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A Community-Curated DokuWiki Resource on Diagnostics, Diversity, Pathogenicity and Genetic Control of Xanthomonads

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fastidiosa

Abstract

Xanthomonads, including *Xanthomonas* and *Xylella* species, constitute a large and significant group of economically and ecologically important plant pathogens. Up-to-date knowledge of these pathogens and their hosts is essential for the development of suitable control measures. Traditional review articles or book chapters have inherent limitations, including static content and rapid obsolescence. To address these challenges, we have developed a web-based knowledge platform dedicated to xanthomonads, inspired by the concept of living systematic reviews. This platform offers a dynamic resource that encompasses bacterial virulence factors, plant resistance genes, and tools for diagnostics and genetic diversity studies. Our goal is to facilitate access for newcomers to the field, provide continuing education opportunities for students, assist plant protection services with diagnostics, provide valuable information to breeders on sources of resistance and breeding targets, and offer comprehensive expert knowledge to other stakeholders interested in plant-pathogenic xanthomonads. This resource is available for queries and updates at <https://euroxanth.ipn.pt>.

Context

Food security is of key importance for the welfare of individuals and communities, and according to the Rome Declaration of 1996, is achieved when ‘all people, at all times, have physical and economic access to sufficient, safe and nutritious food to meet their dietary needs and food preferences for an active and healthy life’ [Aliaga and Chaves-Dos-Santos 2014]. However, food supplies are constantly under threat from a variety of challenges, with plant pathogens being a major cause of severe yield losses. The pressure on food security is expected to increase in the future due to adverse climatic conditions, which in turn will lead to economic and social problems. Climate change is likely to favor conditions for pathogen evolution and higher/faster migration and adaptation potential in pathogens and pathogen vectors [Elad and Pertot 2014; IPCC Secretariat 2021; Raza and Bebbler 2022]. In addition, climate change scenarios predict an increase in the severity of epidemics and a northwards geographic expansion of pathogen distribution in Europe, China and North America [Chaloner et al. 2021; Singh et al. 2023]. Finally, increased human migration and international trade pose an additional risk for the emergence of disease epidemics [Jeger et al. 2021; Simler et al. 2019].

The bacterial genera *Xanthomonas* and *Xylella*, both belonging to the family *Lysobacteraceae* (syn. *Xanthomonadaceae*) and collectively called xanthomonads, harbor some of the most devastating plant pathogens that constantly challenge food security. Collectively, strains of these

taxa infect a plethora of plant species found in agricultural, horticultural, forest or unmanaged ecosystems. Notably, several species of *Xanthomonas*, including pathogens of rice (*Xanthomonas oryzae*), brassicas (*Xanthomonas campestris*), pepper and tomato (*Xanthomonas euvesicatoria*), cotton (*Xanthomonas citri*) and cassava (*Xanthomonas phaseoli*), and the related species *Xylella fastidiosa*, have been listed among the top 10 plant pathogenic bacteria in plant pathology [Mansfield et al. 2012]. A better insight into population structures and virulence mechanisms of these pathogens, as well as research into the molecular mechanisms underlying disease resistance to the pathogen, are essential for the development of durable resistant crop cultivars/varieties.

Currently, information on the various aspects of bacterial plant pathogens, such as appropriate diagnostic tools, studies of the genetic diversity and population structures, mechanisms of pathogenicity and sources of genetic resistance in crops, etc., can be found in numerous scientific publications. Book chapters, review articles in scientific journals and special focus issues compile and summarize these findings, but typically focus on only one aspect and rarely address several species or genera [Catara et al. 2021; White et al. 2009; Yang et al. 2022]. Moreover, new knowledge is generated at such an astonishingly fast rate that such review articles and book chapters quickly become outdated. An additional problem is that the taxonomy of xanthomonads has been revised several times, resulting in changing names of species, which makes it difficult for newcomers and non-experts to fully grasp the available knowledge.

Inspired by the concept of living systematic reviews [Simmonds et al. 2022], we thought of developing a knowledge platform on xanthomonads. This platform is intended to lower the barriers to entry for newcomers in this field, especially early-career scientists, provide continuing education opportunities for students, assist plant protection services with diagnostics, provide valuable information to breeders on sources of resistance and breeding targets, and offer comprehensive expert knowledge on plant pathogenic xanthomonads to other stakeholders. We hope that such a platform of trusted evidence will enable informed decisions for better plant health, thus contributing to achieving the goals of the Rome Declaration.

Building a Community Online Resource and Attracting Contributors

To integrate science on *Xanthomonadaceae* for sustainable plant disease management in Europe, we built a network of researchers with complementary expertise and skills, which was supported by the COST (Cooperation in Science and Technology) Action CA16107 with the acronym EuroXanth [Costa et al. 2023]. During the period from 2017 to 2021, we generated several resources, such as a set of pathogen profiles and a compilation of tools for molecular

diagnostics and diversity studies of phytosanitary regulated xanthomonads [Catara et al. 2021; Costa et al. 2021]. To overcome the static nature of such compilations, we decided to develop an internet-based, community-driven resource. We, therefore, established the EuroXanth DokuWiki, a comprehensive collection of knowledge on bacterial virulence factors, plant resistance genes, and information on pathogen diversity and diagnostics. As initial targets, we identified key virulence traits (specifically, type 3 effectors) and plant resistance genes, for which we developed dynamic fact sheets.

Once we had decided what information should be included in such a fact sheet, we considered how best to engage the scientific community in this endeavor. We followed a three-step process in which the fact sheets were first drafted, then revised in two rounds, first as an internal revision by another colleague from the EuroXanth network, and finally approved by a renowned expert on the specific virulence trait or host plant (Fig. 1). We realized that this goal could only be achieved with a large number of contributors, especially that several rounds of revisions would be required to ensure that the information was accurate and up to date. Therefore, we used the opportunity of COST funding to harness participants of the 3rd Annual Conference on “Integrating science on *Xanthomonadaceae* for integrated plant disease management in Europe” to draft the first versions of the fact sheets, using a standardized template that was shared with them. During the conference in Lednice (Czech Republic) in September 2019, we presented this community science project to the audience and discussed the achievements of the first round of drafting the fact sheets. The project was very well perceived by the vast majority of participants, who volunteered to revise the first drafts in the coming weeks. In this way, the community produced 46 effector fact sheets and 16 plant resistance-gene fact sheets, all but three of which underwent internal revision (see below for details). It proved much more difficult to mobilize external experts who were not associated with the EuroXanth COST Action. Nevertheless, 20 expert reviews were achieved and those without expert review were validated by ourselves. Finally, we considered the quality of the fact sheets to be high and useful for the community. The following sections briefly describe the contents of the fact sheets, followed by a detailed description of the data collection, establishment, implementation and accessibility of the EuroXanth DokuWiki resource.

Virulence Factors

Type 3 effectors are among the most important virulence factors of many bacterial pathogens, including xanthomonads [Khan et al. 2018; Schreiber et al. 2021]. Many phytopathogen effectors act as suppressors of plant defense responses, thereby benefiting the pathogen [Bundalovic-Torma et al. 2022; Landry et al. 2020]. Nevertheless, effectors are considered double-edged

swords because some of them have been shown to trigger strong, often race-specific, defense responses, which is why they are called avirulence proteins [Alfano and Collmer 2004; Grant et al. 2006]. These features, being of key importance but also being recognizable by the plant immune system, make type 3 effectors an important target for resistance breeding, and robust effector identification remains a critical component in the implementation of durable resistance strategies [Lovelace et al. 2023].

In an attempt to harmonize the nomenclature of *Xanthomonas* type 3 effectors, the community met in a roundtable format at the 3rd *Xanthomonas* Genomics Conference in Pingree Park, CO, U.S.A., and discussed rules for naming effectors [Ryan et al. 2009]. Consequently, the then-known effector repertoire of *Xanthomonas* was published following the recommendations of the round table [White et al. 2009]. In parallel, a website was created that not only tabulated the effector repertoires of a few completely sequenced *Xanthomonas* strains but also listed their homologs in other plant-pathogenic bacteria, such as *Acidovorax citrulli*, *Dickeya dadantii*, *Pectobacterium atrosepticum*, *Pseudomonas syringae* and *Ralstonia solanacearum* (<http://www.biopred.net/xanthomonas/t3e.html>). In addition, this website monitored the progress of genome sequencing, updated publications on xanthomonads, provided information on bioinformatic tools for effector prediction and studies of genetic diversity, and listed contact details of agreed experts in the field. Impressively, this website was cited more than 150 times according to Google Scholar (Supplementary Table S1). However, as this website was maintained by a private one-man initiative, it soon became impossible to keep the resource up to date, and the updating of the literature and genome sequences soon ceased. This was another reason to look for a new community-driven format like the one presented here.

Type 3 effectors in *Xanthomonas* have been classified based on their sequence similarity and designated as Xop proteins (except for the well-established AvrBs1, AvrBs2, and AvrBs3 proteins). Xop classes are identified by capital(s) after 'Xop', e.g., XopB, XopC, [...], XopZ, XopAA, XopAB, etc., in alphabetical order. Xop classes with large sequence diversity were divided into families, the members of which are identified by a decimal (Arabic numeral) after the capital(s), e.g., XopJ1, XopJ2, XopAF1, XopAF2. Similar to the effector classification in *Pseudomonas syringae* [Lindeberg et al. 2005], *Xanthomonas* effectors are usually considered to belong to the same family if they share more than 50% sequence identity over at least 60% of their sequence length (Supplementary Table S2). Effectors belonging to the AvrBs3/PthA class, also known as Transcription Activator-Like (TAL) effectors, have a modular, repetitive structure and follow a separate, distinct nomenclature [Grau et al. 2016].

For each effector family, we provide information on the several features in individual fact sheets, as outlined in Box 1.

Currently, our public resource contains information for 54 effector classes (from XopB to XopBA), comprising 73 effector families (Fig. 2). Amino acid sequences of type 3 effectors, representing all effector families, are available in a multi-FASTA format (Supplementary Data S3), and are also available online at <https://euroxanth.ipn.pt/doku.php?id=bacteria:t3e:effectors>.

Resistance Genes

The use of disease-resistant crop cultivars is an economically and environmentally sustainable strategy for plant disease control [Sharma et al. 2022]. Unfortunately, the efficacy of resistance genes is constantly challenged by the emergence of new pathogen strains, necessitating the isolation and exploitation of new sources of resistance and pyramiding them to increase efficacy and durability [Dormatey et al. 2020]. In general, resistance can break down after only a few cropping seasons [McDonald and Linde 2002], and only a few sources of resistance with long durability have been reported [Kusch and Panstruga 2017]. The durability of resistance genes can only be reliably predicted with detailed knowledge of the underlying molecular mechanisms and the evolutionary potential of the pathogen populations. Therefore, the successful development of durable resistant cultivars depends critically on a profound knowledge of the pathogens' identity and genetic diversity, their population structure and their key pathogenicity and virulence factors.

Among the various means of integrated plant disease management, genetic resistance is considered the most effective, ecologically safest and socially best accepted approach. Breeding for resistance has a long history, and modern novel approaches such as genomics-assisted breeding and genome editing have accelerated the generation of resistant elite crop cultivars [Schepler-Luu et al. 2023; Tripathi et al. 2020; Varshney et al. 2021].

We therefore decided to provide an overview of the identified sources of genetic resistance against plant-pathogenic xanthomonads. We started with 16 groups of plants that are affected by *Xanthomonas* spp.: banana, common bean, cassava, citrus, cotton, hazelnut and walnut, forage grasses (e.g., ryegrasses and fescues), mango, pepper, poplar, stone fruit trees (e.g., apricot, peach and sweet cherry), rice, soybean, strawberry, tomato, small-grain cereals (e.g., wheat). For each of these crops, we scrutinized the literature and listed identified resistance genes. Currently, our online resource lists 134 resistance genes, most of which are considered qualitative resistance loci, conferring effector-triggered immunity (ETI) or vertical resistance [Burbano-Figueroa 2020]. For plant species where we did not find characterized resistance genes, we included quantitative

trait loci (referred to as QTL), such as one QTL against angular leaf spot of strawberry, caused by *Xanthomonas fragariae*, and five QTL against bacterial wilt of several forage grasses, caused by *Xanthomonas translucens* pv. *graminis*.

For each plant species, we have first structured the entry by the causal agent, i.e., by bacterial species and pathovars. For each pathogen, we then provide a fact sheet that includes information about the name of the resistance gene, synonymous names, the source of the gene (accession, cultivar), the status of its characterization (i.e., whether identified, mapped, cloned, or sequenced), linked molecular markers, a brief description, and the relevant references. This public resource is open to expansion. For instance, some important host plants are not yet included, sometimes due to the lack of identified resistance genes (e.g., brassica). For further improvement, we also propose to include more QTL and candidate resistance genes. At present, molecular markers are provided for only 50 resistance genes, which can be due to the lack of mapping data for some of the genes. However, it is also possible that we have missed information for some of the mapped loci.

Diagnostics and Diversity

Effective containment and control measures of pathogens require standardized up-to-date detection and diagnostic methods. Within the framework of the EuroXanth COST Action, a systematic and critical review of molecular methods for diagnosis, detection and diversity studies was conducted, with particular emphasis on regulated *Xanthomonas* pathogens in the European Union [Catara et al. 2021; Costa et al. 2021]. The information gathered was organized into three main themes: (i) plant diseases, their regulation and management recommendations, (ii) main protocols described for regulated xanthomonads based on amplification of specific target DNAs, and (iii) tools for molecular typing of regulated xanthomonads. This information was then summarized in tables for easy consultation [Catara et al. 2021].

Following the implementation of the community-curated resource on virulence factors and genetic control of xanthomonads, it was proposed to broaden the scope by including content deemed relevant in this context and already compiled in the EuroXanth COST Action, to make the resource more comprehensive and to make this knowledge more easily accessible and usable by the community. In line with this strategy, the information contained in the previously compiled tables on molecular methods for diagnosis, detection and diversity studies, which had already been peer-reviewed, was included in the platform to facilitate their access and updating [Catara et al. 2021]. After an initial exploration of the data insertion and formatting tools available in the EuroXanth DokuWiki, data insertion into the platform was easy and quick. The most time-consuming part of

the process was to associate each publication with the corresponding hyperlink, a fundamental step in providing users with correct and direct access to the relevant literature. The new web resource was then tested and revised, with occasional intervention by the management committee to resolve some minor issues.

Technical Implementation

A special task force, consisting of the authors of this publication, was formed to establish the essential prerequisites to ensure a smooth launch of this collaborative resource before the 3rd EuroXanth Annual Conference. Two major open-source wiki alternatives were evaluated and tested, namely MediaWiki (<https://www.mediawiki.org>) and DokuWiki (<https://www.dokuwiki.org>). Both platforms have minimal server requirements and are translated into more than 50 languages, making them attractive for building an online community resource with participants from all over the world by facilitating inclusiveness, broad access, and ease of use. Both platforms can also be displayed on smaller devices such as mobile phones or tablets, thus widening the audience when access to a computer is limited. Both platforms also offer the ability to track changes, to restore older entries and to restrict user access, thus ensuring the quality of information hosted in an online community resource. Thanks to the free encyclopedia Wikipedia, MediaWiki is better known and has proven useful for large and complicated wikis, whereas DokuWiki is more oriented towards smaller and simpler wikis meant for documentation (e.g., software manuals and corporate knowledge bases) [Feldman 2020]. MediaWiki appears to be more powerful, more scalable and more flexible but this comes at the expense of ease of use for newcomers. We also appreciated the fact that various tools are available in case one decides to switch from the DokuWiki platform to MediaWiki later on. Switching in both directions is possible, but is rather recommended for small wiki projects. After testing both platforms and weighing their different pros and cons, the task force unanimously decided to use the DokuWiki tool, mainly because of the ease of making updates (e.g., installing extensions) and controlling the user list.

Two standardized templates, one for type 3 effectors (https://euroxanth.ipn.pt/doku.php?id=bacteria:t3e:t3e_template) and one for plant resistance genes (https://euroxanth.ipn.pt/doku.php?id=plant:plant_template), were initially drafted on the DokuWiki platform, underwent an iterative testing process by the task force and were finally converted into Microsoft Word documents. We expected that Word files would increase the acceptance of participants at the 3rd EuroXanth Annual Conference, who were not familiar with such an online tool, to draft satisfactory fact sheets. To motivate the conference participants, who had diverse backgrounds and expertise, we asked them two months before the event to select

their preferred topic from 25 pairs of type 3 effectors and seven pairs of plant resistance genes using an online poll. For each pair, a tandem of editors was thus created. The two templates and three pre-filled examples (two for effectors and one for resistance genes) were then sent by email to the participants. Most of the 57 fact sheets were collected before the conference (i.e., within two months). The Word fact sheets were converted from .docx format to DokuWiki markup format as .txt files using the universal markup converter Pandoc v.2.7.3. The final files were then uploaded on DokuWiki 2018.04.22 installed on a private Network Attached Storage (NAS). This solution offered more flexibility than an institutional solution, with the drawback of eventual downtime mainly due to the lack of redundancy of hardware and of connectivity in such a setting. A subsequent update of this setup to DokuWiki 2020.07.29 also worked flawlessly.

Despite our standardization efforts, it turned out that the fact sheets required additional editing by the task force. The main task was then to ensure consistent formatting of the entries. The references were the main problem. Since numbered references were initially used in the entries, any addition or deletion of a reference would require a change in the numbered sequence. Although DokuWiki reference plugins exist, we realized that scientific references could not be easily maintained centrally. We, therefore, decided to revert the references to an APA formatting style, i.e., the author-date method for in-text citation, to sort the reference list alphabetically, and to provide the Digital Object Identifier (DOI) for each reference as the most reliable external hyperlink. A minor drawback of our approach was that the ability to hyperlink the in-text citation to the entry in the reference list was lost.

Once all of these technical steps were completed, participants were asked to complete the internal revision of their corresponding tandem fact sheet online. This step went smoothly and required minimal input from the task force with a few minor issues when creating a member account to allow editing of an entry. For a second revision, we aimed to involve renowned experts in the field (i.e., on a particular effector family or host plant), based on publication records. This last step took much longer than expected and required more commitment than originally planned, as several reminders or alternative contacts were needed.

Finally, the DokuWiki hosting was migrated from a private to an institutional environment in early 2023. Apart from a few minor issues, this step went smoothly, thanks largely to the BackupTool for DokuWiki v.1.0.1 plugin. On this occasion, the resource was also updated to DokuWiki 2022-07-31 and then to 2023-04-04a without any problem. Snapshots of the EuroXanth DokuWiki resource were taken on 3rd October 2023 and deposited at the CERN Data Centre-backed

research data repository ZENODO for long-term archiving [Costa et al. 2023]. Regular backups will be stored at ZENODO at six-monthly intervals.

Maintenance and Usefulness

The EuroXanth DokuWiki is hosted at the University of Coimbra, Portugal, without the need for funding and will therefore remain alive and active in the longer term. The management committee, consisting of the six authors of this publication, will continue to oversee the further development of the DokuWiki resource, thus ensuring that the high quality of the content is maintained. To do so, all members of the Management Committee meet virtually once a year or on demand, if necessary. In the long term and in case members of the management committee retire or change their field of research interest, we will implement a strategy to actively look for replacements, for instance at the three-annual *Xanthomonas* Genomics Conferences [Ryan et al. 2009].

To keep the EuroXanth DokuWiki up to date, we use the PubCrawler alerting system (Figure 1) [Hokamp and Wolfe 2004]. PubCrawler queries PubMed once a week for the terms 'Xanthomonas' and 'Xylella' in the title or abstract of the publication and sends a notification to the corresponding author, who will check for new publications with relevance to the EuroXanth DokuWiki. In case of a relevant publication, we invite the first or corresponding author of a manuscript to update the corresponding fact sheet (Figure 1). Alternatively, or in case of no response, the fact sheet will be updated by a member of the management committee. Moreover, whenever we encounter new data during our routine work, we consider its inclusion in the DokuWiki resource.

To give an idea of how the EuroXanth DokuWiki may be useful, we have formulated a few questions from everyday scientific life to which our resource may provide an answer, and explain how a search through the website could be carried out (Box 2). We also included links to other websites that we consider relevant in the context of effector research, but also for taxonomy and genetic diversity, such as PhytoBacExplorer (<https://phytobacexplorer.warwick.ac.uk/>), the *Pseudomonas syringae* Genome Resources Page, Ralsto T3E, LINbase, PAMDB, PubMLST, and MLVAbank [Almeida et al. 2010; Grissa et al. 2008; Jolley et al. 2018; Lindeberg et al. 2005; Peeters et al. 2013; Tian et al. 2020].

Outlook

The EuroXanth DokuWiki is a dynamic resource that is open to regular updates with immediate release. As such, its future relies on the expert curation of its content, which is overseen by the management committee. We invite the wider scientific community working on xanthomonads to contribute to the success of this resource. For instance, authors of forthcoming publications with

relevance to the EuroXanth DokuWiki can add their findings themselves (e.g., functional characterization of effectors, novel resistance genes, diagnostic tools for diseases not yet covered) or inform the management committee and ask for assistance (Figure 1). We also envisage that the resource could be used in teaching activities as student's projects, where students systematically screen the literature on distinct effectors or resistance genes and update the corresponding fact sheets in a supervised manner, as tested by us during the EuroXanth Training School on "Molecular typing of *Xanthomonadaceae* – from epidemiological surveillance to outbreak investigation" in 2019 (<https://euroxanth.eu/events/training-schools/training-school-2>). To maintain the high standard of its content, contributors are requested to register at <https://euroxanth.ipn.pt/doku.php?id=start&do=register>. Applications are evaluated by the management committee and are usually approved within a week.

We believe that our EuroXanth initiative can serve as a model for other pathosystems. Hopefully, this resource on xanthomonads and the way it was built will inspire other scientists to build similar resources for other pathogens, such as *Pseudomonas* or *Ralstonia*, but also for fungi and oomycetes, nematodes or insects. Artificial intelligence may one day serve a similar purpose, providing a comprehensive, timely and high-quality presentation of expert knowledge on plant pathogens and their management. However, in our experience, available tools are not yet sophisticated and user-friendly enough, lack proper citations, and their efficient use depends on very clever phrasings of queries. We, therefore, believe that our DokuWiki will serve to share information based on referenced literature and may also inspire and integrate research on an important group of pathogens. This EuroXanth online resource is available for queries and updates at <https://euroxanth.ipn.pt>.

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Legends to the figures

Figure 1. Flow chart of the development and maintenance of the EuroXanth DokuWiki. All five phases were overseen by the management committee, consisting of the authors of this publication. Members of the EuroXanth COST Action contributed to the completion and internal revision of the fact sheets (phases 3 and 4), while internationally renowned experts were consulted for peer revision (phase 5). The resource was made available online after completion of phase 4. For the maintenance, text mining and dedicated workshops will be used to identify fact sheets in need of revision (phase A), which will preferentially involve the authors of a new study on effectors or resistance genes (phase B).

Figure 2. Content of the EuroXanth DokuWiki. Information about 54 effector classes and 134 resistance genes is presented in the form of fact sheets, while diagnostic and diversity tools for 18 pathogens that collectively cause 14 plant diseases are presented in three tables. This EuroXanth DokuWiki is available for queries and updates at <https://euroxanth.ipn.pt>.

Box 1. Features of individual effector fact sheets.

Box 2. Typical questions that can be addressed using the EuroXanth DokuWiki.

Supplementary Table S1. Xanthomonas.org citations. Citations of the ‘xanthomonas.org’ resource, as retrieved from Google Scholar on 6th February and 4th July 2023.

Supplementary Table S2. Classification and sequence comparison of *Xanthomonas* type 3 effectors. All amino acid sequences were compared against each other by BLASTP using default parameters at NCBI, with an expect threshold of 0.05 (<https://blast.ncbi.nlm.nih.gov/Blast.cgi>). Calculated sequence identities and coverage of the sequence alignments are indicated in tables ‘Sequence identity’ and ‘alignment coverage’, respectively. The current classification is given in the table ‘Identity & >60% coverage’, according to the criteria that homologs with less than 50% sequence identity and at least 60% of alignment coverage are usually considered to belong to the different families of the same effector class.

Supplementary Data S3. Amino acid sequences of *Xanthomonas* type 3 effectors. Representatives of each effector family are presented in a multi FASTA format and are also available online at <https://euroxanth.ipn.pt/doku.php?id=bacteria:t3e:effectors>.

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Author-Recommended Internet Resources

EuroXanth DokuWiki – Online resource for xanthomonads diagnostic tools, virulence factors and resistance genes: <http://www.xanthomonas.org>

LINbase – The Life Identification Number® (LIN®) Platform: <https://linbase.org/>

MLVAbank – A genotyping resource for tandem repeat typing, CRISPR typing, sequence typing and single nucleotide polymorphisms: <https://microbesgenotyping.i2bc.paris-saclay.fr/>

PAMDB – A multilocus sequence typing and analysis website and database for identification of plant associated and environmental microbes and for the study of their epidemiology, population genetics, and molecular evolution: <http://PAMDB.org>

PhytoBacExplorer – Online resource for analysing and visualising genomic variation within plant-pathogenic bacteria: <https://phytobacexplorer.warwick.ac.uk/>

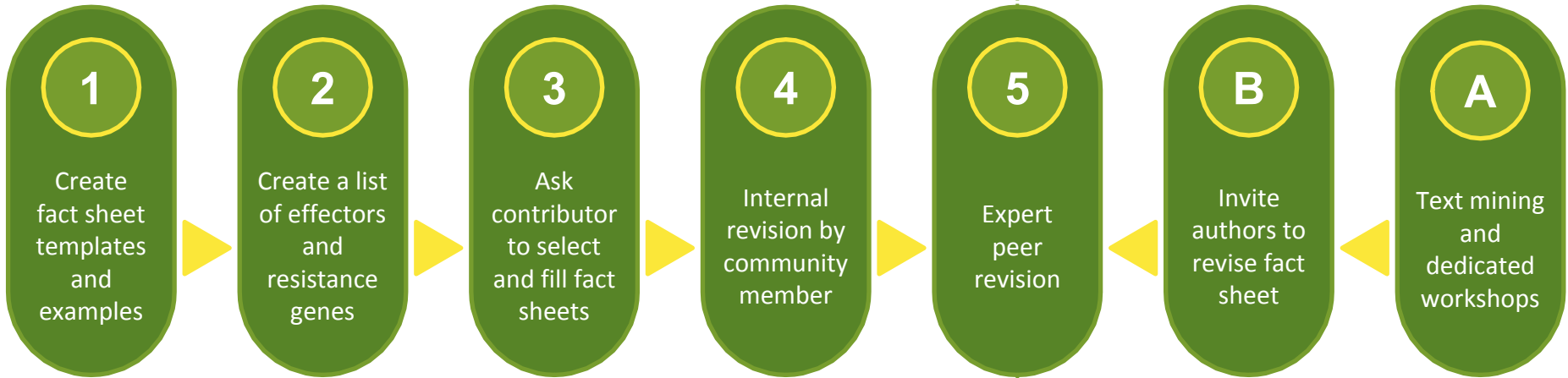
Pseudomonas syringae genome resources Home Page: <http://www.pseudomonas-syringae.org>

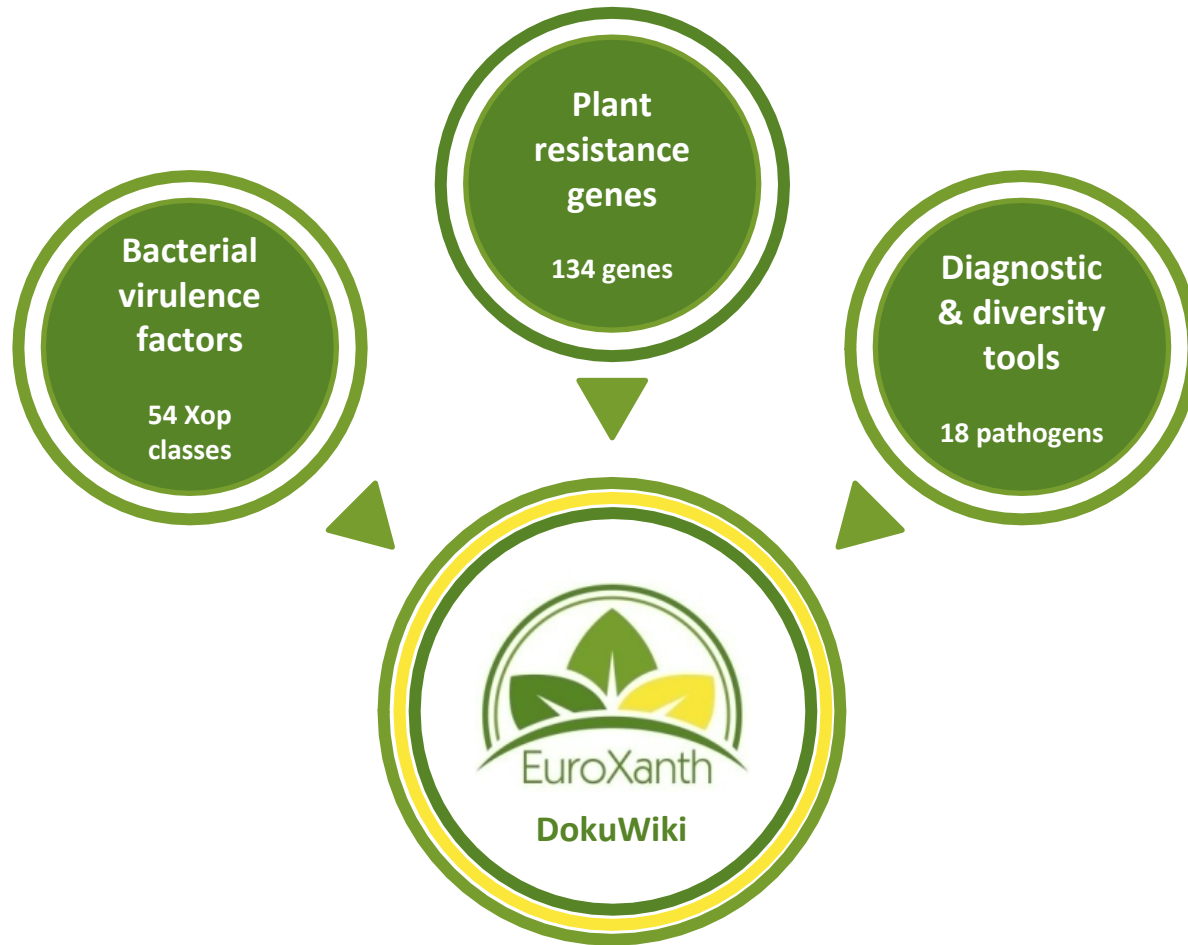
PubMLST – A collection of open-access, curated databases that integrate population sequence data: <https://pubmlst.org/>

RalstoT3Edb – A pangenomic type 3 effector database of the plant pathogenic *Ralstonia* spp.: <https://iant.toulouse.inra.fr/T3E>

Development

Maintenance





Box 1. Features of individual effector fact sheets.

Annotation

- Name of the fact sheet's author
- Name(s) of the reviewer(s)

Overview

- Class, family and synonymous names of the effector
- Prototype effector with GenBank accession number
- RefSeq identifier for the effector
- Three-dimensional structure information, if available

Biological function

- How was the effector discovered?
- What is the (experimental) evidence for being considered a type 3 effector?
- How is the gene regulated?
- Phenotypes of mutants or upon transient or stable transgenic expression
- Information on subcellular localization
- Information on enzymatic function
- Information on interaction partners

Conservation

- In xanthomonads
- In other plant pathogens/symbionts

References

Box 2. Typical questions that can be addressed using the EuroXanth DokuWiki.

(1) Which known type 3 effector genes are present in my new *Xanthomonas* genome sequence? Where can I find a multi-FASTA file with protein sequences to identify them by BLAST search?

- On the left panel, click on "**Type 3 effectors**".
- On the main panel, click on "**Multi-FASTA-formatted list of type 3 effectors from *Xanthomonas***".
- Alternatively, you can retrieve the sequences from GenBank when you click on "**List of type 3 effectors in *Xanthomonas***".

(2) What is known about the type 3 effector XopAJ?

- On the left panel, click on "**Type 3 effectors**".
- In the table of the main panel, click on family "**XopAJ**".
- Information on the sequence, structure, discovery, regulation, function and conservation of the type 3 effector is compiled and the corresponding references of primary literature are given at the end of the page.

(3) Which markers can I use to breed the *Bs2* resistance gene into a pepper cultivar?

- On the left panel, click on "**Plant resistance genes**".
- On the main panel, click on "**Pepper**".
- In the Table of Contents in the upper right area of the main panel, click on "**Resistance gene: *Bs2***".
- Look for the paragraph "**Molecular markers**" and read the information. Corresponding references of primary literature, where the markers are described, are given at the end of the page.

(4) How can I identify a suspect bacterial strain isolated from a barley leaf?

- On the left panel, click on "**Molecular Diagnosis and Diversity for Regulated *Xanthomonas***".
- On the main panel, click on "**Diagnostics: main protocols based on amplification of specific target DNAs**".
- In the table, look for "**Bacterial leaf streak and black chaff of cereals**". Corresponding references of primary literature, where diagnostic protocols are described, are given at the end of the page.

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