EPPO Datasheet: *Xanthomonas oryzae pv. oryzicola*

Last updated: 2022-09-29

IDENTITY

Preferred name: *Xanthomonas oryzae pv. oryzicola*
Authority: (Fang et al.) Swings et al.
Taxonomic position: Bacteria: Proteobacteria: Gammaproteobacteria: Lysobacterales: Lysobacteraceae
Other scientific names: *Xanthomonas campestris pv. oryzicola* (Fang et al.) Dye, *Xanthomonas oryzicola* Fang et al., *Xanthomonas translucens f. sp. oryzicola* (Fang et al.) Bradbury
Common names: BLS, bacterial leaf streak of rice, leaf streak of rice
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EPPO Categorization: A1 list
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EU Categorization: Quarantine pest ((EU) 2019/2072 Annex II A)
EPPO Code: XANTTO

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Notes on taxonomy and nomenclature

Bacterial leaf streak of rice, caused by *Xanthomonas oryzae* pv. *oryzicola*, has quite similar symptoms to bacterial leaf blight of rice, caused by *Xanthomonas oryzae* pv. *oryzae*, **see EPPO Datasheet on *X. oryzae* pv. *oryzae***. Bacterial leaf streak was first observed (but thought for a considerable time to be bacterial leaf blight) in the Philippines in 1918 (Reinking, 1918). It was 'rediscovered' in China in 1957, described as bacterial leaf streak of rice and the causal bacterium was named *Xanthomonas oryzicola* (Fang *et al*., 1957). *X. oryzicola* was reclassified in later years, first as *X. translucens* f. sp. *oryzicola*, and then as *X. campestris* pv. *oryzicola* (Bradbury, 1971; Aldrick *et al*., 1973; Dye, 1978). The combination *Xanthomonas translucens* (Jones *et al*., 1917) f.sp. *oryzae* (Uyeda & Ishiyama, 1928) Pordesimo 1958 has been incorrectly used (see Bradbury, 1971, Aldrick *et al*, 1973).

On the basis of a polyphasic taxonomical study, Swings *et al*. (1990) placed both bacteria as pathogenic varieties within the species *Xanthomonas oryzae* as *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae.*

For a long time, and unlike *X. oryzae* pv. *oryzae*, it was not possible to discriminate pathogenic races for *X. oryzae* pv. *oryzicola* (Ou, 1985), but recently some race variation was reported from Southern China (Yang *et al*., 2020). Variability among *X. oryzae* pv. *oryzicola* strains based on genomic studies is very high (Adhikari & Mew, 1985; Gonzalez *et al*., 2007; Zhao *et al*., 2012; Wonni *et al*., 2011, 2014). Whole genome sequencing was performed with the pathotype strain of *X. oryzae* pv. *oryzicola* (WHRI 5234?=?NCPPB 1585?=?ICMP 5743, isolated in Malaysia in 1964, Michalopoulou *et al*., 2018).

A strain slightly deviating from *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae* isolated from the (invasive) perennial grass weed species *Leersia hexandra* (southern cutgrass or rice swamp grass) was described in 1957 from China by Fang *et al*. (1957) as *X. leersiae*. Based on comparative genomics of strains from China, Burkina Faso, India, Mali and Uganda it was later described as *X. oryzae* pv. *leersiae*. *X. oryzae* pv. *leersiae* is most closely related to *X. oryzae* pv. *oryzicola*, but it is also a close relative of *X. oryzae* pv. *oryzae* (Lang *et al*., 2019).

X. oryzae strains occurring in the United States, and first reported in 1989 (Jones *et al*., 1989), appear to be (slightly) different from *X. oryzae* pv. *oryzicola*, *X. oryzae* pv. *oryzae*, and *X. oryzae* pv. *leersiae*. These strains have low virulence on rice, they have not yet been distinguished at pathovar level and are called (also in this document) *X. oryzae* 'USA' (Xu & Gonzales, 1991; Gonzalez *et al*., 2007; Triplett *et al*., 2011; Hajri *et al*., 2012; Lang *et al*., 2019).

X. oryzae as a species, is genomically closely related to *X. vasicola* pv. *vasculorum*, causing leaf scald of maize, sugarcane and some other Poaceae and *X. vasicola* pv. *musacearum*, causing banana xanthomonas wilt. It is only

distantly related to other *Xanthomonas* species and pathovars pathogenic to Poaceae, such as the host specialized pathovars of *X. translucens* and *X. albilineans* (Rodriguez *et al*., 2012; Hersemann *et al*., 2017; Sapkota *et al*., 2020).

For additional taxonomic and nomenclatorial information see CABI (2022a and b) and Niño-Liu *et al*. (2006).

HOSTS

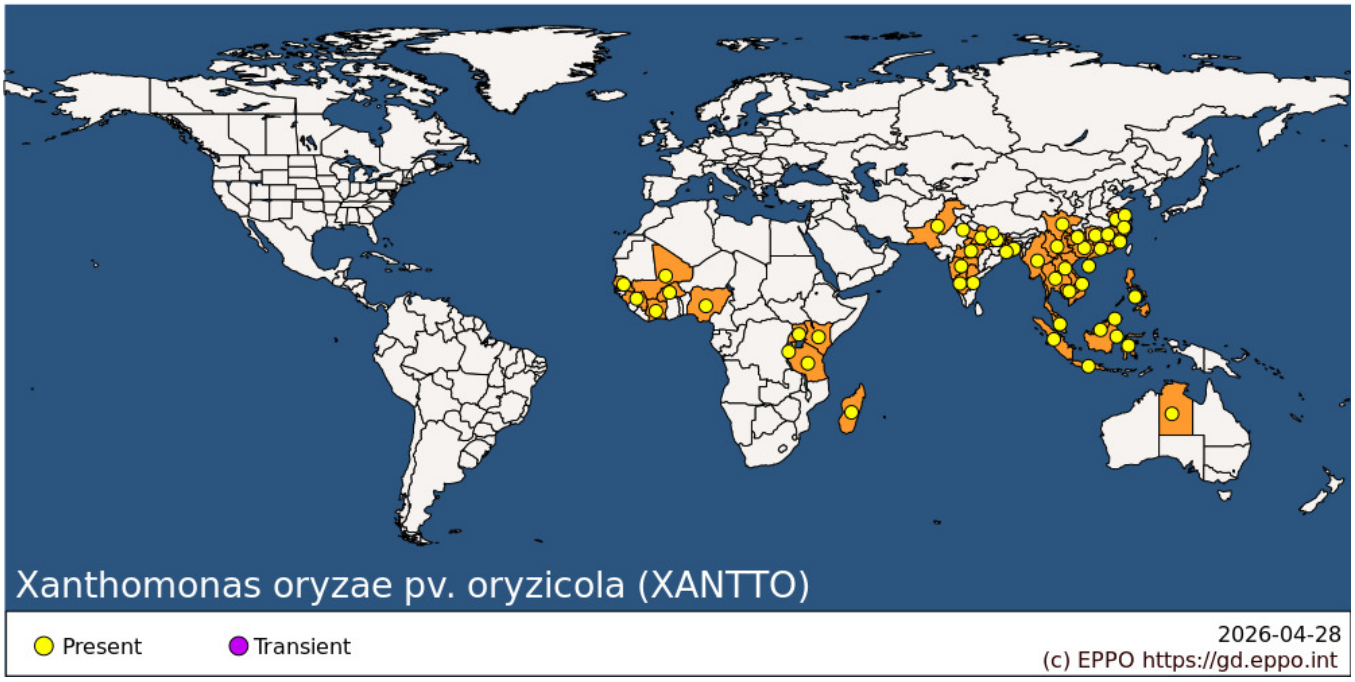
The principal host of *X. oryzae* pv. *oryzicola* is rice, *Oryza sativa*. The sticky, short-grained *O. sativa* subsp. *Japonica* (syn. *O. oryza* subsp. *Sinica*) is less susceptible to *X. oryzae* pv. *oryzicola* than the non-sticky, long-grained *O. sativa* subsp. *Indica*. In Europe, *O. sativa* subsp. *Japonica* is mainly grown (Agri-food Data Portal, 2022; Cai *et al*., 2013; Kraehmer *et al*., 2017).

Other important hosts belong to the Poaceae family, both wild and cultivated, annual and perennial species (Reddy & Nayak, 1975; Leyns *et al*., 1984; CABI, 2021; EFSA, 2018).

Host list: *Brachiaria lata*, *Digitaria horizontalis*, *Echinochloa colonum*, *Eleusine indica*, *Leersia hexandra*, *Leptochloa mucronata*, *Oryza barthii*, *Oryza glaberrima*, *Oryza latifolia*, *Oryza longistaminata*, *Oryza minuta*, *Oryza officinalis*, *Oryza sativa*, *Paspalum scrobiculatum*, *Paspalum vaginatum*, *Rottboellia cochinchinensis*, *Zizania aquatica*, *Zizania palustris*, *Zoysia japonica*

GEOGRAPHICAL DISTRIBUTION

Bacterial leaf streak was first reported in the Philippines in 1918 and is widely present in tropical and subtropical Asia, including China, Malaysia, India, Indonesia, and also in Northern Australia (under the old and incorrect name *Xanthomonas translucens* f.sp. *oryzae*, Aldrick *et al*., 1973) and West and East Africa, including Madagascar (CABI/EPPO, 2015). It has not been reported from temperate regions, and unlike *X. oryzae* pv. *oryzae* (**see EPPO Datasheet on *X. oryzae* pv. *oryzae***) no geographically distinct groups have been determined (Ou, 1985; Mew, 1991).



Africa: Burkina Faso, Burundi, Cote d'Ivoire, Guinea, Kenya, Madagascar, Mali, Nigeria, Senegal, Tanzania, United Republic of, Uganda
Asia: Bangladesh, Cambodia, China (Anhui, Fujian, Guangdong, Guangxi, Guizhou, Hainan, Hunan, Jiangsu, Jiangxi, Sichuan, Yunnan, Zhejiang), India (Andhra Pradesh, Bihar, Haryana, Karnataka, Madhya Pradesh, Maharashtra, Uttar Pradesh, West Bengal), Indonesia (Java, Kalimantan, Sulawesi, Sumatra), Lao People's

Democratic Republic, Malaysia (Sabah, Sarawak, West), Myanmar, Nepal, Pakistan, Philippines, Thailand, Vietnam
Oceania: Australia (Northern Territory)

BIOLOGY

X. oryzae pv. *oryzicola* usually enters the host plant through stomata or leaf lesions caused by insects, heavy rain and/or wind. It multiplies in the apoplast of mesophilic parenchyma cells and spreads actively in the intercellular spaces. It causes linear water-soaked to necrotic leaf streaks, without entering the vascular tissues (Mew, 1993). *X. oryzae* pv. *oryzicola* has a strong cell-wall degrading (cellulose) activity. This differs from *X. oryzae* pv. *oryzae* which mainly infects the plant via hydathodes (water pores, connected to vascular tissue) and multiplies and spreads mainly in the vascular tissue (Tsuno & Wakimoto, 1983; Zou *et al*., 2012, Cao *et al*., 2020).

In severe infections, *X. oryzae* pv. *oryzicola* may produce typical yellow orange (amber-coloured) exudate in the form of tiny droplets from stomata on the leaf surface. The droplets dry in the form of sticky tiny beads with or without small stalks, or also in strands. These strands may be spread by dry wind (Ou, 1985; Mew, 1991).

Both *X. oryzae* pv *oryzicola* and *X. oryzae* pv. *oryzae* can be isolated from the rice seed coat (Sakthivel *et al*., 2001; Niño-Liu *et al*., 2006), but only *X. oryzae* pv. *oryzicola* has been reported to be seed transmitted (Fang *et al*, 1957; Shekhawat, 1969; Mew, 1993; Xie & Mew, 1998; EFSA 2018). The bacterium can survive up to 5 months in seeds stored at 15-30 °C and seed transmission is efficient when sown under conditions of high humidity (Devadath, 1984).

The bacterium can persist from one season to the next on infected leaves and leaf debris, but was found not to survive in non-sterile soil (Devadath & Dath, 1970). The bacteria may survive on and in alternate hosts, such as *Leersia hexandra* and *Zizania aquatica* (Reddy & Nayak, 1975; Leyns *et al*., 1984), but this has been infrequently and/or inadequately reported (Ou, 1985; Niño-Liu *et al*., 2006).

Spread within a crop occurs by mechanical contact and via rain and irrigation water. Under favourable conditions (warm and wet with heavy winds) rapid and severe disease development can occur. The bacterium survives for up to 90 days in water at 15-20°C and up to 60 days at 25-45°C (Devadath, 1984). Contaminated irrigation water may spread the bacterium to adjacent fields (Devadath, 1984).

X. oryzae pv. *oryzicola* occurs mostly in tropical and subtropical climates and causes damage only under very wet conditions. Without continuous rain, secondary infections no longer occur (Mew, 1993; EFSA 2018).

After infection, temperature is the main determinant of disease development. Higher temperatures (26 - 32°C) favour disease development, lower temperature (below 22°C) restrain it (Devadath, 1984). Heavy nitrogenous fertilization favours disease development as is the case for *X. oryzae* pv. *oryzae* (Devadath, 1984). Insects (such as leafhoppers and grasshoppers), humans, and agricultural equipment can mechanically transmit the bacterium (Devadath, 1984). There is an apparent connection with pest damage since the bacterium readily enters insect-damaged tissue, but the exact role of these insects and that of man and machines is poorly understood.

The pathogenicity of *X. oryzae* pv. *oryzicola*, as for *X. oryzae* pv. *oryzae*, is based on a type-3 secretion system, that injects a range of type-3 effectors into rice cells (Niño-Liu *et al*., 2006; Jiang *et al*., 2020). This includes members of the Transcription Activator-Like Effector family (TALEs), major virulence factors, activating susceptibility genes of the host (Hutin *et al*., 2015). Contrary to *X. oryzae* pv. *oryzae*, which has widely present gene-for-gene resistance based on an avirulence gene (bacterium) and a resistance gene (plant), so called avr-R gene interactions, this has not been identified in the *X. oryzae* pv. *oryzicola*-rice pathosystem. Resistant rice varieties therefore only show (partial), so-called quantitative resistance (Niño-Liu *et al*., 2006; Zhao *et al*., 2004; Hajri *et al* 2012; Cai *et al*, 2017). However, to date, the avrRxo1 effector gene was found to be present in all Asian *X. oryzae* pv. *oryzicola* strains, and as it is likely to be involved in fitness/pathogenicity it is therefore important for resistance breeding (Zhao *et al*. 2004).

A high degree of genetic diversity was observed among Asian (Philippines) and African strains of *X. oryzae* pv. *oryzicola*. Strains from Mali were found to be closely related to those from Malaysia, implicating a possible transfer of the bacterium with planting material from Asia to Africa (Raymundo *et al*. 1999; Gonzalez *et al*., 2007; Wonni *et al*., 2014). In an extensive study, using 75 *X. oryzae* pv. *oryzicola* strains from South-West China and 6 differential rice varieties, Wang *et al.* (2010) discriminated 13 race groups, that showed some geographical differentiation. Yang *et al*

. (2020) could discriminate 6 pathotypes of *X. oryzae* pv. *oryzicola* in Southern China, using differential varieties, and these local rice varieties showed various levels of resistance against *X. oryzae* pv. *oryzicola*.

DETECTION AND IDENTIFICATION

Symptoms

Early symptoms are narrow, dark-green, water-soaked, interveinal streaks of various lengths, initially restricted to the leaf blades. The lesions enlarge, often showing a yellow halo and later turn yellowish-orange to brown (depending on the rice cultivar) and may coalesce. Bacterial ooze is often present on the streaks, visible as tiny amber-coloured drops. In advanced stages, the disease is difficult to distinguish from that caused by *X. oryzae* pv . *oryzae* but lesion margins remain linear (rather than wavy for those caused by *X. oryzae* pv. *oryzae*). It can be noted also that both *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae* may occur simultaneously in the same field, and sometimes even in the same plant (Goto, 1992; Mew, 1993). In a final stage, streaks become brown to greyish and may completely wither. Infected florets turn brown or black and the ovary and stamens die. Symptomatic infected seeds show browning of glumes and necrotic endosperm. Symptoms are often associated with those caused by larvae of lepidopterous leaf rollers/folders (e.g., *Cnaphalocrocis medinalis*), and of the rice hispa beetle (*Discladispa armigera*), because bacteria readily enter the damaged tissue resulting from these insect infestations (Ou, 1985; Niño-Liu *et al*., 2006; EFSA, 2018).

Morphology

X. oryzae pv. *oryzicola* is an aerobic, motile, Gram-negative, non-spore-forming, capsulated rod, occurring singly or in pairs, 1.0-2.5 x 0.4-0.6 µm in size, with one polar flagellum (Bradbury 1970, 1986).

Most of the procedures described for the isolation of *X. oryzae* pv. *oryzae* from rice plants, can also be applied for the isolation of *X. oryzae* pv. *oryzicola*. (EPPO, 2007). Faster growing contaminants often occurring on and in diseased tissues, such as species of *Pantoea* or xanthomonad-like saprophytes may overgrow the slow growing *X. oryzae* pv. *oryzicola* colonies and hinder its isolation from diseased material.

Isolation of *X. oryzae* pv. *oryzicola* from symptomatic material is possible on Peptone Sucrose Agar (PSA), Nutrient Broth Yeast Extract agar medium (NBY), Growth Factor (GF) agar or otherwise using semi- selective media (Agarwal *et al*., 1989; Sakthivel *et al*.,2001; EPPO, 2007). A semi-selective medium, called XOS, is available for detection of *X. oryzae* pv. *oryzicola* from rice seed (Di *et al*., 1991; EPPO, 2007). On nutrient agar (NA), after 3 days of growth, colonies of *X. oryzae* pv. *oryzicola* are circular, entire, smooth, convex, opaque, and pale to straw yellow, 1-2 mm in size. Optimum growth temperature is between 25 and 30°C. For growth on other media, see EPPO, 2007.

Detection and identification methods

Detection of *X. oryzae* pv. *oryzicola* in seed, using a detached leaf inoculation method was described by Xie & Mew (1998). The method is based on inoculating leaf segments on agar with seed washings in a moist chamber. For selective recovery from seed, this method and the XOS semi-selective medium of Di *et al*. (1991) can be used.

Furthermore poly- and monoclonal antibodies (genus and pathovar specific) can be used in Immuno-fluorescence and ELISA tests on seed extracts and/or colonies isolated from seeds or leaf/stem material and isolated bacterial cells (Benedict *et al*., 1989). An ELISA kit is commercially available for the detection of *X. oryzae* pv. *oryzicola* (EPPO, 2007). A padlock probe (PLP)-based PCR with dot blot hybridisation was developed for simultaneous detection of *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae* by Tian *et al*., 2014. A specific TaqMan probe for its detection in seed was developed by Zhao *et al*. (2007).

Leach *et al*. (1990) used a repetitive DNA sequence (pJEL 101) to distinguish *X. oryzae* pv. *oryzae* from other pathovars and species of *Xanthomonas*. Kang *et al*. (2008) developed a specific PCR detection system (targeting a membrane fusion protein gene) for *X. oryzae* pv. *oryzicola*. Other specific TaqMan-based multiplex PCRs for detection and discrimination of *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae* were developed and validated by Lang *et al*. (2010), Noh *et al*. (2012), Kang *et al* (2012) and Lee & Vera Cruz (2014).

Lang *et al*. (2014) developed a sensitive and rapid loop-mediated isothermal amplification (LAMP) test, using primer sets to distinguish not only *X. oryzae* pv. *oryzicola* and *X. oryzae pv. oryzae*, but also the Asian and African lines of *X. oryzae* pv. *oryzae*.

A SYBR green-based multiplex PCR for the detection and identification of *X. oryzae* pv. *oryzicola*, *X. oryzae* pv . *oryzae* and *Burkholderia glumae* (causing bacterial grain rot of rice) was developed by Lu *et al*. (2014). Kang *et al*. (2016) also developed a multiplex PCR for the detection of the same three bacteria. Cui *et al*. (2016) developed a multiplex conventional and real-time PCR for the simultaneous detection of six bacterial pathogens of rice, including *X. oryzae* pv. *oryzicola*, *X. oryzae* pv. *oryzae*, *Pseudomonas fuscovaginae* (rice sheath brown rot), *Burkholderia glumae*, *B. gladioli* (bacterial panicle blight of rice) and *Acidovorax avenae* subsp. *avenae* (bacterial brown stripe of rice). A validated multiplex PCR to detect *P. fuscovaginae*, *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae*, *Burkholderia* (both *B. glumae* and *B. gladioli*) as well as *Sphingomonas* and *Pantoea* spp. was published by Bangratz *et al*. (2020).

The two pathovars of *X. oryzae* differ in the symptoms induced (Ou, 1985), phenotypic characters (Reddy & Ou, 1974; Vera Cruz *et al*., 1984; Vauterin *et al*., 1995), polyacrylamide gel electrophoresis protein fingerprints (Mew & Vera Cruz, 1979; Kersters *et al*., 1989), serological behavior (Benedict *et al*., 1989) and phage typing (EPPO 2007). Also, on the basis of rep-PCR using BOX-primers discrimination of *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae* is possible (Raymundo *et al*., 2008).

As for the whole genus *Xanthomonas*, *X. oryzae* is catalase-positive, unable to reduce nitrate and a weak producer of acids from carbohydrates. Pathovars *oryzicola* and *oryzae* can be differentiated by (a) acetoin production (*X. oryzae* pv. *oryzicola*+, *X. oryzae* pv. *oryzae*–), (b) growth on l-alanine as sole carbon source (*X. oryzae* pv. *oryzicola*+, *X. oryzae* pv. *oryzae*–), (c) growth on 0.2% vitamin-free casamino acids (*X. oryzae* pv. *oryzicola*+, *X. oryzae* pv . *oryzae*–) and (d) resistance to 0.001% Cu $(NO_3)_2$ (*X. oryzae* pv. *oryzicola*–, *X. oryzae* pv. *oryzae*+) (Dye & Lelliott, 1974; Reddy & Ou, 1974; Gossele *et al*., 1985; Niño-Liu *et al*., 2006; EPPO 2007). Extensive characterization of *X. oryzae* pv. *oryzicola*, using biochemical, physiological tests and PAGE was performed by Vera Cruz *et al.* (1984). Wonni *et al*. (2014) determined extensive variability between African strains of *X. oryzae* pv. *oryzicola*. Restriction fragment length polymorphism (RFLP) analysis using the effector *avrXa*7 as probe resulted in the identification of 18 haplotypes. PCR using two conserved type III effector (T3E) genes (*xopAJ* and *xopW*) differentiated the strains into an African group where the *xopAJ* was generally not detected, and a group of possible Asian origin.

Six housekeeping genes— *atpD* (ATP synthase ? chain), *dnaK* (chaperone protein), *efP* (elongation factor P), *gyrB* (DNA gyrase subunit B), *lepA* (GTP binding protein), and especially *rpoD* (RNA polymerase ?-70 factor) are useful for identification and phylogenetic studies of *X. oryzae* pv. *oryzicola* strains (Afolabi *et al*., 2014; Wonni *et al*., 2014).

Isolates can be tested for pathogenicity on susceptible rice cultivars. For *X. oryzae* pv. *oryzicola* 30–45-day old plants of cultivars IR24 or IR50 (International Rice Institute) or local, susceptible varieties can be used. Leaf clipping and spray inoculation methods are available for inoculations (Kauffman *et al*., 1973; Cottyn *et al*., 1994; EPPO, 2007; Afolabi *et al*., 2014). Niño-Liu *et al*. (2005) inoculated plants by dipping them in bacterial mixture and incubating in a growth chamber. Symptoms developed within 6 days.

PATHWAYS FOR MOVEMENT

X. oryzae pv. *oryzicola* can only move short distances within infected crops. The bacterium is found in association with weeds, even if their role in the disease cycle is less clear than for *X. oryzae* pv. *oryzae* (Leyns *et al*., 1984; Reddy & Nayak, 1975).

There are little substantiated data on spread or transmission in the field by animals other than insects (Ou, 1985; Niño-Liu *et al*., 2006; EFSA, 2018).

Long distance spread can take place via infected rice seeds, and seed transmission is regarded as the main means of dispersal. The planting of disease-free seed is considered of utmost importance in control (Rao, 1987; Xie *et al*., 1990, 1991; Ming *et al*., 1991; Mew, 1993; Xie & Mew, 1998).

PEST SIGNIFICANCE

Economic impact

Bacterial leaf streak is only of importance in some areas during very wet seasons and where high levels of nitrogen fertilization are used. It does not usually reduce yields if low levels of nitrogen fertilization are applied. In general, bacterial leaf streak is a much less important disease than bacterial leaf blight. In Central India, losses ranged from 5 to 30% depending upon environmental factors and cultivars (Naik *et al*., 1973). In Northern India, disease intensity affecting 80% of leaf area resulted in 61 percent yield loss (Singh *et al*., 1980). In the Philippines, no significant losses were reported in either the wet or dry seasons (Opina & Exconde, 1971).

In West Africa outbreaks of *X. oryzae* pv. *oryzicola* usually showed lower incidence and severity than those of *X. oryzae* pv. *oryzae*, as determined in a 10-year survey (Awoderv *et al*., 1991).

In China, however, *X. oryzae* pv. *oryzicola* has sometimes been more damaging than *X. oryzae* pv. *oryzae*. In Southern China, epidemics of *X. oryzae* pv. *oryzicola* have repeatedly been reported, reducing yield by 10-20% and in some cases reaching up to 40% losses (Xie & Mew 1998; Niño-Liu *et al*., 2006; Cai *et al*., 2017). In Uganda, under favourable conditions (wet/windy/warm temperatures/susceptible varieties) bacterial leaf streak has caused major crop losses (up to 60%) (Andaku *et al*., 2016; EFSA, 2018).

Control

The bacterial leaf streak pathogen hardly requires any particular control measures except the use of healthy seed and prevention measures (see below). Neither treatments nor resistance are mentioned to any significant extent in the literature.

Chemical control

Chemical seed treatment and field sprays have been reported from India (Shekhawat & Srivastava 1971), using a combination of antibiotics (streptomycin sulphate and tetracycline) and copper-oxychloride. It was also reported that when yield is affected, a copper-based fungicide applied at heading stage can be effective in controlling the disease (ICAR/TNAU, 2022; CABI Plantwise, 2022). The use of antibiotics against plant pathogens is not permitted in many EPPO countries, although in Asia their use is still ongoing and resistance against streptomycin has been reported in China (Xu *et al*., 2010). Recently Chen *et al*. (2019) reported a strong bactericidal effect (in vitro and in vivo) of the bactericide melatonin (N-acetyl-5-methoxytryptamine) on *X. oryzae* pv. *oryzicola* and a reduction of disease incidence by 17%.

Heat treatment

Hot water treatment of rice seeds at 52-54°C for 30 min, preceded by 8-10 hour of presoaking at room temperature in water, has been advised and used to cure seeds of *X. oryzae* pv. *oryzae* (Jain, 1970; Reddy, 1983) and is also expected to be effective for *X. oryzae* pv. *oryzicola*.

Biological control

Hata *et al*. (2015) found an antagonistic effect on *X. oryzae* pv. *oryzicola* of *Streptomyces* spp. in vitro. In a follow-up (greenhouse) study two strains showed a suppressive effect on bacterial leaf streak due to induction of systemic resistance and growth promoting activity (Hata *et al*., 2021)

Zhang *et al*. (2012) reported promising biocontrol effect of strain Lx-11 of *Bacillus amyloliquefaciens*. This strain appears also to trigger a systemic immunization activity and significantly reduced disease incidence in field experiments (from 60% to 71%) which was better than the effect of a chemical spray with thiadiazole-copper (a bactericide often used in China).

Plant resistance

In contrast to bacterial leaf blight, native major resistance genes controlling resistance to bacterial leaf streak have not yet been identified in rice. There are, however loci determining quantitative resistance, such as qBLSR-11-1 (Chen *et al*., 2006) and qBlsr5a, which had a relatively large impact in breeding lines, where the broadly effective rice recessive gene xa5 is involved (Xie *et al*., 2020). In a genome-wide resistance-gene analysis in rice Sattayachiti *et al*. (2020) and Thianthavon *et al*. (2021) stated that this recessive xa5 gene is a very promising candidate to be used in breeding for broad-spectrum resistance. A non-host resistance gene, Rxo1, isolated from maize, and present in transgenic rice was shown to confer high level resistance to bacterial leaf streak (Zhao *et al*., 2005; Jiang *et al*., 2020). Using CRISPR/Cas9 gene editing of two rice varieties Ni *et al*. (2021) obtained rice lines that proved to be resistant to *X. oryzae* pv. *oryzicola* and *X. oryzae* pv. *oryzae*. The original agronomic traits of these lines were not diminished. The dominant locus Xo1 apparently confers complete resistance to African strains of *X. oryzae* pv. *oryzicola* (Triplett *et al*., 2016, Cai *et al*., 2017).

Prevention and cultural control

Prophylactic measures (such as use of healthy seeds, adequate fertilization and irrigation, destruction or ploughing under of crop residues, disinfection of machinery and equipment, production of seedlings in boxes and removal of diseased plants and weed hosts from fields and along irrigation canals) have all been found useful in the control of bacterial leaf streak (Devadath, 1984; Goto, 1992; Ou 1985; Shekhawat *et al*., 1972).

Phytosanitary risk

Rice cultivation in Europe occurs in Bulgaria, France, Greece, Hungary, Italy Portugal, Romania, the Russian Federation, Spain, Turkey and Ukraine. About 80% of the European Union rice production takes place in Italy (>220 000 ha and Spain (>115 000 ha), another 12% in Greece and Portugal (some 20-25 000 ha each). The remainder is cultivated in Bulgaria, France, Hungary and Romania, (10-20 000 ha each). In non-EU European countries, rice is grown in the Russian Federation (120 000 ha in the Krasnodar region) as well as in Ukraine (25 000 ha). In those countries all rice fields are under irrigation, planted in spring and harvested in autumn. (Agri-food Data Portal, 2022; Ferrero & Nguyen, 2004; Kraehmer *et al*., 2017).

Resistance of European varieties against *X. oryzae* pv. *oryzicola* is unknown. Non-European varieties are only introduced, in small quantities, for breeding (Cai *et al*., 2013; Kraehmer *et al*., 2017). No interceptions of *X. oryzae* pv *oryzicola* have been reported in the EU from 1995 to April 2022 (European Commission, 2022). However, no systematic surveying and monitoring for *X. oryzae* pv. *oryzicola* takes place in Europe

The main risk of introduction is via imported rice seed (germplasm) used for breeding purposes and therefore direct sowing. Milled rice poses a negligible risk, because hulls are removed, and endosperm infection is very rare. Moreover, milled rice has its main destination outside growing areas.

Once introduced by infected seed, further spread could take place via newly infected seed and contaminated water and the bacterium could survive in stubble, straw, weed hosts and volunteer plants.

PHYTOSANITARY MEASURES

Phytosanitary (quarantine) measures can be implemented to reduce the risk of long-distance dissemination of the pathogen. It can be recommended that consignments of rice seeds should have been produced from pest-free areas, or from pest-free places of production.

General inspection and sampling procedures for imported rice, which include *X. oryzae* pv. *oryzicola* are described in EPPO Standard PM 3/78(2) *Consignment inspection of seed and grain of cereals*. Seed inspections of rice intended for breeding purposes in international trade may assist in preventing spread of the pathogen to areas with no history of the disease. However, visual inspection of imported seeds is not very reliable due to the occurrence of latent infections and therefore, when material is imported from areas where the disease is known to occur, certification for disease freedom via field inspections and laboratory testing are necessary.

A contingency plan to prepare for possible introductions of *X. oryzae* pv. *oryzicola* in the USA, was developed by the USDA (USDA, 2013).

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