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CHARACTERIZATION OF SOME SUPERIOR MUNG BEAN GENOTYPES ON THE AGRONOMIC AND BIOCHEMICAL GENETIC LEVELS

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The present work was undertaken during 2005 and 2006 seasons in newly reclaimed sandy loam soil at the experimental farm of Fac. Agric., Fayoum University. Nine newly bred mung bean genotypes and the check variety Qawmy-1 were evaluated under two irrigation regimes, i.e, irrigation every 12 days (I_1) and every 24 days (I_2). The treatments were arranged into split plots in randomized complete block design with three replications. The work objectives were to identify the most yield improved and drought tolerant genotype(s) and to differentiate among these newly developed genotypes using biochemical genetic technique (SDS-PAGE). The results indicated that all seven agronomic traits were significantly affected in both seasons by irrigation level. Under frequent irrigation (I_1) in the first season, lines 2920, 2020, 1720, 2520 and 1320 surpassed Qawmy-1 for plant height, fruiting zone length, number of branches and pods/plant as well as number of seeds and yield/plant. Also, lines 3430 and 3940 showed higher means than those of Qawmy-1 for most traits. In the second season, the same lines exhibiting superiority in the first season in addition to L3740, surpassed Qawmy-1 for most studied traits. In general, the mean performance of most lines indicated a genetically diverse relations among them.

Under drought conditions, almost all traits were negatively affected by water deficit. But, lines 2020, 1720, 2520, 3740 and 3940 were superior compared with the chick variety over the two seasons, indicating their suitability for direct use or indirectly through further breeding procedure for developing improved and drought tolerant mung bean genotypes.

Protein analysis (SDS-PAGE) revealed that twenty-seven bands were recorded with a polymorphism of 44.4%. From

them, 15 monomorphic bands were recognized and could be considered as common bands in mung bean genotypes. One unique polymorphic band at molecular weight of 39.66 kDa could be used for identifying the related mung bean genotype (L-1320). The results of SDS-PAGE analysis were used for drawing the genetic relationships among genotypes, and the obtained dendrogram showed three different genetic clusters. Finally, by means of field evaluation and biochemical genetic analysis it could be possible to identify some promising drought- tolerant mung bean lines.

Keywords: Mung bean, drought, newly reclaimed lands, protein analysis, banding pattern.

Mung bean (*Vigna radiata* L. Wilczek) is a warm season annual pulse grown mostly as an opportunity crop in rotation with cereals. Mung beans are erect plants with few branches carrying pods borne in clusters near the top of the plant. Pods contain 8–15 green seeds. Its main advantages are, as being a legume, it does not require nitrogen fertilizer application, and it has a short growth duration (75–90 days) which means that it requires less water than many other summer crops and it is easily fitted into rotations. Its main disadvantage is the difficulty to produce premium grade seed that commands top market prices. Mung beans grow on most soils, with a preference for loams with a pH in the range 5.5–7.5. Root growth can be restricted on heavy clays, with a consequent limitation to growth (Imrie and Lawn, 1991). It is a new introduced summer pulse crop in Egypt with short growing season and high nutritive value grown principally for its protein rich edible seeds (Ashour *et al.*, 1992). This crop can be used for both seed and forage production. It plays an important role not only in human diet, but also in improving the soil fertility by fixing atmospheric nitrogen into available form with the help of *Rhizobia* species present in the nodules of its roots (Ashraf *et al.*, 2003). Water deficit is frequently the primary limiting factor for crop production under arid and semi-arid conditions (Hussain *et al.*, 2004). It affects nearly all the plant growth processes. However, the stress response depends upon the intensity, rate and duration of exposure and the stage of crop growth (Wajid *et al.*, 2004).

Attia-Ismail and Afiah (1998) concluded that mung bean can be successfully grown under Egyptian newly reclaimed lands and it seems promising for sheep feeding. Little effort is being made to breed new mung bean varieties, but only one variety (Qawmy-1) is available in Egypt.

The present investigation was carried out to evaluate the performance, yield and its components of nine newly bred lines compared with the released Egyptian mung bean variety under drought stress and to

differentiate these genotypes according to its polypeptide patterns and detect some biochemical genetic markers for drought tolerance.

MATERIALS AND METHODS

Ten mung bean (*Vigna radiata* L. Wilczek) genotypes including nine newly bred lines released through Desert Research Center breeding program (Afiah and Rashed, 2000) and one check Egyptian variety (Qawmy-1) were used in the present study. All genotypes were evaluated under two irrigation treatments (I_1 = every 12 days and I_2 = every 24 days intervals) in newly reclaimed, sandy loam soil at the experimental farm of Fac. Agric., Fayoum University during two successive seasons (2005 and 2006). The two irrigation treatments and the 10 genotypes were arranged in split plot randomized complete block design with three replications, where the main plots contained irrigation treatments and sub-plots contained the genotypes. Seeds of each treatment were planted in hills within five rows, 3.5 m long and 60 cm apart. Thinning for two plants/hill was done one month after emergence. Other cultural practices were executed according to recommendations.

At harvest, 10 guarded plants were randomly sampled from each plot and the following traits were measured; plant height, cm (pl. h), height to first branch, cm (h. 1st Br.), number of branches/plant (Brs), number of pods/plant (Pods), pods weight/plant (Pods wt/pl.), number of seeds/plant (No. S./pl.) and seed yield/plant (SY/pl.). Pods weight/feddan (Pods wt./f) and seed yield/feddan (SY/f) were calculated on the bases of yield/plot and seeds to pods ratio (S:P%). The obtained data were subjected to analysis of variance according to Gomez and Gomez (1984). The treatment means were compared using the New Least Significant Difference (New LSD) as mentioned by Waller and Duncan (1969) and calculated for all traits recorded in both seasons.

SDS-Protein Electrophoresis

SDS-PAGE (SDS-polyacrylamide gel electrophoresis) was carried out according to the method of Laemmli (1970) on samples of 10 plant seeds ground and extracted. Protein extraction was conducted by mixing 0.2 g of seeds composite sample with an equal weight of pure, clean, sterile fine sand and was ground to fine powder using a mortar and pestle and homogenized with 1.5 M Tris-HCl buffer, pH 8.8 in clean eppendorf tube and left in refrigerator over night. Then centrifuged at 10000 rpm for 10 min. The supernatant of each sample (contains protein extract) was kept in deep-freeze until use for electrophoretic analysis. Then, a volume of 25 µl protein extract was added to equal volume of treatment buffer before loading in the gel. After removing the staining solution, gel was covered with 200 ml destaining solution (fresh prepared). This step was repeated several times

until gel background is clear, then photographed. The banding patterns of bulked samples were compared among the tested genotypes. Bands were scored as present (+) or absent (-).

RESULTS AND DISCUSSION

Results presented in tables (1 and 2) show the mean performance and new LSD of the significant cases for 10 traits of mung bean genotypes tested under both irrigation levels in the first and second seasons, respectively. Variation of the performance of legumes, in general and mung bean in particular, from one season to another is quite high (Yadav and Warsi, 1988; Ashour *et al.*, 1992; Abd El-Latif *et al.*, 1998 and Afiah and Mohamed, 2000). In both seasons, mean performance of all traits except seeds/pods % in the second season, were decreased as affected by long irrigation intervals (I_2). The interaction between mung bean genotypes and irrigation intervals was significant for all traits in both seasons, except height of the first branch, number of branches/plant and weight of pods/plant in the first season.

Under normal irrigation level, in the first season (Table 1) lines 2920, 2020, 1720, 2520 and 1320 surpassed the check variety in pl. h, h. 1st Br., Brs, Pods, Pods wt./pl., No. S./pl. and SY/pl. Also, the two lines 3430 and 3940 had higher values than those of Qawmy-1 for most traits. Whereas, line 3740 had the lowest mean. However, in the second season (Table 2) the genotypes showed behaviour differed from that observed in the first season, reflecting their sensitivity to the climatic condition. But the most consistent in both seasons were L-1320, L-1720 and L-3630 especially for Brs, Pods, No.S./pl. and SY/pl., as well as L-2520 and L-2920 for Brs, Pods wt./f, SY/f and S:P%. These results indicated that most of these genotypes genetically related to each other. Lines 2520, 1720, 2920, 2020 and 1320 and 3940, in both seasons, had improved SY/f and S:P% due to their superiority in yield components. These results indicated that most of these newly tested genotypes are promising for releasing improved ones.

Evaluation under drought is a tool enabling to differentiate among genotypes to select the tolerant one(s). Under drought stress, however, all genotypic agronomic traits were affected by water deficit (Tables 1 and 2). Inferiority of genotypic performance traits was early reported by several mung bean investigators (Pandey *et al.*, 1984; Sarkar, 1992; Haqqani and Pandey, 1994; Thomas *et al.*, 2004 and Thalooth *et al.*, 2006). Whereas, Bhanot *et al.* (1994) using two irrigation levels and showed that irrigation had no effect on mung bean yield.

In the first season (Table 1), all genotypes except L-3740 which insignificantly different from Qawmy-1 in all traits had improved means of pl.h, h.1st Br, Brs, Pods and No.S/pl. compared with those of the check variety. Also, lines 1320, 1720, 2020, 2520, 2920 and 3740 surpassed Qawmy-1 variety for No. S/pl and seed yield per plant and per feddan.

Table (1). Mean performance of mung bean samples in the first season.

Genotype		Plant height (cm)	Height of 1st branch (cm)	No. of branches/ plant	No. of pods/ plant	Weight of pods/ plant (g)	Seed yield/ plant (g)	No. of seeds/ plant	Weight of pods/fed. (kg)	Seed yield/ fed. (kg)	Seeds/ pods %
First irrigation level (I_1)											
L-1320		64.89	23.51	5.43	22.12	12.75	8.59	134.67	802.43	410.04	50.98
L-1720		68.39	24.06	5.56	22.71	13.02	8.80	135.61	971.52	543.74	56.12
L-2020		71.26	24.74	5.75	23.53	13.40	9.07	139.35	745.19	413.08	55.73
L-2520		65.75	23.67	5.49	22.40	12.87	8.70	136.54	863.57	585.63	68.31
L-2920		71.31	25.23	5.87	24.05	13.64	9.23	141.68	858.98	482.38	56.26
L-3740		50.79	19.65	4.63	17.23	11.00	7.39	115.73	835.57	438.36	52.49
L-3940		60.87	21.72	5.03	19.57	11.14	7.56	118.22	1184.52	572.13	48.51
L-3430		60.61	22.42	4.82	20.21	11.80	7.95	123.67	795.43	339.11	42.78
L-3630		59.37	21.58	4.67	17.83	11.08	6.97	116.58	699.88	303.72	43.42
Qawmy-1		54.74	20.41	4.71	18.04	10.50	7.04	110.82	726.58	345.10	47.48
Means of the 1st irrig. Level		62.79	22.69	5.19	20.76	12.12	8.13	127.28	848.36	443.32	52.21
Second irrigation level (I_2)											
L-1320		66.05	23.35	5.41	22.15	12.76	8.65	131.40	773.14	314.46	40.67
L-1720		63.24	23.01	5.35	21.78	12.59	8.50	131.40	721.55	366.61	51.11
L-2020		61.09	22.50	5.21	21.16	12.30	8.30	128.60	773.14	392.61	50.81
L-2520		59.78	22.18	5.13	20.81	12.15	8.19	124.70	784.84	328.98	41.92
L-2920		61.56	22.63	5.24	21.29	12.37	8.35	129.22	718.08	364.87	50.77
L-3740		48.43	19.29	4.45	17.85	10.08	7.05	102.87	671.25	294.14	43.82
L-3940		55.70	21.30	4.93	18.84	10.93	7.26	114.01	607.51	248.40	40.89
L-3430		55.17	20.44	5.09	18.03	10.19	6.82	107.78	640.57	277.78	43.49
L-3630		52.71	19.84	4.90	18.88	10.20	7.31	107.94	579.53	234.94	40.54
Qawmy-1		46.91	18.74	4.31	16.26	9.68	6.46	102.80	563.85	230.77	40.83
Means of the 2nd irrig. Level		57.06	21.32	5.00	19.61	11.22	7.58	117.47	683.34	303.36	44.49
New LSD											
Irrig. (I)	0.05	3.40	0.40	0.12	0.21	0.69	0.25	1.18	49.23	15.46	0.87
	0.01	7.84	0.92	0.27	0.48	1.59	0.58	2.71	113.54	35.66	2.01
L x I	0.05	4.21	n.s	n.s	1.43	n.s	0.65	6.31	117.92	71.85	4.03
	0.01	5.65	n.s	n.s	1.92	n.s	0.87	8.48	158.42	96.53	5.41

n.s: not significant at 0.05 probability level

In the second season (Table 2), all new genotypes were better than the check variety for pl.h except L-1320 and L-1720; for No. S/pl except L-3430, L-3630 and L-2920. L-3740 was superior for pl.h, h.1st Br, Pod wt/pl. SY/pl., No. S/pl and SY/f. indicating its drought tolerance. The best yielding genotypes arranged in descending order, lines 2020, 2520, 3740 and 3940. In general, these four genotypes could be used for breeding high yielding and drought tolerant mung bean genotypes.

Table (2). Mean performance of mung bean samples in the second season.

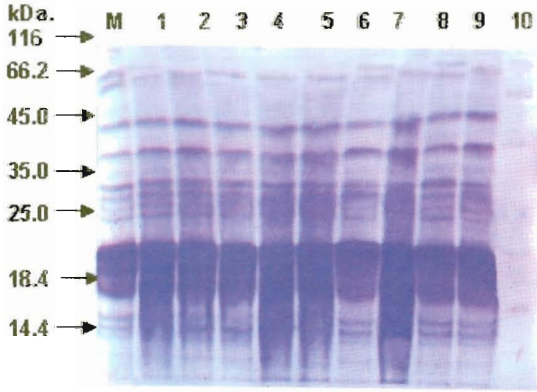
Genotype	Plant height (cm)	Height of 1st branch (cm)	No. of branches /plant	No. of pods /plant	Weight of pods/ plant (g)	Seed yield/ plant (g)	No. of seeds/ plant	Weight of pods/fed. (kg)	Seed yield/ fed. (kg)	Seeds/ pods %
First irrigation level (I_1)										
L-1320	58.78	15.00	5.67	20.11	9.24	5.57	137.44	961.72	465.79	48.43
L-1720	58.89	15.56	6.56	19.67	11.86	7.28	140.33	1005.51	509.70	50.69
L-2020	60.67	24.78	4.45	8.89	6.81	4.18	53.56	888.46	450.72	50.73
L-2520	57.67	13.67	6.00	13.78	13.76	9.36	130.56	908.18	430.18	47.37
L-2920	55.67	19.33	5.22	9.56	8.13	5.09	79.11	1009.85	511.89	50.69
L-3740	63.33	15.89	5.00	16.78	11.09	7.17	138.55	679.62	277.53	40.84
L-3940	54.56	17.83	4.83	8.50	9.98	5.97	71.67	725.95	296.24	40.81
L-3430	59.67	18.67	5.78	11.89	10.04	7.18	97.56	718.95	277.38	38.58
L-3630	65.00	21.67	5.00	18.17	14.20	9.38	140.00	579.53	280.75	48.44
Qawmy-1	56.11	18.11	4.56	14.89	6.72	3.88	108.33	654.41	267.34	40.85
Means of the 1st irrig. Level	59.03	18.05	5.31	14.22	10.18	6.51	109.71	813.21	376.75	46.33
Second irrigation level (I_2)										
L-1320	45.89	14.11	4.33	14.45	7.46	4.79	105.32	467.21	282.72	60.51
L-1720	44.67	16.11	4.33	14.89	7.18	4.09	104.33	415.41	279.28	67.23
L-2020	53.00	16.56	4.22	13.89	9.05	5.24	105.00	649.52	357.00	55.16
L-2520	51.56	16.55	4.33	11.11	9.00	5.95	104.67	597.02	345.63	57.90
L-2920	50.11	19.55	4.33	7.00	6.16	3.81	56.11	414.32	223.46	55.57
L-3740	53.89	23.56	4.22	13.78	8.77	5.43	105.78	550.28	333.33	60.57
L-3940	47.83	17.78	4.22	10.89	7.12	4.55	96.78	633.69	296.67	46.82
L-3430	51.22	21.22	4.67	11.11	7.54	4.71	56.67	358.24	188.53	52.86
L-3630	48.50	17.50	4.17	11.67	6.62	3.90	56.17	692.77	239.17	34.77
Qawmy-1	42.78	14.00	4.11	14.33	3.60	1.73	62.56	486.76	211.14	43.38
Means of the 2nd irrig. level	48.94	17.69	4.29	11.21	6.55	4.02	70.03	546.52	265.99	53.48
New LSD										
Irrig. (I) 0.05	3.53	n.s	0.35	1.19	1.37	0.66	8.02	41.59	39.59	3.09
Irrig. (I) 0.01	8.14	n.s	0.81	2.76	3.15	1.51	18.50	95.94	91.31	7.12
L x I 0.05	5.17	5.85	0.69	2.84	2.19	1.85	17.54	80.02	55.55	8.57
L x I 0.01	6.94	7.86	0.93	3.81	2.94	2.48	23.56	107.5	74.64	11.52

n s: not significant at 0.05 probability level

Protein Analysis (SDS - PAGE)

Figure (1) demonstrated the SDS profile of mung bean soluble protein fractions while, table (3) revealed their computer analysis and represented the occurrence of bands as (+) and absence as (-). Twenty seven bands were recorded in this pattern with polymorphism of 44.4%. From them, 15 monomorphic bands were recognized and could be considered as common bands in mung bean samples under drought conditions. One unique polymorphic band at molecular weight of 39.66 kDa could be used for identifying the related mung bean genotype (L-1320). These results are more or less in harmony with those previously obtained by Bhatty (1982), Khalil (1994), El-Saied and Afiah (1998) and Abou Deif *et al.* (2005).

It is notable that, superiority of L-2520 and L-1720 in seed yield/fed. was correlated with absence of the two bands in molecular weight 94.65 kDa and presence of the band with the molecular weight of 12.1 kDa under drought stress conditions. Also, to discriminate genetic markers that could be used for assisting selection in mung bean for drought stress, more studies on the molecular level must be practiced.



M	Genotype
1	Qawmy-1
2	L-3940
3	L-3740
4	L-3630
5	L-3430
6	L-2920
7	L-2520
8	L-2020
9	L-1720
10	L-1320

Fig. (1). SDS-PAGE of seed storage protein for ten mung bean genotypes tested.

The results generated from SDS-PAGE soluble seed protein fractions under both irrigation levels were pooled for drawing the genetic relationships among the ten tested mung bean genotypes. The similarity indices were estimated for each pair-wise group using SPSS computer program version 11, and the results are given in table (4). The constructed dendrogram tree is present in Fig. (2). The obtained dendrogram revealed three different genetic clusters. The first one includes the three lines L-3430, L. 2920 and L. 3740. The second cluster includes six genotypes i.e. L.2520, L-1720, Qawmy-1, L. 3940, L. 3630 and L-1320, while the third one comprises line 2020.

Table (3). The molecular weights of seed storage protein bands for the ten mung bean genotypes tested.

Molecular weight (kDa)	Qawmyl	L. 3940	L. 3740	L. 3630	L. 3430	L. 2920	L. 2520	L. 2020	L. 1720	L. 1320
106.51	+	+	+	+	+	+	+	+	+	+
94.65	+	+	+	+	+	+	-	+	-	+
85.17	+	+	+	+	+	+	+	+	+	+
70.94	+	+	-	-	-	-	-	-	-	+
65.62	+	+	-	+	-	-	+	+	-	+
63.91	+	+	-	+	-	-	+	+	+	+
60.47	+	+	+	+	-	-	+	+	+	+
53.22	+	+	-	+	-	-	+	+	+	+
49.01	-	+	-	+	-	-	-	-	-	+
41.66	+	+	+	+	+	+	+	+	+	+
39.66	-	-	-	-	-	-	-	-	-	+
36.55	+	+	+	+	+	+	+	+	+	+
32.27	+	+	+	+	+	+	+	+	+	+
30.75	+	+	-	+	-	-	+	+	+	+
29.84	+	+	-	+	-	-	+	+	+	+
29.24	+	+	-	+	-	-	+	+	+	+
27.12	+	+	+	+	+	+	+	+	+	+
24.65	+	+	+	+	+	+	+	+	+	+
23.37	+	+	+	+	+	+	+	+	+	+
22.22	+	+	+	+	+	+	+	+	+	+
20.71	+	+	+	+	+	+	+	+	+	+
19.09	+	+	+	+	+	+	+	+	+	+
18.00	+	+	+	+	+	+	+	+	+	+
16.60	+	+	+	+	+	+	+	+	+	+
15.30	+	+	+	+	+	+	+	+	+	+
12.70	+	+	+	+	+	+	+	+	+	+
12.10	-	-	-	-	-	-	+	-	+	-
Total No. of bands	**24**	**26**	**16**	**25**	**15**	**15**	**22**	**22**	**22**	**27**

(+): present and (-) absent

From the previous results, it can be concluded that, the highest similarity value 0.960 (Table 4), was observed between L. 3430 and L. 2920 indicating that these two lines are closely related to each others in their protein polypeptide patterns. Meanwhile, the lowest similarity values (0.680) were scored between the two newly bred lines L. 3740 and L. 1320 as well as (0.681) between L. 2020 and each of L. 3430 and L. 2920 indicating the wide genetic diversity among them. These results confirmed the above conclusion mentioned in the performance of the genotypes tested under frequent irrigation.

Good results could be obtained if we cross between these five genotypes because there are a wide diverse among them. It is noteworthy that cluster analysis is a valuable tool for subdividing genotypes into groups including similar and dissimilar lines and has a great value from the breeders point of view for initiating mung bean hybrid program. These findings are in

line with those earlier obtained by Afiah and Mohamed (2000) and Hassan (2001).

Table (4). Similarity indices among the ten mung bean genotypes as estimated using SDS protein banding patterns.

Genotype	Qawmy1	L. 3940	L. 3740	L. 3630	L. 3430	L. 2920	L. 2520	L. 2020	L. 1720
L. 3940	0.887								
L. 3740	0.743	0.736							
L. 3630	0.889	0.887	0.743						
L. 3430	0.798	0.738	0.841	0.825					
L. 2920	0.798	0.738	0.841	0.825	0.960				
L. 2520	0.912	0.738	0.743	0.889	0.825	0.825			
L. 2020	0.777	0.801	0.781	0.777	0.681	0.681	0.777		
L. 1720	0.889	0.838	0.743	0.889	0.825	0.825	0.936	0.749	
L. 1320	0.893	0.869	0.680	0.893	0.760	0.760	0.871	0.713	0.871

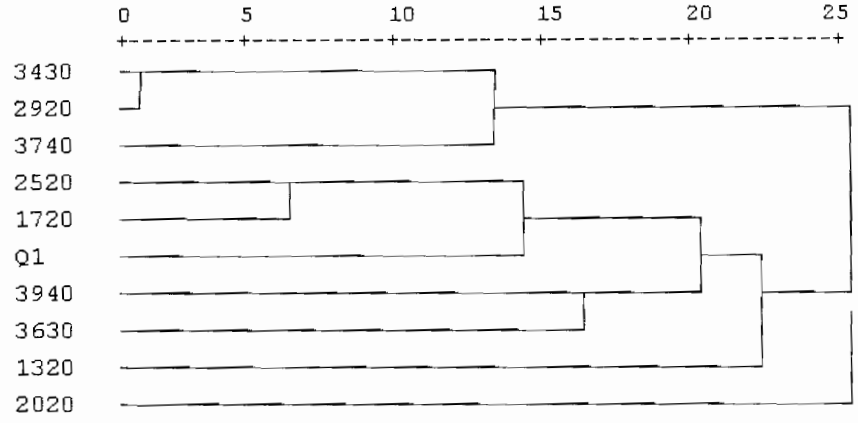


Fig. (2). Dendrogram demonstrates the relationships among the ten mung bean genotypes tested based on SDS-PAGE analysis.

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توصيف بعض التراكيب الوراثية المختارة من فول المانج على المستوى المحصولى والوراثى البيوكيميائى

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أقيمت تجربتان حقليتان فيَ الأرض الجديدة لمزرعة كلية الزراعة بالفيوم (أرض طمييه رملية) خلال الموسمين ٢٠٠٥ و٢٠٠٦ واستخدم في كل منهما تسعة تراكيب وراثية من فول المانج مع صنف المقارنة قومي –١ والذي تم تقييمهم تحت معاملتين للري، الأولى الري كل ١٢ يوم والثانية الري كل ٢٤ يوم ونفذت كل تجربة في تصميم القطاعات المنشقة في قطاعات كاملة العشوائية في ثلاث مكررات ووزعت معاملتي الري في القطع الرئيسية والتراكيب الوراثية في القطاعات المنشقه. وتهدف الدراسة إلى الوصول لأكثر السلالات محصولاً ومقاومة للجفاف تحت ظروف الأراضى الجديدة وكذلك التمييز والتفرقة بينهم باستخدام تقنية كيميائية حيوية.

أظهرت النتائج في كلا الموسمين لكل الصفات تحت الدراسة تأثيراً معنوياً للتفاعل بين التراكيب الوراثية ومعاملات الري عدا طول منطقة التفريع وعدد الأفرع ووزن قرون النبات في الموسم الأول. ظهر تحت ظروف الري العادي في الموسم الأول تفوق السلالات ٢٩٢٠و٢٠٢٠و١٧٢٠و٢٥٢٠و١٣٢٠ على صنف المقارنة قومي–١ في طول النبات وطول منطقة التفريع وعدد الأفرع وعدد القرون على النبات ووزن قرون النبات وكذلك عدد بذور النبات ومحصول النبات. أيضاً وجد ارتفاع في متوسطات معظم الصفات للسلالتين ٣٤٣٠و٣٩٤٠عن قومي–١.

في الموسم الثاني تفوقت السلالات السابقة (في الموسم الأول) بالإضافه للسلالة ٣٧٤٠ على قومي –١ في معظم الصفات المدروسة. عموماً أظهرت النتائج وجود تقارب وراثي بين مجموعات السلالات السابقة ٠ ولوحظ تحت ظروف الجفاف أن معظم الصفات لبعض السلالات تأثرت بنقص المياه ولكن مقارنة بالصنف قومي –١ في الموسمين تفوقت السلالات ٢٠٢٠و١٧٢٠و٢٥٢٠و٣٧٤٠و٣٩٤٠وهذا يشير إلى مناسبتها للاستخدام مباشرة أو بطريقة غير مباشرة خلال طرق التربية للتحسين وتحمل الجفاف في فول المانج.

اظهر تحليل البروتين (SDS-PAGE) وجود عدد ٢٧ حزمه مختلفة من بينها ١٥ حزمة متشابهة بنسبة تباين ٤٤,٤% . كما أوضحت نتائج التحليل والتي استخدمت لرسم علاقات القرابة بين التراكيب الوراثية المستخدمة انتمائها لثلاث مجموعات مختلفة. وفى النهاية ومن خلال التقييم والتحليل الوراثى البيوكيمائى الحيوي أمكن التعرف على بعض السلالات الواعدة والمقاومة للجفاف في فول المانج.