2021-2022 UC Davis Report for Garbanzo Breeding

Contents

Highlights

Highlights of the garbanzo research in Bean Breeding at UC Davis in 2021-2022 include:

- Garbanzo:
    - Advanced generations have been identified with a combination of higher yields and larger seeds [e.g., Pegasus (0905) x 1101 or Sutter x 1101]
    - The study of a population resulting from the cross between a drought-susceptible and drought-tolerant parent is close to completion. Three years of field data have been obtained and a molecular (DNA) genetic map has been developed.
    - Early germination and growth vigor has been backcrossed into California cultivars (generation BC_1F_1).

Additional highlights of the Bean Breeding Program include:

- Lima bean: Much of the breeding work has focused on improving bush Large Lima, in response to comments of the Board
    - The diversity screen identified Lima bean accessions with high level of tolerance to Lygus. These accessions are being used in a crossing program to California varieties, with emphasis on Large Limas.
    - Early generation (F3-F4) identified superior cross-combinations of gene-bank accessions with UC 92 (Large Lima) that are higher-yielding.
    - Backcross combinations involving UC 92 have been tested to make single-plant selections on the basis of yield, seed size, and quality greater than or comparable to UC 92 and Dompe 95.
    - Advanced lines have been tested for yield and seed quality (color, size) and may results in one or two improved lines (yields and 100-seed weight similar to or above UC 92 and Dompe 95)
    - Linamarin, a defense compound of Lima bean, occurs in flowers and developing pods but not (or only to limited levels) in seeds (a positive result for consumers). The presence of Lygus increases linamarin levels in pods but not in flowers.
    - The breeding program has also been active in: 1) development of electronic, high-throughput, constant Lygus monitoring; 2) a discussion about viny plants in a bush Lima field; and 3) re-submission of a pre-proposal to broaden the genetic basis of Lima bean in the U.S. via a germplasm conversion procedure.
- Common bean:

Cooperative Dry Bean Nursery results for a slate of mainly pinto and great northern beans are made available in the report.

Garbanzo Breeding, 2021-2022 Report

Researchers: Antonia Palkovic (Associate Specialist), Claire Spickermann (current MS graduate student), Varma Penmetsa (Associate Research Scientist), P. Gepts (Principal Investigator)

Objective 1. Testing and selection of advanced generation lines;

A. Palkovic, P. Gepts. Funding from CDBAB

Crosses were made by M. Thapa around 2013-2015 to introduce new diversity from the core collection of the USDA (kabuli types) into California cultivars, mainly Sutter and Vega. Crosses were also made by K. Watt, who sought to introduce new diversity from Plant Introduction accessions of the USDA with drought tolerance (**Table 1** of the Garbanzo 2020-2021 report). Some of these progeny lines have displayed very good performance in a one-year trial. Further testing were made in 2022 for seed type (color, wrinkledness, size) and yield to verify this performance.

In 2021, twenty advanced generation (F8) large-seeded kabuli-type selections were planted along with 6 CA varieties as checks (UC 27, UC 15, Sutter, Pegasus, Vega, and Sierra). The breeding trial was planted to moisture in a complete replicated block design with two-row, 50' plots and 3 replicates on March 1. Full replacement ET irrigation was applied weekly using buried drip starting March 30. Plots were harvested from standing mature plants using a Zurn multi-crop small plot combine on June 24 and 25. Stand counts showed seedling germination and survival to be highly uneven, with many plots having 30-50% stands compared to the seeding rate, which was high at ~5 seeds/foot, or one seed every 2.4". The poor stands were likely due to a number of factors, including problems with the planter and uneven soil moisture. It is possible that for this reason, when the yields are analyzed, entry is not a significant predictor of yield. Hundred-seed weight was a significant factor, however, with many lines having seed weights of over 49g/100 seeds.

Table. One-way ANOVA, Garbanzo Yield (lb/a) June 2021

Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Entry	25	4248986.3	169959	1.6885	0.0558
Error	52	5234054.5	100655		
C. Total	77	9483040.9			

Table. Garbanzo Entries 2021, ranked by Mean Yield						
Entry	Pedigree (F3:F8 seed)	Mean 100-sd wt (g)	Mean Yield (lb/a)	Std Error	Lower 95%	Upper 95%
95	0905 x 1101	56.40	1747	183.17	1379.6	2114.7
UC 15	Check	44.60	1575	183.17	1207.0	1942.2
98	Sutter x 1101	43.13	1542	183.17	1174.5	1909.6
94	0905 x 1101	49.97	1475	183.17	1107.7	1842.8
Sutter	Check	40.53	1413	183.17	1045.0	1780.1
111	Sutter x 1104	46.77	1385	183.17	1017.1	1752.2
106	Sutter x 1104	44.87	1359	183.17	991.6	1726.7
102	Sutter x 1121	52.67	1303	183.17	935.8	1670.9
96	0905 x 1101	51.73	1282	183.17	914.9	1650.0
109	Sutter x 1109	45.10	1249	183.17	881.8	1616.9
100	Sutter x PI502998	45.40	1169	183.17	801.6	1536.8
Sierra	Check	51.93	1138	183.17	770.3	1505.4
105	Sutter x 1121	49.30	1121	183.17	753.4	1488.5
97	Sutter x 0901	43.73	1115	183.17	747.6	1482.7
Vega	Check	44.33	1106	183.17	738.9	1474.0
101	Sutter x 1109	45.10	1090	183.17	722.6	1457.8
108	Sutter x PI502998	48.33	1058	183.17	690.7	1425.8
UC 27	Check	49.63	1043	183.17	675.6	1410.7
Pegasus	Check	52.13	1007	183.17	636.1	1371.2
99	Sutter x 1109	49.13	991	183.17	623.3	1358.4
113	Sutter x 1121	52.73	968	183.17	600.1	1335.2
112	Sutter x PI503006	46.63	929	183.17	561.3	1296.4
103	Sutterx1104	45.33	919	183.17	551.9	1287.0
107	Sutter x 1109	49.17	906	183.17	538.5	1273.6
110	Sutterx1121	52.60	890	183.17	522.8	1258.0
104	Sutter x PI503006	49.63	858	183.17	490.3	1225.4

Table. One-way ANOVA, Garbanzo Breeding Lines 100sdwt (g) 2021					
Source	DF	Sum of Squares	Mean Square	F Ratio	Prob > F
Entry	25	1086.7929	43.4717	11.6988	<.0001*
Error	52	193.2267	3.7159		
C. Total	77	1280.0196			

Table. Multiple means comparison for Mean 100-seed weight (g)

Garbanzo F8 Entry										Mean 100 sd wt (g)
95	A									56.40
113		B								52.73
102		B								52.67
110		B								52.60
Pegasus		B	C							52.13
Sierra		B	C							51.93
96		B	C							51.73
94		B	C	D						49.97
104		B	C	D	E					49.63
UC 27		B	C	D	E					49.63
105			C	D	E					49.30
107			C	D	E					49.17
99			C	D	E					49.13
108				D	E	F				48.33
111					E	F	G			46.77
112					E	F	G			46.63
100						F	G	H		45.40
103						F	G	H		45.33
101							G	H		45.10
109							G	H		45.10
106							G	H		44.87
UC 15							G	H		44.60
Vega							G	H		44.33
97							G	H		43.73
98								H	I	43.13
Sutter									I	40.53

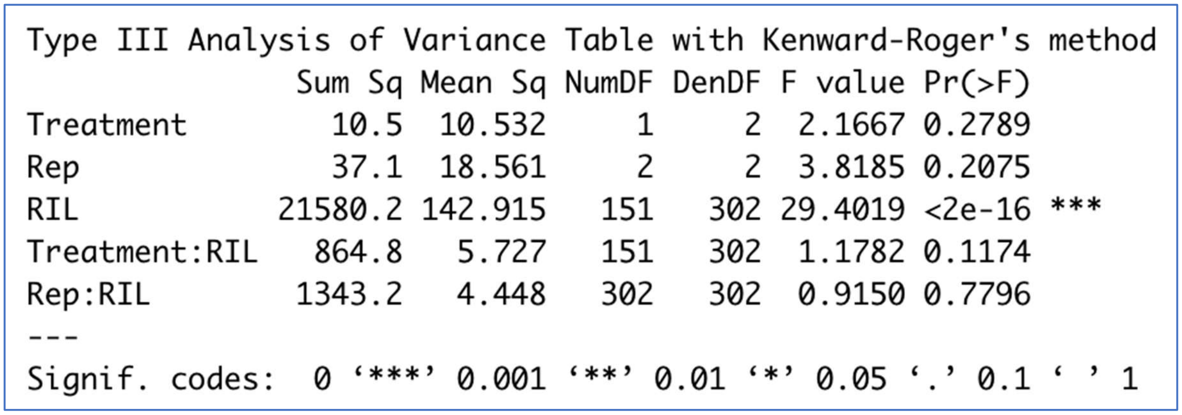
In summary: The results of the 2021 evaluation are exciting because they largely confirm results of the 2020 evaluation (see Figure 2 and Table 1). Entry 95 was the highest yielder in both years and the progeny with the largest seeds. Overall, the cross 0905 x 1101, which gave rise to Entry 95, appears to have captured the excellent traits of both parents: large seed weight of 0905 (now released as Pegasus) and highest seed yield of 1101. Entry 94 is a sister line of Entry 95.

These lines will be tested for a third year in 2022, after which large-plot evaluations will be conducted at UC Davis and with growers, if possible, prior to a possible release.

Objective 2. Testing of the ILC588 (drought-tolerant) x ILC 3279 (drought-sensitive) RI population, shared by ICARDA;
C. Spickermann, A. Palkovic, P. Gepts. ***funding from CDBAB***

The n = 152 lines of this RI population were planted again at UC Davis in February-March 2021 under the same water treatments (drip irrigation for the well-watered treatment and residual moisture for the drought treatment). The drought treatment was irrigated to have had 10 acre-inches of water after precipitation and the irrigated side had 20 acre-inches'. The drought treatment had water cut off in mid-April and the irrigated side had it cut May 14th. There might not have been enough difference in water during the flowering period for there to have been noticeably different, as shown by the lack of significant differences in yield (see below).

Comparing the flowering time (number of days from planting to 50% of the plants in a plot are flowering) for the irrigated and drought treatments showed significant variation in days to flowering among the different lines. Genotypic differences among recombinant inbred lines (RILs) were significant. The differences between irrigation treatments were not considered highly significant statistically. This might be because flowering occurred early enough in the experiment as to not be severely impacted by reduced irrigation due to residual soil moisture from rainfall and previous irrigation that occurred.



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Type III Analysis of Variance Table with Kenward-Roger's method
              Sum Sq Mean Sq NumDF DenDF F value Pr(>F)
Treatment       10.5  10.532     1     2  2.1667 0.2789
Rep             37.1  18.561     2     2  3.8185 0.2075
RIL          21580.2 142.915   151   302 29.4019 <2e-16 ***
Treatment:RIL  864.8   5.727   151   302  1.1782 0.1174
Rep:RIL       1343.2   4.448   302   302  0.9150 0.7796
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
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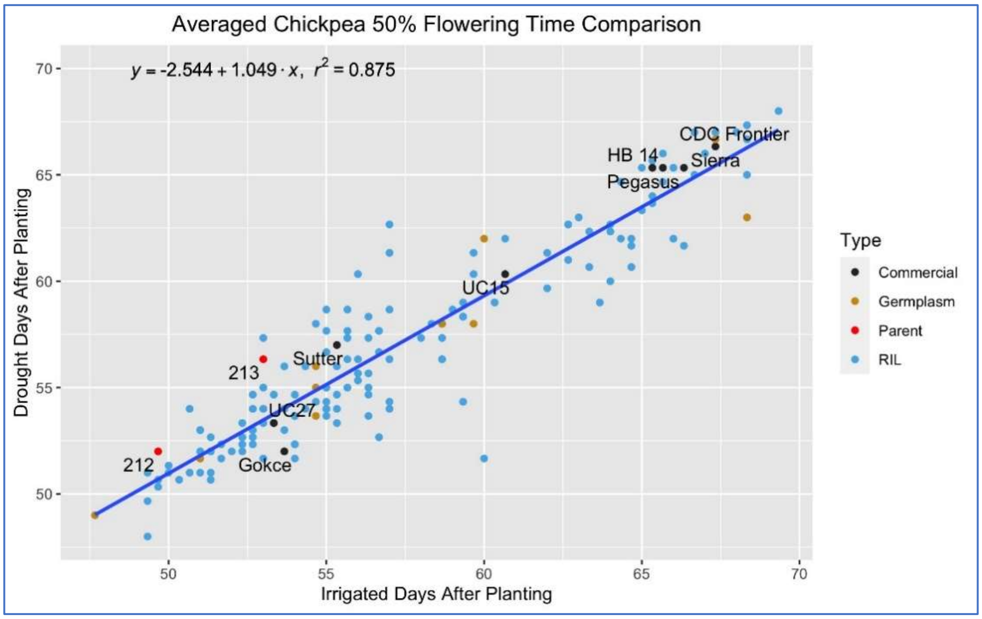
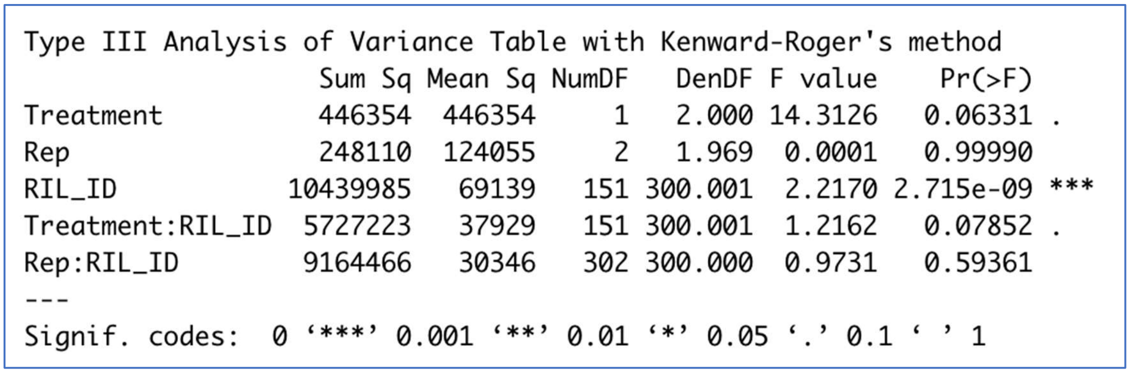
Both parental varieties (red dots) were in the lower left quadrant of the graph indicating early flowering times in both treatments. Several of the recombinant inbred lines descending from the two parents and the germplasm line developed by ICRISAT ICC 4958 (strong germination vigor) also appear in this quadrant indicating early flowering. Alternatively, progeny lines with later flowering can also be selected in this population.



In the comparison of grain yields under the two treatments (irrigation and drought), differences among recombinant inbred lines were significant. Differences between the drought and well-watered treatments were nearly significant.



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Type III Analysis of Variance Table with Kenward-Roger's method
                    Sum Sq Mean Sq NumDF   DenDF F value    Pr(>F)
Treatment           446354  446354     1   2.000 14.3126   0.06331 .
Rep                 248110  124055     2   1.969  0.0001   0.99990
RIL_ID            10439985   69139   151 300.001  2.2170 2.715e-09 ***
Treatment:RIL_ID   5727223   37929   151 300.001  1.2162   0.07852 .
Rep:RIL_ID         9164466   30346   302 300.000  0.9731   0.59361
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Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
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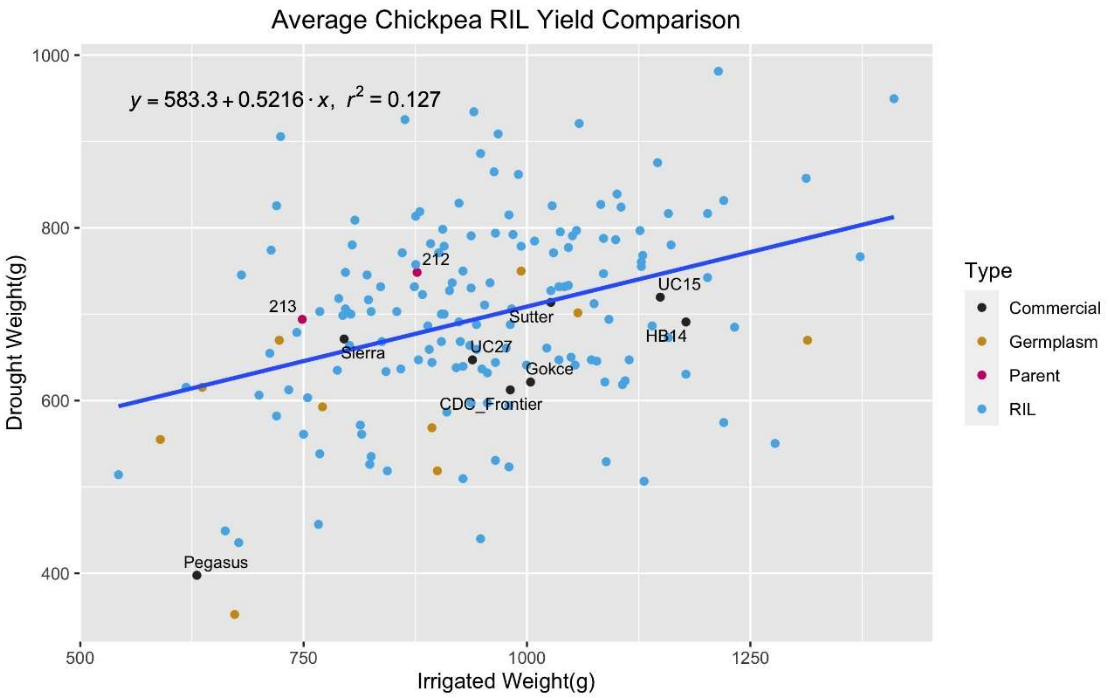
The parental lines (red dots) were in the upper left quadrant indicating that they were less than average for the irrigated yield but higher than average in drought yield. Additionally, several recombinant inbred lines are in the upper right quadrant indicating high yields in irrigated conditions and better than average yields under drought that were outside the parental lines’ demonstrated yield.



This population has also been sequenced at the DNA level, although the data remained to be analyzed. Analysis of the field data and DNA sequences is part of the MS thesis of Ms. Claire Spickermann. She has completed the DNA data processing and has 1) establish a molecular linkage map for this population. She is now conducting a genetic (QTL) analysis to identify genes involved in yield phenology and seed size/weight: genome location, magnitude of their effect.

In summary: This is the third, and final, year of field evaluation of this ICARDA population. The results are positive in that there is a wide range of agronomic traits segregating in this population, including seed yield, flowering time, and seed weight. Many of the progeny lines surpass the two parents for yield both under well-watered and drought conditions. These will provide materials for further breeding.

At the same time, the molecular analysis, which is being conducted by graduate student Claire Spickermann, will assist us in understanding the genetic of yield, flowering and maturity time, and seed weight in garbanzos that are well adapted to California. This will also facilitate the breeding work.

*Objective 3. Increase germination and early vigor (funding from USDA NIFA AFRI and USDA ARS PCHI; **no funding requested from CDBAB)***

R.V. Penmetsa, P. Gepts

Dr. Varma Penmetsa is a grain legume scientist with considerable experience in genetic and breeding of garbanzos. He has been pursuing succesfully outside funding for research that supports the UC Davis Garbanzo Breeding program.

The focus of his USDA-ARS Pulse Crop Health Initiative (**PCHI**) project is to evaluate the potentials of (1) the Indian garbanzo accession ICC4958 to improve early vigor and drought tolerance and (2) of wild chickpeas to provide heat tolerant pod set to US commercial garbanzo cultivars, including from California.

Trait 1: Early vigor in garbanzo (funding from USDA-ARS-**PCHI**)

In 2021 crosses between the early vigor trait donor ICC4958 and the California cultivars UC27 and VEGA were advanced in the greenhouse through F2 to the F3 generation. From mining of genome sequence data we developed and tested four different DNA ('SNP') markers linked to the vigor-conferring genetic region of ICC4958. Two of the four SNP markers proved to be effective in our breeding material. F3 progenies were greenhouse grown in autumn 2021 and screened with these two markers. From marker information individual F3 plants containing the ICC4958 genomic segment were selected and used in winter 2021for the first cycle of backcrossing to California cultivars UC27, and VEGA to generate BC1-F1 generation hybrids.

In 2022, we will conduct additional cycles of backcrossing (BC2/BC3 cycles) to UC27 and VEGA using greenhouses for plant growth and the SNP markers for marker-assisted selection.

Trait 2: Heat-tolerant pod set in garbanzo (funding from USDA-ARS-**PCHI**)

During summer of 2021, 43 F4 progeny families from a cross between a wild chickpea and a cultivated 'desi' chickpea that were previously observed to be segregating for pod set at high temperatures in India were reevaluated in a greenhouse at UCDavis. Greenhouse was set to provide day and nighttime temperatures of 95-98F and 68-72F which are substantially higher than temperatures normally experienced by cultivated chickpea. In this greenhouse trial, elite garbanzo cultivars including the California cultivar UC27 failed to flower (and therefore set pods). By contrast 3 of the 43 F4 families of the wild-cultivated intercross were able to flower, set pods and yield viable seeds which was harvested. In autumn 2021 these 3 potentially heat-tolerant F5 selections were grown in a greenhouse and crossed during winter 2021 with the California cultivars UC27 and VEGA. Hybrid F1 seed from these crosses will be harvested in late winter (in February 2022).

In 2022 we will advance these F1 hybrids with UC27 and VEGA to F2 and F3 generations for evaluation of progenies under higher than normal temperatures for flowering and pod set in 2023.

Trait 3: carotenoid content in garbanzo seed. (funding from USDA NIFA ***AFRI*****;** no funding from CDBAB)

In 2021 BC1-F2s from introgression crosses of the green cotyledon trait (associated with elevated seed carotenoid content) into the California cultivar UC27 were screened for larger seed size, angular seed shape and cotyledon color and advanced to BC1-F3 generation. During autumn 2021 BC1-F3 selections were grown in a greenhouse and backcrossed to UC27. Seed from these crosses (BC2-F1s) is expected in February 2022.

In 2022 these BC2-F1s will be advanced to BC2-F3s for field evaluation in the 2023 field season.

Trait 4: Early flowering/ maturity in garbanzo (no funding from CDBAB)

During 2021, backcross progenies from a cross between the small seeded 'desi' cultivar ICCV96029 with super-early flowering (~25 days after emergence) and maturity (~70-75 days after sowing) and the California cultivar UC27 were generated and advanced to obtain BC1-F3s.

In 2022 these BC1-F3s will be field evaluated alongside UC27 and if observed, single plant selections made of promising individual plants for additional backcrossing cycles or fixation by selfing.

Traits 5 & 6: black seeded, 'eyed' garbanzo. (no funding from CDBAB)

During 2021, F2 progeny from a cross between a small seeded, very late flowering/maturity garbanzo line of Steve Temple with black seed coat and eye-like spots and the super-early flowering/maturity 'desi' chickpea ICCV96029 were field grown and F3 generation seed harvested. Segregation ratios of F3 seed from ~120 F2s suggest that the black seed coat color as being controlled by a single dominant gene, while the eye-like pattern being under recessive genetic control.

In 2022 F3 families will be grown to develop material for genetic linkage mapping of the black seed coat color and eye spot pattern traits. Selected F4 lines may be crossed to UC27 or other experimental lines for trait introgression and to develop additional segregating material for mapping of the two seed coat traits.