

Data Paper

An annotated registry of established forest pathogens in the continental USA, Canada, and Hawaiian Islands

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Abstract

General understanding of disease epiphytotics caused by introduced agents (pathogens) in forest systems, as well as the ability to assess risk of future introductions within a process-barrier framework of biological invasion, are impeded by a lack of systematically compiled information on origins and functional traits of pathogens that have become established outside their range. To address these gaps, substantially update previous registries, and provide critical biosecurity information, we assembled a list of established forest phytopathogens that are present, but not thought to be native in the continental United States (CONUS), Canada, and the Hawaiian islands under working hypotheses of their origins. We restricted the present list to phytopathogens that cause disease on native tree or woody shrub species, excluding the larger number of species of non-native phytopathogens of trees that are exclusive to agricultural and horticultural species and landscapes which are already well-represented in pest databases (e.g., CABI, EPPO, APHIS, etc.). We used previous databases as a scaffold and supplemented those lists with additional taxa by cross-referencing with lists of forest pathogens and hypothetical origins for other regions (Australia and Europe) as well as by reviewing taxonomic, host, and distribution history of pathogen species that have been recorded in both the study area (CONUS-Canada-Hawaii) and at least one other continent. For each of the 93 species in our database, we provide a relational database of a) taxonomic information, b) invasion status in each region, c) first year on record in each region, d) working hypotheses of original range (where possible), e) traits including disease type and name, dispersal mode, and organs and host life stages infected, f) major hosts, g) and > 7,000 chronological records of potential location-year and host-location-year combinations for each pathogen. We also provide a reference-annotated classification system for types of evidence for first years (c), original ranges (d), and major hosts (f). This represents a significant expansion of our knowledge of non-native infectious microorganisms of forest trees compared to previous registries, particularly in terms of its comprehensiveness, precision, and accuracy of information that includes a way to assess and compare the level of uncertainty associated with key information.



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Introduction

Biological invasions are a critical component of global change that interact and synergize with climate warming and environmental degradation (Sturrock et al. 2011; Santini and Ghelardini 2015; Ramsfield et al. 2016; Seidl et al. 2017; Hadziabdic et al. 2022). Invasive pests of plant resources, including arthropod herbivores and pathogenic organisms that cause infectious disease, imperil the sustainability of forests, which are a key resource in the collective effort to slow the impacts of global change (Griscom et al. 2017; Fei et al. 2019).

Prediction of invasion success remains difficult and predicting the impacts of invasions presents an even greater challenge (Raffa et al. 2023; Williams et al. 2023). As pests pass through the successive stages of invasion (introduction, establishment, and invasion/spread), the pest populations themselves, as well as their impacts on ecosystems and society, become simultaneously more visible and increasingly intractable to manage. On the other hand, due to the cryptic biology of many forest pathogen species, a lack of basic knowledge, and general uncertainty associated with their potential spread and impact pose a significant barrier to intervention. This uncertainty extends to well established and even currently invading, destructive pathogens. This tradeoff characterizes the primary challenge associated with slowing forest phytopathogen invasions and reducing the impacts of disease epiphytotics caused by introduced agents (Williams et al. 2023).

Key information that is needed to predict the establishment success and impacts of many plant pathogens in forests includes: identities of pathogens and their invasion histories, origins, key functional traits, and host ranges. A key, innovative solution that has received increased investment in recent years is the monitoring of sentinel trees, particularly in *ex situ* plantings (Paap et al. 2017; Munck and Bonello 2018; Eschen et al. 2019; Mansfield et al. 2019). Sentinel trees are recognized as important tools to be integrated into a larger toolbox along with controlled pathogenicity experiments, modeling, and pest classification (Raffa et al. 2023). Advancement has been made in empirical modeling: particularly in the use of past history of impacts and invasiveness of established and invasive organisms as part of a training set to predict the impacts of future invaders—primarily insects (Mech et al. 2019; Schulz et al. 2021; Uden et al. 2023). This approach is promising but also limited in its utility by the availability of key information on established, non-native organisms, particularly plant pathogens in forests.

To successfully integrate data collected from sentinel trees (i.e., host associations, host specificity, contextual information, etc.) into empirical modeling frameworks, baseline information is needed on both established and invasive pathogens in forest systems along with a way to assess uncertainty associated with key information such as host range and biogeographical region of origin. Currently, much of this information is non-standardized and spread across many databases and literature.

Here, we assembled a database that can be used as a training set for other analyses, and as a general reference and baseline of information on established, non-native forest pathogens. This resource is intended to be updated with input and review from scientific experts and from additional data gathered from other resources. For example, record digitization, molecular data, taxonomic revision, and data sharing agreements with diagnostic labs and networks all can be integrated into the database.

The information currently contained in this first release of the database was drawn from several sources (Table 1). The chosen scope was pathogens not thought to be

native to Canada, Continental United States (Lower 48 and Alaska, CONUS) or Hawaii, which are causing or potentially contributing in any significant capacity to disease (symptoms) on native, woody host species in those regions. These data have been cross-referenced with other lists of non-native pathogens, databases of taxonomic synonyms, and reviewed by experts in the field through an online survey and related workshop in Annapolis, Maryland, USA in 2024 (Williams et al. 2024) and by the Forest Pathology committee of the American Phytopathology Society ahead of its 2025 national meeting in Hawaii. The authors acknowledge that there are caveats about origin hypotheses, whether a pathogen is native or exotic in different regions, taxonomic uncertainty, and other details. This is meant as a best-possible, and critical first effort to assemble the information that is available into one resource that can be updated and used to test scientific hypotheses and inform decisions to protect natural resources in the spirit of a precautionary biosecurity framework.

Metadata

I. Dataset descriptors

A. Dataset original sources

The data were collected using previous databases as scaffolds and curated both manually and with R scripts. The sources are listed in Table 1 and the information they provided are reported in Table 2. Importantly, the working hypotheses of the origins of candidate established, non-native pathogens were evaluated and filtered based on their hypothesized origins. In cases where there was significant doubt that an organism was not native to the region based on conflicting evidence in the literature, differing expert opinion, or unreliable bases of evidence, it was excluded. For example, the *Neonectria* species involved in Beech Bark Disease in North America, which are often discussed as introduced invasive species, have been shown to have most likely originated in North America (Castlebury et al. 2006; Cale et al. 2017), and therefore were omitted from the list. Additionally, there were many pathogens distributed in both North America and Europe that easily could have originated from either region, or that could have circumboreal distributions across both the Nearctic and Palearctic on plants common to both continents; these were excluded from the database in the absence of evidence suggesting they were introduced to North America from Europe. Organisms thought to be introduced—whether or not there is a working hypothesis of their origin—were included, as were organisms that have been moved from one

Table 1. Description of databases and other sources used to construct this database.

Source ID	Name	Reference
1	Peer-reviewed & grey literature, websites, reports	-
2	US Register of Introduced and Invasive Species	Simpson et al. 2022
3	USDA ARS Fungus-Host Database	Farr et al. 2024; https://fungi.ars.usda.gov/
4	Alien Forest Pest Explorer	Fei et al. 2024
5	Plant Pathogens of Hawaii	http://www.hear.org/pph/
6	Global Biodiversity Information Facility (GBIF)	GBIF 2023
7	Species Fungorum	https://www.speciesfungorum.org/
8	EDDMaps	https://www.eddmaps.org/
9	WorldFlora Database	WFO Consortium et al. 2024

region within the study area into another region (e.g., *Geosmithia morbida* and *Cryptostroma corticale* introduced from western to eastern North America and *vice versa*; and pathogens introduced from continental North America to Hawaii).

B. Dataset description and structure

The product is a relational database provided as multiple tab-delimited files consisting of 12 tables of data, two tables of code descriptions, one table of references, and one table of column descriptions for each of the 15 other tables. Table-to-table relationships are included in Table 2 along with table names, sources, and sizes. All pathogen and host names were standardized according to Table M and the WFO Consortium et al. (2024), respectively. A description of all data columns is also included.

Table 2. Description of files included in the dataset including file names, numbers of rows (NR), not including header, number of columns (NC), related tables, and sources (* indicates table also relates to uncertainty codes).

Table ID	Table name	Description	NR	NC	Related Table	Sources (Table 1)
	Description	Column definitions	81	5	A-O	
A	pathogens	Unique pathogens	92	2	A-J,L-M	1–6
B	taxonomy	Taxonomic assignments	92	8	A	1,6
C*	hi_conus_ca	Status and 1 st years with references	92	24	A,N	1,3–8
D*	origins_short	Working hypotheses of pathogen origins	92	5	A,K,N	1,6
E*	origin_working_hyp_annot_long	Table D, long format	121	7	A,K,N	1,6
F	traits	Vectors, disease names, condensed Tables G-K, and host numbers at tax levels	92	20	A,K,N	1,3–7,9
G	traits_dispersal	Dispersal and infection mode	136	3	A	1
H	traits_organ	Host major organ	161	3	A	1
I	traits_guilds	Type of disease caused in major host	102	3	A	1
J*	Koch_evidence	Type and level of evidence for disease causation with references	118	4	A,K,N	1
K	references	Annotation references	230	3	D-E,J	1
L	chronology_all	1 st -year pathogen, host and/or location combinations	7,289	20	A	1,3,6,8
M	synonym_table	Synonymy convention as used in database	438	3	A	1,6,7
N	uncertainty_codes	Uncertainty codes used for classifying evidence for geographic origin, first years, and hosts	17	6	D-E,J	-
O	severity_ranks	Impacts on host productivity, sustainability and/or overall health based on data curator knowledge	9	3	C	

II. Project description

A. Scope and criteria

Overall rationale

The database is intended to represent a comprehensive, biogeographically and functionally annotated record of pathogens established as non-native, introduced organisms within the study regions that infect tree and shrub species that are native to the study region. The rationale for these criteria (further detailed below) is that these data are meant to support research on biological invasion by pathogenic organisms in native ecosystems.

Time period

Available published records to 2024.

Geographic and biogeographic scope

CONUS, Canada, and the Hawaiian Islands. Working hypotheses were generated for the native range of candidate taxa and were excluded if a preponderance of evidence pointed to a native origin within the study area. However, pathogens native to one of our three regions (Canada, CONUS, and Hawaii) and established in another, and pathogens native to one area within CONUS or Canada and established in another (e.g., west and east of the great plains, or the Southeast and Northeast United States), and infecting native species there, were included.

Organismal scope and criteria

We followed a traditional definition of phytopathogens as infectious organisms that cause disease, excluding piercing/sucking insects and microscopic arthropod herbivores such as eriophyid mites. We included some organisms that are not exclusively microscopic, namely the parasitic plants and nematodes (which can reach > 1 mm in length and can be seen with the naked eye). We have included all organisms traditionally studied in plant and forest pathology.

Functional scope and criteria

This dataset focuses on pathogens whose hosts include forest tree and shrub species that grow and regenerate naturally in terrestrial ecosystems. To limit the data to true pathogens, we excluded fungi that cause wood rot only, without being documented as functioning as pathogens of living trees, as well as those species of Ophiostomatoid blue stain fungi not considered to function as pathogens in living trees. We further restricted the scope to pathogens that cause disease in tree and shrub species that have at least part of their native range within the study area. Therefore, we excluded pathogens that primarily impact non-native host species (e.g., exotic agricultural and horticultural cultivars) and/or that are only documented on North American species that are growing outside of their range within North America. However, in the event that a pathogen is predominantly or more frequently found on an introduced species, but also can infect native host trees or shrubs within their native range, pathogens were included.

B. Methods

Assembling the list of forest pathogens

The first step in assembling the database was to compile a list of established forest pathogens for the study area, starting with a review of the US Register of Introduced and Invasive Species (USRIIS) (Simpson et al. 2022). Pathogens were filtered by organism type, individually confirmed to have originated outside of North America, and checked to ensure they met all the criteria in section 11IA. As explained below, we also annotated the type of evidence and reference for each working hypothesis of the native range of each organism in the database. These and the details below were further reviewed by a survey of plant and forest health professionals across the study regions ahead of the Annapolis workshop (Williams et al. 2024).

Taxonomic information and synonymy

We followed standard naming for fungi using GBIF backbone taxonomy and Species Fungorum (Table 1, numbers 6 & 7). Where these conflicted with one another and/or with literature or expert opinion, we consulted experts and followed their consensus taxonomic opinions, which are reflected in `synonym_table`.

We elected to restrict the taxonomic scope of the present list to the rank of species, except in cases where taxonomic concepts associated with an invasion were either definitively more precise, insufficiently precise to do so, and/or complicated by population-level invasion history and reproductive species complexes. This led to one exception at a lower level (*Litylenchus crenatae* subsp. *mccannii*), and two at higher levels (*Ceratobasidium theobromae* s.l. and *Ophiostoma ulmi* s.l.). In the latter case (*O. ulmi* s.l.), two subspecies of *O. novo-ulmi* are recognized, *novo-ulmi* in Europe and *americanum* in North America (Brasier and Kirk 2001), the latter of which includes introgressed populations of *O. ulmi* and *O. novo-ulmi* (Brasier et al. 2021). The two subspecies have hybridized in Europe (Brasier et al. 2021). In at least one case (*Gremmeniella abietina* which comprises distinct subpopulations within North America, and between North America and Europe; Dusabenyagasani et al. 2002), the decision to employ a species-level circumscription may have been less precise than what has been established in scientific literature, but the records used to assemble the database did not necessarily employ such taxonomic concepts. Therefore, instead of attempting to accommodate such complex relationships in every case of every introduced pathogen population, many of which have been subject to bottlenecks, hybridizations, and/or multiple introductions, we elected to use rather broad circumscriptions in this database.

We recognize that in many cases the higher taxonomic circumscriptions applied are neither the most precise nor the most accurate taxonomic concept to describe the invasion. A lower taxonomic delineation may have resulted in an expanded list that would have been increasingly difficult to evaluate with respect to range of origin (e.g., an account of introduced members of *Fusarium solani* species complex). Although invasion is a population-level phenomenon, in many cases historical records preceded modern taxonomic concepts that could distinguish between different populations of the same species or different species within a species complex. Therefore, we elected to use the rank of species to incorporate historical context, despite losing taxonomic precision in some cases. This decision struck a balance between precision/accuracy and information standardization for compiling traits, distributions, chronologies, etc. A valuable lesson to be learned from this process is that there will always be a place for basic research on life history and genetics of fungal pathogens to delineate taxa. The present work is intended to be a step toward systematizing additional information on traits and interactions. As discussed below, experts were given a chance to review this information for accuracy and quality—including taxonomic opinion.

Expert assessment

The expert assessment was conducted by contacting 123 experts, of which 21 replied to the survey and contributed some type of information. The experts were selected to span the organismal groups represented in the database and were asked to review all pathogens for exclusion from the list, to add missing pathogens, and to check invasion status, disease names, pathogen functional traits (plant part, disease type, dispersal), host associations, and years of introduction. An additional

group of 68 experts also attended the Annapolis workshop where they were asked to provide additional feedback on the information in the database. All content was reviewed manually by the first author. This database functions as a working consensus and will be further reviewed by the Forest Pathology committee of the American Phytopathological Society.

No internal conflicts of opinion arose during the expert review. Suggested revisions by experts were verified against the literature, resulting in a consensus between the main author of the database and the experts. If necessary, conflicts that may arise in the future can be resolved by similarly arriving at a consensus through debate and dialogue.

Biogeographic origins

In database tables `origins_short` and `origin_working_hyp_long` in the database, we assigned pathogens to a phylogenetic and biogeographic region of origin based on a range of criteria, ranked by reliability, presented in Table 3 below. Each criterion is accompanied by references. Pathogens lacking evidence to support a working hypothesis of their original range are labelled as “cryptogenic”. We recognize that there are conflicting opinions of origins of many pathogens, and that scientific understanding of taxonomic barriers and invasion history changes over time and/or may never be resolved for some species.

Table 3. Ranked uncertainty codes for evidence supporting working hypotheses of origins for introduced pathogens.

Rank	Code	Meaning	Definition
1	Pop	Population Genetics	Putative origin assigned based on criterion of higher levels of diversity in pest populations, and can include marker-based or specific gene evidence as well as linkage and infraspecific phylogenetic history
2	Nonhost	Nonhost resistance	Origin suggested by lack of resistance in native relatives of host where organism is present
3	Coll	Collection	Assumed origin inferred from more abundant and/or earlier collections for taxonomy and phylogenetics
4	Vector	Vector	Assumed origin inferred from known origin of a vector with which fungus has a well-known association
5	Host Div	Host Diversity & Distribution	Hypothetical origin based on diversity of hosts in potential range of origin
6	Phylo	Pathogen Phylogenetic Diversity or Origin	Assumed origin inferred from higher relative known species richness of clade in region and/or phylogenetic analysis placing the species within a clade of species known only from the region
7	Crypt	Insufficient evidence, cryptogenic	No compelling data to suggest origin, but pathogen is assumed to be introduced

Invasion history and extent

As reported in Tables 1, 4, as well as table `uncertainty_codes` in the database, pathogen-year combinations with host and/or location were collected from several databases including ARS Fungal Databases, GBIF, EDDMaps, and literature. In the case of ARS records, record years were derived from publication years or from the publications themselves.

First years reported in database table `hi_conus_ca` for each study region were derived from available literature and checked against reports in the databases. In some cases, there is a known event that is hypothesized to have resulted in a pest’s introduction, but in many it is the first observation of symptoms attributed to a pathogen. In others it may be a collection record of the causative organism. The evidence type for each detection year in each study area was evaluated individually for each pathogen and assigned one of the uncertainty codes in Table 4 and database `uncertainty_codes`.

Table 4. Ranked uncertainty codes for evidence supporting earliest known presence of organism in study area.

Rank	Code	Meaning	Definition
1	Intro	Introduction	Working hypothesis for initial introduction that led to invasion
2	Coll	Earliest Collection	Earliest date pathogen was collected in the study area
3	Obs	Earliest Observation	Earliest date that disease was observed or noted that would be attributed to the pathogen
4	Recog	Taxonomic Recognition	Pathogen is first distinguished from a related species native outside the study area

Host associations

Host associations were compiled as above but we also classified against available evidence in the literature to evaluate the extent to which a host-pathogen combination is well supported (i.e., with Koch's postulates or some incomplete combination of their individual steps and components). In many cases, Koch's postulates are considered to have been completed, but do not necessarily provide convincing evidence that a given pathogen is consistently or primarily the cause of an observable disease *in situ*. The code definitions are available in Table 5 and in database table `uncertainty_codes`, and this information is reported in database tables `traits` and `Koch_evidence`. Note that evaluations have been made for the major host within the study area (introduced range).

Table 5. Ranked uncertainty codes for evidence supporting pathogen associations with major host in study area.

Rank	Code	Meaning	Definition
1	Maj	Major	Well-established causative link between pathogen and impacts on host observed occurring naturally in the field (step 1 of Koch's postulates well supported, other steps completed)
2	Incomplete	Incomplete	Most of Koch's postulates are complete, including step 1. Typically, step 4 (re-isolation) has not been achieved or has weak support
3	Assoc	Associational	Pathogen is commonly found associated with diseased tissues or surrounding soils but has not been confirmed as the causative agent (only step 1 of Koch's postulates has evidence—may not be isolation based)
4	Compl	Complex	Pathogen is considered to be part of disease complex (with or without Koch's postulates)
5	Sec	Secondary	Pathogen is commonly found associated with disease but possibly as a secondary agent (Koch's postulates may have been achieved, but level of support for step 1 of Koch's postulates does not necessarily indicate the pathogen is the primary cause of a significant disease)
6	Vector	Vector	Well-established links between vector and pathogen, and between vector and host symptoms, and pathogen is thought to play a key role in the disease (Koch's postulates not performed)

C. Sources of funding

This project was supported by a contract to GMW from the USDA Forest Service, International Programs.

Data availability

The database is available on Zenodo at the DOI <https://doi.org/10.5281/zenodo.16121534>.

Data summary

I. Comparison to previous registries

Previously, lists of invasive pathogens of native forest tree species in the study areas contained 37 (USRIIS) and 15 (AFPE) species for CONUS, and 15 species for HI

(USRIIS) based on our criteria. AREP (this database) contains 85 species of pathogen established in CONUS, 44 species of pathogens established in Canada (all present in CONUS), and 27 species in the Hawaiian Islands. Of these, a smaller number are destructive pathogens considered to be invasive, which most likely roughly coincide with the lists in previous databases, with a few recent exceptional additions. In CONUS and Canada, richness of pathogens established were highest in California followed by New York and concentrated on the West coast and Northeastern states and provinces, followed by the rest of the Great Lakes states, and finally the Southeastern states (Fig. 1).

II. Summary of data

Overall, the established pathogens are dominated by phylum Ascomycota in the kingdom Fungi. Basidiomycota, including rusts and root-, stem-, and wood-rot causing agarics are more represented in the warmer regions. Hawaii had the most, Canada the fewest, and CONUS an intermediate number of species of the non-rust (belowground or wood-rotting) basidiomycete forest pathogens (Figs 2, 3). This trend was paralleled by a dominance of rot-causing pathogens in Hawaii compared to CONUS, and even more so compared to Canada which had the fewest rot-causing pathogens relative to total established pathogens (Fig. 3). A similar pattern was found for soil-borne pathogens and those infecting belowground plant parts and stems, which were most abundant in HI, intermediate in CONUS, and lowest in Canada, which in turn was dominated more by foliar and above ground diseases (Figs 3, 4). Overall, foliar diseases and those infecting above ground plant parts dominated the established forest pathogens across study areas (Fig. 4).

Overall, most pathogens were dispersed by spores but many could be dispersed by insects or with multiple modes (Fig. 5A). There was also a trend toward multiple

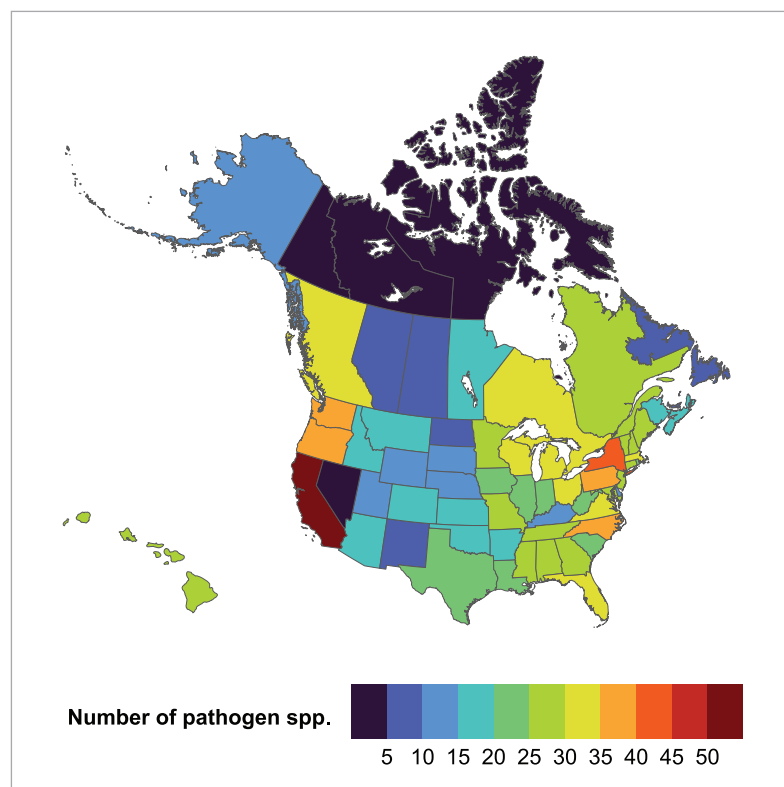


Figure 1. Richness distribution of established forest pathogens in the database across CONUS states, Canada provinces, and Hawaii.

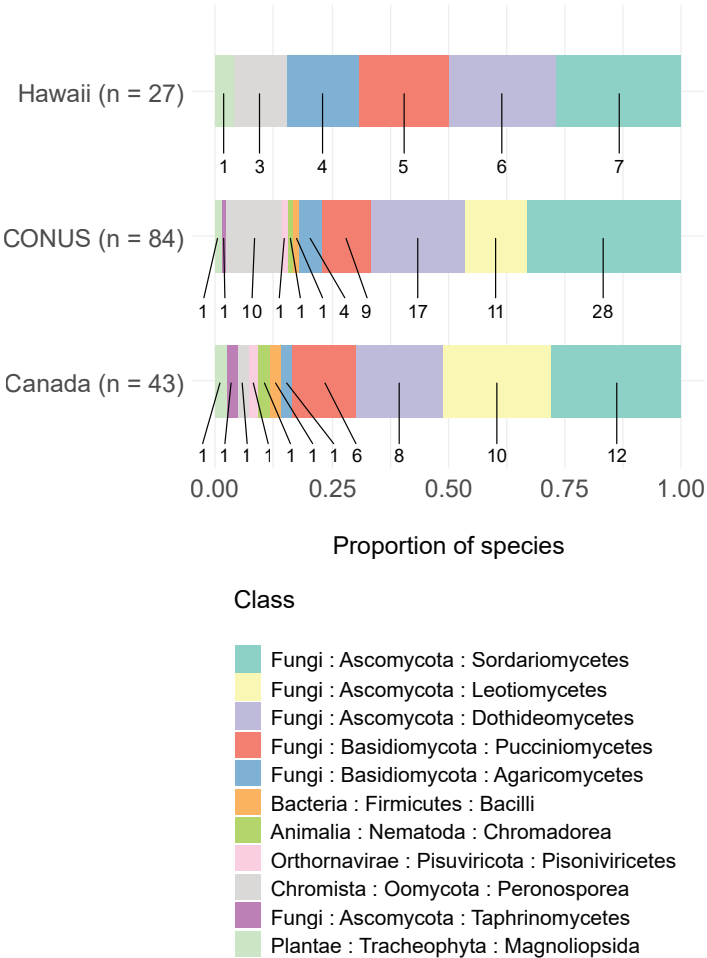


Figure 2. Taxonomic distribution of pathogens in the database, with colors representing major classes of pathogenic fungi, bacteria, microinvertebrates, viruses, oomycetes, and plants. The x axis represents total proportion of established pathogens in each region and the numbers below each section of the bars denote the number of distinct species.

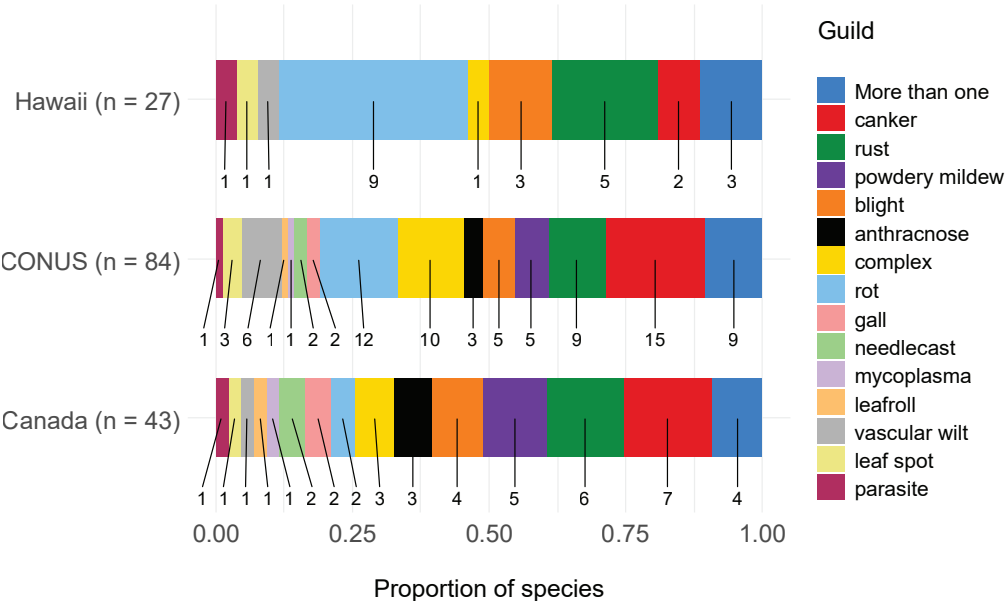


Figure 3. Distribution of pathogen types in the database, with colors representing major guilds of pathogens based on the types of symptoms they cause in descending order, with respect to total guild abundance across the entire study area. The x axis represents total proportion of established pathogens in each region and the numbers below each section of the bars denotes the number of distinct species.

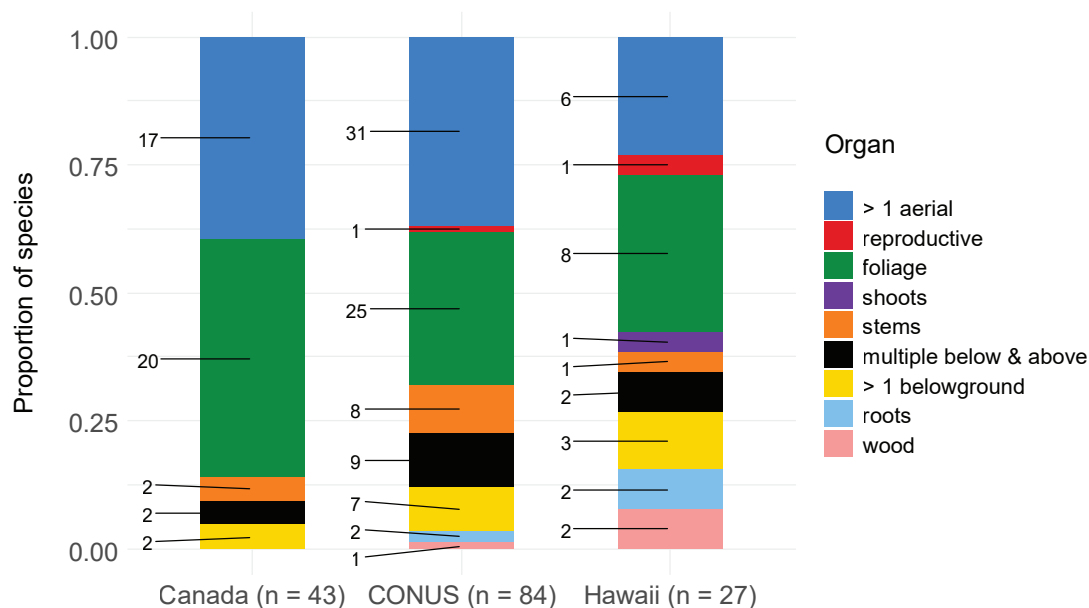


Figure 4. Distribution of plant organs infected by pathogens, from most distal/aerial to belowground, from top to bottom. Colors represent organs or groups of organs. The y axis represents total proportion of established pathogens in each region and the numbers to the left of each section of bars denotes the number of distinct species.

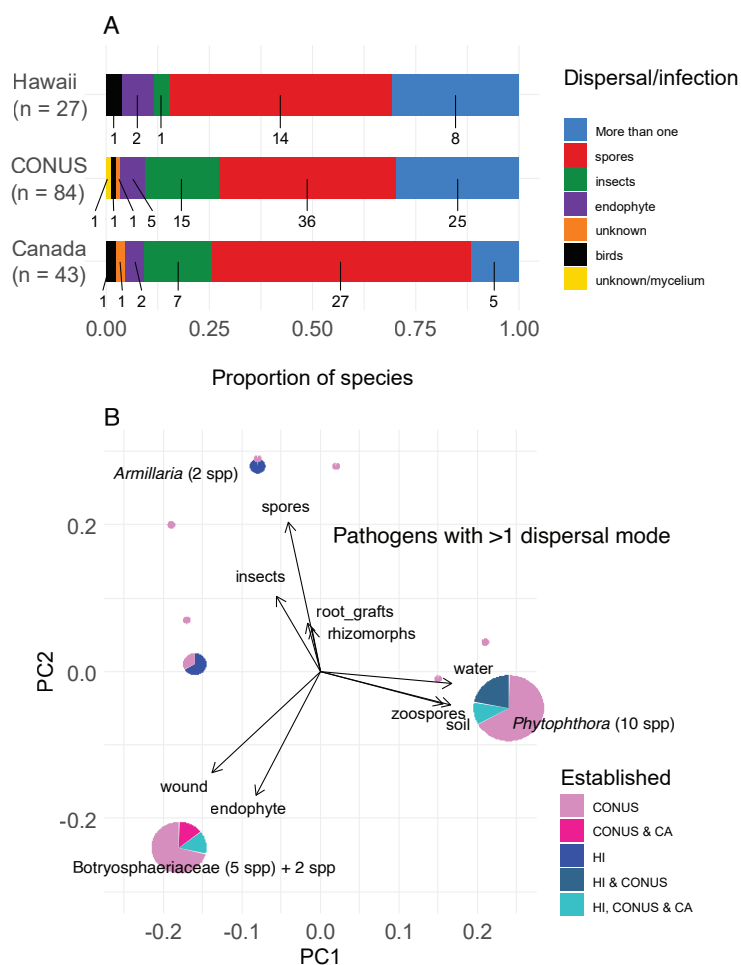


Figure 5. Distribution of dispersal and infection modes of pathogens; **A.** Relative abundance of all pathogen types; **B.** Principal components analysis of pathogen species with more than one dispersal mode, size of pie represents total number of species and % of pie proportional to number of species established in Canada, CONUS, and/or Hawaii.

modes of infection, and fewer pathogens with insect vectors, in Hawaii, as well as fewer in CONUS relative to Canada. Within the pathogens with multiple dispersal and/or infective modes (Fig. 5B), the majority were comprised of either water, soil, and zoospore-dispersing *Phytophthora* spp. or wound/endophytic pathogens (mostly Botryosphaeriaceae). Pathogens with other combinations of dispersal and infection modes involving combinations of infecting spores, insect dispersal, root grafting, and rhizomorphs were largely absent from Canada, while CONUS had the greatest diversity of dispersal and infection strategies.

Hawaii also had more generalist pathogens whereas Canada was most dominated by specialists with narrower host ranges (Fig. 6). CONUS was intermediate, with a more even distribution of host ranges across species and genus-specialist, intermediate, and generalist host ranges. Genus-level host ranges were most common in the database overall with a slightly lower number of family- and species-level host ranges.

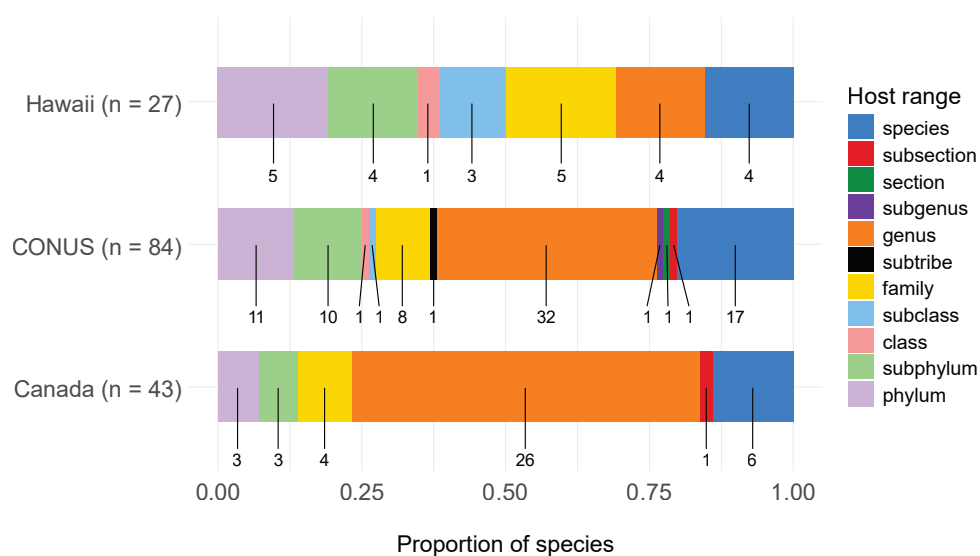


Figure 6. Distribution of host ranges of established forest pathogens in the study areas; host range is denoted by color and considered as the highest rank for a most recent common ancestor among known host species for each pathogen species in the database. The x axis represents total proportion of established pathogens in each region and the numbers below each section of the bars denotes the number of distinct species.

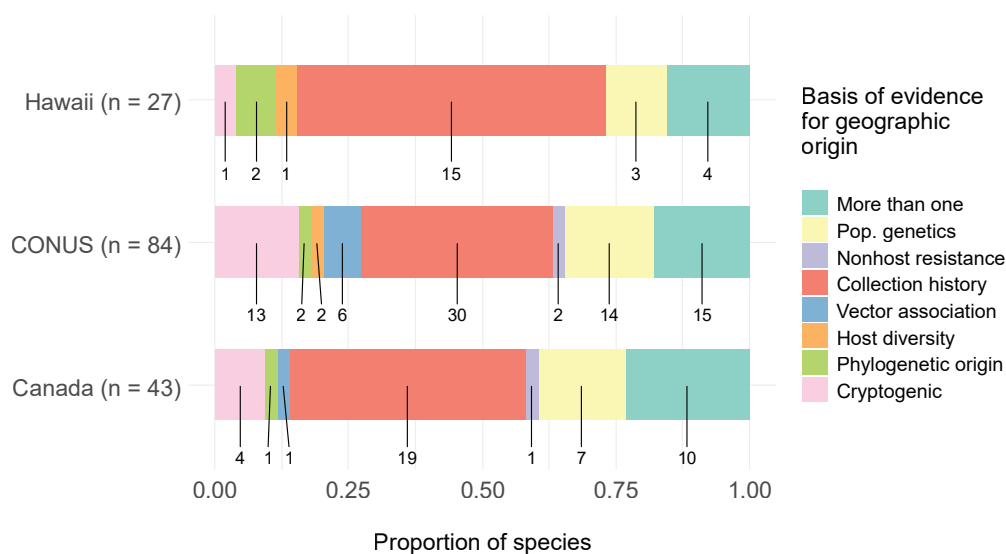


Figure 7. Distribution of evidence bases for working hypotheses of geographic origins of established forest pathogens. The x axis represents total proportion of established pathogens in each region and the numbers below each section of the bars denote the number of distinct species.

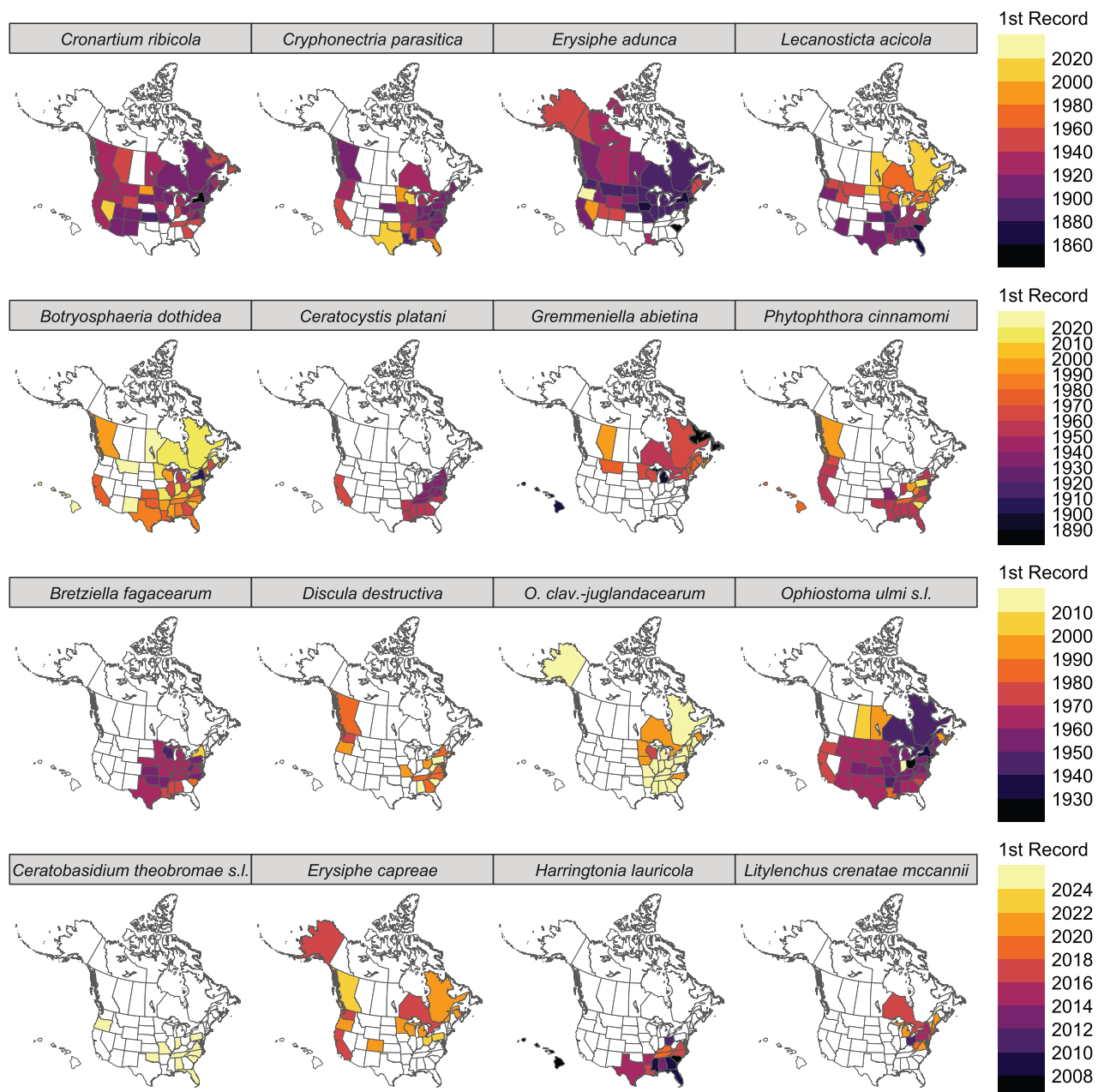


Figure 8. Summary of invasion history and current distribution of selected species. Colors between pairs of years denote time intervals during which records occurred.

The evidence for biogeographic origins for pathogens was dominated by collection histories, followed by population genetics. Several species had working hypotheses of origins supported by multiple lines of evidence. CONUS had the highest proportion of cryptogenic species when compared to Canada and Hawaii (Fig. 7).

Many of the chronological distribution data were limited but several showed patterns of spatial spread over time (Fig. 8), including some examples of pathogens that appear to be tracking climate change (e.g., *Lecanosticta acicola*, *O. ulmi* s.l.) as well as many examples of disjunct distributions between the eastern and western coasts of North America (e.g., *Phytophthora cinnamomi*, *Lachnelulla willkommii*, *Discula destructiva*, *Ceratocystis platani*, *Ceratobasidium theobromae* s.l., etc.). Some of the less continuous records may stem from the method of using publication year

from references in ARS which include many checklists that may themselves cite much earlier literature or records. However, it may also represent lags in detection and/or pathogens jumping invasion fronts (“spotting”).

Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Conceptualization: DRC, RAS, GMW. Data curation: GMW. Formal analysis: GMW. Funding acquisition: RAS. Investigation: KR, JKS, AVG, GMW. Methodology: DRC, MLS, GMW. Project administration: GMW. Resources: SCL. Software: GMW, AVG. Supervision: DRC, RAS, MLS. Validation: GMW, AVG, SCL, JKS, KR. Visualization: GMW. Writing – original draft: GMW. Writing – review and editing: GMW.

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Data availability

All of the data that support the findings of this study are available on Zenodo doi:10.5281/zenodo.16121534 and can be accessed at <https://zenodo.org/records/16121534>.

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