteng province in the high veldt to KwaZulu-Natal, adjoining Mozambique, one of the regions considered most at risk (Nel et al. 2021). Commercial and smallholder farms were surveyed along the roadside at approximately 20 km intervals. Sites with only volunteer maize were sampled at distances no less than 5 km apart. Maize leaves with virus-like symptoms were collected with a maximum of 20 leaves per site depending on the incidence of symptoms. Nucleic acid extraction, sequencing, and phylogenetic analyses were made with the leaf samples. Although some maize viruses and variants were new reports for South Africa, no MCMV or potyviruses were found in the leaf samples.

Meloidogyne spp.

Root knot nematodes are plant parasitic nematodes of the genus *Meloidogyne*. The genus contains more than 90 species with infection in about 2000 host plants.

Core article: Teston et al. (2021).

The root knot nematodes *M. incognita* and *M. hapla* often occur together with other soilborne fungal pathogens in a disease complex. In a survey of 71 protected (high tunnel) tomato production sites in Ohio, USA, soil samples were collected and used for diagnostic bioassay with potted plants and for DNA extraction and PCR assay (Teston et al. 2021). *Meloidogyne* spp., mostly *M. hapla*, were found in 32 of the high tunnels although there was some inconsistency between the diagnostic and PCR assays. Co-infestation or co-infections with other soilborne fungi were common.

Soil samples were taken from ware potato production areas in eight provinces of Turkey in 2018/19 (Evlice 2021), representing some 58% of the potato production and harvested area. A total of 927 soil samples (ranging from 69-226 per site) of 2-3 kg were collected from sites. Root knot nematodes were extracted into suspension and counted, nematode DNA was extracted and amplified with multiplex PCR using primers for six *Meloidogyne* spp. A root knot nematode community analysis was then done for the absolute and relative frequency of each species. Of the 927 soil samples, *Meloidogyne* spp. populations were detected in 84. Most were determined to be *M. chitwoodi* (70), with some *M. hapla* either in single (3) or mixed populations (11) with *M. chitwoodi*.

Cotton is an important cash crop in Pakistan. In Punjab province cotton is reported to be heavily affected by wilt disease. A survey was made of 15 locations in cotton growing areas across Punjab to determine wilt prevalence (% fields with wilt) and incidence (% plants with wilt), and the associated pathogens and presence of root knot nematodes (Naz et al. 2021). Isolation and identification of fungi and of root knot nematodes was made from diseased roots. The maximum prevalence across the locations surveyed was 85%

with a maximum incidence of 15%. The highest frequency of fungi associated with root samples was found to be *Fusarium oxysporum* and, to a lesser extent, *Rhizoctonia* and *Pythium* spp. The dominant root knot nematode found was *M.incognita*. A similar survey was made in Kyber Paktunkhwa province of Pakistan as part of a study on soybean resistance to *M. incognita* (Ramzan et al. 2021). Soil and root samples were taken from 29 soybean fields (2-28 samples per field), giving a total of 453 samples. Root knot nematodes were isolated, cultured and identified. More than half (246) of the fields were infested with either *M. incognita* (86%) or *M. javanica* (16%), the most prevalent being *M. incognita*.

Meloidogyne spp. were found to be the most important plant parasitic nematodes in vegetable fields in Georgia, USA (Marquez et al., 2021). During the spring and fall cropping periods in 2018, some 436 fields across 29 counties were surveyed and sampled for the incidence and abundance of 10 plant parasitic nematode genera in 32 different vegetable crops. The overall incidence of *M. incognita* was about 67%, with a maximum abundance of over 14 000 nematodes per cm^3 soil. Cropping system was found to be more important than environment for plant parasitic nematodes. In Algeria a wide range of endemic nematophagous fungi belonging to eight genera was found in vegetable fields in Algeria and found to have the potential to suppress *M. incognita* and M. *javanica* populations by 70 and 50% respectively (Sabri et al. 2021).

Reports on the occurrence of *Meloidogyne* spp. with other nematode species on specific crops were common; for example, sugar beet (Ashmit et al. 2021); honeybush and rooibos (Daramola et al. 2021); watermelon (Laasli et al. 2021); yam (Abdulsalam et al. 2021); cereals (Özdemir et al. 2021); yam tubers (Okoro et al. 2021); and turfgrass (Mwamula and Lee, 2021). These are listed without further commentary in Electronic Supporting Information, S2.

Pseudomomas syringae pathovars

An overview on the species is given in Straub et al. (2021). Disease symptoms occur on leaves, blossoms, fruits, and woody tissues across a wide range of hosts. More than 50 pathovars have been designated based mainly on the host species. However, pathovar *syringa* can be present with other pathovars on some hosts.

Core article: Kant et al. (2021).

Bacterial blight of pea is associated with two pathovars of *Pseudomonas syringae*: *Ps. syringae* pv. *syringae* (Pss), and *Ps. syringae* pv. *pisi* (Psp). Both pathovars cause indistinguishable symptoms on field pea and require laboratory testing to determine the causal pathovar. In recent years, the more heterogeneous Pss has become the dominant pathovar in Australia causing severe outbreaks and annual surveys are made to determine changes in the causal pathovar. To aid rapid screening techniques that potentially could be used in field surveys, Kant et al. (2021) have developed an accurate and robust LAMP assay for the detection and differentiation of the two pathovars. Branches of sweet cherry cultivars with active and inactive cankers were collected monthly from four locations in Serbia, where the presence of *Ps. syringae* pv. *syringae* and pv. *morsprunorum* had previously been confirmed, to determine the persistence of bacteria in the cankers (Iličić et al. 2021). At the exact locations, isolations were made during February, March and October from healthy leaves and buds to ascertain whether epiphytic populations of Pss and Psm were present. The branch samples showed that both pathovars persisted in cankers in low numbers over the summer and became active in the autumn. Significant epiphytic populations of both pathovars were present in the spring, decreased in the summer and then increased in the autumn. These findings of seasonal activity provide insight into the transition from the epiphytic to parasitic life stages and disease epidemiology but provide qualitative rather than quantitative information.

Pseudomonas syringae pv. *actinidiae* (Psa) has severely affected kiwi fruit production in many producing countries. Most *Actinidiae* spp are dioecious, with male and female plants responding to pathogens in distinct ways in terms of disease susceptibility and phenological development. Male plants are included in orchards predominantly for pollination. Psa causes bacterial canker, but other Ps. syringae pathovars, including pv. *syringae* cause blossom blight in kiwi. Small numbers of male and female plants (five each) were selected from a 1-ha orchard where Psa had been detected and from a 0.5 ha orchard with no Psa detected (Ares et al. 2021). 10 leaves were taken from each selected plant with the sampling procedure done twice on the same plants in June and October. The diversity of the associated bacterial communities was assessed by DNA extraction, amplification of the 16S ribosomal gene, and Illumina sequencing. The leaves of healthy male and female plants shared most of the same bacterial populations, but with some genera increasing from June to October. There were major changes in the bacterial community on Psa-infected female plants with reductions in the relative abundance of genera predominant on healthy plants, less so on male plants. Some of the identified genera have the potential to act as antagonists of Psa.

A significant number of populations within Psa within at least five biovars have been described. Biovar 2 has been found only in Korea, where streptomycin has been used as a control method for 20 years or more, where in 1998 no streptomycin resistance had been found. Four streptomycin-resistant strains were isolated in 2013 and 2014 from symptomatic kiwi plants in different orchards located in Jeju, Korea (little information given), and were examined for genes often found in streptomycin-resistant bacteria (Lee et al. 2021). All four strains of Psa were found to have the stsA/strB gene as a resistance determinant. Further work is required to assess resistance in the soil, rhizophere and phyllosphere microbiome and the possibility of horizontal gene transfer between Psa and other streptomycin-resistant bacteria. Little mention is made of the status of Psa in Korea.

Puccinia striiformis f.sp tritici

Puccinia striiformis f.sp *tritici* is one of three major rust pathogens of wheat, causing yellow or stripe rust disease. Emergence of new pathotypes and virulence patterns continues to cause concern.

Core articles: Perronne et al. (2021), Esmail et al. (2021), Sandhu et al. (2021).

Spatiotemporal changes in varietal resistance of wheat to yellow rust were studied over the period 1985-2018 in 54 French departments (Perronne et al. 2021). Field adult plant resistance levels, race-specific resistance genes, pathogen pathotypes and virulence profiles, and wheat acreages were recorded in annual surveys made at the district level. Over this period, an increase in varietal resistance was found due to a combination of quantitative resistance and accumulation of different race-specific resistance genes. The main conclusion made was that replacement of “newly susceptible” varieties by “still resistant” ones before each seasonal epidemic has had a substantial effect on the increase in overall resistance over these decades.

Surveys of wheat yellow rust in five Egyptian provinces over the period 2018-2020 revealed 42 physiological races, with six new aggressive races detected in the study (Esmail et al. 2021). Field response data indicated that of 15 wheat cultivars tested, only four showed moderate levels of resistance with known resistance genes. Combinations of such genes, both durable and broad-spectrum, would be the best option to avoid large scale rust epidemics in Egypt. A pre-requisite in phenotyping rust resistance in breeding programmes, it is essential to have a reliable disease assessment scale for scoring responses to infection to avoid misclassification in resistance gene characterisation. A high-resolution pictorial scale has been developed for wheat adult plant growth stages (Sandhu et al., 2021) that would prove useful in phenotyping of breeding lines but also in scoring rust symptoms in wider field surveys.

P. striiformis f.sp *tritici* is a heteroecious macrocyclic rust which forms its sexual stage on barberry (*Berberris* spp.) although in many countries which experience wheat yellow rust, it is unclear what role barberry plays in the epidemiology of the disease. Studies made in China (Chen et al., 2021), where yellow rust was first reported in 2010, investigated the role of the sexual stage in providing an inoculum source for infecting wheat.

Leaf samples bearing aecia were taken from naturally infected barberry in two counties of Qinghai province in June, with leaf samples with uredinia taken from wheat at least 100 m distant from the barberry one week after the appearance of aecia on barberry. A total of 375 aecia were taken from 52 barberry bushes at 11 sites in the two counties. Inoculations of wheat differentials with the two inoculum sources were made. Phenotypic and genotypic analysis showed a common ancestry between isolates taken from barberry and wheat and indicated that aeciospores play an important role in the spread of disease from barberry to wheat.

In China, clonal populations can persist where different regions have conditions suitable for over-wintering and over-summering, with migration pathways providing inoculum for spring epidemics. Some 567 isolates of Pst were taken from over-summering (Gansu-Niangxia) and over-wintering (northwestern Hubei) regions from autumn 2016 to spring 2018 (Wang et al. 2021) and genotyped using SSR markers. A greater diversification was found in the spring compared with the autumn population, with only 17 common genotypes found across the 208 determined. Although the amount of inoculum over-wintering may determine the risk of interregional epidemics there was no evidence for extensive genotypic exchange between over-summering and over-wintering regions.

India has had a long history of outbreaks of yellow rust with severe epidemics occurring frequently. The *P. striiformis* f. sp *tritici* population in India, as in many other wheat growing countries and regions, is clonal with dominant lineages emerging through mutations. A total of 951 yellow rust samples were taken from farmers' fields and trap plot nurseries 31 districts across five States and one Union territory (Jammu and Kashmir) in northwest India between 2015 and 2019 and analysed for virulence (Gangwar et al., 2021). The prevalence of the dominant lineage has declined over the sampling period from 62% to just under 50%. The most virulent lineage was present at 6.8% with most of the other characterised lineages present at less than 5%. Such information should prove invaluable for the deployment of resistant cultivars where these are available.

Annual surveys of winter wheat disease in the UK have been made since 1970. Samples from between 250 and 350 randomly selected wheat crops in England and Wales were taken between 1999 and 2019 and assessed for visual symptoms of a range of diseases at a given growth stage (Turner et al. 2021). The incidence of yellow rust remained at trace levels throughout this 20-year period and exceeded 5% of crops affected in only four years, with disease severity exceeding 0.02% leaf area affected in only one year. This is an extremely low prevalence given a high diversity in the rust population, attributed to cultivar use diversification and high uptake of resistant cultivars with no associated breakdown in resistance, and no reduction in efficacy due to the development of fungicide resistance.

Xylella fastidiosa and vectors

Xylella fastidiosa is a xylem-limited bacterium with a wide host range, currently about 600 plant species, including grapevine, citrus, stone fruit, coffee, olive, and oleander. At least four subspecies have been designated with some partial host affiliations. The bacterium is transmitted by several xylem-feeding leafhoppers, in Europe mainly by the meadow spittlebug *Philaenus spumarius*, for which there has been a major range expansion in the last decade.

Core articles: Lazaro et al. (2021), Beale et al. (2021), Bodini et al. (2021), Gargani et al. (2021), Zarco-Tejada et al. (2021), Poblete et al. (2021), Olmo et al. (2021).

Plant health legislation in the European Union requires the implementation of annual surveys for priority quarantine pests, and consequentially to delimit the infested zone of the bacterium *Xylella fastidiosa* where an outbreak has been reported. Official surveys under this legislation have been in place in Alicante, Spain, since 2017 when the first outbreak of *X. fastidiosa* subsp. *Multiplex* occurred on almond. In 2019, the demarcated area in Alicante covered 140000 ha with almost 5000 orchards, and some 75000 trees destroyed. A strategy to optimise the official survey programmes was proposed by Lazaro et al. (2021).

Using the official survey data, a sequential adaptive delimiting scheme based on increasing spatial resolution was developed and optimised using simulation methods. The proposed survey scheme would be adaptive, enabling the inspection and sampling intensities to be modified according to previous information based on coarser spatial resolutions, and would improve the efficiency of the official survey methods.

The meadow spittlebug *Philaenus spumarius* is a vector of *Xylella fastidiosa*. Adult population abundance was assessed in north coast vineyards of California from 2016-2018 using sweep and trap surveys to determine the contribution to epidemics of Pierce's disease of grapevine (Beal et al., 2021). Spittlebug adults were present from April to December but there were significant differences in transmission rates from July to December, with the greatest risk of transmission being in December. This period of infective spittlebugs does not align with historical patterns of epidemic development arising from the spring flights of infective *Graphocephala atropunctata*, a vector considered critical in initiating epidemic development of Pierce's disease in the region. *P. spumarious* may play a secondary role in plant-to-plant spread of the bacterium.

Spittlebug species are the only known vectors of *X. fastidiosa* in Europe. Spittlebug diversity, phenology and host-plant association were assessed over three years in vineyards of northwest Italy (Bodino et al. 2021). These included a 2-year survey of a single site in the province of Asti in Piedmont in 2016-2017, and a further 1-year survey in Asti and two other sites in Piedmont in 2018. *Philaenus spumarius* was the most common species and reached high population levels in vineyards where there was herbaceous coverage for the whole season and only moderate use of insecticides. The extended presence of the vector on grapevine represents a significant risk factor for the spread of *X. fastidiosa* in northwest Italy and elsewhere in Europe. The main vector of *X. fastidiosa* in Europe is the spittlebug *Philaenus spumarius*, although other xylem-sap feeding insects have been investigated for their ability to vector the bacterium. In Italy, the main outbreak area has been in Apulia with subsp. *Pauca* causing olive quick decline syndrome. Following the detection of subsp. Multiplex in *Spartium junceum* in Tuscany in 2018, attempts were made to identify putative vectors by identifying the bacterium in insects that had tested positive (Gargani et al., 2021). Insect collection sites had been established as part of a 5-year survey in Tuscany from 2015 to 2019 with the number of sites ranging from 179 to 263 across these years. Over this period, more than 4000 specimens from the suborder Auchenorrhyncha were collected with no positive insects found. In 2019, subsp. *Multiplex* was found in small numbers (<10) of *P. spumarius* and *Neophilaenus campestris* specimens. The occurrence and distribution of these vectors was assessed at 19 sampling areas in Calabria, neighbouring the main outbreak area of subsp. *Pauca* in olive in Apulia, from August to October 2020 (Lombardo et al. 2021). All 563 individual specimens tested negative for the bacterium.

To date, severe disease outbreaks caused by *X. fastidiosa* in Europe have occurred only in regions predicted using species distribution models to be highly favourable for the vector *Philaenus spumarius* supporting the view that the climatic response of the insect could play a major role in the spread and distribution of the pathogen in vulnerable hosts (Godefroide et al. 2022). The same models also predict that over the period 2040-2060 there may be a decrease in climatic favourability for the vector.

The spread of *X. fastidiosa* around the Mediterranean basin has led to an increased awareness of many neighbouring countries not only of the need to make regular surveys of vulnerable crops but also to assess the economic costs of invasion. Lebanon is the country considered to be at the highest risk in the Middle East and North African region (Frem et al. 2021). Grapevine is an important crop in Lebanon with an average 5-year annual revenue of US$ 22 million. An economic analysis estimated the potential economic losses could be US$ 11 million over four years with replacement of plants to over US$ 84 million over the normal life span of grapevine in which infected plants are not replaced. As well as the private losses to grapevine holdings there would be public costs involved in plant health regulation and risk management of the disease.

The Balearic Islands of Spain hold the greatest diversity of *X. fastidiosa* in Europe with subspp. *fastidiosa*, *multiplex*, and *pauca* found infecting a range of host species including the economically important almond, olive, grapevine, and fig (Olmo et al. 2021). Between November 2016 and December 2020, over 13000 plant samples were analysed by the Official Laboratory of the Plant Health Service of the Balearic Islands based on mandatory monitoring with random sampling required by the European Commission (symptomatic and asymptomatic samples), and results from research projects and samples from farmers and other organisations (only symptomatic samples). Samples were taken from 453 plant taxa representative of crop fields, gardens, and wild communities, weighted according to the land area of the four islands. About 9% of plant samples tested positive for the bacterium with olive, grapevine and almost accounting for more than 60% of the positives (recognising the bias implicit in sampling from these economically significant crops). Olmo et al. (2021) concluded that the eradication and contingency strategies imposed were inadequate largely because the epidemiological history of the epidemics had not been investigated.

Verticillium dahliae is a xylem-limited fungal pathogen that can cause symptoms that can be confounded with water stress and similarly with symtoms arising from *X. fastidiosa* infection. Large scale detection methods using remote hyperspectral and thermal imagery have been used successfully to detect the presence of both pathogens separately, and recently methods have been developed to discriminate infections when both pathogens are present (Poblete et al. 2021). Data sets from 27 olive orchards in Italy and Spain where there had been outbreaks of *V. dahliae* and latterly *X. fastidiosa* over the period 2011 to 2017 were used to develop an algorithm to discriminate the symptoms. The method generated false positive rates of 9% for *V. dahliae* and 4% for *X. fastidiosa*. This type of study was repeated by the same group with over one million trees to disentangle biotically induced symptoms from those caused by abiotic stress (Zarco-Tejada et al. 2021). The results indicated that the uncertainty associated with *X. fastidiosa* detection, estimated from probability distributions was reduced to less than 6% across a range of hosts.

Zymoseptoria tritici

Zymoseptoria tritici is the causal agent of Septoria tritici blotch and one of the most serious diseases of wheat, particularly of winter wheat in western Europe. The disease is particularly difficult to control due to the widespread occurrence of resistance to multiple fungicides, and only partial resistance to the local pathogen population being available in cultivars.

Core article: Garnault et al. 2021.

Fungicide resistance in *Zymoseptoria tritici* causing Septoria tritici blotch of wheat was monitored annually from 2004 to 2017 at about 70 sites in 22 regions of France representing about 25000 km^2, with an average of 4-5 trials/region (Garnault et al., 2021). Changes in resistance frequency were modelled in relation to regional use of fungicides, yield losses, and the area of organically grown wheat. The regional scale was the most appropriate in identifying fungicide use intensity as the main determinant of the dynamics and evolution of resistance. The predictions of the model replicated the spatial and temporal patterns of fungicide resistance in field crops with a high level of confidence. The main conclusion drawn was that fungicide resistance would best be managed at the regional level to complement local action. In the UK, Septoria tritici blotch kas been the most prevalent and severe disease of wheat found in annual surveys of wheat disease since 1999 (Turner et al. 2021). Although there has been no significant change in disease levels over 20 years, there has been an increased reliance on fungicides, but with an accompanying resistance or reduced sensitivity to the major fungicide groups used for control.

A weather-based forecasting model for Septoria tritici blotch epidemics in winter wheat was developed further with the aim of determining when a control threshold would be reached within the period of efficacy of a systemic fungicide (Beyer et al. 2022). Some 40 plots of winter wheat which had received no fungicide treatment were monitored for necrosis caused by *Z. tritici* over the period 2017-2019. Two thresholds were defined based on two wheat growth stages at the date these thresholds were reached was termed the date of epidemic outbreak. Independent data were obtained to evaluate the predictions of the model. Within the efficacy period of a systemic fungicide the model gave correct predictions in about 85% of cases. The predicted and observed dates of epidemic outbreak were highly correlated ($r = 0.92$) with an average deviation of 3 days and maximum deviation of 19 days allowing for the fitted confidence intervals.

Z. tritici forms genetically diverse infections in wheat fields and may cause mixed infections in individual plants. A study was made on the effects of mixed infections on disease development, virulence, and spread/transmission in wheat plants in a glasshouse using one of four single strains or six pairwise combinations of the strains. (Barrett et al. 2021). Overall, the more virulent strains had the greater competitive ability during host colonisation, but less virulent strains had the advantage in transmission. Within-host competition had a major effect on infection dynamics and pathogen population structure and hence would be predicted to have a major effect on the dynamics of Septoria tritici blotch epidemics in wheat crops.

The prevalence of necrotrophic foliar fungal pathogens of winter wheat and triticale in field experiments at eight geographical regions of Poland was assessed from 2015-2020 (Bartosiak et al., 2021). The experiments consisted of 10 winter wheat and 10 winter triticale varieties planted in 10 m long rows. Some 350 leaf samples and infected heads were taken from each plot, giving a total of 8 x 2 x 10 x 350 leaf samples. Isolations were made from lesions on infected leaves, cultured and identified to species level by morphological methods. Over the period of the trials, the most significant pathogen on winter wheat was *Z. tritici* while on triticale *Parastagonospora nodorum* produced symptoms on the largest number of leaves. Only trace levels of *Parastagonospora avenae* f.sp triticeae was found on winter wheat and triticale.

A regional survey of 330 wheat samples was done in 2015-2017 from locations in Denmark, Norway, Germany, and the United Kingdom (50-100 samples per country over the three years) (Justesen et al. 2021. In 2015, a small number of samples was also collected from Latvia, Finland, and Sweden (eight in total). Disease severity was assessed using a rating scale and leaf segments were prepared for qPCR quantification of *Z. tritici* and *Parastagonospora nodorum* targeting the *ß-tubulin* gene and molecular screening for effectors in *Pyrenophora tritici-repentis*. Distinct regional differences were found and 65% of the samples harboured at least two of the three pathogens. The study confirmed that mixed infections of these wheat pathogens are common and carry implications for both disease management and breeding strategies.

The dynamics of *Z. tritici* in microplots of pure stands and three mixtures of two wheat cultivars was monitored in natural epidemics occurring in the cropping seasons 2017/18 and 2018/19 (Orelana-Torrejon et al., 2021). The two cultivars used were Apache with moderate susceptibility and Cellule, a cultivar whose resistance had recently broken-down. Disease severity was used as a proxy for population size and assessed twice, at early and late growth stages, as the leaf area covered by pycnidia, but scored as percentage classes. A mean disease severity index was calculated for each pure stand and the three mixture treatments. A total of 3060 strains were isolated at the two sampling times and five treatments across the two years, characterised for virulence against the major gene *Stb16qp* present in Cellule, one of the cultivars used in the study and phenotype. Disease reductions on both cultivars were observed in the mixtures relative to the pure stands but effects on the pathogen population size, size of the virulent component of the population, and the relative frequency of virulence compared with cultivar Cellule differed according to the mixture ratios used.

A large-scale genome-wide association mapping (GWAS) study was made based on 145 global strains of *Z. tritici* collected in Australia, Israel, Switzerland, and the USA, with all samples made between 1990 and 2001, under comparable field conditions (Dutta et al. 2021). Virulence and reproduction of *Z. tritici* on 12 different wheat hosts and plant responses to abiotic stressors were assessed using GWAS combined with genetic correlation analysis. Of the traits analysed most were governed by polygenic architectures and were highly heritable. There were negative correlations between host colonisation and survival in stressful environments, indicating that genetic interactions could limit host damage by the pathogen in such environments.

Objective 1. Literature review of published articles on disease outbreaks and epidemics (multiple pathogens/cropping systems/production systems)

In many surveys of plant diseases, multiple rather than single pathogens are recorded for a given plant host, cropping system (mixed cropping, rotation, or within season sequential planting), or wild plant populations (both native and invasive). Production may vary from annuals to perennial, with different production systems from seed production to vegetative propagation in plant nurseries to the harvested crop (Table 2). As previously described, comprehensive reviews on multiple pathogens of a single host (e.g., rice, Savary et al. 2022) or a higher taxonomic grouping across multiple hosts (e.g., viruses, Jones 2021) have already been published. The follow sections summarise the results for categories of article from the literature review (see Table 3, bottom section), reporting the categories in alphabetical order.

Aquaculture

Seaweed diseases in aquaculture cropping systems have been mostly ignored by plant pathologists, with most reports on pests and diseases appearing in specialist journals on phycology (from the Greek "seaweed"), often on industrial exploitation, or more general aspects of marine science.

Core article: Mateo et al. 2021

The Philippines is a major producer of farmed seaweed, the red algae *Kappaphycus alvarezii* and *Eucheuma denticulatum*, with many thousands of farmers involved in cultivation, used for the production of carrageenans, which are used as thickening and gelling agents in the food industry. 'Ice-ice' (IID) is a disease condition that arises when seaweed is placed under stress from environmental changes of salinity, temperature, and light intensity and is attacked by a range of bacterial species leading to a characteristic whitening and hardening of seaweed tissues. One of the bacteria implicated in the condition, *Stenotrophomonas maltophilia*, is also a human pathogen. A survey (knowledge-attitudes-practices, KAP) of seaweed farmers in the Philippines on biosecurity practices for pests and diseases showed "fair" ratings for knowledge and practices and "good" for attitudes (Mateo et al., 2021). It was concluded that biosecurity measures could be improved by addressing gaps and appropriate action taken. An extension of the KAP approach on biosecurity was taken in Tanzania (Campbell et al. 2021) and Malaysia (Kambey et al. 2021) in comparison to the Philippines, with generally lower ratings.

Pests and diseases of seaweed were surveyed at 16 farms across major seaweed farming areas in the Philippines (Faisan et al., 2021). More than 5% of individual seaweed plants at each site were visually assessed for disease symptoms. IID was found to be present at all sites at incidences less than 25%. Overall, it was concluded that pests and diseases were major production constraints, and that better surveillance, diagnosis, and management were needed in this major aquaculture industry.

The green macroalga *Caulerpa lentillifera* is cultivated as a seafood delicacy but can be affected by bacterial diseases. The bacterial communities associated with healthy and diseased *C. lentillifera* were investigated at a company farm in Vietnam (Kopprio et al. 2021). Clear differences were found in the microbiome of healthy and diseased algae. Detrimental bacteria were found as operational taxonomic units (OUT) of the family Flavobacteriaceae, but a range of saprophytic and potentially beneficial bacteria were also found.

Crop-associated weeds

In many cases, weed species in or surrounding crops can act as reservoirs for single pathogens and/or vectors. Examples of this are given in the articles for specific pathogens in Tables 1-6: *Plenodomas lingam* spp., Claasen et al. 2021; *Ca.* Phytoplasma vitis, Rizzoli et al. 2021. Pethybridge et al. 2021. In other cases, multiple pathogens are described.

Core article: Korbecka-Glinka et al. (2021), Ahmed et al. (2021), Mwaipopo et al. (2021).

A survey was made of five viral pathogens of solanaceous crops, predominantly tobacco, in six provinces of Poland (Korbecka-Glinka et al. 2021). Totals of 157 samples of tobacco and 600 samples of weeds were taken for DAS-ELISA detection of tomato spotted wilt orthotospovirus (TSWV), cucumber mosaic virus, potato virus Y, tobacco mosaic virus (TMV), and tobacco ringspot virus. Some 29% of weed samples were infected with at least one of the viruses, with TSWV and TMV the most frequently detected. In most cases where tobacco was found to be infected, the same virus was found in weeds. Some weeds were found to be coinfected with all five viruses, especially species in the Asteraceae family.

Malvaceous weeds in the Caribbean basin commonly show symptoms typical of viruses. Leaf samples from *Malachra* sp. and *Abutilon* sp. with golden-yellow mosaic symptoms were collected in Haiti and the Dominican Republic from 2014-2020 (Maliano et al., 2021). *Malachra* was found to be infected with the begomovirus tobacco leaf curl Cuba virus (TbLCuCV), *Abutilon* with a new begomovirus with the tentative name Abutilon golden yellow mosaic virus (AbGYMV). TbLCuCV also induced severe symptoms in *Nicotiana benthamiana* and *Phaseolus vulgaris* in host range studies, but AbGYMV seemed to be well-adapted to Abutilon and did not infect crops.

Tobacco bushy top disease affects tobacco crops in China and is caused by co-infections of several plant viruses. More than 1700 leaf samples collected from field plants, including weeds of 29 species in 13 families across China, were sampled for four viruses known to be associated with the disease (Tan et al., 2021). Some 663 samples were found to contain several co-infecting viruses, with the incidence of tobacco vein distorting virus at the highest frequency of 37.5%. Coinfections of the viruses were also found in commercial crops. Overall, the results indicate that tobacco bushy top disease has a much broader host range than previously reported and that weeds can serve as a natural reservoir of the co-infecting viruses.

In a survey of virus diversity of *Phaseolus vulgaris* in Tanzania, at least 15 different viruses from 11 different genera have been found. A further study was made to investigate the survival of *Phaseolus* viruses between seasons (Mwaipopo et al., 2021). Leaf samples were taken from 1430 wild plants within and around common bean fields across Tanzania. RT-PCR analysis of samples indicated the presence of yam bean mosaic virus and peanut mottle virus in wild leguminous plants. Mechanical transmission of cucumber mosaic virus and a novel bromovirus to common bean was demonstrated.

In most of these studies, multiple weed species have been sampled for their presence and impact on crop populations. More detailed studies have been made on individual species such as shepherd's purse (*Capsella bursa-pastoris*), a summer or winter annual weed distributed across temperate and sub-tropical regions of the world. This weed is known to be a host for pathogens that have been reported to infect annual crops, including fungi, oomycetes, bacteria, phytoplasmas, viruses, nematodes, and parasitic plants. In Canada it has been one of the 20 most prevalent weeds since annual surveys began in 1970 (Ahmed et al. 2021).

Cropping system

Many of the single pathogen species identified in Tables 1-6 on a given host crop are of course still relevant when that crop is grown in a system with mixed cropping, sequential planting within a growing season, or as part of a rotational system. However, the contention here is that the single pathogen should not be considered the nexus of a cropping system, but rather how multiple pathogens interact with multiple crops, the cropping environment, and the agronomic practices prevalent in such systems.

Core article: Hampf et al. 2021,

In many crop production regions of Brazil, maize, soybean, and cotton are dominant crops with early maturing soybean grown at the onset of the rainy season followed by maize or cotton, forming a successional cropping system. In the southern Amazon region, little is known of the pests and diseases affecting these crops and a study was made to map the spatial distribution of diseases affecting soybean and maize and yield and economic losses using a smartphone application *Plantix* that provides recognition of visual disease symptoms (Hampf et al. 2021). Between 2016 and 2020, users of the application collected about 78000 georeferenced pest and disease images. Spatial distribution maps indicated the most common diseases of both crops, which when combined with expert opinion, gave estimates of crop loss of 12% for soybean and 15% for maize.

Maize-soybean rotational systems are widespread and economically important, and by exploiting the presence of N-fixing bacteria these systems are claimed to improve plant growth and health. The interaction between biotic and abiotic factors on the rhizosphere microbiomes, which may contain both beneficial and opportunistic pathogenic species, was studied by Meier et al. (2021). The main effects were due to seasonal changes in the environment and nitrogen fertilization rather than crop rotation. However, it was suggested that the microbial community could be manipulated through plant breeding and field management to provide further beneficial effects and reduce the reliance on pesticides and industrial fertilizers.

Annual rotation of wheat and rice is a common practice in regions of China, with rice transplanted in June and harvested in November, followed by wheat sown in November and harvested in May. The continuous return of crop residues to the system may serve as an organic fertiliser but may also be a source of pathogens; aspects studied in a 2-year rotational field experiment in Zheijiang Province (Shan et al. 2021). An optimal combination of reduced nitrogen application and straw incorporation was found to significantly reduce the incidence and cluster formation of rice sheaf blight (*Rhizoctonia solani*) and false smut (*Ustilaginoidea virens*). Outbreaks of rice yellow mottle virus disease were studied in rice cropping systems from 2011-2013 in Tanzania (Sekiya et al. 2022) with different agronomic practices, including double cropping of rice and rice-maize rotation. Straw removal and crop rotation with maize were found to reduce the probability of local spread of the virus by almost 30 and 50%, respectively.

Cover crops are grown in viticulture for a range of purposes: to reduce soil erosion, improve soil structure, improve nutrient retention, and increase microbial community. A survey of grapevine cover crops, either sown or native weeds, was made across six European countries in 2019/2020 to determine the association with black-foot, a disease complex caused by *Cylindrocladium*-like asexual fungi (Léon et al., 2021). Some 685 plant species were identified and analysed, with almost 10% found to be infected with about 1% of the plated root segments yielding three fungal species. The most frequently recovered fungus, *Dactylonectria torresensis*, was associated with many cover crops in all six countries, suggesting that the cover crops may act as alternate hosts and increase inoculum levels in the soil.

Forest tree pathogens

Forest trees have very different characteristics, production systems and levels of intensive management than crops, including intensively managed fruits. Yet, despite these differences, similar processes affect pathogen population processes, adaptation and evolution in crops and forest trees, often in similar ways (Hessenauer et al. 2021). Examples of tree diseases caused by single pathogens are given in Tables 1-6: *Bretziella fagacearum*, Pellegrini et al. 2021; *Diplodia* spp., Fereira et al. 2021; *Austropuccinia psidii*, Fensham & Radford-Smith, 2021; *Cronatium ribicola*, Dudney et al. 2021; *Diaporthe* spp., Lopes et al. 2021; *Neonectria neomacrospora*, González et al. 2021; *Phytophthora ramorum*, Jung et al. 2021, Rosenthal et al. 2021; *Phytophthora cinnamomi*, Hornero et al. 2021; Shayka et al. 2021; *Phytophthora austrocedri*, Donald et al. 2021; *Bursephalenchus xyophilus*, Atkins et al. 2021, Zhang et al. 2021, Yu et al. 2021; *Raffaela quercus-mongolicae*, Lee et al. 2021. More usual is the reporting of multiple pathogens in multiple tree hosts.

Core articles: Thu et al. (2021), Panzavolta et al. (2021), Spears and Broders (2021)

Forest tree health, globally, is affected by new and emerging pathogens and pests causing environmental and economic damage, with increasing numbers of alien invasive species being recorded in trees, plantations, and nurseries in many countries (Panzavolta et al. 2021). Forest health surveys were made annually from 2011-2020 across eight forested regions of Vietnam with observations on 16 tree species (Thu et al. 2021). Three plots (40 m x 25 m) in each region were put in place at least 20 m from any edge effects from roads, forest edges or gaps. At least 30 trees in each plot were selected randomly and assessed for disease or pest damage, with observations made in spring, summer, and autumn. The number of new and emerging pests and pathogens had increased from 2 in 2011 to 17 by 2020, with three pathogens associated with extensive damage on a range of hosts. Bark and wood samples were taken from symptomatic trees and pathogens were isolated, cultured and identified by microscopy and DNA extraction and analysis. Damage was recorded in both native and exotic species: *Ceratocystis manginecans* in acacia spp. (*Acacia*, exotic), eucalyptus spp. (*Eucalyptus*, exotic), Indian mahogany (*Chukrasia tabularis*, native), and rosewood (*Dalbergia tabulensis*, native); *Fusarium solani* in sweet bamboo (*Dendrocalamus latiflorus*, exotic); and *Phytophthora acaciivora* in acacia species and hybrids. *P. acaciivora* can cause about 20% mortality in acacia nurseries and poses a significant threat to young plantations in Vietnam. The long land and sea borders of Vietnam may have made the national biosecurity and quarantine procedures difficult to implement, and these require improvement.

The widely accepted Janzen-Connell hypothesis attributes the maintenance of tropical forest diversity to host-specialised pathogens (as well as herbivores and pests). Yet, in diverse forests, the rarity of many tree species may favour generalist pathogens with wider host ranges (Spear and Broder 2021). A series of experiments were done in which 27 potential fungal pathogens were isolated from infected tree seedlings in Panama, identified in terms of operational taxonomic units, and tested for pathogenicity on healthy seedlings of 35 tree species. Genera within the Nectriaceae, Clonastachys sp, Mycoleptodiscus spp, and Sordariomycetes sp. were found to have pathogenic associations with up to five of the tree species, leading to morbidity or mortality. Some tree species appeared to be resistant to all fungal isolates tested, whereas other species were susceptible to multiple fungal isolates. Tree species adapted to environments in which there was little disease pressure were more likely to develop the disease when challenged with fungal pathogens. Overall, it was concluded that generalist fungal pathogens can contribute to forest diversity by host-specific effects and the mortality of susceptible or disease-sensitive trees from areas where disease pressure is high.

Wild plants

There has been an increasing interest in the impacts of disease in wild plants as an indicator of environmental health and in the provision of ecosystem services (Gougherty and Davies 2021, Jeger et al. 2021). Studies on single pathogens of wild plants in natural populations are given in Tables 1-6: *Plantago*/powdery mildew (Eck et al. 2022) and *Cakile maritima*/*Alternari brassisicola* (Papaix et al., 2021), In other studies, multiple pathogens in wild plant communities have been studied.

Core article: Halliday et al. (2021)

Foliar symptoms in wild plant communities were surveyed in 220 wild plant communities (0.5 m diameter) across a 1100 m altitudinal gradient in Switzerland in 2019. The study provided field evidence that elevation can affect host community structure and disease (Halliday et al., 2021). The main interpretation of the results was that increasing temperatures at lower elevations increased disease by providing more suitable conditions for pathogen growth and reproduction, determining which species were present at these elevations, and host life-history parameters such as growth rates, reproduction, and dispersal where fast growth rates, rapid reproduction, and high dispersal, may be correlated with a reduced defence against pathogens.

The relationship between host plant diversity and the prevalence and diversity of viruses in populations of *Plantago lanceolata* in agricultural field edges and natural habitats was assessed (Susi and Laine, 2021). Surveys were made of 27 *P. lanceolata* populations (15 field edges, 12 natural landscapes) in the Åland Islands of Finland and five newly identified viruses of *P. lanceolata*. A high level of infection by one or more of the viruses was found in 57% of 267 plants sampled with coinfections present in 17% of plants. There was no significant difference between infection incidence in field edges and natural habitats, although virus species richness (number of virus species present in a population) was higher in the field edges.

Yearly surveys (2017-2020) were made for the occurrence of four fungal pathogens infecting wood anemone *Anemone nemorosa* in an area of about 150 m x 150 m in a nature reserve in Sweden (van Dijk et al., 2021). Initially, 139 spatially distributed patches were established, but these were significantly reduced in number, due to half the study area being clear-cut or had relocated by 2020 due to forest management operations or wild boar destroying patches. Two of the fungi, the rusts *Ochropsora ariae* and *Tranzschelia anemones*, have perennial systemic lifestyles overwintering in rhizomes, whereas a chytrid, *Synchytrium anemones*, and a smut *Urocystis anemones* have annual non-systemic lifestyles. Furthermore, it was found that the rusts usually occupied well-connected plant patches, whereas the chytrid and smut were found equally often in isolated patches and had higher patch occupancies and colonisation rates, due to spore dispersal and infection of new plants.

Wild *Citrus* spp. (China) and *Vitis* spp. (southern Europe) in areas where they are endemic can be infected by viruses and phytoplasmas respectively and are often close to cultivated grapevine and citrus, posing a potential risk to modern citrus and grapevine varieties (Liu et al. 2021, Rizzola, 2021).

Objective 2. Records in the CABI Distribution Database (single pathogens, following manual review)

The follow sections summarise the results for named pathogens identified via the DDB (see Table 4, green highlighted rows), reporting the pathogens in alphabetical order.

Aphelenchoides besseyi

Aphelenchoides besseyi (rice leaf nematode) has a wide global distribution (CABI, 2022a). Manual review of records added to the DDB in 2021 show that four records constitute new reports, although together they refer to just two geographic locations. *A. besseyi* has been found on yam (*Dioscorea cayenensis*) for the first time in two states in Brazil (Noronha et al., 2020; EPPO, 2021). Symptoms, including brown lesions on leaves leading to defoliation, were observed on plants between 2017 and 2019 in the states of Alagoas and Sergipe in eastern Brazil (Noronha et al., 2020). These records are not the first report of *A. besseyi* in Brazil where it has been present for decades (CABI, 2022a).

Apple hammerhead viroid

First identified in China and subsequently reported in countries including Italy, Spain, USA, Japan, and New Zealand (Zhang et al., 2014; Szostek et al., 2018), *Apple hammerhead viroid* (AHVd) is now found on most continents. Manual review of results from the DDB indicated four confirmed first reports were added in 2021 for this pathogen; Tunisia, India, Jammu and Kashmir (India) and Rio Grande do Sul (Brazil).

Sequences of AHVd isolates collected from Tunisia in 2019 were deposited with NCBI GenBank in 2020 (GenBank, 2021). These isolates confirmed the first report of AHVd on apple in Tunisia. Hamdi et al. (2022) subsequently published the findings that relate to these GenBank accessions.

Leaf samples collected from apple trees in 2019 from the Jammu and Kashmir Union territory were analysed and the first report of AHVd in the territory, but also in India as a whole, was confirmed (Nabi and Baranwal, 2020). This report indicates the spread of the viroid to a new region of Asia.

Nickel et al. (2021) published a summary at the 32nd Brazilian congress on Virology confirming the first report of AHVd in Brazil. Samples from apple orchards in Rio Grande do Sul were sequenced and presence of the viroid confirmed, however the year in which the samples were collected is not clear. The authors highlight that more information on the extent and potential impacts of AHVd is needed.

Apple rubbery wood viruses

Recorded in parts of Europe, North America, Asia and Oceania, Apple rubbery wood disease infects species of apple, pear, and quince (CABIa, 2022). The causal agent for this disease has been the subject of much debate. Recently, Rott et al. (2018) detected two viruses, Apple rubbery wood virus (ARWV) 1 and 2 using next-generation sequencing, which they tentatively suggest may be the causal agent. Manual review of DDB records revealed eight records that were considered new reports for these viruses, all of which related to China and provinces in the east of China, including Fujian, Jiangxi, Hubei, and Shandong.

Hu et al. (2021a) report the first confirmed occurrence of ARWV-2 in domestic apples in China after samples from a range of cultivars in Liaoning province were analysed. Hu et al. (2021b) collected 200 samples from leaf and shoots of apple trees in China to test for the prevalence of associated viruses. ARWV-1 was identified for the first time in China in 21 samples from the provinces of Hebei, Liaoning, and Shandong. Coinfection with ARWV-2 was common among these samples.

Records added to the DDB from EPPO Global Database in 2021 also indicate the first report of ARWV-2 infecting pear trees. Wang et al. (2019) identified the virus in leaf samples from *Pyrus pyrifolia* and *P. bretschneideri* in commercial orchards across Fujian, Jiangxi, Hubei, and Shandong provinces.

Biscogniauxia mediterranea

Biscogniauxia mediterranea occurs across North and South America, much of Europe and parts of Africa and Asia (CABI, 2022b). One record added to the DDB in 2021 indicates an expansion in the host range of the pathogen in the USA.

Wright et al. (2022) published the first report of *B. mediterranea* on the host plant *Quercus emoryi* (emory oak) in Arizona, USA after tissue samples taken from hosts in 2019 were analysed. Southwestern states of the USA are becoming increasingly hot and dry due to climate change. With *B. mediterranea* commonly associated with water-stressed trees, increasing incidence of this pathogen is likely and threatens important woodland habitats in the region (Wright et al., 2022).

Candidatus Liberibacter asiaticus (: see also results of Objective 1)*

The Asian form of *Ca*. Liberibacter is the most widespread of the *Ca*. Liberibacter species, which cause citrus greening disease or 'huanglongbing' (CABI, 2022a). The pathogen is not reported to be present in Europe or the Mediterranean but does affect major citrus producers such as Brazil, China, and the USA (CABI, 2022a). One new report was identified by the manual review of DDB records in Bahia, Brazil.

A record added to the DDB from the EPPO Global Database in 2021 shows *Ca.* L. asiaticus was recorded for the first time in the state of Bahia in the east of Brazil (EPPO, 2021). This was based on samples taken from the vector *Diaphorina citri* between 2011 and 2014. Though by no means the first record in Brazil (it was first reported in the country in

2004), EPPO cite a paper by Abreu et al. (2020) which states that citrus greening disease caused by *Ca*. L. asiaticus is a major threat to the citrus industry in the state of Bahia.

Citrus tristeza virus *(*: see also results of Objective 1)*

Globally widespread, *Citrus tristeza virus* (CTV) has been introduced to nearly all citrus-growing regions of the world (CABI, 2022a). Manual review of records added to the DDB in 2021 shows one first report, in Tunisia.

The first report of CTV in Tunisia was confirmed after samples taken in 2018 were analysed (IPPC, 2021). Samples had been collected from the northeast of the country and it is now under official control.

Colletotrichum siamense

Colletotrichum siamense occurs across much of Asia as well as the Americas and Australia (CABI, 2022a). Manual review of distribution records added to the DDB in 2021 show four new reports, one indicating the first report of the pathogen in New Zealand and the remaining three indicating first reports on new host plants.

Hofer et al. (2021) report the first confirmed occurrence of *C. siamense* in New Zealand. It was found on *Persea americana* (avocado) after samples were collected from commercial orchards in 2019. The authors highlight that it is difficult to tell different *Colletotrichum* species apart based only on morphological characters, so sequencing is important and allows more informed decision making in terms of prevention and control (Hofer et al., 2021).

Yang et al. (2021) isolated *C. siamense* in 2019 from leaf samples of *Vernicia montana* (Chinese wood oil tree) in Jiangxi, China. This is the first time it has been identified on this host, but it is already known to cause damage on other important host plants.

The first report of *C. siamense* on *Ocimum basilicum* (Thai basil) in Malaysia was reported by Ismail et al. (2021). Symptoms were observed on inflorescences of basil plants in 2019 and tissue samples analysed. Control measures available for this disease are lacking and it is therefore a high risk to Thai basil cultivation in Malaysia (Ismail et al., 2021).

C. siamense has previously been identified on *Allium cepa* (onion) in India however, Herath et al. (2021) reported the first occurrence of this pathogen on onion in Sri Lanka based on analysis of samples collected from onion plants in mid-2020. The authors highlight that this range expansion poses a threat to onion crops in Sri Lanka and has already led to severe crop losses in onion-producing regions of the country.

Cucurbit chlorotic yellows virus

The distribution of *Curcurbit chlorotic yellows virus* (CCYV) includes Africa (Algeria, Egypt, Sudan), parts of Asia, a handful of countries in Europe (Cyprus, Greece, Spain) and the USA where it has a localized distribution (CABI, 2022a). Distribution records added to the DDB in 2021 indicate first reports of CCYV in 11 geographic locations. These include four countries: India (Kumar et al., 2022), Philippines (Chang et al., 2021), South Korea (Cho et al., 2021) and Spain (Chynoweth et al., 2021). The remaining records are for subnational locations. First reports are all based on observations or samples taken between 2018 and 2020.

The first report of CCYV in India occurred on pumpkin plants in New Delhi (Kumar et al., 2022). Symptoms were observed from August 2020 and the authors highlight a need to complete surveys to understand the extent and impact of infections with CCYV.

The report from Spain suggests CCYV may have spread undetected in the Mediterranean Basin as the symptoms of the disease resemble those of other cucurbit infecting viruses (Chynoweth et al., 2021). Subsequently, Alfaro-Fernandez et al. (2022) reported the first occurrence of CCYV in Tenerife, Canary Islands. The paper states the need for control measures to limit the spread of CCYV within Tenerife and beyond to other nearby islands.

The DDB also contains a record of the first natural infection of pumpkins in mainland China (Hunan Province) in 2020 (Liu et al., 2021). Authors highlight that the rapid evolution and spread of the virus suggests there is potential for it to cause high levels of crop loss in future. They also emphasise the importance of early detection and prevention of CCYV. However, this is not the first record of the virus in China as a whole. It is found in other provinces in the country, and was first reported in 2007 (EPPO, 2021).

CCYV had previously been recorded in the USA in California on melon in 2018 (Wintermantel et al., 2019). Analysis of records added to the DDB in 2021 indicate CCYV has since spread. Reports confirmed the presence of CCYV in four more US states: Alabama, Florida, Georgia and Texas (Mondal et al., 2022, Jailani et al., 2022, Kavalappara et al., 2021, Hernandez et al., 2021 respectively). All of these reports are based on samples collected in 2020.

Erysiphe corylacearum

Erysiphe corylacearum has been identified in parts of Asia and Europe causing disease with powdery mildew symptoms on hazelnut trees (*Corylus* spp.) (CABI, 2022a). A manual review of DDB records for this pathogen showed three records that all relate to first reported occurrences of *E. corylacearum* in Romania.

Chinan and Mânzu (2021), published their report in March of 2021, which was followed by a report by Rosati et al. (2021) in September 2021. The former publication confirms the presence of the pathogen in the Romanian Carpathians and the latter in commercial orchards in Dudeștii Vechi in the far west of the country. Identification by Rosati et al. (2021) was based on samples taken in October 2020 and it is suggested the pathogen may have spread east to west through the Caucasus into Europe due to its presence in Turkey, Azerbaijan, Georgia, and Iran. EPPO (2021) also updated the status of the pathogen in Romania in 2021 because of these publications.

Erwinia rhapontici

Erwinia rhapontici, commonly known as rhubarb crown rot, is present across Asia, Europe, North America and in New Zealand and in some locations has been reported as widespread (Poland, United Kingdom, Israel) (CABI, 2022a). Manual review of records added to the DDB in 2021 highlight one first report on a new host plant.

Wang et al. (2022) reported the first instance of *E. rhapontici* causing stalk rot of celery in China. According to the authors this is the first time *E. rhapontici* has been reported on this host plant. Soft rot symptoms were observed on celery in May 2021 in Hebei Province. Wang et al. (2022) emphasise the threat this poses to local celery production and the need for prevention and control measures to manage it.

This is not the first occurrence of *E. rhapontici* in China overall. It has also been recorded previously in Sichuan Province causing disease in kiwifruit (Wang et al., 2017) and in Hubei province in 2010 associated with roots of the orchid, *Cymbidium faberi* (Chu et al., 2010).

Fusarium oxysporum f.sp. cubense Tropical race 4 (: see also results of Objective 1)*

Known commonly as Fusarium wilt or Panana disease, *Fusarium oxysporum* f.sp. *cubense* Tropical race 4 (TR4) is a soilborne fungus and a major threat to banana production globally (CABI, 2022a). First reported in Southeast Asia it has since been recorded in Australia, the Middle East and Africa (CABI, 2022a). Manual review of records from DDB show a new report of this pathogen in Peru.

In 2021 a press release was published by SENASA (National Agricultural Health Service of Peru) confirming the first report of TR4 in a 0.5-hectare plot of land in the department of Piura in northwestern Peru. Phytosanitary measures were immediately put in place to limit the spread and impact of the outbreak. This included limiting access to the site, destruction of the plants from the plot, training for farmers and increased surveillance in other banana producing locations (SENASA, 2021).

Globodera rostochiensis

Globodera rostochiensis, commonly known as the yellow potato cyst nematode, is widely distributed throughout potato growing regions of the world (CABI, 2022a). Manual review of DDB records showed one new report of this pathogen occurring in Sulawesi, Indonesia.

First recorded in Indonesia itself in 2003, *G. rostochiensis* was shown to be present in Sulawesi for the first time in 2020 (EPPO, 2021). This EPPO record is based on a publication by Handayani et al. (2020) who identified the pathogen in soil samples collected from a potato field in north Sulawesi. The study also found the nematode in fields in Sumatra and Java.

Nothophoma quercina

Following a manual review of DDB records for this pathogen, a first report was found for *N. quercina* on the ornamental plant *Photinia* x *fraseri* in China (Zou et al., 2021). It was identified when bud blight disease was observed on *P. fraseri* in 2017 and 2018 and leaf samples were collected and analysed. Zou et al. (2021) state that this is the first report of the pathogen on this host plant and the first report of the pathogen in China.

Potato spindle tuber viroid

Potato spindle tuber viroid (PSTVd) occurs in Egypt, Ghana, and Nigeria in Africa and in various parts of Asia (CABI, 2022a). Its distribution is patchy with erratic outbreaks in various counties where it then comes under eradication. Successful eradication was reported for Canada and the USA in the mid-2000s (CABI, 2022a). Records added to the DDB in 2021 highlight three new reports of PSTVd. Two in Africa (Uganda and Kenya) and a first report of the viroid on tomato in India.

First reports of PSTVd in Uganda and Kenya were confirmed in seeds of *Solanum* wild relative species (EPPO, 2021). The records from the EPPO Global Database reference Skelton et al. (2019) who report that the seed was tested for PTSVd to confirm it was suitable to be distributed to a centre for pre-breeding research. At the pre-breeding centre, it would have been used to assess genetic diversity of samples to help develop improved crop varieties. The author's state that this demonstrates the potential of pospiviroids to be distributed through non-commercial seed.

Records also indicate the first report of natural infection by PSTVd on tomato in India, this is not the first report of this viroid in India overall but is the first on this host plant in the country. PSTVd is under stringent phytosanitary regulations because it already infects potatoes in India (Natarajamurthy, et al. 2021).

Tomato brown rugose fruit virus

First identified in Jordan in 2016, *Tomato brown rugose fruit virus* (ToBRFV) has since been identified almost exclusively on tomato plants in Asia, Europe and some regions of North America (CABI, 2022a). Manual review of distribution records in the DDB identified through the automated process show 15 confirmed first reports in new geographic locations. Ten of these are for countries in which the virus was observed and sampled in 2021 itself across Europe (Austria, Estonia, Hungary, Malta, Norway, Portugal, Slovenia and Switzerland) and Asia (Iran, Saudi Arabia). For example, Ghorbani et al. (2021) first observed symptoms consistent with the presence of ToBRFV in greenhouses in Iran in August 2021. Infection with ToBRFV was subsequently confirmed and plants destroyed. Sabra et al. (2022) suggest infection of tomato plants in Saudi Arabia may have been caused by imported seed from a country with the virus. Many of these new occurrences have been reported by National Plant Protection Organisations (EPPO, 2021). The virus is currently under eradication in the majority of the countries listed above and has already been reported as eradicated in Estonia (EPPO, 2022).

The remaining five confirmed first reports highlight recent outbreaks that were based on surveys carried out pre-2021, although the reports themselves were published in 2021 or first available online in 2021. In 2017, ToBRFV was confirmed on tomatoes growing in greenhouses in Syria (Hasan et al., 2022). It was confirmed as present in the United States of America in California in 2018 (EPPO, 2021). Although it has since been eradicated from California, records in the DDB show that EPPO now record it as present in the country due to a new record from Florida from 2019 (Dey et al., 2021). In 2020, outbreaks were reported on tomato in Belgium and Uzbekistan and on pepper (*Capsicum annuum*) and tomato plants in Czechia (EPPO, 2021).

DISCUSSION

Although losses in major crops are increasingly well documented (Savary et al. 2019, 2022), the underlying disease dynamics driving these losses are much less well studied. Disease epidemics and outbreaks in minor crops, non-food crops and natural plant systems are particularly poorly characterised. It is of course rather difficult to provide a representative overview of plant diseases patterns on a global scale. However, global changes in trade, land use and climate continue to alter the drivers and in turn distribution of plant disease epidemics. Monitoring and understanding these patterns therefore become increasingly important.

Here we used two contrasting approaches to analyse plant disease epidemics across the world in 2021. The first was a systematic review of the 2021 peer-reviewed literature reporting surveys of plant disease occurrences (our Objective 1). The second retrieved new pest presence records added to the CABI Distribution Database (DDB) in 2021 (our Objective 2). Our study has confirmed the value of taking complementary approaches to identifying current plant disease outbreaks and potential new risks. Our two approaches certainly gave somewhat different perspectives.

Geographically, both approaches revealed the highest numbers of outbreaks and new records in North America, Asia, and Europe, with lower numbers in Africa and South America (Figure 9). There were also similarities in the pathogen taxa identified across the two approaches, with fungi and viruses dominating (Figures 3 & 7). Interestingly however, the two approaches led to essentially distinct lists of specific pathogen species (Tables 3 & 4). Exceptions to this were *Candidatus* Liberibacter asiaticus, *Citrus tristeza virus*, *Colletotrichum siamense*, *Fusarium oxysporum* f.sp. *cubense* Tropical race 4, *Globodera rostochiensis* and *Tomato brown rugose fruit virus*, which were retrieved from both approaches. It is particularly noteworthy that of these pathogens, only three – *Ca.* Liberibacter asiaticus, citrus tristeza virus and *Fusarium oxysporum* f.sp. *cubense* – were reported in at least 5 publications in the 2021 in the results of Objective 1 (Table 3).

Both approaches adopted here were systematic, explicitly designed to avoid bias toward certain crops or pathogens. Although reports in the literature and submitted to the DDB ought to reflect the balance of current outbreaks and new findings, certain sources of bias are difficult to avoid. The biases were driven by various factors. The scientific publications underpinning both the scientific literature surveyed in Objective 1, and most of the reports to the DDB in Objective 2, are written in English, introducing a "Tower of Babel" bias into our results (Grégorie et al., 1995). This is acknowledged to affect the results of studies using similar data (Bebber et al., 2019). Certain pathogens are topical for scientific reasons since they constitute model systems for experiments, for example *A. thaliana* and *P. syringae* (e.g., Karasov et al. 2018). The pathogens that appear in the scientific literature are also driven in part by the need attract research funding, and this does not always necessarily reflect the economic, social, or environmental impact of the disease caused by these pathogens.

We have very likely underestimated the importance of pathogens in the "Global South" (Figure 9). This simply reflects greater surveillance and research effort in richer, more developed countries (Jones et al., 2008). Other pathogens have significant regulatory implications following first discovery, for example *Tomato brown rugose fruit virus*, and still others receive increased attention because of the impacts they might cause. Both these factors make these pathogens more likely to appear in our results.

Conversely sometimes pathogens do not receive very much attention because they are perceived to be unimportant. This can have unintended consequences. As an example, there is a paucity of records on *Xylella fastidiosa* on deciduous tree species in North America. This likely reflects underreporting of the disease in these areas due to perceived low impact. However, precisely this has led to considerable current uncertainty in Europe as to what the impact could be if *X. fastidiosa* spreads in forest trees species present in the European Union (EFSA 2019).

Other issues that impact on reporting of disease include a potential over representation of those diseases that have strong symptom expression and existing tools for diagnosis, as well as time lags between when samples are collected in the field and when laboratory diagnosis occurs. Moreover, our approach does not capture data from the large number of regulatory surveys that are not published nor reported via the DDB, especially for pathogens which are not notifiable.

In Objective 1, we concentrated on published literature reporting the results of surveys. This task would have been made easier if journals specified general guidance for good practice in planning, designing, carrying out, analysing, and writing papers reporting the results of surveys. Such guidance would include reporting the rationale for surveys, the purposes they serve, the questions being asked, and whether surveys were hypothesis-driven or exploratory. Ideally this guidance would encourage at least a partial move away from single pathogen surveys, given the increasing recognition of disease complexes and syndromes and the recent awareness of mixed or co-infections and cryptic species. As we saw here, the increased splitting into various sub-specific forms and other genomic characterisations arising from surveys presents major data analysis challenges and difficulties in biological interpretation.

In Objective 2, we initially automatically extracted records from the DDB. However, manual intervention was required to identify confirmed first reports of pathogens in new geographic locations or on new hosts. This is unsurprising, since confirmed new reports are not the only focus of the DDB. Records required manual review for various reasons, predominantly due to taxonomic revisions and/or differences in the date of addition to the DDB versus the date of the survey itself. On other occasions, the literature cited by records found in the automated stage discusses surveys carried out with the purpose of determining pathogen prevalence, disease severity or pathogen impacts in locations where a given pathogen is already well known to occur. This was not our focus here, and so such records required manual removal.

Certainly, pathogen distributions present a constantly evolving picture, and any study based on a database can only ever provide a snapshot in time. For example, *Tomato brown rugose fruit virus* was first reported as present in 2021 in Estonia, but has subsequently been reported as absent, having been eradicated (EPPO, 2022). The structure of the geographic regions in the DDB also introduced some possibility for bias. For example, *Ca.* Liberibacter asiaticus was reported for the first time in Bahia, a state in Brazil, and this only showed up in our results as “new” outbreak because Brazil is one of the countries for which sub-national geographical resolution is retained in the DDB.

Our results have also been affected by the way in which regulatory surveys for quarantine pests in plant health are principally targeted at substantiating claims for pest freedom. Such surveys could even be argued to provide perverse incentives which in fact reward under-sampling of those pests. Though risk and statistically based survey approaches are increasingly adopted (EFSA 2020, Mastin et al., 2020), detection surveys are often used to establish presence/absence rather than providing representative surveys of disease dynamics. Lack of resources for representative and widespread monitoring of disease has in many cases led to significant outbreaks being undiscovered for decades. For example, *X. fastidiosa* was first reported in France in 2015 but independent studies have estimated it was introduced in the 1980s (Soubeyrand et al., 2018; Dupas et al., 2022). In the United Kingdom, Ash Dieback Disease was first reported in 2012, but *Hymenoscyphus fraxineus* may have been present and spread from ash stock planted as early as 1991 (Wylder et al., 2018).

Clearly more investment is needed in plant health monitoring, not just to accurately characterise presence or absence at country and regional levels, but also to monitor spatial distribution and temporal changes for improved epidemiological intelligence (Ristaino et al., 2021). This is sorely needed to enable rapid responses to new and emerging diseases, particularly in low- and middle-income countries for which the impacts can be particularly severe (Carvajal-Yepes et al., 2019). Better sources of data on disease presence and – perhaps particularly – absence would allow predictive mathematical models to be properly parameterised, which often remains very challenging in practice (Cunniffe et al., 2015). It would also allow targeting of novel outbreaks of re-emerging diseases which can no longer be controlled in traditional ways (Bhattacharya et al., 2017). New detection technologies, for example remote sensing (Zarco-Tejada et al., 2018) are being developed, and could potentially feed into more cost effective and widespread monitoring. There are also opportunities to include diffuse data sources into the information stream concerning the spread of pathogens, including, for example, citizen science (Brown et al., 2020) and landowner reports (Defra, 2020).

Six of the 14 pathogens reported extensively in 2021 in the scientific literature are vectored by insects. The role of vectors in disease transmission, epidemiology and spread needs as much attention as the pathogen. A good example of this concern is the African citrus psyllid *Trioza erytreae*, first recognised as having spread to Europe in the last decade (Cocuzza et al. 2017), and which now poses the risk of allowing huanglongbing to establish. Although the pathogens identified are well-known and characterised, they (or their vectors) continue to spread, e.g., *X. fastidiosa* in Europe, and *T. erytreae*. The question remains which of the pathogens identified as new records in data bases will in future years cause major disease outbreaks and be reported extensively in the scientific literature.

Very few pathogens spread intercontinentally through natural dispersal, mostly rust fungi such as sugarcane rust and cereal rusts (Jeger 1999, Brown and Hovmøller 2002). In many cases the role of international trade in plants and plant products can seed subsequent establishment, spread and impact of pathogens (Brasier et al. 2008, Jeger et al. 2021). A traded plant may carry with it a pathogen to a new location, or a naïve introduced plant may acquire a new pathogen in the new location. Similarly, a vector may move with the traded plant, or an invasive pathogen may acquire a new vector. Numerous examples of the introduction of exotic and emerging pathogens can be found in the listings of pathogens identified in Objective 2 of this review.

Problems remain of delays in reporting, publishing, and communicating plant disease outbreaks and new records for plant health regulation, disease management and farm strategic planning. We suggest that the approach taken in this review provides a mechanism for integrating information and a synoptic view on current plant disease outbreaks and potential future risks and might usefully be adopted regularly in the future.

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