

## Fine Mapping and Candidate Gene Analysis of Novel QTLs for Resistance to TSWV and Leaf Spots in Peanut

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Candidate gene identification and functional characterization through map-based approach requires to fine-map the QTL in a narrow genetic window or genomic regions. Through the years, in collaboration with other researchers, we have identified QTLs and potential genes associated with the resistance to TSWV and leaf spots (early and late) using two genetic mapping populations such as the “S” (SunOleic 97R x NC94022) and the “T” (Tifrunner x GT-C20) **bi-parental** recombinant inbred line (RIL) populations. One significant progress is that we have identified a candidate gene, *PSWD-1*, a peanut spotted wild disease resistance gene to TSWV in peanut breeding line NC94022 through fine-mapping and whole genome re-sequencing of NC94022. The functional characterization by gene cloning is underway. A late leaf spot resistance candidate gene, *pRPP13*, has been also identified using a NAM **multi-parental** population. The long-term **goal** is to identify and characterize the candidate genes controlling these disease resistances through fine-mapping and genome sequencing to narrow the QTLs to a smaller genomic region or to a single gene. By doing this, we will have a perfect marker for marker-assisted breeding for efficient cultivar development with disease resistance. Therefore, we have developed three new populations, two “mutant” populations (the “TL”, Tifrunner x 70-2, 70-2 is a mutant line of Tifrunner and totally lost resistance to leaf spots, and the “GT-C”, GT-C20 x GT-C20D, GT-C20D is a natural mutant of GT-C20 and has fresh seed dormancy), and the peanut **multi-parental MAGIC**. All the seeds have been increased in 2021, and genotyping and phenotyping will be carried out in 2022. The **objectives** in 2022 are focusing on early and late leaf spots, while the TSWV resistance gene cloning and functional characterization is in collaboration with others:

- 1) Conduct greenhouse and laboratory bioassay of these parental lines for resistance and susceptibility to early leaf spot (ELS) and late leaf spot (LLS) pathogens.
- 2) Conduct field evaluation with three replications for these new populations, the “TL”, “GT-C”, and MAGIC, for disease severity of TSWV, ELS and LLS.
- 3) Extract DNA from these populations for whole genome resequencing.

### Publications:

Gangurde, S.S., Nayak, S.N., Joshi, P., Shilp, P., Sudini, H.K., Chitikineni, A., Hong, Y., **Guo, B.**, Chen, X., Pandey, M. and Varshney, R.K. Comparative transcriptome analysis identified candidate genes for late leaf spot resistance and cause of defoliation in groundnut. *International Journal of Molecular Sciences*. 22, 4491:1-23. 2021.

Wang, M.L., Wang, H., Zhao, C., Tonniss, B.D., Tallury, S., Wang, X., Clevenger, J. and **Guo, B.** Identification of QTLs for seed dormancy in cultivated peanut using a recombinant inbred line mapping population. *Plant Molecular Biology Reporter* (published online, 08/30/21) <https://doi.org/10.1007/s11105-021-01315-5>. 2021.