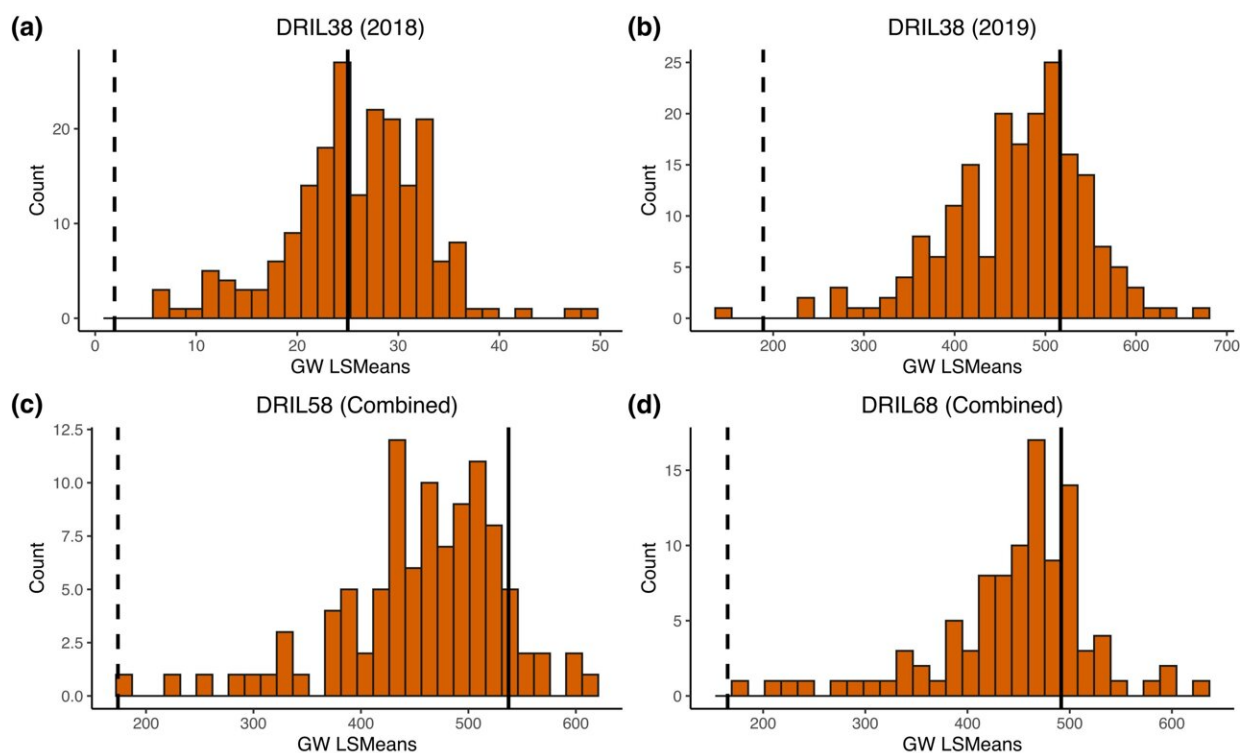


# Study finds corn genome can gang up on multiple pathogens at once

February 7 2024, by Lauren Quinn



Phenotypic distribution of GW in the 3 populations. For the DRIL58 and DRIL68 populations, combined environment LsMeans estimations for AUDPC of the GW data are presented. For the DRIL38 population, there was only 1 rating in 2018 and no AUDPC calculated. Thus, the DRIL38 2018 estimation distribution was not combined with the DRIL38 2019 estimation, which was based on the AUDPC calculated using 3 ratings. The solid line indicates the LsMean of the common recurrent parent Oh7B and the dashed lines indicate the LsMeans of the donor parents, which is different for each population. The donor line for DRIL38 population is Ki3; for DRIL58 population is NC262 and for DRIL68 population is NC304. Credit: *G3: Genes, Genomes, Genetics* (2023).

In a changing climate, corn growers must be ready for anything, including new and shifting disease dynamics. Because it's impossible to predict which damaging disease will pop up in a given year, corn with resistance to multiple diseases would be a huge win for growers. Now, University of Illinois Urbana-Champaign researchers are moving the industry closer to that goal.

Goss's wilt, a bacterial disease, and [fungal diseases](#) gray leaf spot, northern corn leaf blight, and southern corn leaf blight are important to growers across the Midwestern U.S. and, in some cases, globally. The study, published in [G3: Genes, Genomes, Genetics](#), reveals [genomic regions](#) associated with resistance to all four diseases.

"We not only found regions of the genome conferring resistance to each disease but also identified a handful of experimental corn lines that were resistant to all of them. These findings should help the industry develop materials with resistance to multiple diseases at once," said Tiffany Jamann, senior author of the new study and associate professor in the Department of Crop Sciences, part of the College of Agricultural, Consumer and Environmental Sciences (ACES) at U. of I.

The team made several strategic crosses between disease-resistant and susceptible corn lines that let them map resistance traits to specific locations in the genome. For now, those regions are fairly large, comprising hundreds of individual genes. If there are [specific genes](#) with outsized effects, they haven't been identified yet.

Still, identifying important regions is helpful, as disease resistance rarely comes down to a single gene. In fact, the additive or quantitative power

of multiple genes working together can mean more durable resistance. There's a backup if a pathogen finds a way around a given resistance mechanism. Interestingly, this durability may even work against different groups of pathogens.

"We found 19 regions associated with resistance to the [bacterial disease](#) Goss's wilt. Several of those regions are also involved with resistance to [fungal pathogens](#)," Jamann said. "Thus, it is possible to breed for resistance to several diseases at one time using the same genetic regions."

Fungi and bacteria are very different biologically, but both must find ways to get into the plant, travel throughout, and reproduce. Jamann says it's possible that resistance genes trigger changes in the plant's vasculature to make it harder for both kinds of pathogens to move around, but she still can't say exactly how the genes help plants protect themselves. She's working on it, though, thanks to a 2022 grant from the National Science Foundation.

Although the team identified three corn lines with resistance to all four diseases, it will be a while before growers can purchase seed for multiple-resistant [corn](#) as a result of this work. First, Jamann's team will fine-map the regions highlighted in this study to find any major-effect genes, then pass that information off to breeders who can develop hardy new hybrids. Still, Jamann says, multiple [resistance](#) is on its way.

**More information:** Yuting Qiu et al, Identification of loci conferring resistance to 4 foliar diseases of maize, *G3: Genes, Genomes, Genetics* (2023). [DOI: 10.1093/g3journal/jkad275](https://doi.org/10.1093/g3journal/jkad275)

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