

A Synoptic Review of Plant Disease Epidemics and Outbreaks Published in 2022

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Abstract

This scientometric study reviews the scientific literature and CABI distribution records published in 2022 to find evidence of major disease outbreaks and first reports of pathogens in new locations or on new hosts. This is the second time we have done this, and this study builds on our work documenting and analyzing reports from 2021. Pathogens with three or more articles identified in 2022 literature were *Xylella fastidiosa*, *Bursaphelenchus xylophilus*, *Meloidogyne* species complexes, ‘*Candidatus Liberibacter asiaticus*’, *Raffaelea lauricola*, *Fusarium oxysporum* formae specialis, and *Puccinia graminis* f. sp. *tritici*. Our review of CABI distribution records found 29 pathogens with confirmed first reports in 2022. Pathogens with four or more first reports were *Meloidogyne* species complexes, *Pantoea ananatis*, grapevine red globe virus, and *Thekopsora minima*. Analysis of the proportion of new distribution records from 2022 indicated that grapevine red globe virus, sweet potato chlorotic stunt virus, and ‘*Ca. Phytoplasma vitis*’ may have been actively spreading. As we saw last year, there was little overlap between the pathogens identified by reviewing scientific literature versus distribution records. We hypothesize that this lack of concordance is because of the unavoidable lag between first reports of the type reported in the CABI database of a pathogen in a new location and any subsequent major disease outbreaks being reported in the scientific literature, particularly because the latter depends on the journal policy on types of papers to be considered, whether the affected crop is major or minor, and whether the pathogen is of current scientific interest. Strikingly, too, there was also no overlap between species assessed to be actively spreading in this year’s study and those identified last year. We hypothesize that this is because of inconsistencies in sampling coverage and effort over time and delays between the first arrival of a pathogen in a new location and its first report, particularly for certain classes of pathogens causing only minor or non-economically damaging symptoms, which may have been endemic for some time before being reported. In general, introduction of new pathogens and outbreaks of extant pathogens threaten food security and ecosystem services. Continued monitoring of these threats is essential to support phytosanitary measures intended to prevent pathogen introductions and management of threats within a country.

Keywords: data science, diseases in natural plant populations, ecology, epidemiology, global surveillance, pathogen emergence and spread, plant disease outbreaks, scientometrics

Plant diseases continue to cause economic and social insecurities to farmers, food supply chains, and consumers (Djurle et al. 2022), as well as significant environmental damage (Freer-Smith and Webber 2017). These risks are further compounded by the challenges posed by climate change (Chaloner et al. 2021; Singh et al. 2023) and ever-increasing world trade and travel (Spence et al.

2020). The contribution of plant pathogens to crop losses and impacts on ecosystem services remains poorly documented and understood. It is therefore almost certainly underappreciated. In the context of a rapidly growing world population, documenting the distribution of pathogens and their impacts potentially allows policy makers and stakeholders to make more informed decisions on how to allocate their limited resources for management. It is also essential for improved understanding of how plant disease outbreaks are changing with global changes in environment, land use, and management practices (Raza and Bebbber 2022).

Our previous study (Jeger et al. 2023) was a scientometric analysis of major plant disease outbreaks and first reports of pathogens worldwide. It involved a review of the scientific literature published in 2021, where surveys or other quantitative approaches had been

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used to report disease outbreaks or epidemics, and a complementary study interrogating the CABI Distribution Database (CABI DDB) for first reports of plant pathogens in a new location, or on a new host, that had been identified and added to the CABI DDB in the same year. Here, we repeat this protocol for publications and first reports from 2022, assessing what we can learn about pathogen spread in 2022 from these sources, as well as reporting the consistency of results of these two approaches with each other and year-on-year. We did not use expert-based assessment methods (Savary et al. 2019) to avoid the potential for bias in favor of pathogens that are well known or perceived to be important. The aim was to continue to assess such a synoptic approach for understanding ongoing plant disease spread, epidemics, and outbreaks. We also review the properties of these reports, including the most represented taxa, hosts, study types, and affected geographic areas.

New disease outbreaks are detected and reported through a multitude of mechanisms. Formal approaches include the general and specific surveillance activities conducted by National Plant Protection Organizations (NPPOs) to identify and monitor outbreaks. Invasive plant pathogens as alien species pose a threat to many countries (Mulema et al. 2022), and horizon scanning—and the subsequent prioritization of threats—requires a supra-national effort (EFSA et al. 2022). It has been recognized that the coherence and capabilities of NPPOs in many regions of the world vary widely (Gc et al. 2022). In the European Union (EU), it is a requirement to conduct annual surveys for priority pests and multiannual surveys for all other regulated plant diseases to ensure member states remain disease free or that pathogens have not moved from current demarcated areas (Council Regulation [EU] 2016/2031). New plant disease outbreaks may also be reported through ad-hoc reports from members of the public or growers (Brown et al. 2020), as well as via monitoring surveys conducted for research purposes. Although horizon scanning tools (EFSA et al. 2021) and pest and commodity risk assessments (EFSA Panel on Plant Health et al. 2018) synthesize information from ongoing outbreaks, they tend to focus only on a subset of hosts, pathogen types, and areas.

Consequently, although those diseases that cause significant economic or environmental damage are often somewhat well documented, comprehensive information on the frequency and extent of new outbreaks across all pathosystems is rarely synthesized. This means we neglect a clear opportunity to reveal patterns or trends. Because the results of our past study, the first of its type to take a global synoptic approach, were sufficiently informative, it was considered appropriate to repeat the exercise on a regular basis. By so doing, we anticipate building up a body of knowledge reflective of current threats due to plant pathogens and identifying trends that will help to anticipate future threats.

Even though it has only been 1 year since our last article (Jeger et al. 2023), we note that there have been positive developments published in 2022 that may enhance disease management. Focusing only on publications from 2022, developments include relating genomics research to the population dynamics of plant pathogens (Xia et al. 2022), a greater appreciation of the role of wild plants in disease epidemiology (Jeger 2022; Najberek et al. 2022; Singh et al. 2023; Triolet et al. 2022) or their exploitation in plant breeding (Ramirez-Villegas et al. 2022; Tobón-Niedfeldt et al. 2022), and more nuanced approaches to the potential role of microbiota in biological control and plant health more generally (Collinge et al. 2022; Sangiorgio et al. 2022). Detection of plant pathogens, as well as our ability to distinguish between different plant pathogens, has been improved by recent technological innovations (Verma et al. 2022; Zhang et al. 2022), including biosensors (Mohammad-Razdari et al. 2022; Shaw and Honeychurch 2022) and continued advances in artificial intelligence techniques (Garrett et al. 2022). However, use of these tools is not optimal unless combined with the contextual information provided by surveillance, either via traditional national surveys (Elmhirst 2022) or as supplemented by the increasingly wide

range of remote sensing opportunities now available and routinely used (Oliva et al. 2022; Prasanna et al. 2022; Wan et al. 2022).

Methods

Overview of the approach

Unless stated otherwise, we followed the same strategy for information retrieval as in the previous study (Jeger et al. 2023), using two complementary approaches. The first (A) was a search of peer-reviewed journal full-length research articles for 2022 to obtain information, by pathogen, location, and host, on studies of major disease outbreaks published in that year. This was done in two stages (Stage 1 and Stage 2) as further explained below. Second, (B) pathogens were identified for first reports, by location and/or host, that had been added to the CABI DDB in 2022. For clarification, first reports in (A) are all referenced and may originate as short notes in journals or in other sources before being added to the CABI DDB.

Approach A: Published journal articles on disease outbreaks and epidemics

A systematic review was made on Web of Science of journal articles published in 2022 (Database Web of Science Core Collection, Clarivate Analytics, accessed 26 April 2023) following a search protocol based on thematic blocks and search strings. The systematic review included online access of copy edited, but not necessarily typeset, articles prior to full publication (also known as “Early View” or “First Look” or other synonyms). The searches were done in two stages. In Stage 1, the aim was to identify pathogen species, hosts, and locations for which major disease outbreaks had been studied through surveys or other quantitative approaches but, importantly, without making prior assumptions on pathogen species or host plants. In Stage 2, a search was done to provide further context and information on the pathogens identified in Stage 1.

The Stage 1 protocol consisted of six thematic blocks each with comprehensive search strings together with preset exclusion criteria (Fig. 1). The publications recovered in Stage 1 are termed the “core” articles and form the basis for further analysis. The search terms adopted in Stage 1 were slightly broader than those we used for 2021 publications (Jeger et al. 2023), and we anticipated a larger number of articles would be returned. The articles recovered were checked manually for relevance by setting further exclusion criteria, recognizing that in some cases these must necessarily be a matter of judgement rather than absolute criteria. Mainly, and based initially on the abstracts, 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, primer design and genomic approaches, and physiological dissection of host resistance mechanisms. Also excluded, unless linked directly to field observations of disease, were articles reporting analysis of seed samples, small-scale experimental plots using artificial inoculation, analysis of historical culture collections, aerobiological studies, and theoretical mathematical models (i.e., mathematical models that do not have parameters fitted to a particular named disease system). Articles that dealt with functional aspects of microbial communities associated with the natural occurrence of disease in the field were retained, given the current interest in microbiota (Trivedi et al. 2020). Also retained were grower surveys and citizen science that referred to or were combined with field observations of disease. Further articles were then excluded—or not—based on a reading of the full articles.

The articles retained were allocated to categories corresponding to (i) a single named pathogen species, but also including a disease complex with coinfecting, often related, species; and (ii) multiple pathogens for a given host system (i.e., crop, cropping system, forest trees, or wild plant populations). These articles comprise the core articles. Each core article was flagged by host (grouped into the following categories: cereals; pulse, vegetable, roots, and tubers;

forest tree species; fruits, nuts, or berries; ornamentals; and other), pathogen group (fungus, oomycete, bacterium, phytoplasma, virus, and nematode), and geographical origin (region, country, continent, and global) and one of 10 descriptor types for the main motivation of the study, recognizing that many articles were motivated by more than one of these descriptors:

- A. **Detection**, discrimination, and analysis
- B. **Surveillance**, including growers and citizen science
- C. **Emergence** of new pathogens, strains, and vectors
- D. Weeds as **inoculum reservoirs**
- E. Wild **crop relatives**, land races, and genetic resources
- F. **Wild plant** populations and communities
- G. **Disease management**, including host resistance deployment
- H. Natural **biological control**, including microbiota
- I. **Climate change** and variability
- J. **Yield loss** and damage estimation

The text in bold in each descriptor is the short name as used in our result figures.

Again, following the approach from last year (Jeger et al. 2023), a Stage 2 search was then done to provide additional context and information on the pathogen species and complexes identified in Stage 1. The protocol had two thematic blocks and the search strings: <pathogen name> AND (survey OR epidemic OR outbreak), restricted to 2022 publications. The intention was to recover articles reporting on an epidemic or outbreak of a given pathogen but without reporting a survey, and vice-versa. Where the pathogen had a wide host range, the Stage 2 search was restricted to the host(s) specified in the core articles. The articles recovered in Stage 2 comprise the “supplementary” articles. A similar approach was followed for the multiple pathogen categories identified in Stage 1, but with an appropriate thematic block defined for the host system rather than the single pathogen name. Articles recovered in the Stage 2 search were allocated and added to the categories defined from Stage 1.

Approach B: First reports of plant pathogens

The CABI DDB was used to identify pathogens that had been reported for the first time in new locations and/or on new hosts in

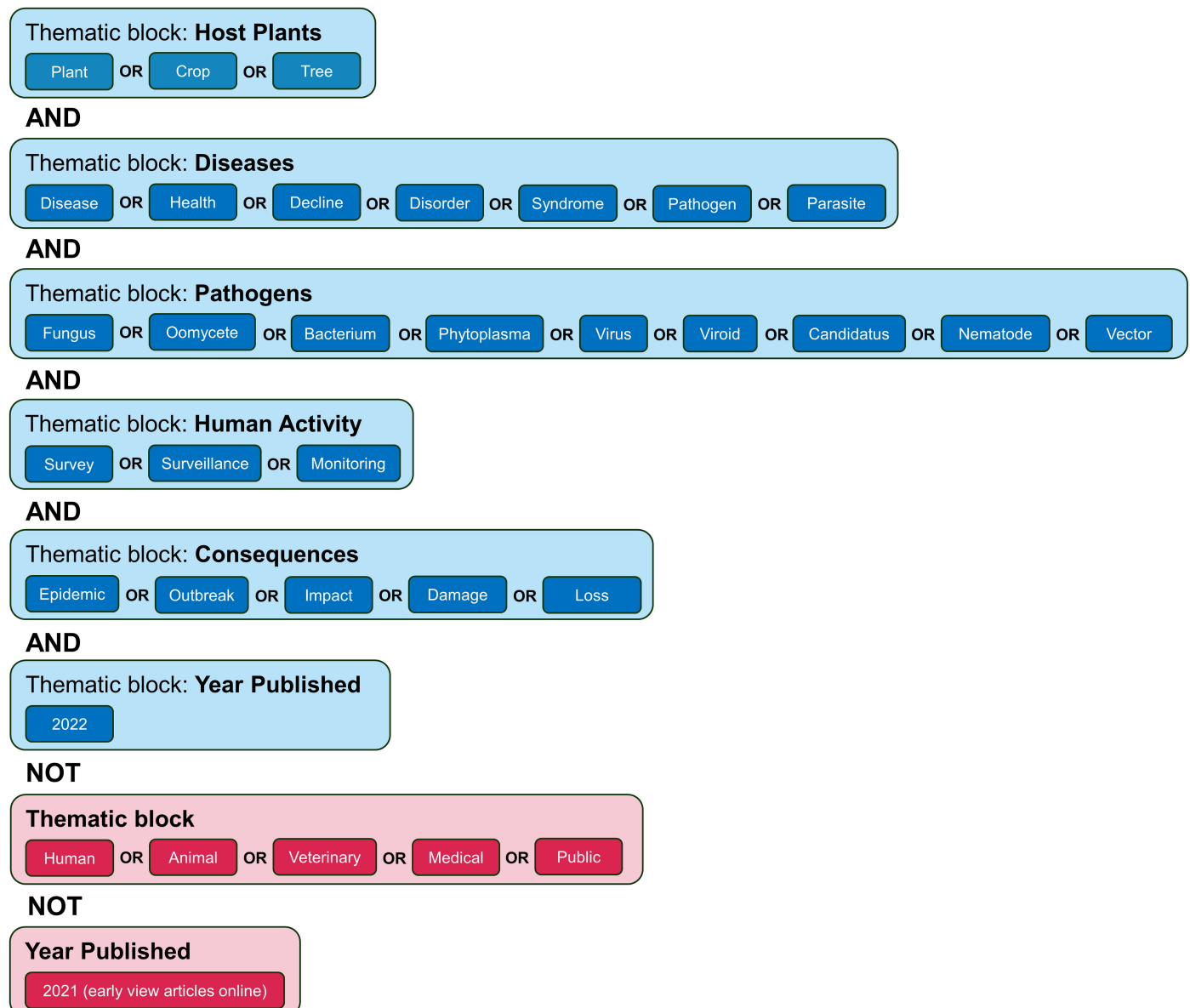


FIGURE 1

The search protocol for 2022 publications based on thematic blocks and search strings to identify pathogens, locations, and hosts for which major disease outbreaks had been studied.

2022. The method very closely followed that of Jeger et al. (2023), consisting of an automated identification of distribution records that indicated potential first reports of pathogens and a manual review of those records to confirm their status as first reports.

Automated identification of potential first reports of pathogens. Records added to the CABI DDB during 2022 (and for which the reference for the record was published in 2022) were extracted from the database, considering only those with a status of “Present” and without any flags indicating the record was of poor quality. If a record did not have a year indicated for the cited reference but was added to the database between 1 January 2022 and 31 December 2022, it was also included in the dataset. The records were then filtered to include plant pathogens only, based on taxonomic group, following the method outlined in Jeger et al. (2023).

A total of 26,956 distribution records, covering 903 plant pathogens, were identified in this initial step. These records were then compared with “pre-2022” records for each organism and geographic location (i.e., all records that existed in the CABI DDB for a pathogen prior to 2022). Only those pathogens with no previous record of presence for the location were classified as potential first reports. A list of 1,123 distribution records (potential first reports), covering 838 plant pathogens, was the result of this automated step.

Plant pathogens with five or more records identified in the automated step were selected for manual review (751, 67% of the potential first reports). This threshold was chosen as a balance between maximizing the size of the dataset while remaining practical with the human resources available to review articles.

Manual review. The source publications for a total of 751 distribution records (potential first reports) from the CABI DDB were manually reviewed. The aim was to identify those reports that could be classified as confirmed first reports of a pathogen in a new geographic location where it had not been recorded before or on a new host plant on which it had not been identified previously.

This included records for some pathogens that did not meet the threshold of five potential first reports but that were identified in the Stage 1 search of peer-reviewed journal articles described in Approach A. This cross-check between approaches allowed us to consider whether there was any overlap in the pathogens that were emerging or spreading to new locations/hosts and those that were causing diseases outbreaks or epidemics. Some of these pathogens

were part of species complexes. In these cases, where the CABI DDB covered individual species within a complex, these individual species were combined, and records were reviewed and reported at the level of the species complex (e.g., *Meloidogyne* species complexes).

Any duplicate records identified in the CABI DDB dataset for manual review were flagged and excluded from subsequent analysis to avoid overinflation of results. This occurred when the CABI DDB cited a journal article as well as a record from a third-party database whose original source was the same journal article.

The year of publication for a record had to be 2022 for inclusion in the dataset for the study (an exception was made where a publication had been available online in 2022, and therefore added to the CABI DDB in 2022, but with a publication year of 2023). The date of a confirmed first report was taken as the year that symptoms were first reported, or when samples of the pathogen or affected host plant were collected, not the year of the publication. The confirmed first reports were then reviewed to determine their significance in terms of their likely impact on plant health and relevance to risk assessment and management.

Results

Approach A: Published journal articles on disease outbreaks and epidemics

A total of 251 articles were recovered in the Stage 1 protocol (Fig. 1). Applying the manual exclusion criteria yielded a total of 179 distinct core articles, listed in Supplementary Material S1 (130 articles concerning single pathogen species or species complexes) and Supplementary Material S2 (49 articles concerning multiple pathogens affecting a crop or cropping system).

Core articles for single pathogen species or species complexes allocated to categories, hereafter “named species,” are tabulated in Supplementary Material S1 for fungi, oomycetes, bacteria, phytoplasmas, viruses, and nematodes. The greatest number of named species was for fungi (42 named species, 54 articles, and 59 unique species and location combinations), followed by viruses and viroids (19, 22, and 23); bacteria, including mollicutes (6, 21, and 17); nematodes (8, 19, and 16); and oomycetes (4, 6, and 6) (Fig. 2). The dominant article type for named species was for detection, discrimination, and analysis of pathogens (32 articles), followed by

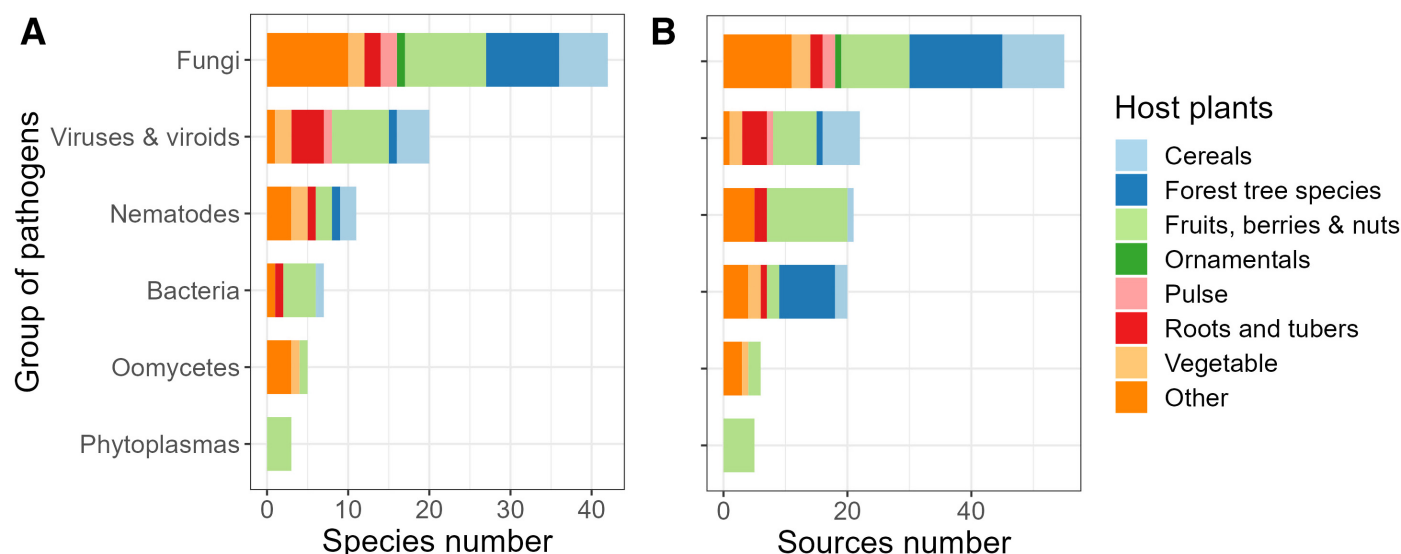


FIGURE 2

Number of single named species and number of core articles in which species were identified in Stage 1 of the review of published articles on disease outbreaks and epidemics classified by a group of host plants. **A**, Number of species by pathogen taxon. **B**, Number of sources by pathogen taxon.

disease management, including deployment of resistant cultivars and biological control (27); disease surveillance, either remote or ground-based (25); emergence of new pathogens, strains, and vectors (23); yield loss and damage estimation (10); climate change and variability (6); and across all articles for wild plant populations, weeds, and wild relatives (3). Regarding host plant species, the largest number of core articles referred to pathogens found in the fruits, berries, and nuts host category (27 named species, 40 articles), followed by other (18, 24), cereals (13, 19), forest tree species (11, 25), roots and tubers (8, 9), vegetable (7, 8), pulse (3, 1), and ornamentals (1, 1) (Supplementary Material S6).

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 perennials, with different production systems from seed or vegetative propagation to the harvested crop. Core articles relevant in this context included multiple pathogens of individual crops (32 articles), tree/forest systems (8), wild plants (7), crop-associated weeds (1), and aquaculture (1) (Supplementary Material S2). Because of the diversity of studies where multiple pathogens were concerned, there was no allocation of article type.

Of the 63 hosts covered in the 179 core articles, only pathogens of pine (9 articles), maize (8), potato (8), grapevine (8), rice (7), pepper (6), citrus (6), wheat (5), and cucurbits (5), where hosts have been grouped to reflect common pathogens, were reported in at least five articles (Fig. 1). Geographically, the core articles reported

studies in 54 countries, with eight articles relevant at the regional or intercontinental level. Most articles described studies done in the United States (30 articles) and China (29). At the continental scale (Fig. 3A), the comparable numbers were for Asia (60 articles), Europe (51), North America (35), Africa (21), Australasia (8), and South America (3).

Accounting for articles that reported multiple pathogen species-location pairs, as well as articles that took a worldwide focus and so were relevant to every continent, allowed us to project a graphical summary of the results onto a global map showing species counts per taxonomic group and continent (Fig. 4). The largest number of unique location and species combination records was reported from Asia (42), followed by Europe (33), North America (21), and Africa (18). Records from Australasia, from South Africa, and with global remit accounted for 7, 3, and 3 unique reports, respectively.

The dominant types of articles were related to detection, discrimination, and analysis (32 articles, 36 unique species and location pairs); emergence of new pathogens, strains, and vectors (25, 31); surveillance, including growers and citizen science (27, 24); and disease management, including varietal resistance (23, 21).

Combining the results of Stage 1 and Stage 2, and so considering all results returned by our literature review, resulted in identification of 25 categories for named species or species complexes with five or more articles (Table 1). These included seven fungal pathogens (or complexes): *Raffaelea lauricola*, *Fusarium oxysporum* formae speciales, *Puccinia graminis* f. sp. *tritici*, *Hemileia vastatrix*, *Magnaporthe oryzae*, *Fusarium* spp. complexes, and

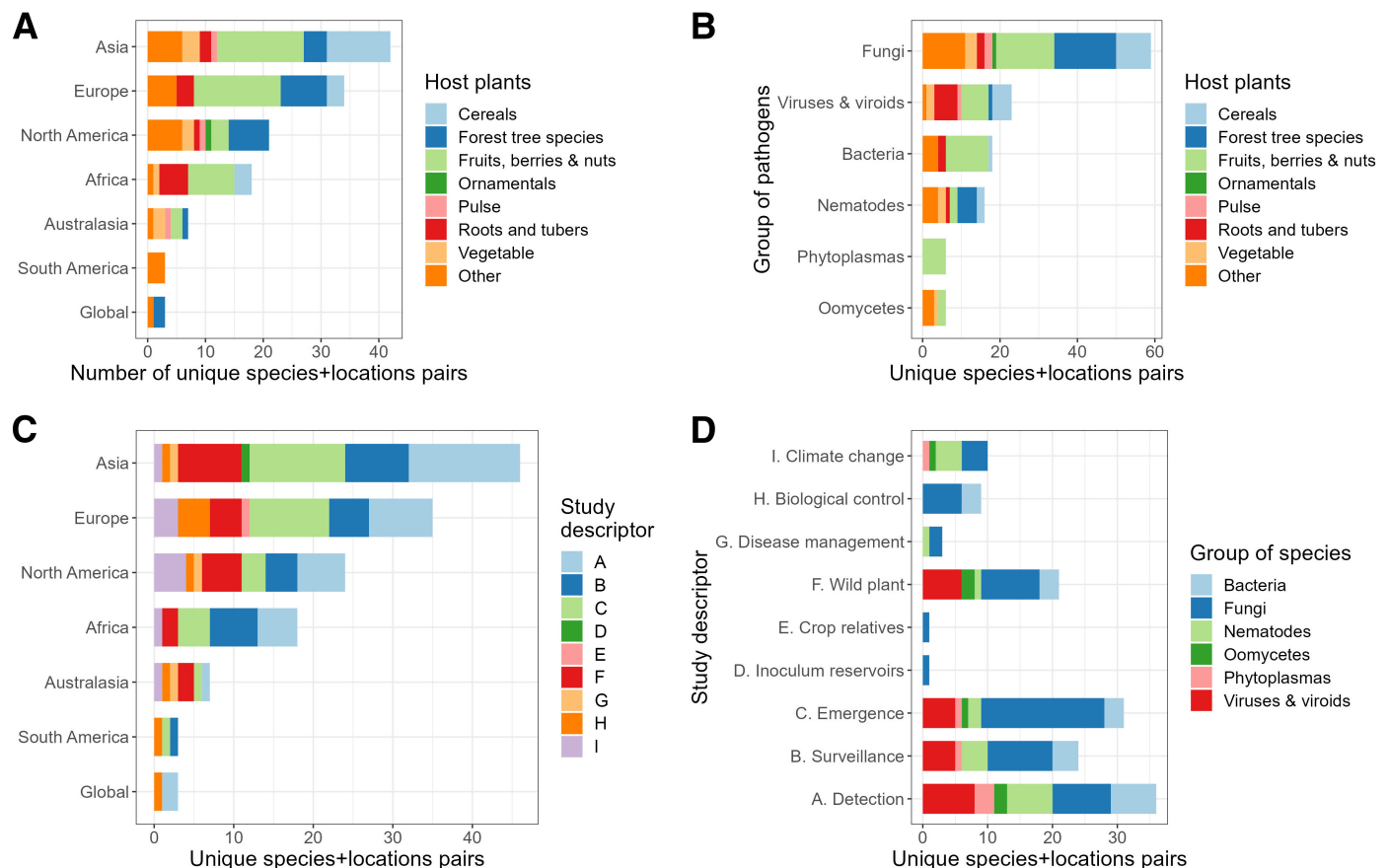


FIGURE 3

Categorization of core articles on single named species identified in Stage 1 of the review of published articles on disease outbreaks and epidemics. Locations refer to geographic areas, most commonly a country. **A**, Number of unique pathogen and locations species per host plant category per continent where retrieved pathogen species were observed. **B**, Number of unique pathogen species and locations pairs per group of pathogens and host plants on which they were observed. **C**, Number of unique pathogen species and locations pairs per continent and study descriptor. **D**, Number of reported unique pathogen species and locations pairs grouped by study descriptors and pathogen group.

Neofusicoccum mediterraneum; three oomycetes (or complexes): *Phytophthora ramorum*, *Phytophthora* spp. complexes, and *Plasmopara viticola*; six bacterial pathogens: *Candidatus Liberibacter asiaticus* (and vectors), *Xylella fastidiosa* (and vectors), *Erwinia amylovora*, *Pectobacterium* spp., *Pseudomonas syringae* pvs., and *Xanthomonas oryzae* pv. *oryzae*; two phytoplasmas: ‘*Ca. Phytoplasma solani*’ and ‘*Ca. Phytoplasma vitis*’ (flavescence dorée); five viral pathogens (and vectors): cucumber mosaic virus, potato virus Y, cassava mosaic viruses, grapevine leaf roll-associated virus, and cucumber green mottle virus; and the nematodes *Bursaphelenchus xylophilus* and *Meloidogyne* spp. complexes.

Where articles were grouped into multiple pathogen categories of crops or cropping systems, combining the Stage 1 and Stage 2 searches resulted in seven categories with three or more articles (Table 1). The host categories identified were pepper (*Capsicum*), grapevine, cucurbits, eucalypts, spruce, and ribwort plantain (*Plantago lanceolata*). Where there were at least three core articles in a category, brief summaries of the main findings and study periods of these articles are tabulated in Electronic Supplementary Material S3 for the seven highlighted pathogen species categories and Supplementary Material S4 for the four highlighted multiple pathogen categories. The supplementary articles for each of these categories are listed in Supplementary Materials S3 and S4 without further commentary.

Approach B: First reports of plant pathogens

The 751 CABI DDB records manually reviewed covered 62 plant pathogens. This included three *Ralstonia* species and the *Ralstonia solanacearum* species complex. A decision was made to retain the records for the species complex and to exclude records from the individual species to avoid duplication in the results. After these records and other duplicate records were removed from the dataset, 582 records remained for manual review (59 pathogens). After manual review, a list of 58 records (29 pathogens) was considered as

our final list of confirmed first reports of a pathogen in a location or on a novel host plant (Table 2; Fig. 5).

This dataset included six pathogens that were manually added, as they had been identified in Approach A through the Stage 1 search of peer-reviewed journal articles and had at least one confirmed first report in the CABI DDB. These were *Meloidogyne* species complexes, *Erwinia amylovora*, *Fusarium culmorum*, *Neofusicoccum mediterraneum*, *Pseudomonas viridiflava* (included in the broader category of *Pseudomonas syringae* pathovars), and *Raffaelea lauricola*. A causal agent of grapevine yellows, *Phytoplasma vitis*, was identified in both the CABI DDB and the Stage 1 search of peer-reviewed journal articles.

Comparing the results obtained using Approaches A and B

Combining the focal results obtained from the literature review (Approach A, Stages 1 and 2) and the analysis of the CABI DDB (Approach B), the vast bulk of papers/records corresponded to reports of pathogens in Asia, Europe, and North America (Fig. 6). There was also a preponderance of fungal pathogens, although, as expected, relatively large numbers of viruses, bacteria, and nematodes were also identified.

Only ‘*Ca. Phytoplasma vitis*’ was present in both sets of results obtained with the two approaches. Six articles were identified for this pathogen in peer-reviewed journal articles (Stage 1 + Stage 2), and the criteria for manual review of the CABI DDB results were met, with seven records flagged by the automated step as potential first reports new in 2022. Of these, two were confirmed to be first reports after manual review.

Most of the pathogens indicated with an asterisk in Table 2 did not meet the threshold for manual checking of CABI DDB results (<5 new 2022 records) and so would not have appeared in the CABI results by default. However, as described above, because they were identified in peer-reviewed journal articles in Approach A, the records in the CABI DDB for these pathogens were also manually checked. Six of these pathogens had confirmed first reports in 2022:

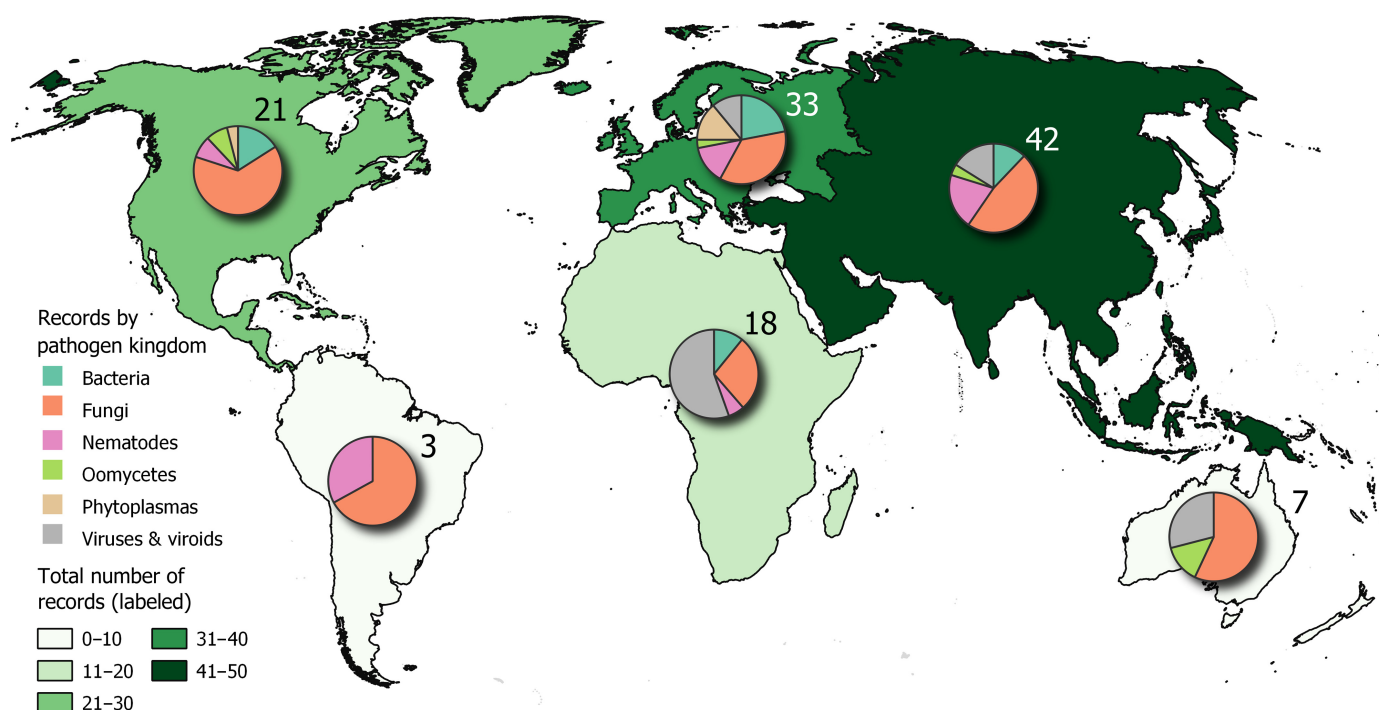


FIGURE 4

Map of literature review records summarized by continent. Counts represent unique country-pathogen reports. Pie charts show a breakdown of pathogen types on each continent. There were three records with global coverage, which are not represented on the map.

TABLE 1
Combined results with five or more articles following Stages 1 and 2 from the review of published articles^a

Category	Core articles (Stage 1)	Number of articles (Stage 1 + Stage 2)	Pathogen taxon
Named species or species complex			
<i>Xylella fastidiosa</i> and vectors	8	23	Bacterium
<i>Bursaphelenchus xylophilus</i> and vectors	9	17	Nematode
<i>Meloidogyne</i> species complexes ^b	5	14	Nematode
' <i>Candidatus Liberibacter asiaticus</i> ' and vectors	7	13	Bacterium
<i>Raffaelea lauricola</i>	6	12	Fungus
<i>Fusarium oxysporum</i> formae specialis ^c	3	10	Fungus
<i>Puccinia graminis</i> f. sp. <i>tritici</i>	3	9	Fungus
<i>Hemileia vastatrix</i>	2	8	Fungus
' <i>Candidatus Phytoplasma solani</i> ' and vectors	2	8	Phytoplasma
Potato virus Y and vectors	1	8	Virus
Cassava mosaic viruses and vectors ^d	1	8	Virus
<i>Pectobacterium</i> species ^e	2	7	Bacterium
<i>Phytophthora ramorum</i>	1	7	Oomycete
<i>Pseudomonas syringae</i> pathovars ^f	1	7	Bacterium
' <i>Candidatus Phytoplasma vitis</i> ' flavescence dorée	2	6	Phytoplasma
<i>Plasmopara viticola</i>	2	6	Oomycete
<i>Magnaporthe oryzae</i>	1	6	Fungus
<i>Phytophthora</i> species complexes ^g	1	6	Oomycete
Grapevine leaf roll-associated virus	1	6	Virus
<i>Erwinia amylovora</i>	2	5	Bacterium
<i>Fusarium</i> spp. complexes ^h	2	5	Fungus
Cucumber mosaic virus and vectors	2	5	Virus
Cucumber green mottle virus	1	5	Virus
<i>Neofusicoccum mediterraneum</i>	1	5	Fungus
<i>Xanthomonas oryzae</i> pv. <i>oryzae</i>	1	5	Bacterium
Multiple pathogens			
Aquaculture	Eelgrass (<i>Zostera marina</i>)	5	Multiple
Crops	Grapevine	3	11
	Pepper (<i>Capsicum</i>)	3	6
	Cucurbits	2	5
Forest trees	<i>Eucalyptus</i> spp.	3	5
	<i>Picea</i> spp.	1	5
Wild plants	<i>Plantago lanceolata</i>	3	5

^a Core articles (Stage 1) are cited in Supplementary Material S1 and S2. Categories (named species/species complex or multiple pathogen) with at least three core articles are in bold.

^b *M. incognita*, *javanica*, *enterolobii*, *arenaria*, *hapla*, *ethiopia*, *luci*, *haplanaria*, *inornata*, *chitwoodi*, *fallax*.

^c *F. oxysporum* f. spp. *fragariae*, *cubense*, *cyclaminis*, *vasinfectum*, *albedinis*.

^d *Bemisia 'tabaci'* cryptic species and *B. afer*; Sri Lankan cassava mosaic virus, unnamed begomovirus species causing cassava mosaic disease.

^e *P. parmententieri*, *versatile*, *aquaticum*, *brasiliense*, *punjabense*, *caratovorum*, *atrosepticum*, *fontis*, *quasiaquaticum*, *polonicum*, *aroidiarum*, *betavascularum*, *cacticida*, *odoriforum*, *peruviense*, *wasabiae* (excludes *Dickeya* spp.).

^f pvs. *syringae*, *morsprunorum*, *tomato*, *savastanoi*; also *P. actinidiae*, *P. viridiflava* (*P. syringae* species complex).

^g *P. cambivora*, *chlamydospora*, *plurivora*, *pini*, *cinnamomi*, *cambivora*, *irrigata*, *gonapodyides*, *cactorum*, *pseudosyringae*, *hydropathica*, *stricta*, *xstagnum*, *caryae*, *intercalaris*, '*bitahaiensis*', *heveae*, *citrophthora*, *macilentosa*, *cryptogea*, *riparia*, *heveae*, *virginiana*, *multibullata*, *P. × vanyensis*.

^h *F. citrullicola*, *melonis*, *oxysporum*, *solani*, *culmorum*, *bubalinum*, *hainanense*, *sulawesiense*, *tanahbumbuense*, *andiyazi*, *fujikuroi*, *proliferatum*, *pseudocincinatum*, *sacchari*, *grosmichelii*, *redolans*, *avenaceum*, *tricinctum*, *culmorum*, *equiseti*, *ipomoea*, *compactum*, *sporotrichioides*, *graminearum*, *citri*, *asiaticum*, *verticilliodes*, *acuminatum*, *glycines*, *temperatum*, *ameniacum*, *flagelliforme*, *annulatum*.

(i) *Meloidogyne chitwoodi*, *M. enterolobii*, and *M. javanica* (collectively *Meloidogyne* species complexes); (ii) *Erwinia amylovora*; (iii) *Fusarium culmorum* (included in *Fusarium* spp. complexes); (iv) *Neofusicoccum mediterraneum*; (v) *Pseudomonas viridiflava*; and (vi) *Raffaelea lauricola*.

Which pathogens are actively spreading and/or emerging?

In the previous study (Jeger et al. 2023), we used the criteria of at least two confirmed first reports in 2021, representing 25% or more of all records for that pathogen in the CABI DDB. If this was applied for 2022, then our analysis would identify no pathogens as

actively spreading/emerging once we discount the artifact of recent taxonomic changes for the *Ralstonia solanacearum* species complex. We therefore relaxed the second criterion and considered all pathogens for which the confirmed first reports in 2022 represented more than 10% of all records in the CABI DDB. However, we retained the restriction to pathogens with at least two first reports. This led to three pathogens being identified as showing a signature of active/emerging spread: grapevine red globe virus, sweet potato chlorotic stunt virus, and ‘*Ca. Phytoplasma vitis*’. In interpreting these results, it is important to remember that there might be a disconnect between the year in which a pathogen is first reported and

TABLE 2
Records from the CABI Distribution Database (CABI DDB) indicating the number of first reports of plant pathogens published in 2022^a

Pathogen species or complex	Number of DDB records			Percentage of first reports from 2022	Emerging and/or spreading ^b	Pathogen taxon
	Pre-2022 records	New automated 2022 records	First reports in 2022 after manual review			
<i>Meloidogyne</i> species complexes*	307	8	5	2%		Nematode
<i>Pantoea ananatis</i>	52	9	5	9%		Bacterium
Grapevine red globe virus	13	10	4	24%	x	Virus
<i>Thekopsora minima</i>	49	10	4	8%		Fungus
<i>Globodera rostochiensis</i>	106	5	3	3%		Nematode
<i>Phyllachora maydis</i>	30	9	3	9%		Fungus
Sweet potato chlorotic stunt virus	21	6	3	13%	x	Virus
Citrus tristeza virus	169	5	2	1%		Virus
<i>Colletotrichum fructicola</i>	26	29	2	7%		Fungus
<i>Gymnosporangium yamadae</i>	32	6	2	6%		Fungus
‘ <i>Candidatus Phytoplasma vitis</i> ’*	16	7	2	11%	x	Phytoplasma
<i>Phytophthora vexans</i>	107	10	2	2%		Oomycete
<i>Ralstonia solanacearum</i> species complex ^c	0	239	2	100%		Bacterium
Tomato brown rugose fruit virus	54	8	2	4%		Virus
Tomato leaf curl New Delhi virus	39	11	2	5%		Virus
Tomato mottle mosaic virus	20	8	2	9%		Virus
Apple stem grooving virus	93	9	1	1%		Virus
<i>Elsinoë fawcettii</i>	129	8	1	1%		Fungus
<i>Erwinia amylovora</i> *	119	1	1	1%		Bacterium
<i>Fusarium culmorum</i> *	116	2	1	1%		Fungus
<i>Guignardia citricarpa</i>	43	7	1	2%		Fungus
Impatiens necrotic spot virus	81	5	1	1%		Virus
<i>Mycosphaerella dearnessii</i>	79	5	1	1%		Fungus
<i>Neofusicoccum mediterraneum</i> *	7	1	1	13%		Fungus
<i>Phytophthora frigida</i>	5	5	1	17%		Oomycete
<i>Pseudomonas viridiflava</i> *	66	1	1	1%		Bacterium
<i>Raffaelea lauricola</i> *	16	1	1	6%		Fungus
Tomato fruit blotch virus	0	6	1	100%		Virus
<i>Trichoderma afroharzianum</i>	0	18	1	100%		Fungus

^a The records for 62 plant pathogens were manually reviewed. A total of 29 pathogens had confirmed first reports in a new location or on a new host. Pathogens with an asterisk (*) were included due to being identified in the literature review and did not meet the threshold of five new 2022 records required for manual review, except ‘*Ca. Phytoplasma vitis*’, which was found in both methods. The “Percentage of first reports from 2022” column was calculated by taking “First reports in 2022 after manual review” as a percentage of “Pre-2022 records” + “First reports in 2022 after manual review.”

^b Pathogens were marked as “Emerging and/or spreading” if they had at least two first reports in 2022 and if records from 2022 made up at least 10% of all records in the CABI DDB.

^c The lack of records for the *Ralstonia solanacearum* species complex before 2022 and the high number of records added to the CABI DDB in 2022 is an artifact of recent taxonomic changes for this pathogen and a subsequent change to how it is stored in the CABI DDB. It is not therefore considered an emerging or particularly actively spreading pathogen based on these data.

its time of first arrival/establishment in a location. We return to this idea in the Discussion.

New reports of grapevine red globe virus came from Japan (Yamamoto et al. 2022), Portugal (Candresse et al. 2023), Slovenia (Miljanić et al. 2022), and the United Kingdom (Dixon et al. 2022). Although infected plants very often remain asymptomatic (Martelli 2014), at least some of the first reports were the result of samples being sent to national diagnostic laboratories after detection of nonspecific symptoms (Dixon et al. 2022). Despite, in our view, the rising number of reports probably being more reflective of an increasing capacity for high-throughput sequencing rather than any important consequences of this virus, the potential for economic impacts when grapevines are coinfecting with other viruses cannot yet be discounted (Jarugula et al. 2021).

Sweet potato chlorotic stunt virus was newly reported from Belgium (EPPO 2022c), Hungary (EPPO 2022d), and the Netherlands (EPPO 2022e), with planting material being the suspected entry pathway in all three cases (whiteflies are the vector in the field). Symptoms of sweet potato chlorotic stunt virus are variable, and infection is very often asymptomatic (Gibson and Kreuze 2015). However, the virus is worrying because coinfection with sweet potato feathery mottle virus leads to sweet potato virus disease. This occurs in many sweet potato-producing areas worldwide and is well known to be extremely economically damaging, with yield losses of up to 100% reported (Qin et al. 2014). Concern over sweet potato virus disease has led to sweet potato chlorotic stunt virus being a quarantine pest in Europe (Kiemo et al. 2022), and although the status of the attempted eradication in Belgium is unknown to us, we note that plant protection organizations have recently reported successful eradication in the Netherlands (EPPO 2023) following the initial report we identify here.

'*Ca. Phytoplasma vitis*' was newly reported in Czechia and Slovakia (EPPO 2022a, b). This phytoplasma—cause of flavescentia dorée—is vectored by the leaf hopper *Scaphoideus titanus*. The pathogen has been present in France since the beginning of the twen-

tieth century, having more recently spread through wine-producing European regions, including Austria, Croatia, Hungary, Portugal, and Switzerland (Oliveira et al. 2019), following establishment and spread of the vector after an accidental introduction thought to be from North America (Adrakey et al. 2022). Impacts of the pathogen on grapevine include color aberrations, which vary with grape cultivar on foliage; reduced fruit setting, with brown and shriveled bunches; and berry drop. No cultivars are resistant to flavescentia dorée, and the recommended control involves removal of infected vines (i.e., roguing) augmented with intensive vector control (EFSA Panel on Plant Health et al. 2016). This makes reports in new regions worrying, particularly because the newly infected countries extend the northern range of this phytoplasma disease, and so the most recent spread may be due to an extended range of the vector. However, because most wine-cultivating regions in Europe with suitable climate for the vector are already affected, we suspect more significant impacts would only be realized if the pathogen were to begin to spread outside the EU.

Discussion

We have presented a synoptic review of plant disease epidemics and outbreaks in 2022. This is a continuation of our previous study (Jeger et al. 2023), in which we took a similar approach, focusing on 2021 publications. Following the methodology introduced last year, retrieval of information for this review employed two approaches: (A) a search of the peer-reviewed scientific literature for accounts of disease epidemics and major outbreaks published in 2022 and (B) first reports of plant pathogens from new geographic locations or on new host plants made in 2022 and added to the CABI DDB. Analysis of results from journal articles was made according to country, crop and/or host species, and pathogen taxon grouping, as well as the type and purpose of the published study. In interpreting the results from the CABI DDB, we focused on identifying pathogens with multiple first reports in new locations or on new hosts, as well as

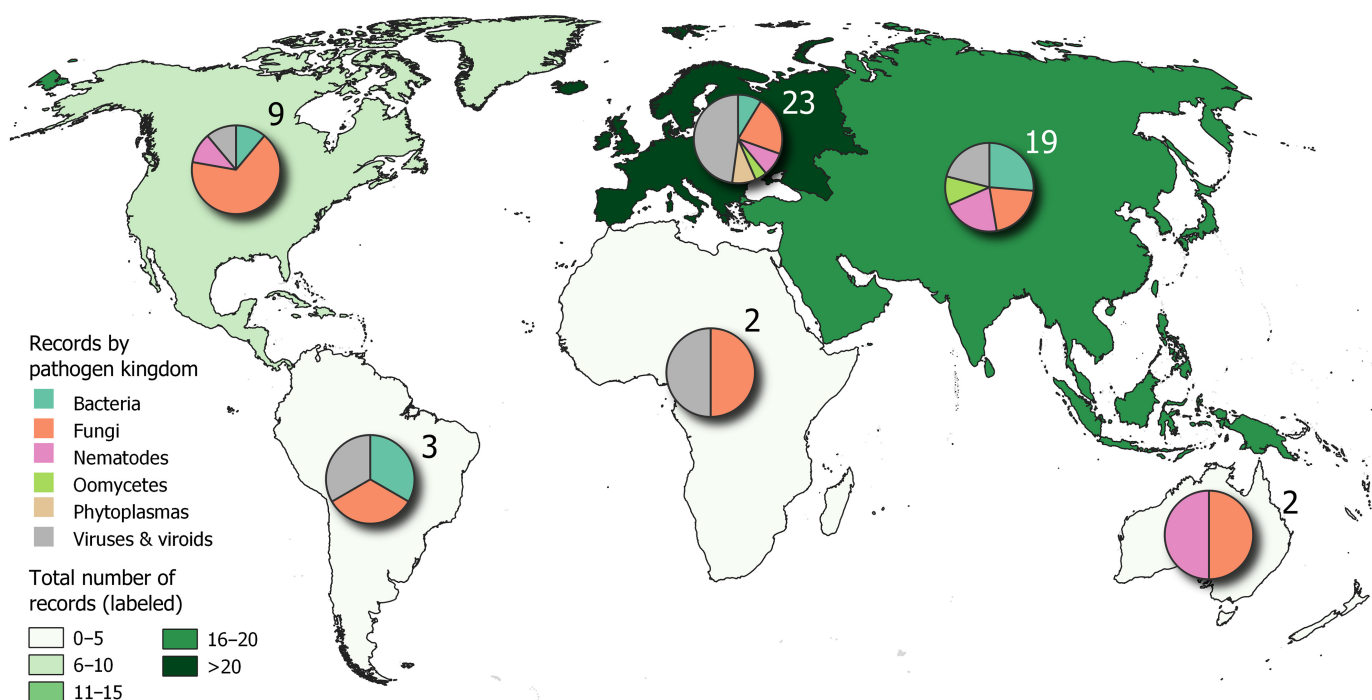


FIGURE 5

Map of CABI Distribution Database records following manual review summarized by continent. Counts represent unique geolocation (countries and sub-national areas)-pathogen reports. Pie charts show a breakdown of pathogen types on each continent.

attempting to detect pathogens actively spreading or emerging in new locations.

To what extent are results consistent between the two sources of information?

Last year's exercise (Jeger et al. 2023) revealed little overlap between the sets of pathogens identified from the literature review and the CABI DDB, with only six pathogens—*Ca. Liberibacter asiaticus*, citrus tristeza virus, *C. siamense*, *F. oxysporum* f. sp. *ubense* TR4, *Globodera rostochiensis*, and tomato brown rugose fruit virus—returned by both approaches last year. This year, as we hypothesized in advance based on our experience from last year, there was again little overlap. Indeed, the disconnect was even more stark this year, with only *Phytoplasma vitis*—the phytoplasma that causes flavescence dorée on grapevine—appearing in the results of both approaches. As we identified last year, this lack of concordance is because first reports of a pathogen species will tend to precede epidemics or major outbreaks that might be reported in the scientific literature (see below).

To what extent are results consistent with last year's exercise?

An important comparison that is possible for the first time this year is assessing the degree of consistency from year to year in the results returned (by both approaches). As in Jeger et al. (2023), most studies returned by this year's literature review were retrieved from North America, Asia, and Europe, followed by Africa, South America, Australia, and, finally, Central America (Fig. 3). The top three pathogen taxa were also the same both this year and last, with fungal pathogens being the causal agent of most records, followed by viruses and bacteria. In contrast to last year, however, more nematodes and fewer oomycetes were reported (Fig. 3). In the combined results from the two approaches last year, despite fungal pathogens dominating overall, they only constituted the bulk of all records in North America and Australia. However, this year, we found that

fungal pathogens now dominate in almost all continents. The only exception to this is Africa, in which viral pathogens are the cause of most records (Fig. 6). We note, however, that trends are partially confounded by differences in the geographic distribution of records retrieved from the literature review (Fig. 4) and the CABI DDB (Fig. 5).

For the first reports from the CABI DDB, there is little overlap at the species level, although we find general similarities between the results from 2021 and 2022 in terms of the geographic distribution and groupings of pathogens retrieved. Only four pathogens were identified in both years: *Globodera rostochiensis*, citrus tristeza virus, *Ralstonia solanacearum* species complex (referred to as *Ralstonia pseudosolanacearum* in the 2023 publication), and tomato brown rugose fruit virus. When we filtered the CABI DDB records to identify those pathogens that could be considered as actively spreading/emerging, we retrieved three pathogen species (cf. four last year), even though this year, we used slightly more relaxed criteria (Table 2). Strikingly, there was no overlap between species assessed to be actively spreading in this year's study and last year's.

Relationship between first reports of pathogens and outbreak reports in the scientific literature

The lack of correspondence in results between our two approaches raises a series of questions, potentially important for future work aimed at identifying trends in the spread, impact, and mitigation of emerging plant diseases.

1. What are typical time lags between first reports in new locations and major disease outbreaks caused by that pathogen? Are these time lags reflective of failures in making risk management decisions?
2. What proportion of first reports at a given location are followed by major disease outbreaks? As a corollary, what proportion of major disease outbreaks were preceded by first reports?

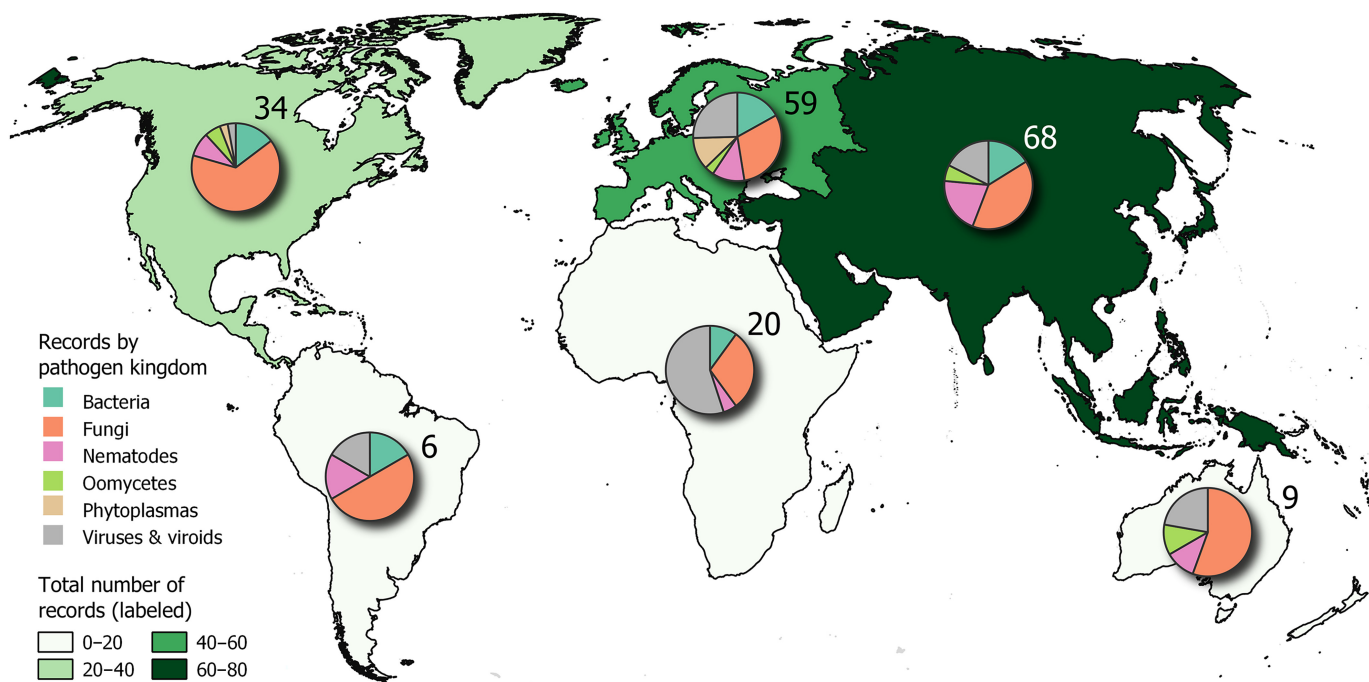


FIGURE 6

Map showing combined results from the literature review and CABI Distribution Database (DDB). Counts represent unique country-pathogen reports (DDB records were summarized to country level from the more granular geolocations before combining). Pie charts show a breakdown of pathogen types on each continent.

- How long does it take for plant health regulation to be put in place following first reports and risk assessments based on such reports? Can plant health regulation claim to be responsible for prevention of major disease outbreaks after a first report of a pathogen?

These questions are much easier to pose than to answer.

In terms of time lags between first reports and major outbreaks, almost by definition, a long period is necessary for comparisons to be made. The basis for first reports being made is often obscure and depends on whether a pathogen was identified as part of an official survey or instead detected serendipitously based on unstructured observations. In many cases, what is found may simply be a consequence of a survey made for other purposes. This is particularly the case for pathogens that cause minor symptoms or that cause non-economically damaging symptoms (particularly on non-crop hosts). In such cases, there might in fact be a significant delay before any first report, and it is entirely possible that a particular pathogen might have been endemic in a given location for some time before this is recognized. Whether or not a major disease outbreak is reported in the scientific literature depends on the journal policy on types of papers to be considered, whether the crop is major or minor, and whether the pathogen is of current scientific interest in the plant pathology community. For these reasons, our approach to the synoptic review attempted to avoid as much bias as possible. We avoided the use of specific economically important host plant species in the search terms, and our results do cover a very wide range of crops and other plant hosts (Figs. 2 and 3). However, of course, there is still the possibility of bias and underrepresentation of diseases affecting less commercialized crops, or pathogens of wild plants, simply because they are less often studied or surveyed. However, this is somewhat unavoidable, and it is important to note that the synoptic approach adopted here avoids the more significant biases toward only well-known or “important” pathogens that might affect studies using expert-based assessment methods (Savary et al. 2019).

Other measures can be considered as possible proxies for both first reports and published accounts of major epidemics, at least in some regions of the world. Information concerning the year any EU emergency measures were put in place for a given pest/pathogen species is in the public domain (European Commission 2023a) and can be compared with country-specific data on the year that any pathogen was first reported (e.g., by the EPPO reporting service; available online at <https://gd.eppo.int/reporting/>). Making this comparison for a few select pathogens showed that the lag can sometimes be an extended period (e.g., 4 to 6 years in the case of *Meloidogyne graminicola*, potato spindle tuber viroid, and *Gibberella circinata*) or relatively short (e.g., 1 year or less in the case of *Phytophthora ramorum*, *Pseudomonas syringae* pv. *actinidiae*, tomato brown rugose fruit virus, and *Xylella fastidiosa*). It should also be noted that EU emergency measures have occasionally been put in place prior to any new report being made (e.g., for the insect pest *Spodoptera frugiperda*) (European Commission 2023b). For certain pathogens, EU emergency measures were introduced based simply on a pest alert and in the absence of any first report in the region: An example is rose rosette virus (syn. *Emaravirus rosae*) in 2019 (and revised in 2022; see European Commission 2022).

Of course, first reports result from the introduction of pathogens into new locations, although there can often be uncertainty over how long a pathogen has been present before it is reported (Lovell-Read et al. 2023; Mastin et al. 2022; Soubeyrand et al. 2018). Introduction of novel and/or nonindigenous pathogens continues to be associated with increased global trade in plants and plant parts (Brasier 2008; Liebhold et al. 2012; Sikes et al. 2018). However, aside from the idea that certain routes will be important, there has been an unfortunate paucity of concrete information and data on pathogen introductions, whether introductions are validated and reported in a timely man-

ner, whether major disease outbreaks follow, and what management measures have been put in place in mitigation.

Pleasingly, a recent study (Rosace et al. 2023) has begun to rectify this and has compiled a comprehensive dataset on 278 plant pest species, including many pathogens, introduced into the EU over the period of 1999 to 2019. As well as the spatial location of each introduction—defined according to the International Standards for Phytosanitary Measures 5 Glossary of Phytosanitary Terms (FAO 2023) as “the entry of a pest resulting in its establishment”—potential pathways of entry that may have led to each introduction are collated. This dataset is very valuable because it provides a base for further analysis to understand the factors associated with new outbreaks and to help to determine priority areas in which the likelihood of pest entry is higher. The information can also feed into future “pathway models” that aim to provide quantitative estimates of introduction risks (reviewed in Douma et al. 2016). The Rosace et al. (2023) study therefore provides a very valuable resource for those working on pathogen introductions, particularly because the authors were ambitious enough to tackle the very large spatial scale of the whole of the EU over a 20-year period.

Are some first reports more “meaningful” than others?

Whereas some first reports may be the precursor of future outbreaks and epidemics, others may be less informative. We identified five first reports of *Pantoea ananatis* (Cui et al. 2023; Lao et al. 2023; Resende et al. 2022; Reshma et al. 2023; Yu et al. 2022), but all of these describe cases in which the pathogen was already known to be in the country in question, and although it affected a new host in that location, in four cases, it was known to be a pathogen on that crop elsewhere. In only one case is *P. ananatis* recorded on a new host (Lao et al. 2023) and another being new to the area of the first report (Reshma et al. 2023). However, these observations do not diminish the fact that the pathogen is affecting hosts in new ways (Yu et al. 2022).

Other first reports might not lead to significant problems because the pathogen will almost certainly fail to establish. An example is *Elsinoë fawcettii*, cause of citrus scab, in the Azores (EPPO 2022k). Despite previous records of the disease in southern Europe (Ciccarone 1957), it has never become established despite favorable climatic conditions in some locations, although future climate change might render such thinking naive (EFSA Panel on Plant Health (PLH) et al. 2017). In other cases, pathogens are very likely to be eradicated after the first report following prompt action by plant health authorities. *Ralstonia pseudosolanacearum* has been reported in Italy (EPPO 2022f), and it is now subject to active eradication measures (EPPO 2022f).

We note that the artificial inoculation methods used in some papers may have inadvertently bypassed natural host defenses by wounding or infiltration of inoculum concentrations well outside the range that would be encountered in natural environments. Indeed, deliberately avoiding the host natural defenses is the intention in some inoculation methods (Zhang et al. 2018). It is possible that this rendered otherwise benign microorganisms pathogenic in some of the reports.

As we noted last year, the ever-increasing availability—and ever-decreasing cost—of molecular techniques continues to affect our results. High-throughput sequencing has led to new detections of grapevine red globe virus in Japan (Yamamoto et al. 2022), Portugal (Candresse et al. 2023), Slovenia (Miljanić et al. 2022), and the United Kingdom (Dixon et al. 2022). It would be no surprise if “new” reports of this virus continue, albeit without this signifying any active pathogen spread and despite the lack of specific symptoms on grapevine (Dixon et al. 2022). Indeed, in general, our results might be biased toward pathogens of high-value crops because these are most likely to be regularly surveyed by trained agronomists with skills to pick up deviations from the norm.

As another example of molecular techniques leading to new findings, citrus tristeza virus was reported in Bangladesh for the first time in 2022 (Akhter et al. 2022). We note that Bangladesh is surrounded by countries in which citrus tristeza virus is endemic and so from which aphids (the arthropod vector of citrus tristeza) may only require a short flight to bring the pathogen into the country. Because transmission is semi-persistent, with aphids potentially remaining viruliferous for up to 24 h (Raccach et al. 1976), natural spread from neighboring countries is at least somewhat plausible. It is perhaps even possible that the virus has been present in Bangladesh for some time and has only recently been detected, particularly because the report was made from near the geographic center of Bangladesh. Similarly, various root-attacking oomycetes share similar morphology and are difficult to distinguish by morphology alone. Therefore, although this year's reports of *Phytophthora frigida* on *Cassia fistula* (the golden shower tree) (Das et al. 2022) and *P. niederhauserii/vexans* on almond (Beluzán et al. 2022) might indeed be new combinations of host and pathogen, they might instead simply reflect our increasing ability to isolate and identify oomycete root pathogens at the species level using DNA.

Were there any sources of potential bias caused by our study protocol?

Another potential source of bias, acknowledged last year (Jeger et al. 2023), is that our literature review focused exclusively on studies retrieved from Web of Science. In turn, this restricts our results to literature written in English. Although at least 95% of scholarly articles in scientific fields are now in English (Ammon 2012; Hamel 2007; Liu 2017), and a similar proportion of systematic reviews do not report results in any other language (Jackson and Kuriyama 2019), the potential for bias might be significant in a worldwide study of the type done here. We therefore welcome recent suggestions around how increased use of machine translation tools can make science more globally representative (Steigerwald et al. 2022).

In the initial stages of this year's study, we did attempt to explore available non-English language databases such as China National Knowledge Infrastructure (<https://oversea.cnki.net/index/>) and J-Stage (Japan Science and Technology Information Aggregator, Electronic) (<https://www.jstage.jst.go.jp/>). Although in both cases we were able to retrieve records absent from English-language sources from these foreign language databases, because we lack both expertise and resources to replicate keyword searches across multiple languages, we were not able to systematically investigate this further. It is important to recognize this limitation to our results and that the comprehensiveness of our reported trends might be affected.

A final potential source of bias is caused by the threshold used in our analysis of the CABI DDB results. A total of 1,123 distribution records (potential first reports) were identified by our automated analysis, but unfortunately, it was not possible to manually review all these records. A threshold of five or more records was therefore chosen to maximize the size of the dataset within the constraints on resources available for this study. This initial set of 751 distribution records was also augmented with a small number of additional records relating to pathogens identified in the literature review. Nevertheless, it is possible that actively spreading pathogens with a small number of new reports were filtered out by this aspect of our methodology.

Were any of our results surprising?

That some pathogens were found only during regular/routine surveys was surprising because these pathogens are well known to cause characteristic symptoms as well as significant damage. For example, *Erwinia amylovora* causes fire blight on apple and pear, with extreme symptoms, involving necrotic leaves that do not detach and so remain visible for an extended period, identifiable by

anyone with any training in plant pathology. However, this pathogen was only detected in Azerbaijan as part of a general survey (EPPO 2022i). Similarly, five of the eight reports of nematodes were discovered as a "side effect" of more general surveillance, despite very characteristic and striking symptoms (galls in the case of *Meloidogyne* or cysts in the case of *Globodera*). *Ralstonia solanacearum* (the cause of bacterial wilt on numerous *Solanaceous* species) was detected in water samples in Hungary from three geographically distinct areas (EPPO 2022i). However, the pathogen has not been reported as causing disease anywhere in that country. This would indicate that either the crop symptoms (rapid wilt initially without yellowing) have not been recognized as a disease or there is a considerable inoculum source from an alternative, unidentified source.

Where and why are pathogens moving?

Spread of certain pathogens continued to be rather predictable, for example, three further first reports of *Phyllachora maydis* (tar spot of maize) in different states of the United States, where it has been spreading rapidly since its first introduction in 2016 (Ruhl et al. 2016). There are also examples of short-distance spread across national borders, allowing very plausible transmission pathways to immediately be inferred. An example is again *E. amylovora*, which was reported in Azerbaijan near the border with Georgia, a country in which the pathogen is known to be present. A second example is *Lecanosticta acicula* (*Mycosphaerella dearnessii*), for which the new record from Ukraine appears to simply show the continued spread of this pathogen across Europe, despite continued phytosanitary regulations (Tubby et al. 2023).

Other first reports might, perhaps, reflect recent changes in cropping practice. For example, the yellow potato cyst nematode, *Globodera rostochiensis*, was found for the first time in new areas of China (Jiang et al. 2022; Peng et al. 2023). The Chinese government has introduced various initiatives to encourage the cultivation of potato (Ware and Merino 2022), which may have led to more potato being planted with tighter crop rotations and, in turn, to greater densities of the yellow potato cyst nematode. Increased interest in potato as a crop may also have led to more extensive surveys, including the survey that led to these first reports. Similarly, Australia (Government of Western Australia 2022), Brazil (Araujo et al. 2022), and the United Kingdom (Latham et al. 2022) have all reported first discovery of *Pucciniastrum minimum* (*Thekopsora minima*) attacking blueberry. In each of these countries, there has been a huge increase in blueberry production (de Oliveira et al. 2022; FarmingUK 2019; Hasham 2022). It would therefore be reasonable to presume that commercial interests are driving increased crop monitoring and so, in turn, an increased likelihood of detection of the disease. Increased blueberry production, of course, also provides a plausible entry pathway (i.e., potentially contaminated germplasm). Other pathogens we have identified in our results are highly likely to have been spread anthropomorphically. Apple stem grooving virus and grapevine red globe virus have no known vectors (Barba et al. 2015; Beuve et al. 2015), nor are they mechanically transmitted. They therefore appear to be entirely reliant on spread by humans. Human transport is also implicated in the spread of *Meloidogyne chitwoodi* to Romania, where it was detected on seed potatoes imported from the Netherlands (EPPO 2022g). In other new reports involving nematodes (Jiang et al. 2022; Peng et al. 2023), there can be less certainty, but contaminated plant and planting material is probably the most likely pathway for any international movement of nematodes (Lambert and Bekal 2002).

As always, the movement of seed and seedborne disease remains particularly troubling, particularly when it affects a major crop. Tomato mottle mosaic virus was first characterized in 2009 in Mexico (Li et al. 2013) and has spread widely across the globe since then. We identified two first reports of tomato mottle mosaic virus, one from Mauritius affecting tomato plants (EPPO 2022h)

and another found in seeds imported from Asia, although the exact location was not determined (Fowkes et al. 2022). It seems likely the Mauritius outbreak was initiated from contaminated seed. We also note the continued spread of tomato brown rugose fruit virus (EPPO 2022j; Orfanidou et al. 2022), one of the pathogens we identified as actively spreading last year (Jeger et al. 2023). The unparalleled stability of tobamoviruses outside their host, where they can survive on inert surfaces (such as the seed coat) for a very long time, and in soils for years (Caruso et al. 2022), makes these viruses considerable threats to tomato production worldwide (Ishibashi et al. 2023).

Toward a worldwide protection and prediction system for plant diseases

The areas of vast monoculture created by agriculture is an artificial phenomenon that promotes pests and pathogens. The world's crops are under threat from within and without. There are pests and pathogens that are not present within a country/region but that would prosper on arrival, and there are those that are already present and become damaging when conditions are suitable. This review covers both these threats. A complementary distinction can be made between (i) protection of the world's plants from pathogens, mostly by the promotion of phytosanitary measures (e.g., quarantine regulation) to prevent the spread of exotic pathogens between, sometimes within, countries and regions where the pathogen had previously been absent and (ii) prediction of endemic pathogens in a country/region, which poses a regular or periodic threat to crop production. Again, we cover both areas here.

Invasive pathogens. The prevention of pest/pathogen movement is an international effort coordinated by the International Plant Protection Convention (<https://www.ippc.int>). The International Plant Protection Convention oversees a network of international partners, including 10 Regional Plant Protection Organizations that coordinate NPPOs. They have developed and promoted International Standards for Phytosanitary Measures as the main tool in protecting sustainable agriculture, the environment, forests, and biodiversity, as well as facilitating economic and trade development.

The International Plant Protection Convention promotes pest risk analysis (PRA), which involves evaluating the evidence to determine whether an organism has pest status and whether its movement should be regulated by means of phytosanitary measures. To assist in the production of a PRA, CABI has produced various online tools intended to enable horizon scanning (<https://www.cabi.org/horizonscanningtool>), a free open access tool that assists in determining which invasive species are a threat to any given country with additional data on pests for CABI Compendium subscribers) and a PRA Tool that guides the user through a formal PRA according to International Standards for Phytosanitary Measures 11 using the CABI held databases. CABI currently provides a gratis subscription to the CABI Compendium with a premium Horizon Scanning Tool and the PRA Tool to NPPOs of 117 lower- and middle-income countries.

These PRAs can be considered as early warning systems (Noar et al. 2021) and have been developed nationally and regionally for Europe and Mediterranean countries (<https://gd.eppo.int/reporting/>) and North America (<http://pestalerts.org/>), as well as globally (ProMED, <https://promedmail.org/>). Evidence is accumulating that there is potential for these systems to be predictive of high-risk pathogens, plant commodities, and regions of origin (Montgomery et al. 2023).

Endemic pathogens. Regional-scale early warning systems for endemic diseases have a long history (Isard et al. 2005; Zadoks 1981). More recent applications tend to follow funding sources by targeting low- to medium-income countries, including highly sophisticated systems linking epidemiological and dispersion modelling with new sources of field and citizen science data (Allen-Sader et al. 2019). Understanding risks over all potentially epidemic-causing plant pathogens is of clear interest to policy mak-

ers (Baker et al. 2014; Magarey et al. 2009). Global surveillance systems to do this have been mooted for plant pathogens (Carvajal-Yepes et al. 2019; Ristaino et al. 2021), but—precisely as for animal (Perez et al. 2011), zoonotic (Hassan et al. 2023), and human (Kamalrathne et al. 2023) diseases—concrete progress here involves significant challenges. Nevertheless, recent trends, including better availability of trade and other entry pathway data (Rosace et al. 2023), as well as new sources of remote sensing information (Oerke 2020), are promising. We also note that, following successes during the Covid pandemic (COVID-19 Genomics UK (COG-UK) Consortium 2020), genomic surveillance of human respiratory viruses is becoming ever more routine (Makoni 2023), and there are significant opportunities for similar advances in plant disease monitoring.

Conclusion

It is clear there is a great potential—and great need—for monitoring which pathogens are spreading or emerging and where they are doing so. Here, we have again reviewed the scientific literature and CABI distribution records to find evidence of major disease outbreaks and first reports of pathogens in new locations or on new hosts, focusing on publications/reports from 2022. Although our approach once again reveals the value of different perspectives on current and future disease risks, consistency of results both between our two approaches and on a year-on-year basis was quite low. Although this might simply reflect the fast-changing and highly variable nature of emerging outbreaks in plant health, this might also be because of inconsistencies in survey coverage and effort over time, as well as sometimes significant delays between the first arrival of a pathogen in a new location and its first report. Understanding the drivers of the variability in results between years will reveal whether the type of analysis presented here might, in time, be a component of a real-time global scale system on emerging threats for use by policy makers, or instead that it is more valuable as a purely retrospective analysis (in which case, considering publications/reports over longer time scales—e.g., 5, 10, or even 25 years—would certainly lead to less variability in the results).

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