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Unusual genetic structure confers major disease resistance trait in soybean

October 11 2012, by David J. Tenenbaum

Nematodes attack a soybean root in the laboratory of Andrew Bent, in the department of plant pathology at the University of Wisconsin–Madison. Roots and nematodes were dyed red during experiments to explore how multiple copies of a three-gene structure allow soybeans to resist soybean cyst nematodes, the most devastating disease of soybeans. The two thick lines are younger nematodes, the two sausage shapes are older nematodes. Credit: David Cook, University of Wisconsin–Madison

Scientists have identified three neighboring genes that make soybeans resistant to the most damaging disease of soybean. The genes exist side-by-side on a stretch of chromosome, but only give resistance when that stretch is duplicated several times in the plant.

"Soybean cyst nematode is the most important disease of soybean, according to yield loss, worldwide, year after year," says senior author Andrew Bent, professor of plant pathology at University of Wisconsin-Madison. "As we try to feed a world that is going from 6 billion toward 9 billion people, soybean is one of the most important sources of protein and food oil."

The nematode is a tough opponent, able to live for years in the soil, and chemicals that kill it are highly toxic and persistent, Bent says. Planting soybeans bred to contain a genetic structure called Rhg1 is the preferred defense against the cyst nematode, currently in use on millions of soybean acres worldwide.

Until now, scientists knew few details about how Rhg1 works. In a study published today in the journal *Science*, Bent, graduate student David Cook, and collaborators including Matthew Hudson of the University of Illinois, showed that Rhg1 actually houses three genes that work together to confer nematode resistance. Although a single copy of Rhg1 does not make the plant resistant, plants with 10 copies of this three-gene structure do grow well in a field infected with the nematode.

The new finding is noteworthy for several reasons beyond the fact that Rhg1 limits a disease that still causes over $1 billion in U.S. soybean yield losses every year, says Bent. "Having several genes right next to each other that all control the same trait is really common in microbes and fungi, but it's very uncommon in multicellular higher organisms."

Second, although the phenomenon of "multiple copy numbers"—repeats of a stretch of DNA—has been seen before, "this is a demonstration that the multiple copies are what make the genes practically effective."

Third, the multiple copies concern a three-gene sequence rather than an individual gene. "We have known that genes get duplicated, but it's very unusual to have a small block of genes duplicated so many times," Bent says. "This is an odd structure."

Many details remain to be worked out, including exactly how the three genes fight the nematode. Because two of the genes are involved with transporting chemicals inside and between cells, "an obvious theory is that the plant is transporting something differently," Bent says, "but we don't know if this is a compound that is toxic to the nematode or something the nematode needs. We can't assume that the plant is poisoning the nematode. It may not be cooperating with a parasite that relies on plant chemicals for survival."

Apparently, it's the sheer number of the triple-genes that makes soybeans resistant, Bent says. "We have evidence that what confers the resistance is higher expression of all three genes," not a mutation in the genes. "The fact that the genes are making more of their product is what makes for resistance."

Identifying the genes needed for resistance should help plant breeders quickly identify resistant plants, speeding the quest to breed soybeans with stronger nematode resistance.

Biotechnologists can also now work with these genes to achieve better nematode resistance.

More broadly, Bent notes that multiple gene copies are being found more commonly, so finding repeats of a string of genes with a single function "may not be a one-shot thing. Is this the tip of the iceberg? Is there a lot more of this going on than we know?"

As gene sequencing gets cheaper and faster, "people are discovering that these copy number variations are much more common than we suspected, especially in plants," Bent says. "Now, we have given a concrete example of a useful trait, that is explainable due to the copy number variation of a string containing several active genes."

More information: "Copy Number Variation of Multiple Genes at Rhg1 Mediates Nematode Resistance in Soybean," by D.E. Cook, *Science*, 2012.

Provided by University of Wisconsin-Madison

Citation: Unusual genetic structure confers major disease resistance trait in soybean (2012, October 11) retrieved 25 April 2024 from https://phys.org/news/2012-10-unusual-genetic-confers-major-disease.html