Identification and utilization of new sources of resistance to White Mold in wild tetraploid Arachis for peanut improvement

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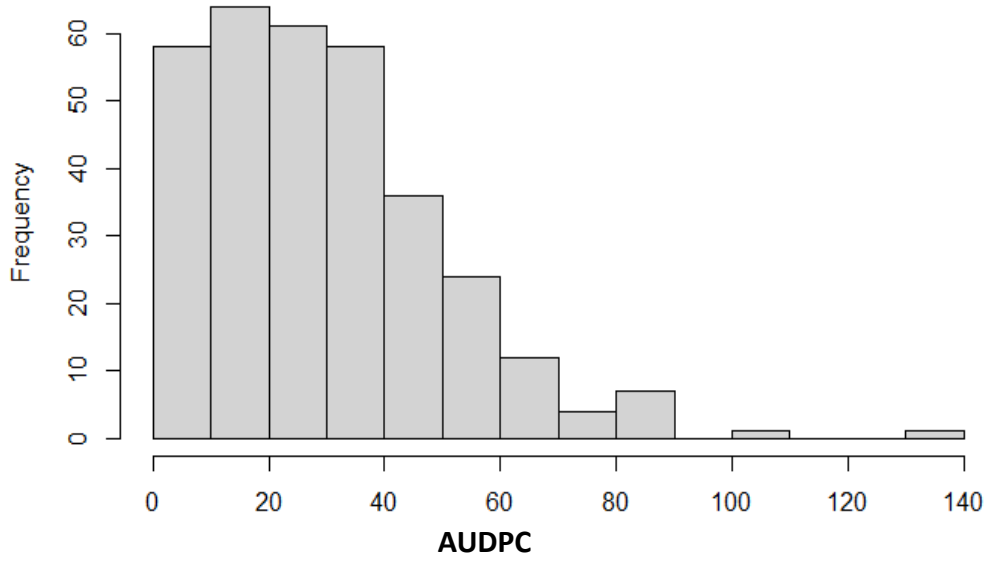
Overview

Peanut lacks strong sources of resistance against important diseases, and therefore is one of the most expensive crops for farmers to grow. Wild relatives of peanut, on the other hand, have strong resistances to several fungal and viral diseases, and nematodes. Wild-derived tetraploids are promising sources of resistance to white mold, but because their architecture is so different from cultivated peanuts, methods that gave meaningful comparisons needed to be developed. With the support of the GPC and other funders, our group has devised two methods: a greenhouse bioassay method and a field method both of which can be used to test wild-derived 'hybrid peanuts' with diverse growth habits against white mold. We have begun to test wild tetraploid hybrids for breeding and identification of genome regions that confer resistance. The production of peanut varieties with increased resistance to white mold will reduce the need for application of fungicides and increase productivity.

Results

We have developed two methods to evaluate white mold resistance suitable for wild peanut hybrids with diverse growth habits, one using cuttings in a greenhouse, and one in the field. This work was written as a scientific publication to allow other researchers and breeders to use it, and it is published in "Phytofrontiers". Using these methods, we have identified the hybrid ValSten as the most promising of wild tetraploid hybrids for white mold resistance. In order to map the regions that confer this resistance, we created an F_2 population using TifGP-2 x allotetraploid ValSten1. The population was evaluated at the Blackshank Farm in Tifton, Georgia. It was also genotyped using the Thermofisher Axiom v02. Analyses revealed several genomic regions that confer minor resistance, meaning that have not yet been able to identify strong resistance to stem rot using this population. We have developed a different population using another wild species: *Arachis microsperma*. The population is called TVM. 267 F_2 individuals were evaluated in greenhouse using the method aforementioned. Large segregation was seen in the resistance to stem rot. Sister lines were also evaluated in the "Banana Field' (by the PhD student D Matisunek and Dr T Brennemman). DNAs of these > 500 lines were extracted and will be sent for genetic analyses soon. We hope to be able to identify genomic regions that confer resistance. Most resistant lines will be crossed with highly productive cutlivars to start a backcrossed program of cultivar development.



AUDPC of white mold lesion on stems of F_2 lines of the population TMV.