Science Societies

Using immune receptor genes to inform rice, maize, and sorghum breeding programs

September 21, 2026



A diseased sorghum plant. Photo courtesy of Xiaocui Chen.

Crop diseases are a major threat to stable food production, making the ability of crops to recognize and defend against pathogens an important target for breeding. Nucleotide-binding leucine-rich repeat (NLR) genes encode a large family of immune receptors that play central roles in plant disease resistance.

Rice, maize, and sorghum are closely related grass crops that contribute substantially to global food security, yet the diversity and evolution of their NLR genes across species remain poorly understood. A clearer picture of this variation could help identify new sources of disease resistance.

Using genomic resources from 75 rice, maize, and sorghum genomes, researchers compared their NLR gene repertoires and evolutionary patterns. The three crops showed broadly similar NLR domain structures but differed in the number and genomic distribution of these genes. Cross-species comparisons also revealed distinct proportion of shared NLR genes and substantial lineage-specific innovation in each crop.

The results reveal how related crops have both conserved and crop-specific immune receptor diversity. This comparative resource provides a foundation for discovering and exploiting NLR variation to strengthen disease resistance in major grass crops.

Dig deeper

Wang, Y., Dorjee, T., Wang, Y., Peng, D., Chen, L., Wei, C., Sun, S., Duan, M., Li, H., Hathorn, A., Mace, E., Jordan, D., Wu, X., Chen, X., & Tao, Y. (2026). *P*an-NLRome analysis uncovers genetic diversity and evolutionary dynamics among rice, maize and sorghum. *The Plant Genome*, *19*, e70257. https://doi.org/10.1002/tpg2.70257

More science

Back to issue

Back to home

Member Hub

Text © . The authors. CC BY-NC-ND 4.0. Except where otherwise noted, images are subject to copyright. Any reuse without express permission from the copyright owner is prohibited.