Science Societies

Molecular markers unlock breeding for complex disease

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On the move for stem rot inoculation. Photo courtesy of Peggy Ozias-Akins.

Using conventional phenotyping methods, it is difficult to breed for resistance to crop diseases with complex development in the field. Finding molecular markers to select for quantitative resistance to these diseases require precise genotypic and phenotypic methodologies.

Stem rot disease, caused by the fungus *Sclerotium rolfsii*, is devastating for peanut farmers in the U.S. Breeding for resistance to stem rot has been limited by the lack of effective phenotyping methods and molecular markers to select for resistance.

In a recent article in *Crop Science*, researchers report their use of a novel phenotyping method combined with next-generation sequencing to identify genomic regions that control field resistance to stem rot in cultivated peanut. The researchers used markers to select for these regions and tested the selected lines. Their tests demonstrated a significant increase in stem rot resistance using only two markers for selection.

With these markers as tools, peanut breeders can now easily select for a very complex trait and deploy resistance in cultivars that will save the peanut industry (growers, shellers, and manufacturers) millions of dollars per year. This work demonstrates a powerful way geneticists and breeders can face new threats to food security.

Dig deeper

Cui, R., Clevenger, J., Chu, Y., Brenneman, T., Isleib, T.G., Holbrook, C.C., & Ozias-Akins, P. (2020). Quantitative trait loci sequencing–derived molecular markers for selection of stem rot resistance in peanut. *Crop Science*, *60*. **https://doi.org/10.1002/csc2.20047**

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