CURRENT REVIEW

Closing the Information Gap Between the Field and Scientific Literature for Improved Disease Management, with a Focus on Rice and Bacterial Blight

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A path to sustainably reduce world hunger, food insecurity, and malnutrition is to close the crop yield gap and, particularly, lower losses due to pathogens. Breeding resistant crops is key to achieving this goal, which is an effort requiring collaboration among stakeholders, scientists, breeders, farmers, and policymakers. During a disease outbreak, epidemiologists survey the occurrence of a disease after which pathologists investigate mechanisms to stop an infection. Policymakers then implement strategies with farmers and breeders to overcome the outbreak. Information flow from the field to the lab and back to the field involves several processing hubs that require different information inputs. Failure to communicate the necessary information results in the transfer of meaningless data. Here, we discuss gaps in information acquisition and transfer between the field and laboratory. Using rice bacterial blight disease as an example, we discuss pathogen biology and disease resistance to point out the importance of reporting pathogen strains that caused an outbreak to optimize the deployment of resistant crop varieties. We examine differences between infection in the field and assays performed in the laboratory to draw awareness of possible misinformation concerning plant resistance or susceptibility. We discuss key data considered useful for reporting disease outbreaks, sampling bias, and suggestions for improving data quality. We also touch on the knowledge gap in the state-of-the-

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art literature regarding disease dispersal and transmission. We use a recent case study to exemplify the gaps mentioned. We conclude by highlighting potential actions that may contribute to food security and to closing the yield gap.

Keywords: bacterial pathogenesis, management, plant-pathogen interactions, resistance genes, rice, susceptibility

During the COVID-19 pandemic, many laypersons learned about epidemiology. Early after the SARS-CoV-2 outbreak in Wuhan, COVID-19 spread rapidly in Asia, but only a handful of cases were reported in Europe. When the first few cases were reported in Europe (Spiteri et al. 2020), based on the limited data during the early phase, it was difficult to determine the extent of the threat and whether Europeans were susceptible or resistant to the virus. Conclusions had to be delayed until the disease spread much further. It did not take long until the disease spread rapidly in Europe and the rest of the world, and we learned that the early snapshot of infection (or lack thereof) could not provide reliable information on the susceptibility of a population. Among the key challenges in the early stages of a disease outbreak were sample scarcity, the lack of tools for monitoring, and the limited knowledge of doctors and officials. Especially at times shortly after an outbreak was detected, data are necessarily biased due to sample selection (i.e., initial analyses are carried out at the site where the first cases were detected) (Zhao et al. 2021). Sampling bias is considered a major potential issue in the later stages of a rapidly spreading disease (Liu et al. 2022).

Another of the important lessons that many laypersons learned from the COVID-19 pandemic was that it is important to know which variants or strains of the virus were present in a particular country or region. The first SARS-CoV-2 strain detected in Wuhan evolved into several strains that are geographically separated before emerging as the Delta strain that caused the second deadly COVID-19 wave in 2021 (https:// www.who.int/director-general/speeches/detail/who-directorgeneral-s-opening-remarks-at-the-media-briefing-on-covid-19-30-july-2021). While many were vaccinated against the early variants of SARS-CoV-2, the vaccines were not protective against the newly emerging strains, including the Delta strain



(Brown et al. 2021; Kumar et al. 2022). To date, booster shots are constantly being developed to offer protection against the virus (https://www.fda.gov/news-events/press-announcements/fdaauthorizes - updated - novavax - covid - 19 - vaccine - formulatedbetter-protect-against-currently; https://www.verywellhealth. com / covid - 19 - booster - shots - what - you - need - to - know -5202116). Geo-epidemiology is extremely important but challenging because of the difficulty in obtaining reliable data that might help to decide the best measures for protection from the virus. In principle, a lot of what could be learned from the COVID-19 pandemic may also be relevant in the context of the emergence and spread of crop diseases in agriculture.

In this opinion piece, we try to draw lessons from the COVID-19 pandemic and exemplify rice bacterial blight (BB) disease caused by *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) to draw attention to the gaps in current literature in reporting meaningful and useable data that can be used for tackling BB. We hope that such lessons are transferable to other crop studies as well.

Potential Gaps in Reporting Information on Pathogen Strains: Classification of Resistance Requires Specification of Pathogen Strain

A disease is typically not caused by a singular, genetically homogenous strain. Rather, considering geography and evolution, pathogens constitute highly diverse populations. Variability between strains can be very high and is often highest at the point of origin and differentiating with geographical distance. For instance, the endemic *Xoo* strains that cause BB in Asia, Africa, and the Americas are evolutionarily very different (Oliva et al. 2019). Whole genome sequencing and pathotyping have shown that these bacterial strains evolve rapidly. Consequentially, pathogen populations are structured according to geographical origin and year of collection (Diallo et al. 2023).

Analogous to COVID-19, BB outbreaks also do not deal with a single strain of Xoo but instead populations of diverse strains, some of which can break a particular resistance gene. While vaccination protects against the strains for which the vaccine was generated, it is less effective on the escapes (Andreano et al. 2021). Xoo injects specialized effectors called transcription activator-like effectors (TALes) to induce the expression of SWEET sugar transporter genes. As a result, SWEETs mediate sugar export to Xoo presumably for feeding and proliferation. In the case of SWEET-based BB susceptibility, we deal with "genefor-gene interactions", meaning that disease can progress only when a TALe matches a particular gene product variant in the host (i.e., the TALe PthXo1 for the induction of OsSWEET11; PthXo2 for OsSWEET13; and PthXo3, AvrXa7, TalC, and TalF for OsSWEET14) (Chen et al. 2012). Since different Xoo strains have different TALes and different rice varieties may carry variants in the TALe binding site, a particular rice variety may be susceptible to one strain but not another (Antony et al. 2010; Zaka et al. 2018). So, the classification "resistant" is not generalizable. It is therefore important to provide strain information (i.e., TALe repertoire) with resistance classification (McDonald and Linde 2002).

Publications and labels differ substantially regarding the depth of description for rice varieties. Typically, descriptions provided for a rice variety do not provide information on the pathogen strains tested. Below, we provide three arbitrarily chosen examples from the Philippine Seedboard (PSB) (https://www.pinoyrice.com/rice-varieties/), the Tanzanian Agricultural Research Institute (TARI, https://www.tari.go.tz/tari-dakawa/technologies/improved-rice-varieties), and a manuscript (Mackill and Khush 2018):

- NSIC 2014 Rc352 (Tubigan 27)- "...Intermediate reaction to Blast and BLB..." (Note: BLB abbreviation for bacterial leaf blight is an alternative name for BB.)
- TXD306 (SARO 5)- "Points of merits: ...resistant to diseases such as Bacterial Leaf Blight (BLB) and Rice blast..."
- "IR64 is resistant to Bacterial Blight (BB) disease (caused by *Xanthomonas oryzae* pv. *oryzae*) and possesses the major gene *Xa4* for resistance...".

Notably, a reference provided in the manuscript by Mackill and Khush (2018) provides the necessary information, that is, both geodata and the exact strains that were used for determining susceptibility ("strain IRN987 was used in 1988, and PX086 of race 2 was used in 1990" as listed in Adhikari et al. [1994]); however, the statement that IR64 was resistant to BB disease in Asia is not fully accurate as shown by recent reports showing that IR64 is susceptible to other *Xoo* strains from Asia (Eom et al. 2019; Mackill and Khush 2018). Similarly, a recent BB outbreak in Tanzania has proven the susceptibility of SARO-5 towards new Xoo strains (Schepler-Luu et al. 2023). Scientific literature that carefully describes the resistance traits of a rice variety along with the strains tested and their origin should be exemplified as a good practice (Kam et al. 2018; Mutiga et al. 2017; Yugander et al. 2017). We suggest that it will be useful to provide more detailed statements regarding which strains were tested, or at least where the tests were performed, combined with information on the locally prevalent strains. In countries such as India or the Philippines, Xoo populations have been monitored over many decades (Laha et al. 2016; Mew et al. 1992; Quibod et al. 2020), and strains have been classified into races. Classification of Xoo races is based on the ability of a particular strain to infect different rice cultivars (Mew 1987; Shanti et al. 2010) (described below). Thus, if molecular characterization of a strain is not possible, information on the location/origin of the strains could at least allow speculation regarding the genetic basis of resistance and the virulence mechanisms. We cautiously note that due to the variability of strains and their virulence mechanisms, the description of a variety would best be always accompanied by information on the strains used for testing susceptibility or resistance.

Suitable facilities can help in genotyping the pathogen strains and infer their relatedness with other pathogens through genetic diversity studies, allowing the assessment of bacterial dispersal patterns and the development of proper control strategies. Multi-locus variable number of tandem repeats (VNTR) analysis (MLVA) based on the analysis of tandem repeats used for showing the relatedness of a bacterial strain is a widely used method for epidemiological analysis (Catara et al. 2021). An MLVA scheme based on 16 VNTR loci has been implemented for X. oryzae pathovars, allowing for local to global spatial scale analysis of Xoo dispersal patterns (Poulin et al. 2015). In parallel, Xoo race analysis may be useful to guide the optimal deployment of suitable resistance rice lines in a given region. The International Rice Research Institute (IRRI) has, to that end, developed a set of near-isogenic rice lines each carrying a single R gene against known Xoo virulence genes that allows for testing of the resistance of a particular *Xoo* strain and thus discriminates strains into races (http://www.knowledgebank. irri.org/ricebreedingcourse/Breeding for disease resistance Blight.htm). A recently developed kit that uses a set of rice lines with variants in the TALe binding sites is useful for determining the TALe repertoire of an Xoo strain (Liu et al. 2024). An additional reason for genotyping includes that symptoms caused by some bacterial Pantoea species, for example, are difficult to distinguish from those caused by *Xoo* (Mondal et al. 2011).

Potential Gaps in Reporting Disease Susceptibility or Resistance: Reporting Resistance with High Reliability

To evaluate the virulence of a particular Xoo strain on a specific rice variety, scientists developed a reliable and highly predictive assay called the leaf-clipping assay decades ago (Kauffman et al. 1973). As the author states: "In a replicated yield trial, 135 entries were inoculated 60 days after seeding on one side of each plot... the clipping inoculation score and the natural disease score were highly correlated." The assay introduces a severe wound by clipping the tip of the leaf with scissors dipped in bacterial suspension, thereby introducing a high bacterial titer (typically > 10^7 colony forming units [CFU]) that are in the logarithmic growth phase directly into the wound. Such an "overkill" assay tests whether a particular Xoo strain can cause disease under an extreme infection condition than what could typically occur in the field. Disease symptom formation is then observed over 2 weeks. The extent of the damage is scored based on the length of the lesion caused by Xoo or, in other words, the efficacy with which Xoo were able to invade and spread in the host tissue (Fig. 1).

One concern regarding Kauffman assays has been that the high bacterial titers in the optimal growth stage are conditions that do not typically occur in nature. The assay likely underestimates the actual resistance of a rice cultivar, since the assay overlooks various steps in the infection process that contribute to successful infection in the field. However, the high correlation between the Kauffman assay conducted in the greenhouse and field performance has been vastly reported (Adhikari et al. 1995; Fred et al. 2016; Padmaja et al. 2017). The IRRI has established a scale for the Kauffman assay to classify resistance: a plant with a lesion length <5 cm is considered resistant; 5 to 10 cm is moderately resistant; 10 to 15 cm is moderately susceptible; and >15 cm is susceptible (lesion length is measured at the maximum tillering stage and 14 days after infection; http://www.knowledgebank.irri.org/ricebreedingcourse/ Breeding_for_disease_resistance_Blight.htm). The scale is true for an infection assay conducted under controlled conditions



Fig. 1. Disease symptoms for bacterial blight (BB)-susceptible and -resistant rice varieties based on Kauffman's leaf-clipping assay. **A**, Leaves from *Oryza sativa* L. cultivar Komboka infected either by the *Xanthomonas oryzae* pv. *oryzae* (*Xoo*) strain PXO99^A[ME2] (a *PthXo1* knockout derivative of PXO99^A) or PXO86 (containing *avrXa7*). While PXO99^A[ME2] is not virulent, Komboka is fully susceptible to PXO86, as indicated by lesions along the leaf. **B**, Leaf-clipping assay performed in the greenhouse: *O. sativa* cultivar Improved Samba Mahsuri (*xa5* + *xa13* + *Xa21*) is fully resistant to the Indian *Xoo* strain IX-020 (Yugander et al. 2017). Note: only local lesion at the clipping site.

(i.e., in growth chambers or greenhouses). In the field, however, a rice variety is considered resistant even if the lesion length is about 5 cm. A lesion length of 5 cm caused by hypersensitive responses (due to defense activation against the Xoo strain) may extend lengthwise over time but not the diseased leaf area (indicating successful disease suppression). In contrast, diseased leaf areas on susceptible rice plants will expand lengthwise and widthwise under a conducive environment over an incubation period of 2 or more weeks. One could, thus, understand that the timing of infection is also an important aspect when sampling for disease and resistance traits. It is also important to note that, in the context of early timepoint sampling, disease severity will depend on both the bacterial titer and timing of the infection in a field (i.e., low titers of bacteria introduced at late stages of crop development will likely only cause minor harm). Moreover, at late stages of plant development, symptoms cannot be distinguished from senescence, possibly leading to false negative classifications. Generally, to reliably classify the resistance trait of a rice variety, survey and field sampling should be performed at the peak of the epidemic, preferably over several time points, in addition to distinguishing lesion length and types (hypersensitive response or diseased area).

Potential Gaps in Reporting Disease Incidence and Severity, Sampling Bias, and Disease Monitoring

Similar to COVID-19, sampling during the early phases of an outbreak will initially be scarce, not systematic, and performed locally at the site of disease observation. Once the disease severity is realized, data collection will expand with the recognition that there is a serious threat to the harvest. In the case of the outbreak in Tanzania, the disease outbreak has spread all across Tanzania within just 3 to 4 years (Schepler-Luu et al. 2023) (Fig. 2). The consequence is sampling bias, which can occur for many reasons, such as the lack of outbreak information from previous years, late sampling during the season, the inability to survey across large areas due to budget or personnel constraints, and initially limited expertise of the surveyors.

The two key parameters for evaluating the disease are incidence and severity. Incidence describes the extent to which the disease has been established in a given field or, in essence, the percentage of plants with symptoms. Severity provides information on how severely individual plants are affected, usually expressed as a percentage of diseased leaf area (% DLA) per leaf of representative plants (Fig. 2). Standardized approaches for BB survey and sampling have been established (Ardales et al. 1996; Vera Cruz et al. 1996). At early stages of BB infection in a field (i.e., when the disease has not spread throughout the field), first symptoms are often observed along the irrigation flow. A likely reason is that the inoculum (bacterial ooze from leaves) is carried with the irrigation water, causing field-to-field transmission. Thus, at early stages, it is worth focusing on the locations where symptoms emerge. For low disease incidences during the early stages, it is challenging to use unbiased designs for surveying and sampling in a field plot. Under conditions of a random distribution of the infection across a particular field (i.e., at the later stages of infection), disease scoring and sampling should be performed following a W-shaped pattern or by using diagonals across the field plot. For each $1-m^2$ area along the W or diagonal, count the number of infected hills and estimate the percentage of plants with different levels of severity scored according to the standard scale by the IRRI (1 to 5% DLA, scale 1; 6 to 12% DLA, scale 3; 13 to 25% DLA, scale 5; 26 to 50% DLA, scale 7; and 51 to 100% DLA, scale 9). Subsequently, statistical analyses can be obtained from the W or diagonal sampling design to provide an accurate picture of disease incidence and severity. The same procedures will be useful for systematic genotyping approaches (e.g., to evaluate the diversity and evolution of *Xoo* strains in a field setting) (Ardales et al. 1996; Vera Cruz et al. 1996).

Unlike the collaborative worldwide effort in reporting cases of COVID-19, outbreaks of a crop disease do not involve a well-developed alert system (https://www.who.int/emergencies/ disease-outbreak-news). Breeders, farmers, and surveyors may not be able to recognize a new disease nor have the tools for diagnosis and surveillance. In most cases, it may be difficult to distinguish the disease symptoms from a nutrient deficiency (Fig. 3). Many countries lack an effective alert system, except for Locust Watch and RustSPORE (https://www.fao.org/agriculture/ crops/rust/stem/rust-report/en/). Strategies will have to be developed based on the epidemiology of the disease and how it spreads (aggregate or random). An alert system and a rapid response are critical in the context of crop disease outbreaks because the introduction of resistance genes into susceptible rice lines by conventional breeding can take up to 14 years or can be cut down to 7 years by marker-assisted background breeding (MABB) (Gopala Krishnan et al. 2022). Efficient monitoring of crop diseases as performed in India (Laha et al. 2016; Oliva et al. 2019) and the United States (https://www.npdn.org/) should be exemplified. An international team of breeders and scientists recommended global surveillance by geographic information systems (GIS) as an important tool for the early detection of disease outbreaks and as a means for improving food protection globally (Carvajal-Yepes et al. 2019; Hu et al. 2023; Oliva et al. 2019; Parnell et al. 2017). The EM-PHASIS project by the European Union concluded effective early disease detection and disease monitoring with sentinel plots (https://emphasis.plant-phenotyping.eu/). Plant Village

Fig. 2. An example for sampling bias during the early outbreak of bacterial blight (BB) in Tanzania. Before 2019. BB was not considered a serious disease in Tanzania. In 2019, severely infected fields were reported for the first time in the Morogoro region. Local sampling was repeated in this area in 2021. In 2022, the surveys and sampling were expanded to locations across Tanzania. From these data, the exact route of disease spread cannot be deduced; also, the severity reported will be affected by the time of observation and the titer of bacteria. Map modified from Schepler-Luu et al. (2023) and reused under the terms of the CC BY 4.0 license.

(https://plantvillage.psu.edu/projects), a joint initiative from the United Nations Food and Agriculture Organization (UN FAO), the Consultative Group on International Agricultural Research (CGIAR), and other publicly funded institutions, is developing artificial intelligence (AI)-based systems for some diseases including cassava blight but not rice diseases. The systematic implementation of airborne imaging-based survey technology (e.g., using hyperspectral imaging) may be the most promising option for effective monitoring and avoidance of sampling bias in the future (Shi et al. 2023). This manuscript does not provide a comprehensive review of the rapidly developing analytic tools, airborne monitoring systems, or deep-learning and AI systems and modeling approaches. Interested readers are conferred to a select set of annotated references in Box 1.

Potential Gaps in Understanding Disease Transmission and Dispersal

Presently, neither the prevalent transmission mechanism(s) nor the complex infection of the rice xylem by *Xoo* is fully understood. Multiple transmission sources have been invoked, including the bacterial ooze on leaves in the late stages of infection of a rice plant and *Xoo* that survived on rice stubble, straw, or hulls (Box 2). Transmission via seeds, although not shown to date, can also not be excluded. Alternative hosts might serve as reservoirs between planting seasons. The dispersal of the pathogen itself can be mediated by strong wind, animals, and humans or by seed distribution systems. New infections can be caused by contaminated irrigation water, plant-plant transfer, entry into hydathodes, or via wounds (Mew 1987; Mew et al. 2004, 1993). Careful surveys combined with modeling approaches used for analyzing medical epidemics could be an



option to identify the prominent sources and transmission pathways and provide means for reducing disease incidence through improved management practices.

Case Study: A BB Outbreak in Tanzania

In 2019, several rice fields in Dakawa, Tanzania, that showed BB symptoms were identified (Schepler-Luu et al. 2023). Phylogenetic analysis of the Xoo strains isolated from the infected field indicated a high probability that the new strains introduced to Tanzania (iTz) were recently introduced from Asia since their closest homologs are strains from southern China. Unlike typical Xoo strains found in Africa, iTz uses virulence mechanisms that resemble the Asian Xoo strains, which African rice varieties are susceptible against (Schepler-Luu et al. 2023). Initial sampling for Xoo could only be carried out in rice fields that were infected. In subsequent years, BB was also observed in adjacent fields in the neighboring Lukenge. Notably, in 2021, field sampling was limited to Dakawa and Lukenge (Fig. 2). These findings triggered more comprehensive surveys at multiple sites across Tanzania in 2022, resulting in the detection of BB with different levels of severity. In 2023, one may consider surveying even more sites. Observations on disease progression and severity were made by teams of experts who traveled from site-to-site, so they collected information only at a single time point. Since BB had not been observed in previous years in these regions, one would hypothesize that the outbreak originated in Dakawa between 2018 and 2019. However, due to the severe sampling bias, this hypothesis must be considered with extreme caution and cannot be used for modeling. The rice variety SARO-5 was grown in most areas that were surveyed and was shown to be susceptible to iTz strains. In 2022, BB symptoms were detected on the Komboka rice variety grown close to the southeastern border of Tanzania. The infected Komboka plants in this field



Fig. 3. Comparison between nutritional stress and disease symptoms on rice leaf. Strikingly similar symptoms caused by nutritional stress and diseases result in difficult, and often wrong, interpretations of symptoms. Photo sources (with permission; original images were cropped to focus on symptoms): ^a http://www.knowledgebank.irri.org/ (Dobermann and Fairhurst 2000); ^b https://infonet-biovision.org/PlantHealth/MinorPests/ white-tip-nematode; ^c Sharma et al. (2023); ^d https://www.yara.com.gh/ crop-nutrition/rice/; ^e Sethy et al. (2020).

showed only moderate severity. However, leaf-clipping assays in the greenhouse demonstrated that Komboka was fully susceptible to the iTz strains (Schepler-Luu et al. 2023).

What can be implemented to break the BB outbreak in Tanzania and its neighboring countries? Effective monitoring of an outbreak and its spread across the globe is relevant. GIS systems such as PathoTracer can be implemented (Eom et al. 2019). CGIAR developed PathoTracer as a platform that integrates early-season pathogen disease diagnostics to accurately define breeding priorities and guide coordinated actions to man-

Box 1

Some select publications regarding new technologies for surveying, monitoring, and predictive modeling

- Hu et al. (2023) provide deep learning-based, multi-scale dual-branch structural pest identification models for rice diseases including blight and blast.
- Dionisi et al. (2023) review modeling approaches for agroecological protection of the rice crop.
- Xing et al. (2020) highlight the relevance of hubs (seed distribution centers, trade locations, etc.) and pathways that connect croplands for disease spread. They recommend that due to the limited availability of capacities for surveying, "cropland connectivity risk maps" can help to pinpoint hubs and "cropland bridges" as sites where surveillance and management should be prioritized.
- Bebber et al. (2019) developed predictive models for current pest distributions. They conclude that the probability of the presence of the disease increases with host abundance, as well as the occurrence of the disease in neighboring regions; global prevalence is also a potential key factor. By comparison, the probability for the presence of the disease decreases with the distance from coastlines and with crop use. Their model may also help to quantify pseudoabsence (the false assumption that the disease is absent due to lack of information).
- Mastin et al. (2019) developed a generic framework that can be for comparing disease detection technology. Their analysis indicates that, for the United Kingdom, visual inspection of the infection by *Phytophthora ramorum* may be more cost-effective relative to diagnostic tests.
- Ristaino et al. (2021) discuss an integrated approach, including tools for disease surveillance; predictive modeling and data analytics; the role of data mining and big data for geographic monitoring; the role of transport routes of plant material by using network analysis; the identification of hubs as sites that carry risk and that could be prioritized for testing and monitoring; population genomic surveillance for monitoring emerging pathogens; extension and digital advisory services for small-scale producers regarding plant disease; and new technologies such as sensors for the detection of infections.
- Parnell et al. (2017) address key ideas such as what the likely disease incidence directly after the first report of an invading pathogen is; pseudoabsence; spatially explicit stochastic models to optimize targeting of surveillance and control; innovative detection and diagnostic technologies; passive surveillance networks (e.g., citizen science); and how improved efficacy of surveys can be provided by epidemiological insights based on the dynamics of disease spread (location and timing).

age crop diseases in real-time for key diseases in Asia and Africa. The toolkit helps identify genetic strains of *Xoo* in particular regions to assist in the selection of suitable resistance profiles of rice varieties for deployment to manage local outbreaks (http://webapps.irri.org/pathotracer/). A global task force, led for example by the FAO that follows the lessons learned by the World Health Organization (WHO), may be useful for tackling key crop diseases. Given that the iTz strains are distinct from endemic *Xoo* strains from Africa and most similar to strains from

Box 2

Potential transmission routes of Xanthomonas oryzae pv. oryzae (Xoo)

- Bacterial blight (BB) symptoms include sequestration of bacterial ooze. Ooze with high bacterial titers is likely one of the major sources of transmission (Mew et al. 1993).
- Irrigation water can be a source of infection and transmission; the layout of irrigation systems may be a means to reduce downstream transmission (Kouassi et al. 2005).
- Xoo can persist for extended periods on straw, hulls, husks, and stubble; field management and hygiene measures can be taken to avoid contamination (Mew et al. 1993).
- Xoo has alternative hosts, which may serve as a reservoir (Lang et al. 2019; Mew et al. 1993; Noda and Yamamoto 2008). Removing alternative hosts may help protect from the disease.
- Wounding during transplanting in the presence of *Xoo* is suspected as a potential cause. Avoidance of transplanting could be beneficial.
- 6. Storms are considered a potential route for transmission. Dispersal of *Xoo* and infection through hydathodes, which may require that individual bacteria carried in aerial droplets to be sufficient for infection. Although the presence of windbreaks has been reported to successfully reduce the spread of *Xanthomonas citri* pv. *citri*, whether storms predominantly impact local spread (Bock et al. 2010) or whether they can carry *Xoo* across long distances remains to be tested.
- Plant-to-plant transfer is likely a factor for spreading within fields (Mew et al. 1993), especially in storms. Lower plant density could help reduce spread but comes at reduced yield per area.
- Animals can cause transfer by causing wounds and carrying bacteria from ooze via fur. Reducing the prevalence of small animals such as rats could help reduce spread.
- Humans can cause transfer by causing wounds, using contaminated farming tools, and carrying bacteria from ooze on clothes. Management practices could possibly reduce spread.
- 10. Infection can be caused via seed import or distribution (e.g., seed centers), with the pathogen on seeds or hulls (Andersen et al. 2019). Implementing suitable hygiene (e.g., efficient removal of hulls before distribution and treatment in hot water) could reduce transmission along this path.
- Rigorous import controls and sterilization before planting could be beneficial to improve plant protection and quarantine (PPQ).

Asia, iTz has possibly been introduced inadvertently (Schepler-Luu et al. 2023). Therefore, one should also consider improvements in guarantine and measures to reduce chances for unintended introduction and transmission within a country without harming trade and exchange. Systematic surveys at the same locations and at different time points with careful analyses of the plant growth stage and yield losses and continuous genotyping of the causative strains may provide a basis for long-term strategic management of the disease. Recent analytical methods allow the reconstruction of epidemics (Voznica et al. 2022) that may help in the deployment of adapted successful control strategies. Similar surveys will have to be coordinated across the borders to neighboring countries to evaluate the spread. The generation of genetic resistance, through classical breeding, marker-assisted breeding, and new breeding technologies, needs to be implemented immediately to protect local rice lines from outbreaks (Dossa et al. 2015; Schepler-Luu et al. 2023). The rice tracer and/or diagnostic SWEET^R-kit may help local scientists identify the best path to resistance breeding (Eom et al. 2019; Liu et al. 2024). The kits include tools that help to identify which TALes the new Xoo strain carries and which SWEET susceptibility gene is targeted (Eom et al. 2019). Importantly, quarantine measures and coordination between countries must be improved; task forces must be established; education and training for farmers, breeders, and scientists must be strengthened; continuous effective monitoring of diseases is necessary; and pipelines for rapid resistance breeding training must be implemented. Importantly, it is necessary to empower the locals.

Summary and Outlook

Climate change and disease transmission by international trade, aid, and travel will likely impact the occurrence, spread, and severity of crop diseases (Duku et al. 2016; Laha et al. 2016). More needs to be done for disease prevention and plant protection from the pathogen to curb yield losses. Geoepidemiology is highly relevant in the context of both human and crop diseases. Despite the fundamental differences, the plant field can learn vastly from medical epidemiology. Early sampling bias is unavoidable, but global preparedness, diagnostic tools, GIS systems, knowledge and education, and awareness of the issues pertaining to sampling bias are important. Careful data analysis and reporting (e.g., in the context of the genetics of plant-pathogen interactions) appears highly relevant. As a costeffective measure and to fully harvest information from the field, we recommend that governments worldwide provide funding to enable surveyors to define pathogens better and to require a more detailed description of newly registered breeding material regarding resistance to specific pathogen strains. Hygiene brought about major advances in human health; likewise, proper crop management can likely play a similar role in protecting crops from diseases (Mew et al. 2004). Improved management requires adequate information for farmers and training. Efficient plant pest quarantine is also relevant to reduce the risk of the introduction from other states, countries, or continents. Since the cost of disease outbreaks is immense, it seems economically reasonable to invest in improved plant pest quarantine, especially in countries where small-scale food producers are so dependent on healthy crops.

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