

**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 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. We identified the regions A06 and B02 as contributing to LLS resistance. In 2022 we planted all BatSten BC₃F₄s and ValSten BC₁F₃s in Midville on sprayed and non-sprayed conditions for further disease and agronomic trait evaluation. KASP markers were designed for the disease-related A06 and B02 regions and were validated. on the BatSten derived lines. The best ValSten BC₁F₃s were selected for backcrosses. The best performing lines were sent to the winter nursery in Puerto Rico for seed multiplication. We also mapped a very strong rust resistance locus on chromosome B02 (below).

Progeny code	8_15_1	8_15_2	8_15_3	8_15_4	8_15_5	8_15_6	8_15_8	8_15_9	8_15_10	8_15_11	8_15_12	8_15_13	8_15_14	8_15_15	8_15_16	8_15_17	8_15_18	8_15_19	8_15_20	8_15_21	8_15_22	8_15_23	8_15_24
Rust response	R	R	S	S	R	R	R	R	S	R	R	R	S	R	R	S	R	R	R	R	S	R	R
B02 locus	+/-	+/+	-	-	+/+	+/-	+/-	+/+	-	+/-	+/-	+/+	-	+/+	+/+	-	+/-	+/+	+/-	+/-	-	+/-	+/-