

Final Report for 2021 National Peanut Board funding to the Texas Peanut Producers Board.

I. Subject area: Molecular Genetics & Breeding

Project Title: Breeding to Increase Peanut Yields and Production Efficiency by Developing Breeding Lines with Improved Drought and Heat Tolerance combined with Multiple Disease Resistance

Funding Year: 2021

Co-PIs:

John M. Cason, Assistant Professor, Texas A&M AgriLife REC, Stephenville, TX 76401. j-cason@tamu.edu

Mark D. Burow, Professor, Texas A&M AgriLife REC, Lubbock, 79403; and Dept. of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409. mburow@tamu.edu

Michael R. Baring, Assistant Research Scientist, Dept. of Soil and Crop Sciences Dept. Texas A&M University College Station, TX. 77843. m-baring@tamu.edu

Charles E. Simpson, Professor Emeritus, Texas A&M AgriLife REC, Stephenville, TX 76401. c-simpson@tamu.edu

Paxton Payton, Research Plant Physiologist, 3810 4th Street, Lubbock, TX, 79415; *Adjunct Assistant Professor*, Dept. of Plant and Soil Science, Texas Tech University, Lubbock, TX 79409. paxton.payton@ars.usda.gov

Waltram Ravelombola II, Assistant Professor, Texas A&M AgriLife REC, Vernon, TX 76384. wraelom@uark.edu

Hanh Pham, Postdoctoral Research Associate, Texas A&M AgriLife REC, Lubbock, TX 79403. Hanh.Pham@ag.tamu.edu

Proposal Coordinator:

John M. Cason, Assistant Professor, Texas A&M AgriLife REC, Stephenville, TX 76401. j-cason@tamu.edu Phone: 254-396-0653

Sub-Project I-1 Multiple Disease Resistant Runner-type trials

The TAMU Peanut project had replicated yield trials located in South Texas, (Pearsall, Dilley, and Derby), in Central Texas (Stephenville), in West Texas, (Seminole, Seagraves, and Plains), the High Plains (Wellington) and in the Rolling Plains (Vernon). We conducted 5 small plot Advanced Line Tests (ALT's) and 2 large plot Combine Trials across Texas in 2021 as well as two replicated screening nurseries for Sclerotinia and Leafspot resistance. We narrowed down lines developed for drought tolerance to one high performing line in our ALT test to continue collecting accurate information on the line's performance across the state. Two top performing candidates were included from previous year's results. Thirteen new breeding lines were included from top candidates for the 2021 Multiple Disease Resistance Test and from the High Yield and Grade tests, and 5 commercial checks Georgia 16HO, AG18, Georgia 09B, Georgia 14N, Webb and NemaTAM II is a combined analysis of the small plot ALTs across Texas. Testing in 2021 was met with cool, wet weather at the beginning of the season and caused us to lose 2 planting locations. An alternate site was located but wild hog pressure ended up damaging the test making our results statistically insignificant. Then the year ended with a prolonged dry spell. Across the state results for individual test were statistically revealing. but, when combined the yield and value per acre results did not prove to be statistically significant. However, for brevity, the combined analysis is presented for discussion (**Table 0**).

Table 0. Combined Advanced Line Test 4 locations in 2021

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		Splits	
Cultivar												
TP 200606-3-10	5610.7	A	1029.98	AB	74.2	BCDEFG	66.5	EF	684	EFG	2.6	EFG
TP 200610-3-2	5546.4	AB	1046.66	A	76.5	AB	67.8	DEF	673	EFGH	3.9	BCD
TP 200606-2-9	5476.4	ABC	1027.53	AB	75.2	ABCDE	67.9	DEF	673	EFGH	2.3	FG
TP 200625-3-2	5430.9	ABC	981.02	ABC	73.8	CDEFGH	63.6	FGH	715	CDE	4.4	AB
Tx144370	5379.5	ABC	989.58	ABC	74.0	BCDEFGH	64.2	FGH	713	CDE	4.5	AB
TP 200606-7-10	5248.9	ABC	969.45	ABC	75.3	ABCD	76.8	A	593	J	2.6	EFG
TxL100212-03-03	5161.6	ABC	950.44	ABC	74.5	ABCDEFG	69.1	CDE	659	FGH	3.3	CDE
TP 200610-1-2	5148.5	ABC	984.48	ABC	76.7	A	58.7	I	777	AB	2.8	EFG
TP 200606-2-14	5092.8	ABC	910.08	ABC	72.2	GH	75.1	AB	608	J	2.3	FG
TP 200608-1-6	5043.1	ABC	900.81	ABC	71.6	H	69.6	CDE	656	FGH	3.3	CDE
Georgia 14N	5042.9	ABC	952.29	ABC	75.8	ABC	60.0	HI	763	AB	3.1	DEF
TP 200608-1-14	4971.4	ABC	904.85	ABC	72.8	EFGH	68.9	CDE	661	FGH	3.0	DEFG
Georgia 16HO	4894.7	ABC	885.14	ABC	73.7	CDEFGH	71.2	BCD	640	GHI	4.2	ABC
Georgia 09B	4864.6	ABC	894.05	ABC	73.8	CDEFGH	65.3	EFG	697	DEF	4.9	AB
AG18	4861.5	ABC	908.38	ABC	74.7	ABCDEF	61.3	GHI	744	ABC	2.0	G
TP 200607-1-2	4850.8	ABC	885.76	ABC	73.8	CDEFGH	62.0	GHI	737	BCD	4.7	AB
NemaTAM II	4762.4	ABC	861.02	ABC	72.2	FGH	72.3	ABCD	630	HJ	4.5	AB
TP 200609-1-5	4758.1	ABC	883.27	ABC	73.2	DEFGH	71.6	BCD	641	GHI	5.1	A
TP 200606-6-10	4553.1	BC	843.45	BC	75.9	ABC	72.6	ABC	633	HJ	2.6	EFG
TP 200607-1-17	4452.1	C	798.57	C	74.4	ABCDEFG	57.9	I	787	A	3.1	DEF
Mean	5057.5		930.34		74.2		67.1		684		3.5	
CV(%)	25.6		27.3		4.4		11.4		11.2		43.6	
Entry "F"	ns		ns		0.0007		<.0001		<.0001		<.0001	

Although yield was not statistically significant, numerically the two top release candidates, Tx144370 and TxL100212-03-03, performed better than all commercial checks with yields of

5379.5 lbs/ac and 5161.6 lbs/ac. Additionally, each performed statistically equal to or better than all commercial checks at 74.0% and 74.5% respectively. TP200606-3-10 was numerically the top yielding breeding line for yield at 5610.7 lbs/ac, while the top grading line for the combined analysis was TP200610-3-2 at 76.5%.

We also conducted 6 replicated trials for various traits of interest. Two trials were high yield and grade trials with materials bred specifically for increased yield and grade. While 4 other trials were for combination of multiple disease resistance traits. This is the first year of testing for some of this material with lines that performed well in 2020 being in test 1 or 2 of either the high yield and grade trials or the multiple disease resistance trials. All these new tests were significant and are presented in summary charts 1-6, although in some cases variability between replications were higher than we would have liked, which, again, we are attributing to environmental effects during the season. TP200608-1-8 performed at the top of the West Texas location (**Table 1**) for yield with a total of 4423 lbs/ac. The top grading line in the test was TP200606-2-1 with a grade of 78.0%. Results continued to be encouraging with the new breeding lines performing well in this test.

Table 1. Yield Test #1 in West Test for 2021

Cultivar	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		SS%	
TP200606-1-8	4423	A	882.63	AB	73.3	DEFGH	78.9	ABCDEF	579	BCDEF	2.8	CD
TP200607-1-16	4405	A	908.44	A	75.4	BCD	73.3	CDEFG	624	ABCD	3.2	BCD
Georgia-09B	4041	AB	839.17	ABC	76.2	ABC	76.6	BCDEFG	602	ABCDE	5.4	A
TP200606-7-12	4033	AB	814.68	ABCD	73.7	DEFGH	90.0	A	505	F	2.5	D
TP200606-6-10	3949	ABC	822.96	ABCD	75.6	ABCD	82.1	ABCD	558	CDEF	3.4	BCD
TP200606-3-6	3877	ABC	772.40	ABCD	72.9	EFGH	71.6	DEFG	642	ABC	3.0	BCD
Txl44370	3873	ABC	804.60	ABCD	75.5	BCD	74.7	BCDEFG	621	ABCD	3.3	BCD
TP200606-6-15	3836	ABC	772.46	ABCD	73.3	DEFGH	72.3	CDEFG	634	ABC	2.6	D
TP200606-2-4	3730	BC	762.57	ABCDE	73.8	CDEFGH	68.6	EFG	661	AB	1.9	D
TP200606-7-11	3699	BCD	748.82	BCDE	74.5	BCDEF	85.3	AB	535	DEF	2.3	D
TP200606-2-1	3673	BCD	780.50	ABCD	78.0	A	72.8	CDEFG	631	ABCD	2.1	D
TP200606-4-5	3643	BCD	748.60	BCDE	75.1	BCDEF	73.9	BCDEFG	623	ABCD	2.5	D
TP200606-3-8	3641	BCD	753.26	BCDE	75.2	BCDE	83.2	ABC	547	CDEF	3.2	BCD
TP200607-1-14	3590	BCD	736.85	BCDEF	74.2	BCDEFGH	67.6	FG	671	AB	2.1	D
TP200606-3-7	3504	BCD	708.95	CDEF	76.3	AB	85.3	AB	537	DEF	4.4	ABC
AG-18	3471	BCD	696.88	CDEF	71.9	GH	65.6	G	695	A	2.0	D
TP200606-6-4	3407	BCD	673.97	DEF	72.7	FGH	75.1	BCDEFG	606	ABCDE	3.1	BCD
TP200606-6-13	3353	CD	678.10	DEF	73.7	DEFGH	88.3	A	517	EF	2.7	D
Georgia 16HO	3330	CD	594.72	F	71.9	H	78.9	ABCDEF	579	BCDEF	4.5	AB
NemaTAM II	3037	D	615.17	EF	74.3	BCDEFG	79.5	ABCDE	581	BCDEF	5.7	A
Mean	3726		755.79		74.4		77.2		597		3.1	
CV(%)	12.6		14.3		2.6		13.0		13.0		42.8	
Entry "F"	0.0171		0.0124		0.0006		0.0079		0.0183		0.0005	

The second yield trial was conducted in Central Texas but due to early rain it necessitated us finding another location to grow the trial. The location chosen was on the Texas A&M AgriLife Research and Extension Center at Stephenville. During the confusion, a mistake was made during planting and was not realized until processing which caused the results to be inconclusive.

In addition to conducting trials for improved yield and grade we also continued testing several new populations that were created in an effort to combine sclerotinia resistance and nematode resistance. Multiple Disease Resistance Trial #1 (**Table 2**) was grown in South Texas and contained lines from several years of crossing programs and represents the lines that have been tested in multiple seasons. Weather conditions in the area in 2021 were conducive for fungal diseases. The best yielding line at this location was the release candidate Tx144370 which yielded 6710 lbs/ac and was statistically equal to Georgia 09B which yielded 6620 lbs/ac. The top grading breeding line was TP200606-2-11 with a grade of 77.1% which was statistically equal to the high grading check Georgia 14N which graded 77.3%.

Table 2. Multiple Disease Resistance Test #1 South Texas

Cultivar	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		SS%	
Tx144370	6710	A	1232.37	A	73.4	GHI	60.7	EFG	747	DE	2.9	CDEF
Georgia 09B	6620	AB	1234.02	A	74.5	DEFGH	65.8	BCD	690	FGH	2.2	DEF
TP200609-2-15	6417	ABC	1186.22	AB	72.9	HI	60.1	EFGH	759	CDE	3.9	CD
TP200610-2-13	6309	ABCD	1206.35	A	76.7	ABCD	59.3	EFGHIJK	766	BCDE	3.8	CD
TP200610-4-5	6058	ABCDE	1155.41	ABC	76.3	ABCDE	58.7	FGHIJK	773	ABCDE	7.8	A
TP200610-2-2	6047	ABCDE	1136.89	ABCD	75.1	ABCDEFGH	55.8	JK	813	AB	3.8	CD
TP200610-3-3	5975	ABCDEF	1119.14	ABCD	74.0	FGHI	61.7	DEF	741	DEF	4.3	BC
TP200610-3-1	5890	ABCDEF	1098.59	ABCD	75.5	ABCDEFG	66.0	BC	688	FGH	4.2	BCD
TP200610-2-3	5848	BCDEF	1105.67	ABCD	74.9	BCDEFGH	55.3	K	822	A	3.5	CDE
TP200610-4-6	5839	BCDEF	1080.22	ABCD	74.1	EFGHI	63.0	CDE	722	EFG	4.1	CD
Georgia 14N	5801	BCDEF	1122.65	ABCD	77.3	A	59.0	EFGHIJK	769	ABCDE	3.5	CDE
TP200610-3-12	5789	BCDEF	1081.31	ABCD	74.8	BCDEFGH	59.6	EFGHIJ	762	BCDE	3.3	CDE
TP200610-1-16	5753	CDEF	1092.74	ABCD	75.7	ABCDEFG	57.3	GHIJK	792	ABCD	3.7	CD
TP200610-2-8	5691	CDEFG	1092.01	ABCD	76.3	ABCDE	56.0	HIJK	810	ABC	3.4	CDE
TP200610-1-13	5629	CDEFG	1079.39	ABCD	76.9	ABC	55.8	IJK	813	AB	4.1	CD
TP200610-3-6	5584	CDEFG	1048.54	BCD	75.8	ABCDEF	69.9	AB	649	H	2.8	CDEF
TP200610-3-14	5565	DEFG	1047.90	BCD	74.7	CDEFGH	59.6	EFGHIJ	761	BCDE	6.2	AB
Georgia 16HO	5421	EFG	1009.73	CDE	74.8	CDEFGH	71.2	A	637	H	2.9	CDEF
TP200606-2-11	5140	FG	985.64	DE	77.1	AB	66.5	BC	682	GH	1.5	EF
AG-18	4862	G	886.15	E	72.0	I	60.0	EFGHI	756	DE	1.2	F
Mean	5847		1100.05		75.1		61.1		748		3.7	
CV(%)	11.1		11.1		2.4		8.2		8.0		49.0	
Entry "F"	0.026		0.0219		0		<.0001		<.0001		<.0001	

Multiple Disease Resistance test #2 and #4 were grown in South Texas as well (**Table 3-4**). At these locations several new breeding lines performed very well with respect to yield; within Test #2 TP200610-2-6 yielded the most at 5721 lbs/ac. It was also in the top statistical grouping for grade with a TSMK of 73.5%. This line numerically and statistically outperformed the commercial checks Georgia 09B and AG18 for both yield and grade, which were 4150 lbs/ac and 3824 lbs/ac respectively and in the top statistical grouping for the grade (Table 3). In Test #4 TP200609-3-14 yielded 7104 lbs/ac and graded 77.1% TSMK, which was also statistically better than Georgia 09B and AG18 for yield and grade (**Table 4**).

Table 3. Multiple Disease Resistance Test #2 in South Texs in 2021

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		SS%	
Cultivar												
TP200610-2-6	5721	A	1060.72	A	73.5	ABC	55.8	DE	814	AB	2.6	DEF
TP200609-1-2	5640	A	1022.57	A	71.6	BCD	53.6	E	848	A	4.1	ABCD
Georgia - 14N	5527	AB	1015.40	AB	73.7	ABC	58.2	DE	780	ABCD	1.6	F
TP200610-2-10	5444	ABC	1014.41	AB	74.4	AB	58.4	DE	777	ABCD	2.6	CDEF
TP200608-3-7	5279	ABCD	997.50	ABC	75.3	A	63.8	BCDE	719	BCDEF	3.1	BCDEF
TP200610-1-17	5173	ABCD	943.89	ABCD	72.9	ABC	58.5	DE	781	ABC	1.9	EF
TP200610-2-4	5125	ABCD	961.68	ABCD	73.8	ABC	72.2	ABC	628	FGHI	2.8	BCDEF
TP200610-4-4	5104	ABCD	949.95	ABCD	73.9	ABC	64.9	BCDE	700	CDEFG	4.5	AB
TP200609-2-11	4968	ABCDE	910.85	ABCDE	73.6	ABC	67.4	BCD	674	DEFGH	2.6	CDEF
TP200610-4-9	4740	BCDEF	851.06	CDEFG	71.9	ABC	63.5	BCDE	715	BCDEFG	4.3	ABC
Georgia 16HO	4654	CDEFG	861.52	BCDEF	74.7	AB	75.4	AB	610	GHI	3.7	ABCD
TP200609-3-11	4594	DEFGH	822.96	DEFGH	71.3	BCD	72.5	ABC	639	EFGHI	1.4	F
TP200608-2-4	4528	DEFGH	812.80	DEFGH	70.5	CD	80.5	A	575	HI	2.9	BCDEF
TP200609-2-1	4486	DEFGH	821.18	DEFGH	73.2	ABC	83.4	A	555	I	3.7	ABCD
Georgia - 09B	4150	EFGH	769.05	EFGH	74.6	AB	65.7	BCDE	691	CDEFG	4.1	ABCD
TP200609-3-18	4077	FGH	710.68	FGH	68.5	D	59.1	DE	785	ABC	3.9	ABCD
TP200610-3-5	3990	FGH	730.97	FGH	73.3	ABC	65.7	BCDE	691	CDEFG	5.0	A
AG-18	3824	GH	700.11	GH	72.7	ABC	67.6	BCD	678	CDEFGH	2.9	BCDEF
Tx144370	3809	H	688.46	H	71.9	ABC	61.2	CDE	741	ABCDE	3.4	ABCDE
TP200610-4-1	3777	H	699.74	GH	74.1	AB	60.6	CDE	749	ABCD	3.8	ABCD
Mean	4730		867.28		73.0		65.4		707		3.2	
CV(%)	15.9		16.7		3.2		15.2		13.3		39.2	
Entry "F"	<.0001		<.0001		0.0483		0.0004		<.0001		0.01	

Table 4. Multiple Disease Resistance Test #4 in South Texas in 2021

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		Splits	
Cultivar												
TP200609-3-14	7104	A	1364.70	A	77.1	AB	73.1	ABC	623	HI	1.7	DEF
TP200628-1-1	6913	AB	1273.59	AB	73.9	CDEF	65.8	BCDE	701	EFGHI	1.6	EF
TP200625-3-1	6440	ABC	1182.63	ABC	74.7	CDE	75.3	AB	603	HI	3.7	BC
TP200645-1-3	6201	ABCD	1075.94	BCD	67.8	G	54.8	EFGHI	832	BCDEF	2.4	BCDEF
TP200613-6-1-3	5868	ABCDE	1069.04	BCD	72.3	EF	53.7	FGHI	852	BCD	3.0	BCDEF
TP200627-5-1	5851	ABCDE	1062.57	BCD	71.9	F	57.6	EFGH	791	BCDEFG	1.8	DEF
Tamrun OL18L	5767	BCDEF	1035.15	CD	72.3	EF	69.7	ABCD	655	GHI	3.4	BCDE
TP200624-3-2	5750	BCDEF	1066.55	BCD	74.1	CDEF	65.3	BCDEF	709	DEFGH	2.9	BCDEF
TP200615-2-2-3	5607	CDEF	997.21	CDE	68.8	G	48.8	HI	933	AB	2.8	BCDEF
Georgia 16HO	5159	DEFG	951.71	CDE	74.7	CDE	69.5	BCD	656	GHI	2.3	CDEF
Georgia - 14N	5016	DEFG	947.99	CDE	75.1	BCD	62.0	CDEFG	738	CDEFGH	2.3	BCDEF
TP200615-2-2-1	4839	EFG	856.11	DE	68.8	G	51.8	GHI	877	BC	2.7	BCDEF
Tx144370	4802	EFG	876.42	DE	73.5	DEF	62.7	CDEFG	736	CDEFGH	4.1	AB
Georgia - 09B	4667	EFG	875.83	DE	76.1	BC	64.1	BCDEF	711	DEFGH	2.4	BCDEF
TP200629-3-1	4662	EFG	867.50	DE	74.5	CDE	54.2	EFGHI	845	BCDE	5.6	A
AG-18	4649	EFG	845.81	DE	74.4	CDE	65.4	BCDEF	703	EFGHI	1.2	F
TP200613-5-1-1	4537	FG	878.68	DE	78.9	A	81.6	A	562	I	2.7	BCDEF
TP200626-2-1	4309	G	787.28	E	73.8	CDEF	65.8	BCDE	696	FGHI	3.7	BC
TP200629-2-2	4141	GH	780.36	E	75.9	BCD	59.3	DEFGH	782	CDEFG	3.5	BCD
TP200643-1-1	2958	H	527.01	F	68.5	G	44.2	I	1038	A	1.2	F
Mean	5262		966.10		73.3		62.2		752		2.8	
CV(%)	22.2		22.6		4.3		17.7		18.2		52.8	
Entry "F"	<.0001		<.0001		<.0001		<.0001		<.0001		0.0048	

In closing for this section, 2 large plot combine trials were conducted, one in the High Plains and one in South Texas. In our program, large plot trials are used as a final look before release to evaluate how candidate breeding lines perform. The High Plains combine trial contained all the lines evaluated in the small plot Advanced Line Trial but only yield data was collected (**Table 5**). TP 200606-7-10 was the top yielding breeding line in the test at 5090 lbs/ac. Additionally, the release candidate TxL100212-03-03 performed in the same statistical grouping and both lines as well as the multiple disease resistant line TP 200625-3-2 also performed statistically above all commercial checks.

Table 5. Large plot combine trial on the High Plains in 2021.

Pods/Ac Lbs.		
Cultivar		
TP 200606-7-10	5090	A
TP 200625-3-2	4868	AB
TP 200606-2-14	4416	ABC
TxL100212-03-03	4360	ABC
TP 200607-1-2	4293	ABCD
TP 200608-1-6	4095	BCDE
AG18	4027	BCDE
NemaTAM II	3960	CDEF
TP 200606-3-10	3845	CDEFG
TP 200608-1-14	3809	CDEFG
TP 200606-2-9	3754	CDEFG
TP 200610-3-2	3647	CDEFGH
TP 200606-6-10	3643	CDEFGH
Tx144370	3615	CDEFGH
Georgia 09B	3425	DEFGH
Georgia 16HO	3401	EFGH
TP 200607-1-17	3092	FGH
TP 200610-1-2	3048	GH
TP 200609-1-5	3017	GH
Georgia 14N	2799	H
Mean	3810.1184	
CV(%)	19.669025	
Entry "F"	0.0001	

The South Texas combine trial included specific lines that are under consideration for release (**Table 6**). Release candidate TxL100212-03-03 was the top yielding breeding line in the test at 9711 lbs/ac. which was numerically and statistically greater than Georgia 09B, which yielded 8480 lbs/ac. Similarly TP200610-3-2 had a TSMK% of 76.5% which was numerically and statistically higher than both of the commercial checks NemaTAM II and Georgia 09B, which had grades of 72.4% and 72.1% respectively.

Table 6. Large plot combine trial planted in South Texas in 2021.

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		Splits	
Cultivar												
NemaTAM II	10176	A	1825.06	A	72.4	B	71.1	A	639	C	15.7	A
TxL100212-03-03	9711	AB	1793.86	A	75.4	AB	65.5	B	694	AB	13.3	B
TP 200606-7-10	9518	AB	1773.78	A	75.9	A	72.6	A	629	C	9.8	C
Tx144370	9080	BC	1672.43	AB	74.1	AB	63.4	B	719	A	14.6	AB
TP 200610-3-2	8812	BC	1640.18	AB	76.5	A	68.1	AB	667	BC	13.0	B
Georgia 09B	8480	C	1508.04	B	72.1	B	63.8	B	712	AB	15.3	A
Mean	9296		1702.22		74.4		67.4		677		13.6	
CV(%)	9.9		10.0		3.6		7.8		7.7		17.7	
Entry "F"	0.0368		0.0543		0.1		0.0044		0.0055		<.0001	

Specific lines considered for release will be discussed later.

Spanish-type Yield Trials

We continued testing advanced Spanish-type lines in West Texas during the 2021 growing season with new breeding lines entering testing for the first time. All breeding lines represent true Spanish growth habit. Several crosses are in early generation development with the hybrid Spanish growth habit and will enter testing in 2022. Growing conditions were excellent in West Texas and the test results reflected these conditions. During the 2021 season we conducted 2 Spanish tests consisting of 30 advanced Spanish breeding lines, three commercial checks: OLin, Schubert, and Tamnut OL06, and 4 historic varieties for disease evaluation.

Spanish Test #1 (**Table 7**) contained 17 breeding lines with various combinations of nematode and sclerotinia resistance. All three checks performed in the top grouping for yield with OLin having the highest numerical yield at 6021 lbs/ac followed closely by the breeding line TP 200641-5-1, which yielded 5980 lbs/ac and was statistically equal (Table 7). OLin also tied for the highest numerical grade in the test with a TSMK% of 77.1%, which was also the grade for TP 200641-2-1 and was significantly better than the Schubert, which graded 73.3%. TP 200641-5-1 was significantly equal to OLin but smaller than Schubert with g/100 seed of 57.3, 54.6 and 61.6 respectively. TP 200641-2-1 was somewhat smaller with a g/100 seed of 50.7.

The Spanish Test #2 (**Table 8**) was located in the same area in West Gaines Co. and produced similar results as the Spanish Test #1. The top yielding and grading line in the test was TP 200656-2-1 with a yield of 5868 lbs/ac and a grade of 79.4%. The size of the breeding lines varied greatly. Again, with TP 200656-2-1 being the largest seeded line in the test at 64.9 g/100 seed, which was statistically equal to Schubert at 62.4 g/100 seed. In contrast the smallest sized line in the test was a sister line from the same original cross, TP 200656-3-2, which had a g/100 seed weight of 40.1.

As mentioned, this was the first year of testing for all these breeding lines. The best performing of the lines from both tests will be carried forward into 2022 with continued testing and new lines will be added.

Table 7. Spanish Test #1 in West Texas for 2021

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		Splits	
Cultivar												
OLIN	6021	A	1138.05	A	77.1	A	54.6	C	831	HI	6	GHIJ
TP200641-5-1	5980	A	1091.40	AB	73.3	CDE	57.3	BC	793	IJ	5	HIJ
TP200640-2-1	5865	A	1113.74	A	77.1	A	50.7	D	896	GH	7	EFGHI
TP200641-4-3	5852	A	1069.63	ABC	73.4	CDE	39.1	GH	1161	CD	14	B
TP200652-2-3	5745	A	1061.82	ABC	75.3	ABC	39.9	FGH	1137	DEF	14	B
Schubert	5741	A	1034.19	ABC	73.3	CDE	61.6	A	737	J	5	IJ
TP200641-4-1	5708	A	989.22	ABCD	70.4	GH	39.6	FGH	1146	DE	12	BCD
TP200655-3-2	5569	A	1028.34	ABC	74.8	ABCD	42.6	F	1064	F	9	EFG
TP200653-2-2	5401	AB	1019.03	ABC	75.9	AB	46.6	E	974	G	8	EFGH
TP200641-1-1	5391	AB	953.07	ABCDE	69.0	H	36.7	HI	1237	BC	8	EFGHI
TP200655-1-1	5369	ABC	995.70	ABCD	74.4	BCD	40.3	FG	1130	DEF	10	DE
Tamrun OL06	5365	ABC	963.08	ABCDE	73.2	CDEF	60.0	AB	757	IJ	3	J
TP200652-2-1	5200	ABC	972.38	ABCDE	76.1	AB	50.3	D	903	GH	10	DEF
TP200652-1-1	5168	ABC	974.61	ABCDE	76.2	AB	42.2	FG	1077	EF	14	B
TP200655-3-1	5084	ABC	919.67	BCDE	72.9	DEF	40.0	FGH	1137	DEF	10	CDE
TP200655-1-3	5065	ABC	899.84	CDE	70.9	FGH	41.0	FG	1109	DEF	8	EFGHI
TP200655-1-2	4531	BC	800.94	E	71.7	EFG	42.2	FG	1076	EF	6	FGHIJ
TP200652-1-2	4464	BC	817.97	DE	74.5	BCD	42.4	FG	1071	EF	13	BC
TP200641-4-2	4442	BC	797.09	E	70.2	GH	35.4	I	1284	AB	9	DEF
TP200641-4-4	4411	C	832.71	DE	75.3	ABC	34.2	I	1330	A	18	A
Mean	5319		973.62		73.8		44.8		1043		9.5	
CV(%)	13.5		14.1		3.6		18.3		16.7		43.1	
Entry "F"	0.012		0.0073		<.0001		<.0001		<.0001		<.0001	

Table 8. Spanish Test #2 in West Texas in 2021.

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		Splits	
Cultivar												
TP200656-2-1	5868	A	1259.24	A	79.4	A	64.9	A	699	J	3.8	IJ
Tamnut 74	5740	A	1173.34	A	75.1	BC	49.1	FG	924	EF	9.4	E
Tamrun OL06	5596	AB	1123.18	AB	73.9	CDE	59.8	BC	759	IJ	3.7	IJ
TP200656-3-2	5542	AB	1085.45	AB	70.3	FG	40.1	K	1134	A	11.5	D
Tamspan 90	5524	AB	1165.72	A	77.1	AB	51.6	EF	880	FG	5.1	HI
Schubert	5499	AB	1114.89	AB	74.5	BCDE	62.4	AB	727	J	2.8	J
OLin	5494	AB	1126.83	AB	75.2	BC	55.6	D	816	HI	7.3	FG
GP of Toakson	5263	ABC	984.75	BC	71.8	EFG	61.9	AB	734	J	7.3	FG
TP200631-4-1-1	4853	BCD	969.03	BC	72.8	CDEF	49.4	FG	919	EF	9.1	EF
TP200656-2-4	4557	CD	895.73	CD	69.6	G	42.2	IJK	1076	AB	12.8	BCD
TP200641-4-1	4482	CDE	885.82	CD	72.5	CDEF	40.9	JK	1109	A	13.8	BC
TP200633-3-1	4438	DE	877.88	CD	71.9	DEFG	51.0	EFG	890	EFG	8.7	EFG
Spanco	4386	DEF	883.95	CD	74.4	BCDE	56.8	CD	802	HI	4.6	IJ
TP200631-2-1	4275	DEF	826.40	CDE	70.4	FG	50.4	EFG	902	EFG	7.7	EFG
#00-16	4144	DEFG	818.80	CDE	71.1	FG	53.8	DE	844	GH	4.4	IJ
TP200639-4-1	4036	DEFG	839.99	CDE	74.6	BCD	45.6	HI	998	CD	6.9	GH
TP200641-4-2	3675	EFG	752.68	DE	74.1	CDE	44.4	IJ	1023	BC	19.9	A
TP200656-2-2	3613	FG	726.18	DE	72.6	CDEF	48.2	FGH	944	DE	7.8	EFG
TP200656-3-1	3403	G	697.61	E	74.1	CDE	50.7	EFG	895	EFG	14.3	B
TP200656-2-5	1988	H	398.84	F	70.8	FG	47.9	GH	950	DE	12.1	CD
Mean	4619		930.32		73.3		51.3		901		8.6	
CV(%)	22.8		23.7		3.8		14.2		14.1		51.4	

Leafspot Resistant Spanish-types

We increased a population BC3-43-09-03-02 × Schubert to introduce leafspot resistance into Spanish peanuts. These materials were segregating for market type, with most of the materials being runners (because runner type is dominant to Spanish type). We harvested the different plant types separately and planted Spanish selections where possible for increase in 2020. These materials were planted at Yoakum in 2021 for leaf spot evaluation. If need be, we will backcross resistant runner selections with Spanish varieties and use selection for leaf spot resistance markers to obtain additional resistant Spanish breeding lines.

Nematode Resistant Spanish-types

We continue to cross with breeding line Tx144432 which is high oleic and nematode resistant lines from a Spanish MDR program. The seed size of the lines is below average and further crossing is needed. In our 2019 and 2020 spring crossing program we made several crosses with released varieties OLIn, Tamnut OL06, and Schubert as well as other selected germplasm. These were increased in our greenhouses over the summers of 2019 and 2020 as well as some individual plants that were planted in Yoakum. These continue to be advanced for evaluation beginning in 2021.

Spanish/Valencia Test

A test of advanced Spanish and Valencia breeding lines was conducted in Gaines and Lubbock Counties. Unfortunately, the seed lots of several accessions and check varieties had poor germination and are not shown. Several accessions, however, had yields statistically equal to TamVal OL14 and grades that were as high as 75% TSMK (**Table 9**). Seed size ranged from small Spanish (45 g/100 SMK) to larger (57g / hundred SMK).

Table 9. Spanish and Valencia advanced lines, 2021.

Genotype	Pod Yield (lb/ ac)	Value (\$/ ac)	Seed Weight (g/ 100 SMK)	Shellout (% TSMK)
TL076224-08	4055 a	615 ns	49.21 d-f	69.22 ns
TL076225-04	3571 ab	574	45.56 f	68.70
TL076225-28	3537 ab	602	49.01 d-f	71.70
TamValOL14	3257 a-c	632	56.46 ab	71.14
TL076240-01	3111 a-c	418	57.16 a	68.39
TL076239-16	3100 a-c	539	51.76 b-d	71.31
TL076239-12	3070 a-c	462	54.86 a-c	70.63
TL076231-002	2799 b-d	502	56.86 a	72.85
TL076229-53	2735 b-d	501	51.01 c-e	72.21
TL076221-34	2730 b-d	502	45.71 f	71.66
TL076232-004	2660 b-d	451	57.46 a	71.64
TL076233-003	2559 b-d	408	54.81 a-c	71.27
TL076221-06	2431 b-d	385	46.01 ef	70.47
TL076238-01	2294 cd	412	49.56 d-f	71.48
TL076225-49	2276 cd	363	51.26 cd	73.55
TL076238-16	1820 de	345	45.56 f	72.08
TL054529-48	1707 de	317	55.46 a-c	70.53
TL076236-04	1607 de	262	54.01 a-d	74.35
TL076226-18	909 e	153	52.56 a-d	75.59
p	0.002	0.229	0.001	0.52
Mean	2674	444	51.80	71.51
LSD	1192		5.02	
CV	24.0%	31.4%	4.5%	3.3%

Finally, we continue to develop new materials for our breeding program. In 2021 we conducted 42 unique cultivated hybridizations for combinations of drought tolerance, disease resistance and improved yield and grade. As part of this we increased several hundred F₁ plants, several thousand F₂ plants, and selected 300 for increase as F₃ for future testing. We also continue to develop prebreeding germplasm from our wild species collection to incorporate new sources of resistance.

Sub-Project I-2 Drought Tolerant Runner-type yield trials

This and the second population have been grown and tested at two locations – the USDA-ARS in Lubbock and the Lubbock AgriLife Center. The materials at the ARS have been photographed using weekly UAS overflights scheduled by Dr. Payton. We expect that when aerial images are analyzed and correlated with ground-based measurements and pod yield at harvest this will give us new ways to measure and select for favorable responses of peanut to water deficit stress.

Runner trials – First population. The first population was developed to combine tolerance to water deficit stress with high oleic seed content. Previously, the number of breeding lines required growing this as three separate tests, but selections for yield, grade, and seed size were made, and the best lines from each of the three previous tests were combined into one. The test was performed under water deficit at two locations. The trial was conducted in West Texas, at a target of 25% ET replacement

(essentially dryland) from June through August. These were chosen to represent the times of greatest water deficit on farms with limited irrigation. The low yields, grades and seed weights demonstrate the degree of water deficit stress the test was under, and we do not expect growers to grow their peanuts with so little water. what is important is that yields of several of the breeding lines under these harsh conditions were significantly (40% to 100%) higher than Georgia 09B, Flavorrunner 458, and Tamrun, suggesting that some of these could be more tolerant to water deficit than standard varieties.

Table 10. Yield of the Runner Drought population #1, 2021.

Accession	Pod Yield (lb/ ac)	Seed Weight (g/ 100 SMK)	Shellout (% TSMK)
100225-03-05	1509 a	58.5 c-i	61.4 ab
100225-03-08	1418 ab	61.8 b-f	65.6 a
100212-05-10	1388 a-c	58.4 c-i	53.0 a-f
100212-03-03	1321 a-d	76.7 a	61.8 ab
100225-03-02	1275 a-e	54.1 f-n	57.2 a-f
100212-07-04	1200 a-f	61.0 b-g	59.6 a-d
100212-07-01	1178 a-g	49.9 l-o	54.3 a-f
100225-06-07	1107 a-h	63.1 b-d	55.6 a-f
100225-05-07	1088 a-h	58.6 b-i	59.6 a-d
100225-05-02	1086 a-h	57.8 c-j	53.4 a-f
100225-03-04	1072 a-h	57.6 c-k	50.5 b-f
Georgia09B	1065 a-h	51.9 i-n	52.6 a-f
...			
FlvRun458	882 c-i	52.1 i-n	43.9 fg
...			
TamrunOL02	751 f-i	57.1 c-l	49.2 b-f
...			
100212-03-11	533 i	53.6 q-n	51.5 b-f
p	0.071	0.016	0.096
Mean	958	56.8	53.1
LSD	523	7.7	13.2
CV	33.4%	7.8%	9.1%

As in previous years, yields of many breeding lines were statistically superior or at least numerically equal to those of the check varieties. Among the best lines combining yield and grade were TxL100212-03-05, TxL100212-03-08, TxL100212-03-03, and TxL100212-07-04 (**Table 10**). TxL100212-03-03, which also performed very well under full irrigation (**Tables 0, 5, and 6**). ,was

among the better lines in the drought test for yield. We expect to write up this entry for release as a drought-tolerant runner variety. Over several years, there appear to be some runner lines with better drought tolerance but may not yield as well under water deficit. This is consistent with what we have seen in earlier drought tests – the best lines under full irrigation are not the ones with the greatest drought tolerance. The opposite is true also. We plan to obtain another year or two of data before deciding if any of the runner lines in this test, other than TxL100212-03-03, could be released as a better option for cultivation when water is scarce.

Table 11. Yield of the new selections under water deficit stress, 2020.

Accession	Pod Yield (lb/ ac)	Seed Weight (g/ 100 SMK)	Shellout (% TSMK)
TL144301-131	4545 a	79.4	68.5
TamrunOL18L	4414 a	79.7	71.2
TL144301-155	3836 ab	45.6	56.3
TL144301-117	3716 a-c	72.6	70.6
TL144301-103	3644 a-d	71.0	69.2
TL144301-170	3643 a-d	78.0	72.0
TL144301-099	3468 a-e	62.4	56.9
TL144301-035	3426 a-e	84.4	66.9
...			
FlvRun458	3050 b-q	70.9	73.2
Mean	3026	71.5	67.2
LSD	1143		
CV	23.1%		

Second runner population.

This population was developed to combine tolerance to water deficit, nematode resistance, and the high oleic trait. Previously, we found several breeding lines better than check varieties for yield under water deficit, but none of the breeding lines graded well. We have begun a marker-assisted backcrossing scheme, using markers for drought tolerance, to cross back with varieties that grade better.

Table 12. Yield of Leading Virginia release candidate lines and checks, 2021.

	(\$/ ac)	(lb/ac)	(% Fancy)	(g/100 SMK)	Shellout (% TSMK)
TxL090105-38	911 a	4970 ns	81.8 d	91.2 cd	72.1 a-c
TxL090106-15	890 a	4816	86.9 a-c	90.8 cd	72.0 a-c
Wynne	877 a	4732	91.7 a	100.7 ab	70.7 a-e
Bailey	799 ab	4682	89.4 a	99.6 a-c	70.4 a-e
NC-7	718 a-c	4647	88.1 ab	102.9 a	68.9 c-e
Champs	737 a-c	4457	87.7 ab	96.2 a-c	67.8 e
TxL090106-05	820 ab	4434	82.7 cd	86.5 d	72.3 ab
TxL090105-07	758 a-c	4379	87.9 ab	92.9 b-d	69.7 a-e
TxL090206-41	660 a-c	4353	79.9 d	95.7 a-c	68.4 de
Tx107844-5	694 a-c	3979	89.3 a	100.3 ab	72.5 a
TxL090106-52	599 bc	3943	80.5 d	84.1 d	69.1 b-e
08X09	751 a-c	3913	84.0 b-d	95.7 a-c	69.1 b-e
TxL090105-18	523 c	2850	88.6 ab	102.9 a	71.4 a-d
p	0.096	0.113	0.001	0.004	0.093
Mean	749	4320	86.0	95.3	70.3
LSD	258	1207	4.8	8.8	3.3
CV	17.3%	16.7%	2.8%	4.7%	2.4%

In the meantime, we found that progeny of the reciprocal cross (cross made in the opposite direction) had better shell out. We intended to test this for a second year under water deficit. However, yields suggested that the test had been given significantly more water than planned, perhaps an error in nozzling. Nevertheless, it appeared that some of the accessions yielded as well as or better than cultivated varieties and had comparable grades. A small subset of the data is presented in **Table 11** to demonstrate this. We are repeating the test this year, but under water deficit.

Virginia trials. We continued testing of leading high oleic Virginia release candidates to gather additional data to select one of the candidates for writing up for release later this year. We grew Virginia lines at three locations in West Texas. Data is shown in **Table 12**. The two leading release candidates, TxL090105-07 and TxL090106-15, did well overall, with yields and grades similar to commercial checks. Line TxL090105-18 had significantly larger seeds and percentage of fancy pods, but yield was subpar in 2021; by contrast, it was at the top of the list in 2020.

Spanish Peanut with Tolerance to Water Deficit.

We conducted the first year of testing of a Spanish population developed for high oleic oil and tolerance to water deficit. The donor parent was a variety used in West Africa, but low oleic; a sister line of Schubert was the parent adapted to Texas. **Figure 1** shows a plot of grade vs. yield. The drought-tolerant parent 55-437 yielded better than the Schubert sister line TxL054520-27 but had poor grade. Schubert did not perform well for yield or grade under water deficit.

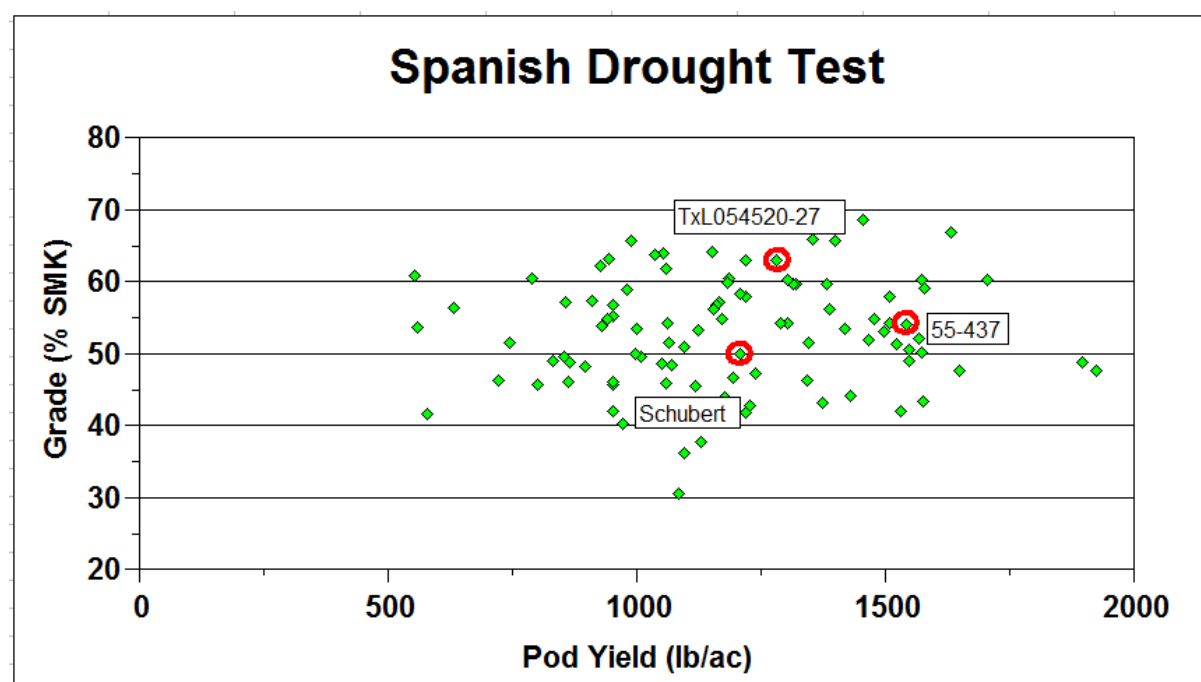


Figure 1. Comparison of yield and grade for Spanish accessions under water deficit stress.

By comparison, several lines possess a good combination of both traits, with yields at the top of the test and grades superior to th 55-437 and equal to or better than the TxL054520-27 high-oleic parent. There are many breeding lines (maybe $\frac{1}{4}$ of the population) as comparable or better in both

yield and grade under water deficit than Schubert. Some of the better lines, along with hundred seed weights, are shown in **Table 13**. This was the first year of testing and will be repeated in 2022 to see if results are consistent across years.

Table 13. Listing of some of the better lines from the Spanish drought test. Selections having grade or hundred seed weight in the top 20% are highlighted.

Genotype	Pod Yield (lb/ ac)	Shellout (% TSMK)	Seed Weight (g/ 100 SMK)
14GAF1424	1924 a	47.7 l-A	36.2 d-q
14GAF1412	1899 ab	48.9 j-A	38.6 c-p
14GAF1367	1706 a-c	60.4 a-n	42.2 b-k
14GAF1458	1649 a-d	47.7 l-A	41.1 c-m
14GAF1373	1633 a-e	66.8 ab	39.3 c-p
14GAF1358	1579 a-f	59.2 a-q	38.3 c-q
14GAF1466	1576 a-g	43.3 t-B	35.6 e-q
14GAF1422	1574 a-g	50.2 f-A	37.3 c-q
14GAF1411	1574 a-g	60.3 a-o	37.4 c-q
55-437	1569 a-g	52.2 c-y	38.7 c-p
14GAF1428	1550 a-h	49.1 i-A	34.7 g-q
14GAF1413	1549 a-h	50.5 f-A	43.1 b-i
14GAF1408	1542 a-h	54.1 b-y	41.5 c-l
14GAF1420	1533 a-i	41.9 w-B	45.6 a-f
...			
14GAF1366	1455 a-n	68.6 a	41.6 c-l
14GAF1332	1430 a-n	44.2 r-B	42.8 b-j
14GAF1314	1419 a-n	53.5 b-y	44.9 b-g
14GAF1348	1400 a-o	65.7 a-e	30.2 n-q
...			
TxL054520-27	1281 a-q	63.0 a-j	42.2 b-k
...			
Schubert	1210 c-s	50.1 f-A	41.8 c-k
p	0.09	0.005	0.01
Mean	1184	53.0	38.3
LSD	668	14.3	10.7
CV	22.8%	10.3%	10.7%

Developing Wild Species Pathway for Introgression of Drought Tolerance

This project continues as part of the long-term drought project. It was first funded internally but has been absorbed into our overall drought program. The initial phase of this project was to identify 14 candidate genes associated with drought tolerance by conducting an imposed drought transcriptomics study. Specifically, we identified transcription factors that occur early in genetic pathways and represent excellent candidates for marker development. We received funding for the Peanut Research Foundation to validate the presence of the candidate genes in the original drought tolerant species and to expand the study to include other related species. Sequencing and analysis are currently underway. This project remains a vital part of our overall drought program. Transcriptomics is a powerful tool that can not only tell if a gene is present but can also determine how strongly a gene is expressed. Once the genes are validated for expression, level marker

development can be conducted and used to aid in introgression of genes into our elite material.

Crossing and chromosome doubling continues as part of the wild species introgression pathway and is under development. When completed this will allow identified genes to be moved into the cultivated peanut. At this point, we have made the initial cross and confirmed hybridization. The next step in pathway development is to double the chromosome number. This is proving to be very challenging. We are exploring alternate pathways using other species and or accessions to move the genes. One related complex hybrid has already been doubled and has cultivated materials that are being backcrossed into more advanced materials. Tamrun OL11 is the recurrent parent in this crossing program, however, several more backcrosses are needed to make the lines commercially viable.

Identify Markers for Drought Tolerance in Mini-core Collection

Minicore accessions were sent for analysis on the peanut community SNP chip. Of 47,837 SNPs 8,189 SNPs were selected for analysis. We performed Genome-Wide Association Scanning (GWAS) analysis using these SNPs on the U. S. minicore collection with phenotypic data from TX, OK, and VA in 2017. This reduced set of SNPs was selected from the larger set based on standard selection criteria. Using the Tassel program, we identified 120 SNPs at p -value $< 10^{-4}$ and 558 SNPs at p -value $< 10^{-3}$ (**Table 14**) significantly associated with the phenotypic data. Of these, 71 SNPs are significantly associated with more than one trait. Overall, 163 SNPs are considered the most reliable and are significantly associated with either different locations, multiple traits, or both. For the sake of comparison, we would expect 0.8 false positives per trait and location at $p < 0.0001$. The Manhattan plot of association by field across locations is shown in **Figure 2**. Once completed, we will go back with these markers to screen advanced progeny and backcrosses in our breeding population.

Table 14. Number of SNP marker-trait associations (p -value = 10^{-3}) for various traits (ALL = all locations, TX = Texas, OK = Oklahoma, VA = Virginia). Trait abbreviations: SCMR- SPAD chlorophyll content, NDVI, normalized difference vegetation index, ELK- extra-large kernels, Temp- canopy temperature, CTD,

Trait	ALL	TX	OK	VA	Sum
Paraheliotropism	5		3		6
Flowering		90	71	14	161
Height				3	3
SCMR	1	53	16		69
Width	3		8	20	30
Wilt		1	2	1	4
Yield	57	30	84	26	148
NDVI				78	78
Temp		1			1
Wgt100SMK		28	71		79
%ELK		41			41
%Mid		7			7
%No1		9			9
CTD				6	6
Others				15	15
Sum					558

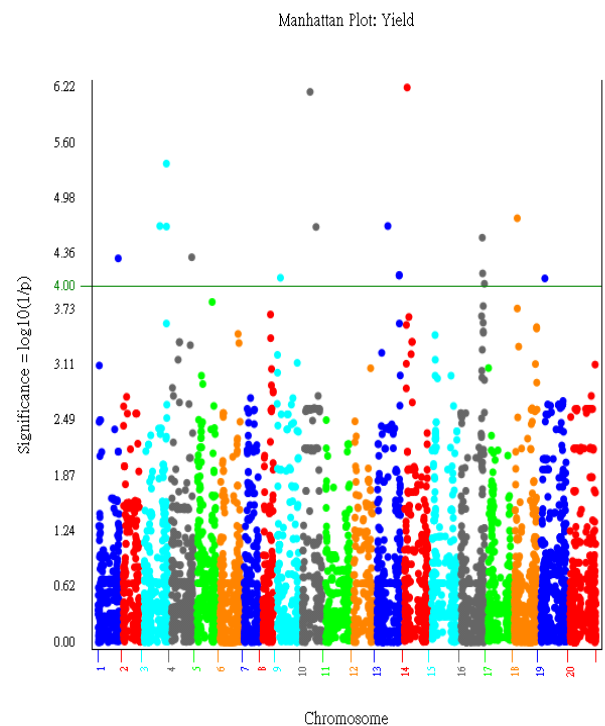


Figure 2. Manhattan plot of association by field across locations shows 17 significant SNPs for yield above the threshold (P -value = 10^{-4}).

We previously sent DNA of the minicore collection and additional accessions to the Texas A&M AgriLife Bioinformatics and Genomics Center for RAD-Seq sequencing on 144 accessions. An additional 72 accessions have been prepared but will be sent to the TAMU-Corpus Christi genomics center because AgriLife has discontinued its RAD-Seq service. We will add the new data to complete the data set and use this for analysis of an additionally drought tolerance minicore data set. To date, we obtained 3,265 SNPs from RAD-Seq using the GATK software. However, some researchers think that the data from RAD-Seq analysis may have some advantages over SNP chip data. To date, we have identified more SNPs by the SNP chip than by RAD-Seq; however, the SNP chip interrogates a single nucleotide and lacks data on flanking sequences. It is expected that there may be more false SNPs in the SNP chip data due to the presence of unexpected closely related (“paralogous”) genes that are present in other places of the peanut genome. RAD-Seq may be better at identifying and filtering out false positive data because it gives flanking sequences. We plan to test this hypothesis while working to identify additional markers for tolerance to water deficit.

Current Releases

We have received final approval for a nematode resistant runner variety from the Texas A&M Plant Release Committee, to be named NemaTAM II, which is a high-yielding, high oleic fatty acid, runner-type peanut cultivar with resistance to root-knot nematodes. The cultivar was developed to provide growers with a replacement option for the former Webb cultivar which had excellent nematode resistance, but also had a very large vine size that made harvest difficult for peanut farmers. Like Webb, NemaTAM II maintains resistance to root-knot nematodes, but has equal to or better yield, higher grade potential and a shorter canopy for easier digging and inverting at harvest. In 2021 approximately 30 acres of foundation seed are being grown at the Texas A&M Foundation Seed offices in Vernon, TX.

We received final approval for release of two early maturing runners from our early maturity program. Tamrun OL18L and Tamrun OL19. Tamrun OL18L is a high yielding, high-oleic, early maturing runner-type peanut cultivar with a larger than average seed size. Its maturity is comparable to Tamrun OL12 which matures 14 days earlier than Flavorrunner 458. Yield is similar to Georgia 09B but is higher than Tamrun OL11. The seed size is similar to Tamrun OL07 and Webb. Tamrun OL19 is a high-yielding, high oleic, early maturing runner-type peanut cultivar that matures approximately 7 days earlier than Tamrun OL07 but 7 days later than Tamrun OL12, as observed from five years of testing. Yield is similar to Georgia 09B but is higher than Tamrun OL11. The seed size is similar to Tamrun OL11, but larger than Georgia 09B. There were no differences in flavors noted in flavor analysis between Tamrun OL18L and check cultivars. We grew ¼ ac breeders seed increases in 2021 but were unable to have the material shelled in 2022 because of damage to the sheller at Vernon. We expect to have the next increase performed in 2023.

Future Runner Releases

The Tx144300's were developed for resistance to Root knot nematodes and Sclerotinia. While they performed lower in yield to the drought lines mentioned above, Tx144370 has performed well in South Texas, which is where they were developed to give growers a nematode

resistant line with better characteristics than the previously released Webb and NemaTAM II variety. These two lines have yielded 400-600 lbs/ac better than Webb and graded 1-3 percentage points higher. Additionally, they have a much shorter growth habit than NemaTAM II and a slightly smaller seed size in most of the trials over the past four years. The decision was made to move forward with the breeding lines for release. Tx144370 is in plant row increase in the 2021 season.

Of the materials developed from the runner drought testing, several lines have done well in irrigated trials. In particular, TxL100212-03-03 (see above) has been in advanced trials for a couple of years now and has consistently done well. We tested this line again under water deficit stress in 2021 and it continued to do well there. We plan to release it because of its high yield potential both under irrigation and water deficit. It was in a $\frac{1}{4}$ ac row increase last year and is being increased again this year in anticipation for release. We expect to write up the release proposal either later this year or early next year.

We are continuing to test runner lines combining tolerance to water deficit, resistance to root-knot nematodes, and high oleic oil. We are conducting marker-assisted backcrosses of water deficit tolerant, nematode-resistant lines selected earlier by higher-grading varieties because the first set of lines in this population had grades that were too low to release. Fortunately, the reciprocal cross has produced several lines with grades equal to check varieties. We will conduct additional testing with the goal of release for one of these as a new variety in the next couple of years.

Sub-Project IV. SNP Marker Development

This year, we have focused our development efforts on three objectives: (1) Developing a high-density marker map of the TxAG-6 x Florunner backcross population for the purpose of using markers for breeding for resistance to leaf spots, (2) developing a less-expensive marker system, called resequencing, and (3) writing up markers identified for drought tolerance in the minicore collection. We will present results on (1) and (2), as for (3), we reported the results last year and will report any new results next year.

1. Identifying Markers for Leafspot Resistance from Wild Species Introgression Lines

Table 15. Summary of the SNP chip analysis of the BC1 TxAG-6 x Florunner population.

Marker Type	Number of Markers
Other	18,669
Poly High Resolution	9,589
Other Variants	8,677
No Minor Homology	5,450
Monomorphic High Resolution	5,052
Call Rate Below Threshold	400

We have already identified ca. 20 markers for resistance to leaf spots and rust, and for yield in backcross introgression lines. However, there are some gaps in the map and some questions about which markers are linked to each other, that is, are inherited together. This is because the current map (ca. 180 SNP-based markers) does not have enough markers to distinguish all chromosomes. For this purpose, we are developing a higher-density linkage map, which will then be used to refine the markers for resistance to leaf spots.

To do this, we sent DNA from the first backcross generation for genotyping on the peanut community Arachis AxiomArray2 SNP chip. Received data is presented in **Table 15**. The first three lines show classifications of single-nucleotide polymorphisms found among the progeny. The results agree with results that we obtained many years ago using older (and now-obsolete) marker types, showing that about 70% of the markers could distinguish the two parents of the population. The difference is that, previously we had only a few hundred possible markers, but from the SNP chip, there are perhaps as many as 35,000 or so, which is far more than needed). The type of markers that are classified as “Poly[morphic] High Resolution” are considered to be the best, with a generally clear distinction in genotyping calls in the population. An example of such a marker is shown in **Figure 3**.

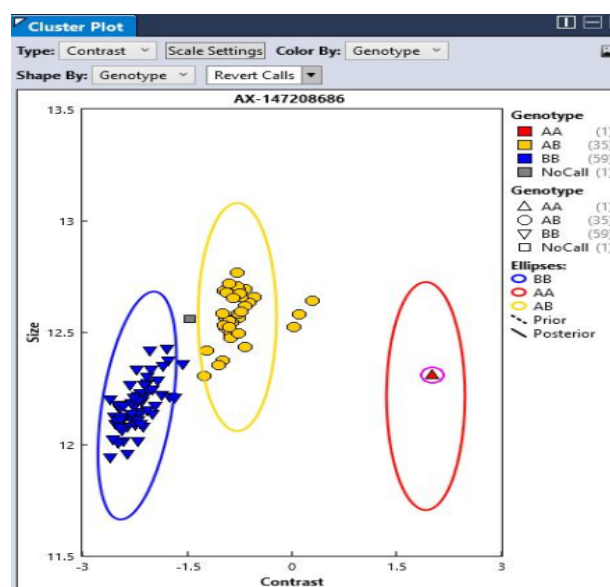


Figure 3. Sample SNP chip marker, where about half the peanut backcross lines match the Florunner recurrent parent, half are intermediate (sharing markers from both parents), and then TxAG-6 stands out by itself.

2. Developing a lower-cost resequencing system.

The ability to identify such a large number of markers in a single experiment is one of the benefits of the peanut genome sequencing project. However, the large number of markers identified is far more than we need and would be useful to have a smaller number at a lower cost. Our goal is to reduce the cost of identifying markers in populations of several hundred individuals by half, from ca. \$30 per sample for 30,000 targets to \$10 or \$15 per sample for 2,500 to 5,000 targets. the markers on the SNP chip were chosen more-or-less randomly. it would be more useful to target genes from specific biochemical pathways, like oil production. For this, a genotyping system called “targeted resequencing” would be useful.

We met with representatives of several companies that have developed such technologies and decided to try Tecan Inc.’s “Allegro” system, which has already been applied to 60 different plant and animal species. This same system is being developed for cotton by researchers at Texas A&M, with the sequencing being done for several species in College Station.

We looked over DNA sequence data and generated an initial set of 2,904 sequence target regions on peanut chromosomes. (We have identified several thousand more targets since then). Of these, Tecan determined that they could design probes for 95% of the targets (**Table 16**). These were then used to sequence DNA targets from 48 peanut varieties and closely related breeding lines to see if the system worked. Differences (“polymorphisms”) were found for 56% of the probes that were designed. The system proved to work, so we will test an additional 144 peanut accessions.

Table 16. Target and probe design statistics.

Stage	# of Targets
Target Information Sent to Tecan	2,904
Successful Design by Tecan	2,770 (95%)
Recovered by Sequencing (48 Accessions used)	1,547

The DNA accessions selected included several sets of closely related sister lines in the AgriLife breeding program from crosses within different market classes of peanut. These were chosen to test whether it would be possible to distinguish closely related lines and see if there were enough polymorphisms (sequence differences) to be used to identify new markers for new traits in the future. We estimate that a few hundred differences would be needed among ca. 300 individuals of a population. Results show between 40 and 114 differences among three individuals, and so we expect that there will be several hundred differences among a population of a few hundred individuals (**Table 17**).

Table 17. Examples of SNP differences between populations of closely related breeding lines within a market class.

Accession	Market Class	Comments	# of SNPs
TxL054529-27	val	Valencia sister lines.	114 SNPs
TxL054529-33	val (TamvalOL14)		
TxL054529-48	val		
TxL080243-06	run (TamrunOL19)	runner sister lines.	64 SNPs
TxL080287-05	run		
TxL080256-02	run (TamrunOL18L)		
TxL090106-15	vir	Virginia sister lines.	49 SNPs
TxL090105-07	vir		
TxL090206-41	vir		
TxL054520-27	spa	Spanish sister lines.	40 SNPs
Schubert	spa		

Screening for Root Knot Nematode Resistance

A total of 480 seeds representing 36 breeding lines were re-screened by SNP markers to test the purity of breeding lines with resistance to root-knot nematodes, drought, and high oleic seed. In addition, we screened breeding lines made by the Stephenville program to incorporate nematode resistance.

Screening for the High O/L Trait

As part of our continued efforts to develop high-oleic varieties and maintain purity of breeding lines and TAMU varieties, 2,558 seeds were tested for the high oleic trait by NIR (**Table 18**). A few additional seeds were scored using DNA markers instead, mainly where we were testing for hybridity for early-generation crosses with markers at the same time (**Tables 19 and 20**).

Table 18. Numbers of Seeds screened by NIR for the High Oleic Trait.

Experiment	Seeds Screened
Valencia Increase (potential release)	669
Virginia Purified Seeds for Bulk Increase (source in 2021)	240
High Oleic and <i>Aspergillus flavus</i> Resistance Peanut	129
West African Spanish Drought Lines	60
AgriLife Stephenville Breeding Lines	1460
Total	2,558

Table 19. Numbers of Seeds screened by KASP Marker Genotyping for Hybridity and for Varietal Identification in Peanut.

Experiment	Seeds Screened
Screening Peanut for Hybridity and for Varietal Identification	384
Total	384

Table 20. Numbers of Seeds screened by KASP Marker Genotyping for the High Oleic Trait.

Experiment	Seeds Screened
<i>Aspergillus flavus</i> Resistance Peanut	48
West African Spanish Drought Lines	117
Total	165

Sub-Project IV. High Throughput Phenotyping

Unmanned Aircraft System (UAS) and sensors is an emerging remote sensing technology that provides imagery datasets with exceptional spatiotemporal resolutions.. UAS can collect images quickly and repeatedly under appropriate weather conditions for agricultural applications. UAS-based imagery data also provides advanced phenotypic data using image processing and computer science algorithms, which is very useful and practical to extract crop traits. In 2021, UAS data was collected, and UAS-based Hight Throughput Phenotyping system was adopted to extract various crop parameters such as canopy cover, plant height, vegetation indices, etc. The project hit a snag in late July of 2021 when a burglary of our Field Headquarters led to the theft of all our Stephenville UAS equipment. These UAVs were never recovered. However, the UAS program at the Texas A&M AgriLife Research and Extension Center at Corpus Christi graciously loaned us 2 older UAVs from their inventory allowing us to continue collecting data. Thanks to their quick response only one data collection during the season was lost. However, issues with the borrowed post kinematic survey system did prevent late season collection of disease index data. For the beginning of the 2022 season, we will continue borrowing the Corpus Christi UAS until Stephenville A&M AgriLife Research can obtain new equipment, We hope to be collecting data with new machines later in the 2022 season.

UAS Data Collection

Texas A&M AgriLife Research at Stephenville conducted UAS data collection using DJI Phantom 4 Pro and DJI Matrice 200 equipped with Slanrange 4P+ to acquire RGB and multispectral images, respectively. The UAS data collection protocol developed by Texas A&M AgriLife Corpus Christi was followed to collect high quality UAS data. This protocol included UAS flights at 25–30-meter altitude with 80-85% overlaps, depending on the sensors used and proper installation of Ground Control Points (GCPs). **Table 21** shows a summary of UAS data collection for 2021.

Table 21. Summary of UAS data collection schedule for 2021.

Date	Platform	Sensor
07/23/2021	DJI Matrice 200	Slanrange 4P+
08/20/2021	DJI Matrice 200 & DJI Phantom 4 Pro	RGB and Slanrange 4P+
09/03/2021	DJI Matrice 200 & DJI Phantom 4 Pro	RGB and Slanrange 4P+
09/13/2021	DJI Matrice 200 & DJI Phantom 4 Pro	RGB and Slanrange 4P+
09/29/2021	DJI Matrice 200 & DJI Phantom 4 Pro	RGB and Slanrange 4P+
10/25/2021	DJI Matrice 200 & DJI Phantom 4 Pro	RGB and Slanrange 4P+

UAS Data Processing

The overall UAS image processing pipeline developed by our team is divided into three levels and presented in **Figure 4**. The workflow starts with the collection of raw images (Level 0 data product from different sensors and platforms). Level 0 data are then processed using the Structure from Motion (SfM) algorithm to generate Level 1 geospatial data products, such as Digital Surface Model (DSM), orthomosaic images, and 3D point cloud data. Level 2 data products are generated from the Level 1 data products and represent relevant biological crop features, canopy height, canopy cover, various vegetation indices, such as Normalized

Difference Vegetation Index (NDVI), Soil Adjusted Vegetation Index (SAVI), and Excessive Greenness Index (ExG).

All raw data collected from UAS was processed to generate an orthomosaic and DSM. We adopted the Agisoft Metashape software (Agisoft LLC, St. Petersburg, Russia), which is one of the famous commercial software to stitch UAS raw images using SfM GCPs' GPS coordinates were also input in image stitching process for removing distortion and precise geo-referencing.

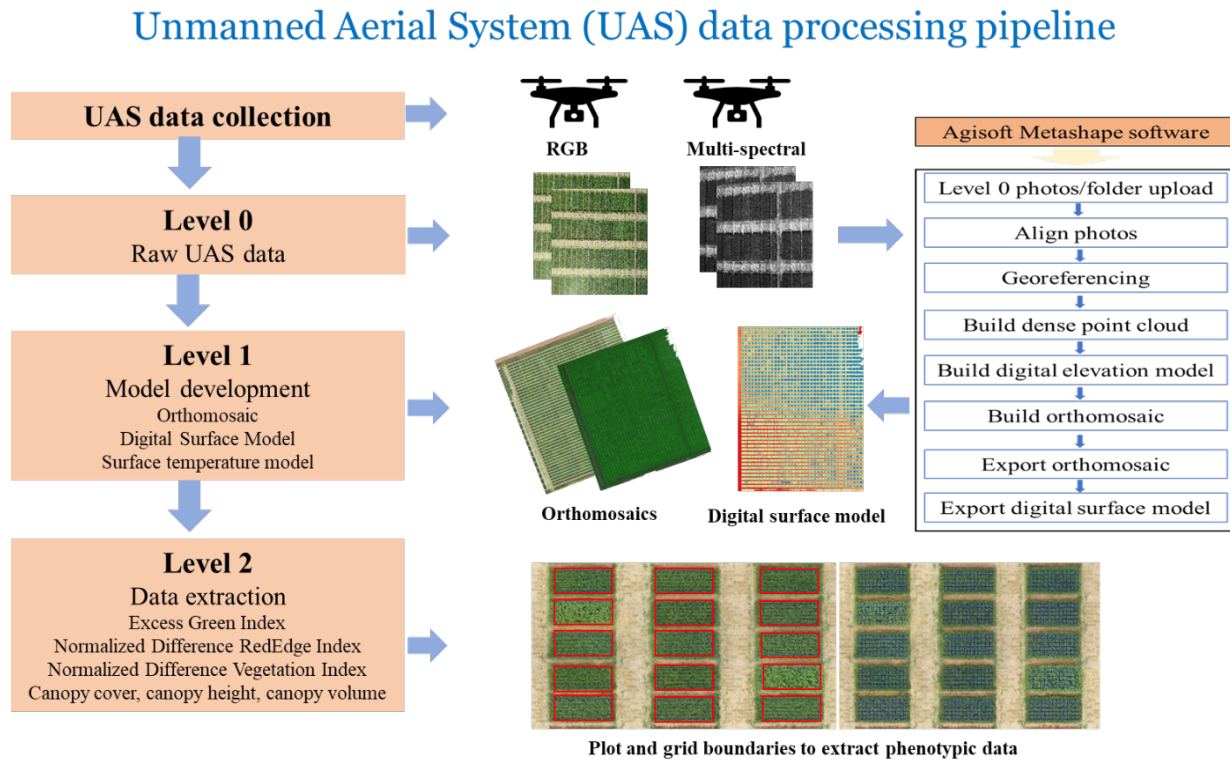


Figure 4. Overall UAS data processing pipeline used to process raw images and obtain phenotypic information

Once the orthomosaic is generated, canopy features such as canopy height, canopy cover, and vegetation indices were obtained. **Canopy height (CH)** is generated from the DSM, which represents the surface elevation of objects on the ground. To estimate CH for each flight date the Crop Height Model (CHM) is generated by subtracting the Digital Elevation Model (DEM) from the DSM. The DEM is generated from UAS data acquired prior to plant emergence. A classification algorithm will be used to obtain **canopy cover (CC)** from orthomosaic images. The classification algorithm uses red, green, and blue spectral bands of orthomosaic images and Red Green Blue Vegetation Index (RGBVI) to generate a binary classification that separates canopy areas from non-canopy areas on the image. A plot boundary file with plot/grids will be created and overlaid on the CHM to obtain height measurements and to calculate percentage of green pixels (CC) within each grid/boundary. **Canopy volume (CV)** provides an estimate of plant biomass as a combination of canopy size and height. CV for individual grids is calculated as the sum of pixels classified as canopy multiplied by the individual pixel height. We also

calculated multi-spectral and RGB-based vegetation indices to assess canopy efficiency and canopy health.

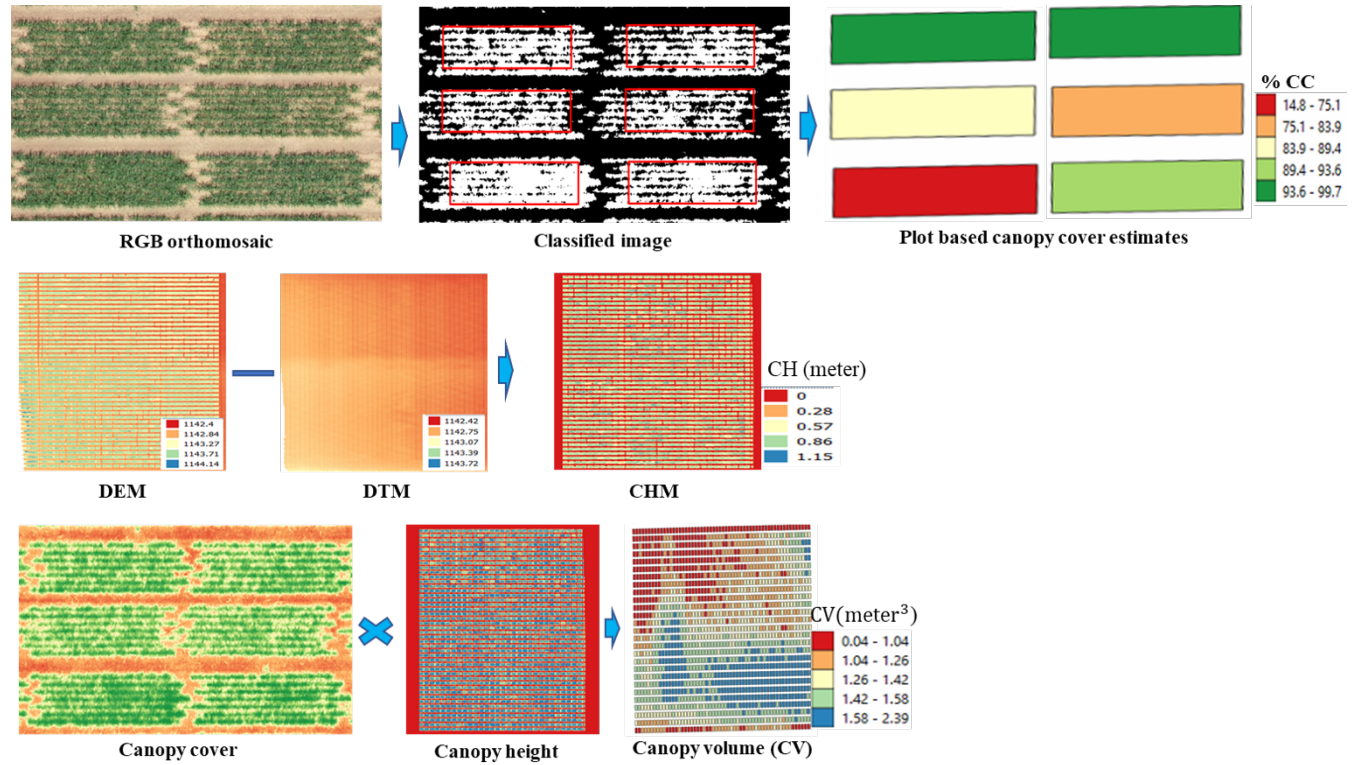


Figure 5. Estimating canopy cover (CC), canopy height (CH), and canopy volume (CV) from Unmanned Aerial Systems (UAS)-based orthomosaic and digital surface models (DSMs)

Data extraction and analysis

Data analysis is ongoing, however, preliminary data for canopy cover, canopy height, excess green index, and canopy volume has been calculated. Overall, canopy cover measurements from the data collection date ranged from 20% to 70% coverage of the plot area. It is our supposition that this information will be helpful to determine time to lapping and estimate plant vigor. The excess green index (ExG) ranged from 0.2-0.5. In other crops this index has been correlated to yield and/or plant health. Our intention is to use this information in a similar manner. Canopy height (CH) ranged from 20 to 45 cm depending on the time of data collection. Similarly, canopy volume ranged from 0.2 to 0.85 m³ per plot. For a breeding program both of these measurements are critical for making selections based on plant type. Average value for canopy features and vegetation indices extracted from plots are plotted in Figure 5-8. As mentioned, data analysis is ongoing and additional information will be extracted and compared to the 2020 season data.

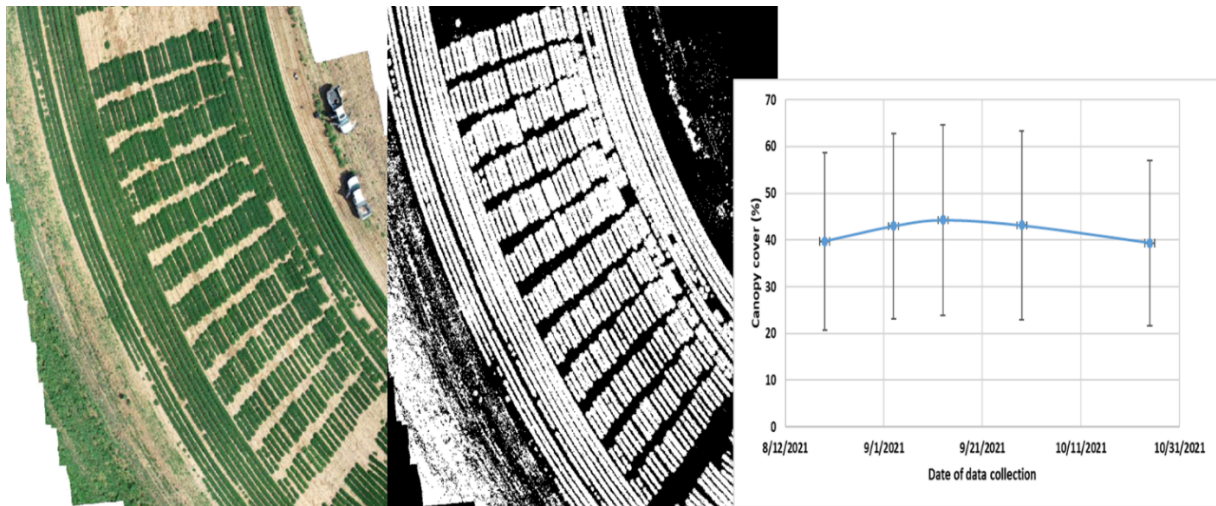


Figure 6. Orthomosaic, classified image, and extracted canopy cover data for all the plots in the study area. Each data point is an average across all the plots in the study.

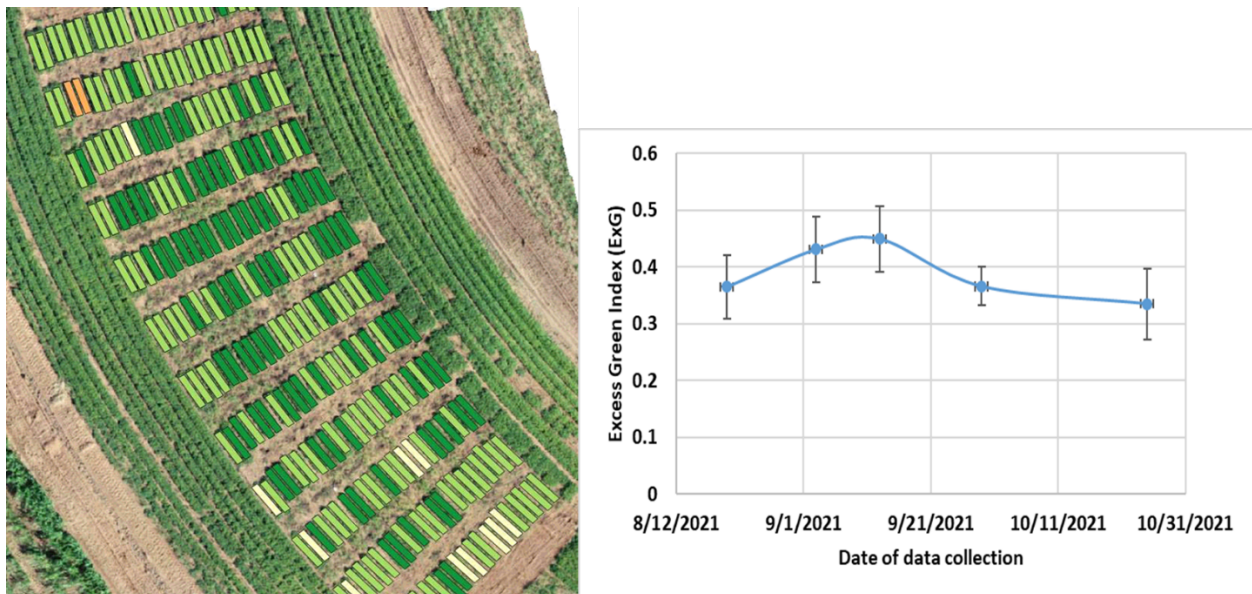


Figure 7. Excess green index map and extracted data across different data collection dates. Each data point is an average across all the plots in the study.

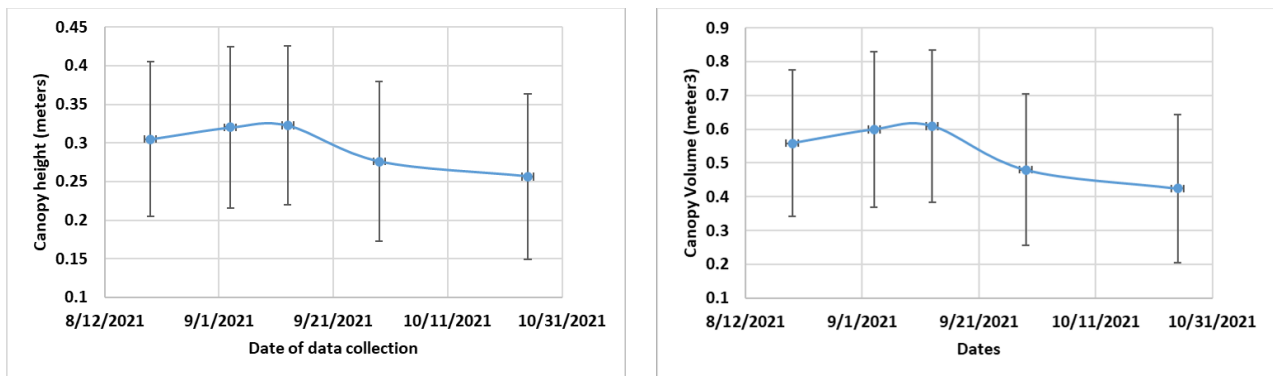


Figure 8. Plot level canopy height and canopy volume extracted across different data collection dates. Each data point is an average across all the plots in the study.

Sub-Project V. Organic Breeding

We initiated an organic breeding program in the spring of 2019 before the funding for this sub-project began and have continued the program for 2021. Initial crosses were grown as plant rows in 2021. In addition, we evaluated some of our current elite breeding lines in certified organic fields in Terry County and Wilbarger Co. As part of this evaluation, we included 2 Spanish lines that are nematode resistant and one historic germplasm line that is known to be pod rot resistant. The released materials performed very well in the challenging organic environment with TamVal OL14 at the top of the study for 2021 with a yield of 5412 lbs/ac and Olin producing the highest grade at 75.6% (**Table 22**).

Table 22. Organic Test in West Texas in 2021.

	Pods/Ac Lbs.		Value/Ac \$		TSMK %		Seed Wt g/100		Seed/Lbs		SS%	
Cultivar												
TamVal OL14	5412	A	981.01	ABC	71.4	EFG	60.9	BC	746	EFG	3.0	EFGHI
TxL076239-16	5391	A	1088.67	A	74.8	ABC	56.7	CDE	800	DEF	2.0	GHI
TxL076239-12	5304	AB	1074.96	AB	75.0	ABC	57.5	CD	789	DEF	1.4	HI
TxL076225-28	5231	ABC	1047.56	ABC	73.3	CDE	51.8	EFGH	876	ABC	4.4	CDEF
TxL076221-06	5050	ABC	1041.78	ABC	75.5	AB	53.9	DEFG	842	BCD	3.9	DEFG
TxL076224-24	5049	ABC	1014.94	ABC	73.7	ABCD	55.8	DEF	818	CDE	4.5	CDEF
TxL076221-34	5018	ABC	1010.19	ABC	73.4	BCDE	50.8	FGH	895	AB	4.3	CDEF
TxL076229-53	4864	ABC	954.46	ABC	72.1	DEF	51.6	FGH	880	ABC	3.8	DEFG
OLin	4837	ABC	991.86	ABC	75.6	A	56.7	CDE	813	CDEF	4.6	CDE
TxL076225-48	4787	ABC	956.50	ABC	73.7	ABCD	54.2	DEF	838	BCD	6.0	BC
TxL076225-24	4644	ABCD	918.58	ABCD	73.1	CDEF	54.8	DEF	828	BCD	4.0	DEF
TxL076236-04	4620	ABCDE	938.30	ABC	75.1	ABC	54.4	DEF	834	BCD	1.7	HI
Schubert	4596	ABCDE	882.85	ABCD	69.9	G	63.5	B	715	G	4.0	CDEF
Tx144923	4470	ABCDE	915.47	ABCD	74.6	ABC	48.6	H	936	A	3.3	DEFGH
TxL076225-04	4258	BCDE	856.68	BCD	74.5	ABC	49.1	GH	926	A	2.6	FGHI
TxL076224-08	4195	CDE	830.90	CD	74.5	ABC	55.3	DEF	821	CD	5.0	CD
GP of Toalson	3649	DEF	701.72	DE	71.0	FG	61.1	BC	743	FG	10.2	A
TxL076226-18	3564	EF	712.93	DE	73.3	CDE	51.8	EFGH	876	ABC	1.3	I
Tamnut OL06	2798	F	515.82	E	67.1	H	57.0	CD	798	DEF	11.2	A
Mean	4664		926.62		73.2		55.9		820		4.4	
CV(%)	18.7		19.6		3.2		10.7		9.8		62.1	
Entry "F"	0.0005		0.0004		<.0001		<.0001		<.0001		<.0001	

A second organic test was planted at the Vernon Research and Extension Center under dryland conditions due to an unexpected, limited irrigation situation. Surprisingly, some of the lines performed fairly well due to the higher-than-normal rainfall. In these situation the historic and current lines again performed at the top of the test for yield with Toalson yielding 4879 lbs/ac. followed by Schubert with a yield of 3484 lbs/ac.

Sub-Project VI. Leafspot Screening and Sclerotinia Screening

Table 23. Advanced Line Test Leafspot Rating in South Texas in 2021.

Cultivar	Rating	
Georgia 09B	5.8	A
TP 200625-3-2	5.8	A
TP 200606-2-9	5.3	AB
TP 200606-3-10	5.3	AB
TP 200607-1-17	5.3	AB
TxL100212-03-03	5.2	AB
NemaTAM II	5	AB
TP 200606-2-14	5	AB
TP 200608-1-6	5	AB
TP 200609-1-5	4.8	ABC
Tx144370	4.8	ABC
TP 200608-1-14	4.5	ABCD
TP 200610-3-2	4.5	ABCD
TP 200606-6-10	4.3	ABCDE
TP 200610-1-2	4.2	ABCDE
TP 200607-1-2	3.8	BCDEF
Georgia 14N	3.2	CDEF
AG18	3	DEF
TP 200606-7-10	2.7	EF
Georgia 16HO	2.3	F
Mean	4.5	
CV (%)	29.8	
Entry "F"	0.0074	

Disease screening is an important part of the multiple disease resistance program. The year-to-year screening gives a good picture of the overall resistance package that is present in breeding lines. Year to year the variability is high in screening nurseries, so it is essential to evaluate lines for several years for a comprehensive picture of their resistance. For the 2021 season we screened for leafspot in our most elite lines in our nursery. During the season leafspot developed late and was relatively light in comparison to other years. Breeding line TP200607-7-

10 was rated at 2.7 on the Florida leaf spot scale which was numerically and statistically less than the commercial check NemaTAM II and Georgia 09B, which were 5.0 and 5.7 respectively (**Table 23**). This test is conducted in an effort to establish Leafspot resistance in our most elite materials. The Advanced Lines Test was planted at the Texas A&M Yoakum Research sub-Station in Yoakum, TX.

Crossing and marker development for improved leafspot resistance from the Burow lab continues with ongoing projects under other funding and will be evaluated in the field in 2022 (see Leafspot-resistant Spanish types section above). The Cason group will also be moving forward with population development from a different genetic background in additional materials. Crosses were made in 2021 and were grown as F1 plants in the greenhouses of Texas A&M AgriLife. These show promise for leafspot resistance and will be followed with testing and molecular marker development work. Crosses are ongoing that focus solely on leafspot resistance as well as incorporation into the multiple disease resistance program. As field rating and marker development continues, the information gathered will help us determine the best candidates to include in our 2021 leafspot crossing program.

Table 24. Advanced Line Test Sclerotinia Rating in Central Texas in 2021

Breeding Line/Cultivar	Hits/Plot	
Tx144370	14.0	A
Georgia 16HO	13.0	AB
TP 200625-3-2	10.7	ABC
TxL100212-03-03	10.0	ABCD
TP 200610-1-2	9.7	ABCDE
TP 200609-1-5	9.0	ABCDE
NemaTAM II	8.0	BCDE
TP 200606-2-9	7.7	BCDE
TP 200606-6-10	7.3	CDE
TP 200606-7-10	7.3	CDE
TP 200606-2-14	6.0	CDE
TP 200607-1-17	6.0	CDE
AG18	5.7	CDE
Georgia 09B	5.7	CDE
TP 200606-3-10	5.3	CDE
TP 200608-1-6	5.0	DE
TP 200610-3-2	5.0	DE
Georgia 14N	4.7	DE
TP 200607-1-2	4.7	DE
TP 200608-1-14	4.3	E
Mean	7.45	
CV (%)	53.7	
Entry 'F'	0.022	

Finally, in related testing, **Table 24** presents the same advance lines that were evaluated for yield and grade as well as leafspot. The lines were also evaluated for *Sclerotinia minor* resistance as part of an ongoing screening nursery. Cool, wet weather late in the season causes excellent disease pressure. TP 200608-1-14 was numerically the lowest entry in the test with a hits per plot of 4.3 in 10 row feet. This was both statistically and numerically lower than the Commercial check Georgia 16HO, as well as the two release candidates Tx144370 and TxL100212-03-03 which were 13.0,14.0 and 10.0 respectively.

Leafspot Resistant Spanish Peanuts.

We planted two populations at Yoakum for the first year of evaluation for leaf spot resistance. The first population was a cross between a leafspot-resistant, low oleic Virginia bunch variety (NkatieSARI) from West Africa and was crossed with Schubert. **Figure 9** shows that most of the breeding lines were more resistant than Schubert. We had made selections previously for Spanish growth habit, and of 137 breeding lines tested, 102 were Spanish in growth habit; others were runners or Virginias. Based on selection in the F₂ and F₃ generation, 85 of the breeding lines were selected as high oleic, and the remainder were segregating high and low oleic seeds. The best 20% of the lines based on response to leaf spots were saved and replanted in 2022 for additional evaluation.

A second population consisting of a cross between a wild species introgression line (BC3-43-09-03-02) with some resistance to early leaf spot x Schubert, was also evaluated at Yoakum (**Figure 10**). The donor parent had an intermediate rating, which was higher than expected. Again, most breeding lines had leafspot ratings less than or equal to Schubert. Spanish materials were selected, and the best 20% of the materials were saved for evaluation in 2022.

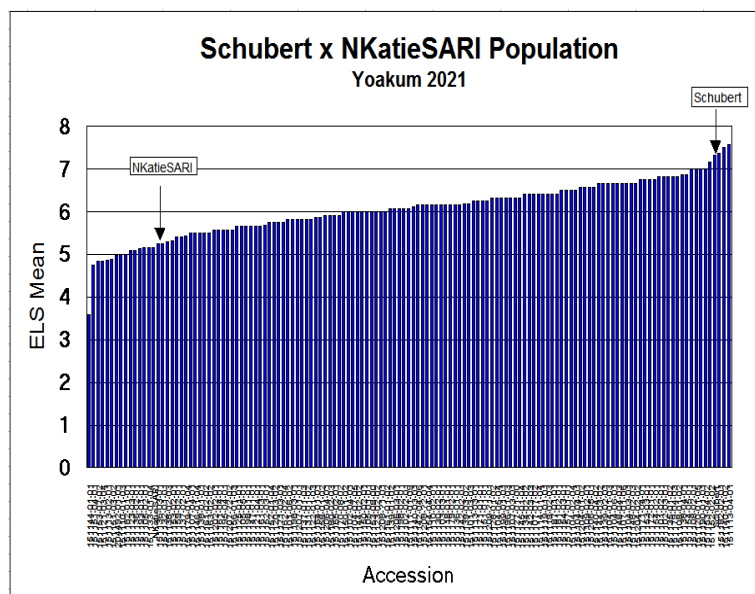


Figure 9. Early leafspot ratings for progeny of the Schubert x Nkatie SARI cross at the Yoakum TX disease nursery in 2021. ELS ratings shown are the average of two ratings, using the Florida 1-10 scale.

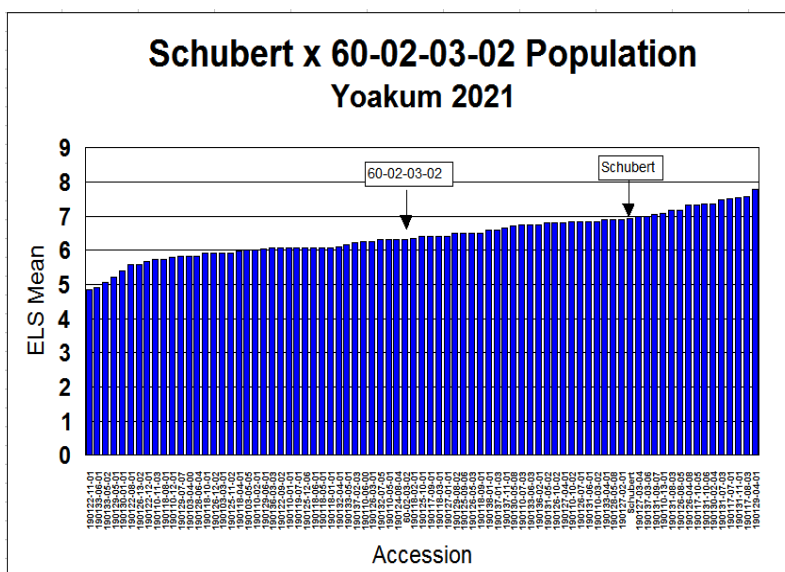


Figure 10. Early leafspot ratings for progeny of the BC₃ x Schubert cross at the Yoakum TX disease nursery in 2021.

Closing Comments

The 2021 season was marked by excessive rain during planting to the point that some off station locations did not plant, and alternate sites had to be identified. This was followed by an extended dry spell that stretched into the 2022 season. The coronavirus pandemic also continued to hamper our progress, although to a much lesser degree as travel began to open back up. The burglary of the Texas A&M AgriLife Field Headquarters in Stephenville would have been disastrous for the program if it were not for the quick response of law enforcement in the recovery of our vehicle and Texas A&M AgriLife's willingness to replace much of the stolen equipment. Finally, with the tireless work of our dedicated staff, we were able to continue to increase the total plot numbers we had for the season.

Many exciting projects are underway. Development of germplasm and algorithms will continue on the 3 new sub-projects, keeping our program at the cutting edge of research and variety development. Projects in high throughput phenotyping using UAS and handheld Raman spectroscopy are underway, as well as development of new populations for drought, yield, leafspot and organic production. In addition, we are starting new projects that specifically deal with nutrition and health of the peanut that could enable peanuts to become a superfood by restoring 2 limiting essential amino acids. The Texas A&M AgriLife Foundation Seed sheller construction, which began in 2020, was officially opened in the fall of 2021 with a ceremony at the Vernon, Tx facility. The construction of a dedicated peanut sheller for the Texas A&M University System will allow the breeding program to provide high quality seed to the peanut industry. Finally, during the summer of 2021 we began development of a project involving high oil content peanuts for the Chevron Corporation. As this project unfolds it has the potential to be transformative in peanut production in Texas as well as Texas Agriculture in general.