식물병연구

Note | Open Access | Fast Tract

Res. Plant Dis. 31(4): 426-430 (2025)
https://doi.org/10.5423/RPD.2025.31.4.426

Diversity and Distribution of the Rice Blast Races in Korea between 2023 and 2024

Dan-Dan Zhao[†], **Hyunjung Chung**[†*], **Nam-Gu Kim**, **Soo Yeon Choi**,
Shinhwa Kim, **Jung-Wook Yang**, **In-Jeong Kang**, **Sang-Min Kim**, **Yul-Ho Kim**,
and Jang-Ho Lee

Crop Environment Research Division, Department of Crop Science, National Institute of Crop and Food Science, Rural Development Administration, Wanju 55365, Korea

***Corresponding author**
Tel: +82-63-238-5343
Fax: +82-63-238-5335
E-mail: chunghyunjung@korea.kr
ORCID
https://orcid.org/0000-0001-9375-3981
https://orcid.org/0000-0001-7258-6977
https://orcid.org/0000-0001-5758-5749
https://orcid.org/0009-0009-4763-7299
https://orcid.org/0000-0003-2187-9336
[†]D.-D. Zhao and H. Chung contributed equally.

Received November 26, 2025
Revised December 15, 2025
Accepted December 16, 2025

Rice blast, caused by *Magnaporthe oryzae*, is one of the most damaging diseases limiting rice production worldwide. Developing and deploying resistant cultivars remains the most reliable strategy for managing the rice blast disease. However, resistance in rice cultivars is often short-lived because the blast pathogen rapidly evolves and adapts to newly released cultivars. This makes continuous surveillance of pathogen populations and their virulence dynamics essential. To assess the current population structure and shifts in resistance effectiveness in Korea, 736 isolates were collected from seven provinces between 2023 and 2024 and evaluated for their pathogenic reactions on the susceptible cultivar 'Lijiangxintuanheigu' (LTH) and 27 LTH-based monogenic resistance lines. The results showed that *Piz-5* and *Pita*-CP1 exhibited over 90% resistance to rice blast isolates collected in 2023 and 2024. The findings of this study improve our understanding of pathogen population dynamics and provide valuable guidance for developing rice cultivars with enhanced blast resistance in Korea.

Keywords: Blast resistance, Monogenic resistance lines, Pathogen populations, Rice blast

Rice (*Oryza sativa* L.) serves as a staple food for more than half of the world's population, and maintaining stable yields is essential for global food security. In Korea, rice production represents a major component of the agricultural sector, with a substantial proportion of farmers, over half engaged in rice cultivation (Jeong et al., 2021). Among the biotic stresses affecting rice cultivation, rice blast, caused by the fungal pathogen *Magnaporthe oryzae*, is regarded as the most destructive (Miah et al., 2017). Rice blast is capable of infecting almost all growth stages, and under favorable environmental conditions, it causes severe yield losses (Nalley et al., 2016). Deploying resistant cultivars remains the most practical and effective strategy for managing rice blast (Miah et al., 2013). However, the durability of resistance is frequently compromised by the rapid evolution and regional diversity of pathogen populations (Chung et al., 2022; Wang et al., 2017).

In Korea, rice blast epidemics continue to emerge intermittently, with notable outbreaks such as nationwide epidemics of rice blast disease, especially in Yeoju in 2020, and widespread panicle blast in Jeonbuk state in 2021, reflecting the high genetic diversity and adaptability of the pathogen (Chung et al., 2022, 2023; Lee et al., 2022). As the previous study, the isolates collected during the 2020 Yeoju outbreak were predominantly avirulent to several resistance genes, including *Piz-t*, *Pik-h*, *Piz-5*, *Pi7(t)*, *Pik-p*, *Pik-m*, *Pik,* and *Pita-2* (Chung et al., 2022). The 2021 Jeonbuk state outbreak was characterized by a different predominant race composition (Chung et al., 2023). These observations highlight pronounced temporal and regional changes in pathogen

Research in Plant Disease
eISSN 2233-9191
www.online-rpd.org

populations, emphasizing that continuous monitoring of race diversity and resistance gene effectiveness is essential for maintaining stable resistance in rice cultivars (Kim et al., 2017; Mutiga et al., 2021; Shim et al., 2012).

Rice blast resistance is governed by the dynamic interaction between rice resistance genes and the corresponding avirulence genes of *Magnaporthe oryzae*, as described by the gene-for-gene theory (Silué et al., 1992). Based on this concept, the International Rice Research Institute (IRRI) and a collaborative research project with Japan developed monogenic resistance lines to characterize the races of rice blast fungus (Fukuta et al., 2004; Tsunematsu et al., 2000). These monogenic resistance lines were developed using the genetic background of the susceptible *Japonica* variety Lijiangxintuanheigu (LTH) and collectively contain distinct resistance genes (Fukuta et al., 2009). In resistance evaluation, these lines serve as differential hosts to determine the virulence patterns of rice blast isolates, allowing researchers to identify the specific races present in a given population. By testing rice blast isolates on this set of monogenic resistance lines, it is possible to assess the effectiveness of individual resistance genes and monitor changes in pathogen virulence over time, providing crucial information for breeding programs aimed at deploying durable resistance in rice cultivars (Khan et al., 2016; Nguyet et al., 2020). Therefore, to investigate the diversity and population dynamics of the rice blast fungus in Korea, we collected isolates from seven major rice-growing provinces between 2023 and 2024. Single spores were isolated from rice leaves and panicles exhibiting typical blast lesions. Spores were induced from infected tissues by incubating them on water agar (15 g agar l^{-1}) at room temperature for 24 hr, as described by (Hayashi et al., 2009). Single germinated conidia were isolated under a microscope and transferred to potato dextrose agar (PDA; MB-P1102; Kisanbio, Seoul, Korea) to obtain pure cultures. For long-term preservation, each isolate was cultured on rice bran agar (RBA; 20 g rice bran, 20 g sucrose, and 20 g agar l^{-1}) at 26°C for 5 days. Sterile Advantec paper discs were placed on the RBA surface until overgrown by mycelia, then air-dried at room temperature for 20-25 days and stored in Eppendorf tubes at -80°C. In total, 736 single-spore isolates were successfully obtained and maintained for further analyses (Supplementary Table 1).

To assess the diversity of the rice blast pathogen, we used a set of 27 monogenic resistance lines, as previously described, each carrying a single *Pi* gene, to evaluate the virulence spectrum of the collected isolates. The monogenic resistance lines each carry a distinct resistance gene, including *Pita*-CP1, *Piz-t*, *Piz-5*, *Pik-m*, *Pi20(t)*, *Pi19(t)*, *Pita-2*-Pi, *Pik-h*, *Pi12(t)*, *Pi9(t)*, *Pita*-K1, *Pish*-B, *Pi7(t)*, *Pik-p*, *Pik*, *Pit*, *Pi11(t)*, *Pita*-CT2, *Pi3(t)*, *Pik-s*-S, *Pik-s*-F5, *Pita-2*-Re, *Pib*, *Pi5(t)*, *Pish*-S, *Pi1*, and *Piz* (Supplementary Table 2). Seeds of each monogenic resistance line were sown in 72-cell seedling trays filled with sterilized nursery soil and grown in a greenhouse environment until the four-leaf stage, when plants were used for inoculation experiments. Infection assays were conducted on the monogenic resistance lines using individual isolates. Each isolate was initially cultured on PDA for 7 days and subsequently subcultured on RBA for 10 days. Conidia production was induced by exposing the cultures to ultraviolet light for 3 days. The harvested conidia were suspended in sterile water containing 250 ppm Tween 20 (CAS: 9005-64-5) and adjusted to a final concentration of 1×10^5 conidia/ml. Rice plants were inoculated with the conidial suspension and incubated in a dew chamber at 26°C for 24 hr in the dark, followed by growth in a greenhouse under a 16-hr light/8-hr dark cycle. Disease severity was assessed seven days post-inoculation using a 0-5 scale: score 0 (no visible lesions), 1 (dark brown pinpoint lesions), 2 (small lesions with darker brown margins and distinct tan centers), 3 (small eyespot lesions approximately 2 mm in length, with tan centers surrounded by dark brown margins), 4 (intermediate eyespot lesions approximately 3-4 mm in length) and 5 (large eyespot lesions approximately 5 mm in length) (Valent et al., 1991). Scores of 0-3 were classified as a resistant reaction, and scores of 4-5 were considered susceptible reactions. The reactions of all 736 isolates evaluated on the monogenic resistance lines are summarized in Supplementary Table 3.

In 2023, monogenic resistance lines carrying the *Piz-t*, *Pita*-CP1, and *Piz-5* showed resistance frequencies exceeding 90% against the collected isolates. However, by 2024, only *Piz-5* and *Pita*-CP1 maintained resistance levels above 90%. In addition, three monogenic resistance lines (*Pi1*, *Pi5(t)*, *Pish*-S) exhibited more than 80% susceptibility in 2023, whereas five lines (*Pi5(t)*, *Pik-s*-F5, *Pik-s*-S, Pi1, and *Pit*) displayed over 80% susceptibility in 2024, further reflecting increased virulence and diversification of the pathogen population (Fig. 1).

Although isolates were collected from seven provinces, only five provinces were evaluated over the 2 years, while Chungcheongnam-do and Gangwon state were evaluated

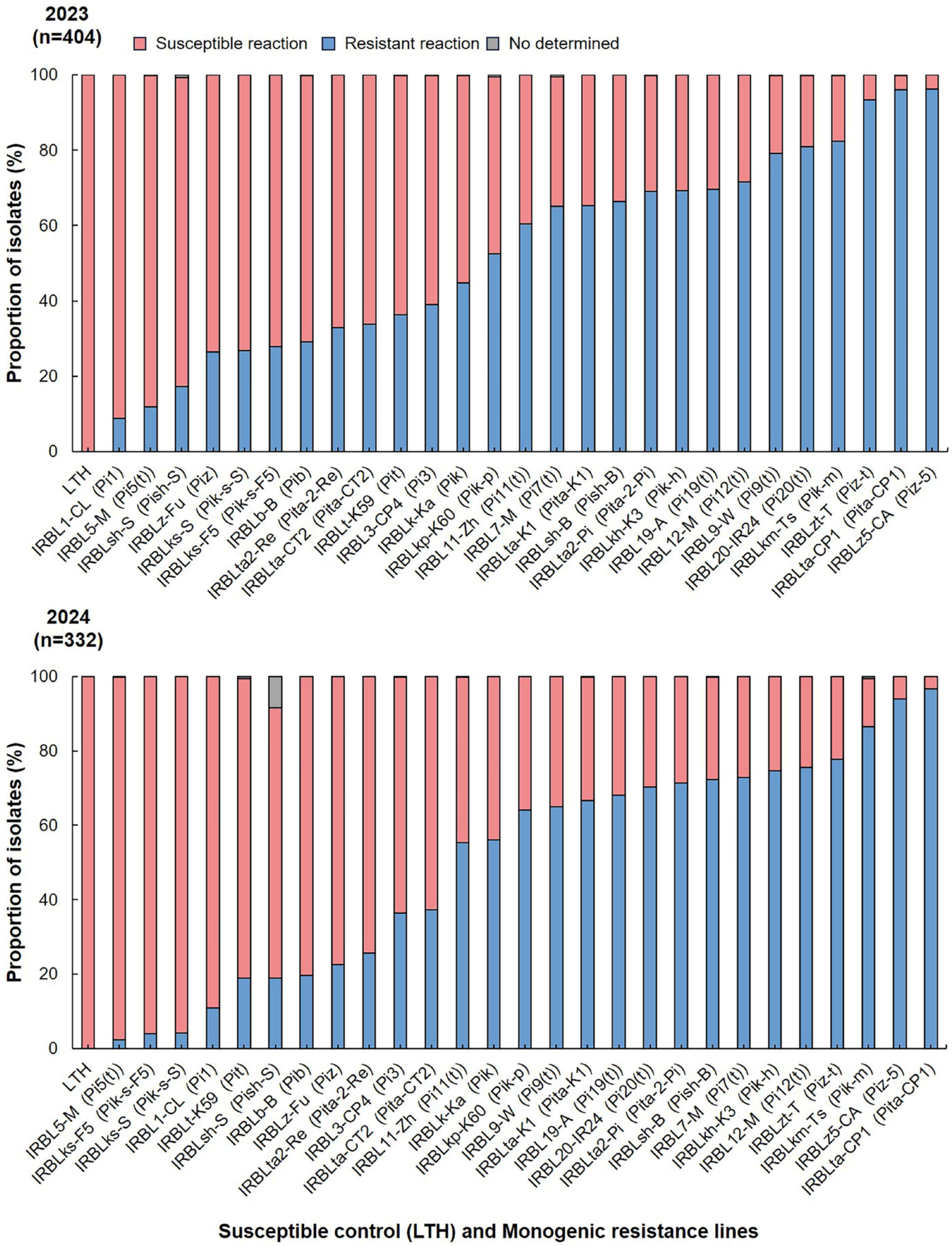

Fig. 1. Proportion of the *Magnaporthe oryzae* isolates showing the resistant and susceptible reaction to the susceptible rice cultivar 'Lijiangxintuanheigu' (LTH) and 27 monogenic resistance lines. A total of 404 isolates collected in 2023 and 332 isolates collected in 2024 were evaluated their pathogenicity.

only in 2023. Regional evaluation of resistance reactions revealed substantial year-to-year variation. In Gyeonggi-do, only one monogenic resistance line (*Pita*-CP1) exhibited >90% resistance in 2023, but this number increased sharply to eight lines (*Pik-h*, *Piz-5*, *Piz-t*, *Pi12(t)*, *Pi7(t)*, *Pik-p*, *Pish*-B, and *Pita*-CP1) in 2024. In Jeonbuk state, four lines (*Piz-t*, *Pita*-CP1, *Piz-5*, and *Pik-m*) showed >90% resistance in 2023, compared with 13 lines (*Pik-h*, *Piz-t*, *Pi12(t)*, *Pi19(t)*, *Pita*-CP1, *Pik*, *Pish*-B, *Pik-p*, *Piz-5*, *Pi7(t)*, *Pik-m*, *Pita-2*-Pi, and *Pi9(t)*) in 2024. In Jeollanam-do, two lines (*Piz-5* and *Pita*-CP1) consistently displayed >90% resistance in both years. In Gyeongsangnam-do, two lines (*Piz-5* and *Pita*-CP1) exceeded the 90% resistance threshold in 2023, increasing to five lines (*Pita*-CP1, *Pik-m*, *Piz-5*, *Pi12(t)*, and *Pita-2*-Pi) in 2024. In Gyeongsangbuk-do, three

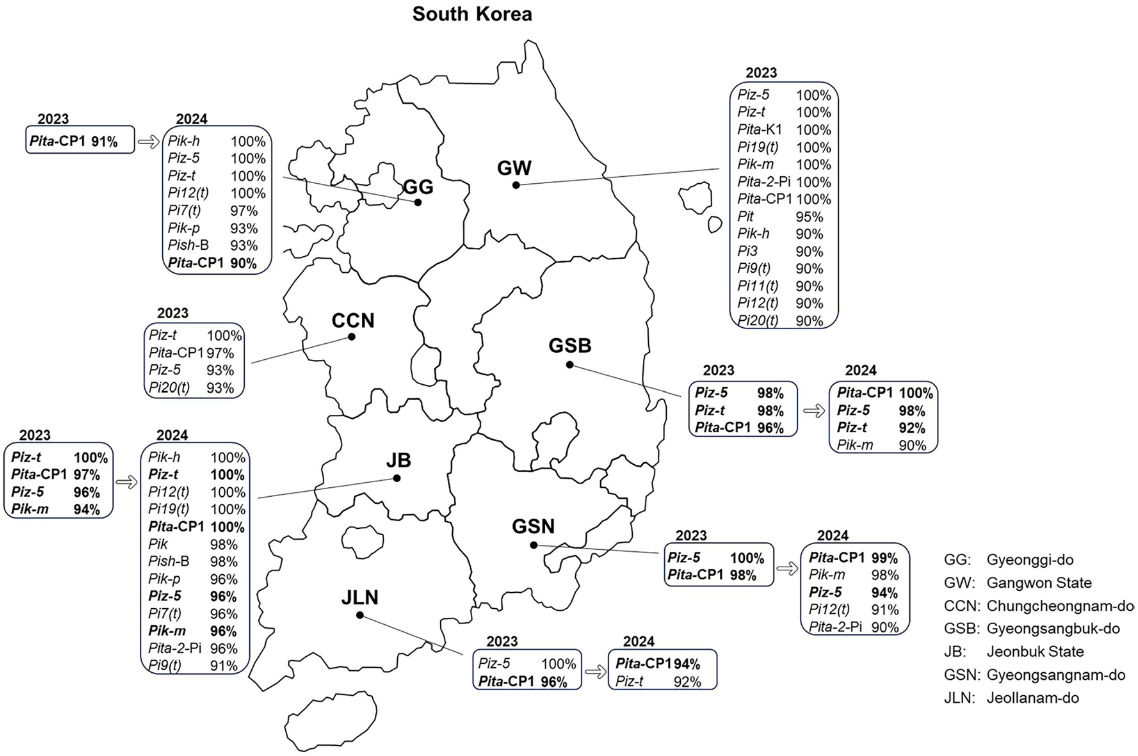

Fig. 2. Candidates of effective resistance genes and proportion of the isolates showing resistant reactions against the monogenic resistance lines in different provinces. The value indicates more than 90% of the isolates showing resistant reactions against the monogenic resistance lines. *n*=the number of the tested isolates collected from each province. Bold text highlights resistance genes that consistently showed >90% effectiveness in both 2023 and 2024. GG, Gyeonggi-do; GW, Gangwon State; CCN, Chungcheongnam-do; GSB, Gyeongsangbuk-do; JB, Jeonbuk State; GSN, Gyeongsangnam-do; JLN, Jeollanam-do.

lines (*Piz-5*, *Piz-t*, and *Pita*-CP1) in 2023 and four lines (*Pita*-CP1, *Piz-5*, *Piz-t*, and *Pik-m*) in 2024 showed >90% resistance. For provinces surveyed only in 2023, Chungcheongnam-do and Gangwon state had four (*Piz-t*, *Pita*-CP1, *Piz-5*, and *Pi20(t)*) and fourteen (*Piz-5*, *Piz-t*, *Pita*-K1, *Pi19(t)*, *Pik-m*, *Pita-2*-Pi, *Pita*-CP1, *Pit*, *Pik-h*, *Pi3*, *Pi9(t)*, *Pi11(t)*, *Pi12(t)*, and *Pi20(t)*) highly resistant lines, respectively (Fig. 2). Overall, across the 2-year evaluation period, *Piz-5*, *Pita*-CP1 consistently exhibited broad-spectrum and durable resistance, highlighting their continued value for resistance deployment in Korea rice breeding programs. In contrast, the effectiveness of other resistance genes varied considerably among regions, underscoring the importance of region-specific resistance strategies.

Conflicts of Interest

No potential conflict of interest relevant to this article was reported.

Acknowledgments

This work was carried out with the support of the "Research Program for Agriculture Science and Technology Development (Project No. PJ017573012025)", Rural Development Administration, Republic of Korea. This study was supported by 2025 the RDA Fellowship Program of the National Institute of Crop and Food Science, Rural Development Administration, Republic of Korea.

Electronic Supplementary Material

Supplementary materials are available at Research in Plant Disease website (http://www.online-rpd.org/).

References

Chung, H., Jeong, D. G., Lee, J.-H., Kang, I. J., Shim, H.-K., An, C. J. et al. 2022. Outbreak of rice blast disease at Yeoju of Korea in 2020. *Plant Pathol. J.* 38: 46-51.

Chung, H., Lee, W.-I., Choi, S. Y., Choi, N.-J., Kim, S.-M., Yoon, J.-Y. et al. 2023. Outbreak of rice panicle blast in Jeonbuk province of Korea in 2021. *Plant Pathol. J.* 39: 136-140.

Fukuta, Y., Telebanco-Yanoria, M. J., Imbe, T., Tsunematsu, H., Kato, H., Ban, T. et al. 2004. Monogenic lines as an international standard differential set for blast resistance in rice (*Oryza sativa* L.). *Rice Genet. Newsl.* 21: 70-72.

Fukuta, Y., Xu, D., Yanoria, M. J. T., Hairmansis, A., Hayashi, N. and Kobayashi, N. 2009. Genetic characterization of universal differential variety sets developed under the IRRI-Japan collaborative research project. In: Advances in Genetics, Genomics and Control of Rice Blast Disease, eds. by G. L. Wang and B. Valent. Springer, Dordrecht, The Netherlands.

Hayashi, N., Kobayashi, N., Vera Cruz, C. M. and Fukuta, Y. 2009. Protocols for the sampling of diseased specimens and evaluation of blast disease in rice. Japan International Research Center for Agricultural Sciences, Tsukuba, Japan.

Jeong, O.-Y., Park, H.-S., Baek, M.-K., Kim, W.-J., Lee, G.-M., Lee, C.-M. et al. 2021. Review of rice in Korea: current status, future prospects, and comparisons with rice in other countries. *J. Crop Sci. Biotechnol.* 24: 1-11.

Khan, M. A. I., Ali, M. A., Monsur, M. A., Kawasaki-Tanaka, A., Hayashi, N., Yanagihara, S. et al. 2016. Diversity and distribution of rice blast (*Pyricularia oryzae* Cavara) races in Bangladesh. *Plant Dis.* 100: 2025-2033.

Kim, Y., Kang, I. J., Shim, H.-K. and Roh, J.-H. 2017. Pathotype classification of Korean rice blast isolates using monogenic lines for rice blast resistance. *Res. Plant Dis.* 23: 249-255. (In Korean)

Lee, K. T., Jeon, H.-W., Park, S.-Y., Cho, J. and Kim, K.-H. 2022. Comparison of projected rice blast epidemics in the Korean Peninsula between the CMIP5 and CMIP6 scenarios. *Clim. Change* 173: 12.

Miah, G., Rafii, M. Y., Ismail, M. R., Puteh, A. B., Rahim, H. A., Asfaliza, R. et al. 2013. Blast resistance in rice: a review of conventional breeding to molecular approaches. *Mol. Biol. Rep.* 40: 2369-2388.

Miah, G., Rafii, M. Y., Ismail, M. R., Sahebi, M., Hashemi, F. S. G., Yusuff, O. et al. 2017. Blast disease intimidation towards rice cultivation: a review of pathogen and strategies to control. *JAPS* 27: 1058-1066.

Mutiga, S. K., Rotich, F., Were, V. M., Kimani, J. M., Mwongera, D. T., Mgonja, E. et al. 2021. Integrated strategies for durable rice blast resistance in sub-Saharan Africa. *Plant Dis.* 105: 2749-2770.

Nalley, L., Tsiboe, F., Durand-Morat, A., Shew, A. and Thoma, G. 2016. Economic and environmental impact of rice blast pathogen (*Magnaporthe oryzae*) alleviation in the United States. *PLoS One* 11: e0167295.

Nguyet, N. T. M., Long, H. H., Ngoc, N. B., Nhai, N. T., Thuy, N. T. T., Hayashi, N. et al. 2020. Diversity and distribution of rice blast (*Pyricularia oryzae* Cavara) races in Vietnam. *Plant Dis.* 104: 381-387.

Shim, H., Yeh, W.-H., Yoo, B.-J., Myung, I.-S., Hong, S.-K. and Lee, S. 2012. Pathogenic races of *Pyricularia oryzae* isolated from various rice cultivars on the blast nursery and paddy field in different locations. *Res. Plant Dis.* 18: 324-330. (In Korean)

Silué, D., Notteghem, J. L. and Tharreau, D. 1992. Evidence of a gene-for-gene relationship in the *Oryza sativa-Magnaporthe grisea* pathosystem. *Phytopathology* 82: 577-580.

Tsunematsu, H., Yanoria, M. J. T., Ebron, L. A., Hayashi, N., Ando, I., Kato, H. et al. 2000. Development of monogenic lines of rice for blast resistance. *Breed. Sci.* 50: 229-234.

Valent, B., Farrall, L. and Chumley, F. G. 1991. Magnaporthe grisea genes for pathogenicity and virulence identified through a series of backcrosses. *Genetics* 127: 87-101.

Wang, X., Jia, Y., Wamishe, Y., Jia, M. H. and Valent, B. 2017. Dynamic changes in the rice blast population in the United States over six decades. *Mol. Plant Microbe Interact.* 30: 803-812.