Selection of A. stenosperma-derived advanced lines with strong resistance to LLS using association analyses

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Overview

Peanut lacks strong sources of resistance against important diseases, and therefore is one of the most expensive row crops for farmers to grow. In contrast, wild relatives of peanut such as *Arachis stenosperma*, present strong resistances to several fungal and viral diseases, and nematodes. We have identified peanut lineages highly resistant to Late Leaf Spot which incorporate genetics from *A. stenosperma*. We are performing genetic analyses on these lineages, using advanced tools developed by the peanut genome sequencing project. This will identify the genetic regions that confer the resistance and create specific LLS resistance-associated DNA markers for breeding. This will allow the development of Georgia-adapted cultivars with much superior late leaf spot resistance, and the reduction of spraying regimes, making cultivation of peanuts more economically and environmentally favorable.

Results

We evaluated more than 1,500 progeny derived from elite peanut lines (TifNV-HO, 13-1014, 5-646-10) backcrossed with wild species-derived tetraploids BatSten and ValSten in field trials in Midville, Tifton and South Carolina. In the 2021 season there was severe disease pressure of Late Leaf Spot, providing excellent conditions for disease screening. We scored disease progression through the season manually, and by processing images captured by drone. Within the field design delineated in an array of squares, green and brown pixels from successive images made through the season could be quantified to give accurate measures of disease severity and plant growth. Just over 500 plants within 42 lineages showed better Late Leaf Spot Resistance than the best of our elite pure pedigree peanut controls, thirteen of these lineages had exceptional resistance. DNA was collected from all plants and genotyping and genetic analyses are currently underway.

