

Research Note

Selection of early segregating progeny lines of chickpea (*Cicer arietinum* L.) for high yield under terminal drought stress conditions

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Abstract

Drought is one of the most devastating abiotic stresses, spreading around the world and limiting the productivity of chickpea. The present study was carried out to select the high yielding progeny lines of chickpea to combat terminal drought stress conditions. Parameters that were measured included phenological traits; yield and yield- related traits viz. number of branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, 100 seed weight and biological yield in F₃ progeny lines of cross HC-1 × RSG 931 along with parental chickpea genotypes. The data was analyzed using statistical program and all yield-related traits were found to be positively correlated with seed yield. Four progeny lines viz. P9, P15, P17 and P18 had higher seed yield plant⁻¹ than drought tolerant parental chickpea genotype, RSG 931 under terminal drought stress conditions. These superior progeny lines could be incorporated in chickpea breeding program to increase yield under terminal drought stress.

Key words

Progeny lines, Phenological traits, Terminal drought stress, Chickpea, Seed yield

Chickpea (*Cicer arietinum* L.) is a self-pollinating legume crop with a diploid set of chromosomes (2n=2x=16) and has a genome size of 738 Mb (Varshney *et al.*, 2013). In addition to having highly digestible protein content (23%), chickpea is also rich in carbohydrate (64%), starch (47%), fiber (6%), and minerals (phosphorus, calcium, magnesium, iron and zinc). Its lipid fraction is also high in unsaturated fatty acid (William and Singh, 1987; Jukanti *et al.*, 2012), thereby, it could be helpful in lowering the risk of coronary heart diseases (Hu *et al.*, 2001). Chickpea is used as protein rich animal feed and its vegetative biomass is also used as a fodder. It can fix up to 140 Kg nitrogen ha⁻¹ to meet upto 80% of nitrogen requirement from symbiotic nitrogen fixation (Saraf *et al.*, 1998).

After soybean, chickpea is world's second most important food legume crop. Globally, chickpea was cultivated on an area of 14.80 million hectares (mha) with an annual production of 14.23 million tons (mt) (FAOSTAT, 2014). Further, among chickpea growing countries, India alone contributes to 70% of the world's total production. In India, chickpea was grown on 10.74 mha areas producing 9.8 mt (FAOSTAT, 2014). In the last four decades, chickpea productivity has consistently increased in India and Mexico while, it has declined in Turkey, Pakistan, and Iran (Upadhyaya *et al.*, 2012). The increase in productivity is mainly due to more availability of seeds of high yielding varieties and good agronomic practices. However, the productivity of chickpea is still low in India (945 kg ha⁻¹) as

compared to other chickpea producing countries like Mexico (1809 kg ha⁻¹), Australia (1268 kg ha⁻¹), and Ethiopia (1265 kg ha⁻¹) (Sewak *et al.*, 2012). This is mainly due to various kinds of biotic stresses including Fusarium wilt, Ascochyta blight, *Helicoverpa armigera* and abiotic stresses such as drought, heat and salinity. Among abiotic stresses, drought is considered as major constraint to chickpea production. Drought stress limits the chickpea production by preventing the crop plants from expressing their full genetic potential. Chickpea is mostly grown on residual moisture from monsoon rains on the Indian subcontinent and crops mature under progressively declining soil moisture (Turner *et al.*, 2001). Annually, 40–50% reduction in seed yield of chickpea has been reported worldwide as a result of terminal drought stress (Ahmad *et al.*, 2005). Further, the damage due to drought is supplemented by heat stress in South Asia where temperature increases towards seed developmental stage.

Efforts to breed drought tolerant varieties in past have not been rewarding because of quantitative and temporal variability of available moisture across years, low genotypic variance, inherent methodologies, difficulties in evaluating component traits, and using yield as an empirical selection criterion (Ludlow and Muchow, 1990; Saxena, 2003). A narrow genetic base and sexual incompatibility of chickpea with its wild relatives, which are known to carry the genes for various abiotic stresses tolerance, also contribute to the limited progress in the improvement of chickpea yield (Choudhary *et al.*, 2012). Keeping these

things in minds, the present study was planned and carried out in drought microplots with rainout shelter using two diverse chickpea genotypes. The objective of the present study was screening of the segregating F_3 progeny lines for high yield that can combat terminal drought stress conditions.

Selection of parents for crossing: Drought tolerant chickpea genotype, RSG 931 and drought sensitive genotype, HC-1 were selected as parents and crossed to make hybrid HC-1 $\times$ RSG 931. HC-1 is a very popular chickpea variety of Haryana, performing very well under irrigated condition but its performance get reduced under drought stress (Summy *et al.*, 2015). Whereas, RSG 931 is a high yielding variety of chickpea under drought stress conditions (Kumar *et al.*, 2012). So, a cross was attempted between HC-1 and RSG 931 during *rabi* 2010-11 to transfer drought tolerant trait from RSG 931 to HC-1.

Development of segregating populations: The crossing was done between parental chickpea genotypes viz. HC-1 and RSG 931 at the research farm of Pulses Section, CCS Haryana Agricultural University, Hisar, India. The seeds set on plants of female parent HC-1 were harvested as F_1 seeds. F_1 seeds were sown next year to get F_1 plants and these were selfed to get F_2 and F_3 segregating populations in subsequent years.

Screening for terminal drought tolerance: Eighteen F_3 progeny lines along with parental chickpea genotypes were grown during *rabi* 2012-13 in specially constructed facilities of concrete microplots (6 m long, 1 m wide and 1.5 m deep connected with iron gates and washing tanks) filled with sandy soil and irrigated up to field capacity at Crop Physiology Field Lab, Agronomy Research Farm, CCS Haryana Agricultural University, Hisar. Parental genotypes were sown in three rows of 1 m length with inter row spacing of 30 cm and plant spacing of 10 cm under two environments, namely Irrigated (I: two irrigations of 6 cm depth, one at pre flowering and another at pod filling stage) and Drought (D: one irrigation of 30 mm equal to long-term average seasonal rainfall). Eighteen F_3 progeny lines of the cross HC-1 $\times$ RSG 931 were grown only in drought stress conditions. All the recommended agronomic practices were followed for raising the crop. The soil moisture content was measured at different soil depths (0-15, 16-45, 46-75, 76-105 and 105 -140 cm) using gravimetric methods (Dirksen, 1999).

Three plants from each progeny lines were randomly taken to record the data. Mean of three plants data was analyzed for computing mean, standard error, range and coefficient of correlation using online Statistical Analysis Package (OPSTAT, Computer Section, CCS Haryana Agricultural University, Hisar, Haryana).

The experiment was performed in drought microplots and drought conditions were maintained during the experiment. At 120 days after sowing (DAS), the soil surface in drought microplots was almost dry with less than 5.1% soil moisture content. However, soil moisture content in drought microplots at 120 DAS in the depth range of 76-105 cm and 106-140 cm was recorded to be 8.1% and 10.1%, respectively. The maximum water was absorbed from the soil depth in the range of 46-140 cm at 120 DAS (i.e. at physiological maturity). To select chickpea superior progeny lines under terminal drought tolerance, the data was recorded for the various phenological and yield-related traits within F_3 progeny lines of cross HC-1 $\times$ RSG 931 along with their parental genotypes.

Phenological traits of parental chickpea genotypes of cross HC-1 $\times$ RSG 931: Phenology plays a critical role in the adaptation of chickpea genotypes to different environmental conditions (Berger *et al.*, 2011). The observations recorded for phenological traits viz. days to 50% flowering, days to 50% podding and days to physiological maturity were higher in drought tolerant genotype, RSG 931 than drought sensitive genotype, HC-1 under both irrigated as well as drought stress conditions (Table 1). There was reduction in days to 50% flowering, podding and physiological maturity in both HC-1 and RSG 931 under drought stress conditions but the percent reduction was less in RSG 931 than HC-1. Being a post-rainy season crop, early maturity is important parameter in escaping the terminal drought stress in chickpea (Gaur *et al.*, 2008). Kumar *et al.* (2012), Summy *et al.* (2015) and Hussain *et al.* (2015) also reported that there was reduction in the values of phenological traits under drought stress conditions.

Phenological traits of F_3 progeny lines of cross HC-1 $\times$ RSG 931 under terminal drought stress conditions: Eighteen F_3 progeny lines of cross HC-1 $\times$ RSG 931 were grown only under drought stress conditions and phenological traits showed large variation in F_3 progeny lines. The days to 50% flowering, days to 50% podding and days to physiological maturity varied from 80-92, 99-113 and 120-144 days, respectively. This could be attributed due to genetic difference in progeny lines. The progeny line, P12 (80 days) took less days to reach at 50% flowering, P6 (100 days) and P12 (99 days) took less days to reach at 50% podding and P6 matured earlier (120 days) than drought sensitive parental chickpea genotype, HC-1 (Table 2). Most of the F_3 progeny lines matured earlier than drought tolerant parental genotype, RSG 931 (139 days) under drought stress conditions except three progeny lines viz. P1 (140 days), P2 (142 days) and P18 (144 days), which matured later than drought tolerant parental chickpea genotype, RSG 931.

Yield and yield-related traits of parental chickpea genotypes of cross HC-1 × RSG 931: Seed yield and yield-related traits such as number of pods, seeds pod⁻¹, biological yield, 100 seeds weight decreased under drought stress conditions due to reduction in reproductive phase of chickpea plants. But, the reduction was less in RSG 931 as compared to HC-1 (Table 3). Leport *et al.* (2006) also reported a decrease in the biomass and yield of chickpea genotypes under drought stress conditions. Drought stress also resulted in decrease rate of photosynthesis, due to which there was less accumulation of photosynthetic resources for growth and yield of plants (Mafakheri *et al.*, 2010). However, the reduction in seed yield plant⁻¹ was less in RSG 931 (25.86%) than HC-1 (47.2%) which may be due to cumulative effect of yield-related traits. Our results are in agreement with the previous reports of Kumar *et al.* (2012) and Summy *et al.* (2015) where they also found the similar results.

Yield and yield-related traits of F₃ progeny lines cross HC-1 × RSG 931 under terminal drought stress conditions: The data on various yield and yield-related traits viz. number of branches plant⁻¹, number of pods plant⁻¹, seeds pod⁻¹, biological yield, 100 seeds weight and seed yield plant⁻¹ of F₃ progeny lines of cross HC-1 × RSG 931 showed a large variation. Maximum number of pods plant⁻¹, seeds pod⁻¹, 100 seeds weight, biological yield, and seed yield plant⁻¹ were recorded in P17, P7, P17, P9 and P17, respectively and the values were higher than that of drought tolerant parental chickpea genotype, RSG 931 (Table 4).

Seed yield plant⁻¹ was recorded maximum in progeny line, P17 (14.09 g) which was 25% higher than drought tolerant parental chickpea genotype, RSG 931 (11.27 g) while minimum seed yield was found in progeny line, P1 (6.07 g) under drought stress conditions. The seed yield plant⁻¹ in 18 F₃ progeny lines of cross HC-1 × RSG 931 varied from 6.07 to 14.09 g under drought stress conditions. Four progeny lines viz. P9 (11.93 g), P15 (13.33 g), P17 (14.09 g) and P18 (11.39 g) had higher seed yield plant⁻¹ than drought tolerant parental chickpea genotype, RSG 931 (11.27 g) under drought stress conditions. Hence, these four superior progeny lines could be used for development of high yielding chickpea genotypes under terminal drought stress conditions.

Yield-related traits *i.e.* number of branches plant⁻¹, number of pods plant⁻¹, number of seeds pod⁻¹, 100 seeds weight and biological yield showed a significant positive correlation with seed yield of F₃ progeny lines of cross HC-1 × RSG 931. Tripathi *et al.* (2012) and Summy *et al.* (2015) also reported positive correlation among yield-related traits in chickpea. Among these traits, 100 seeds weight had highest significant positive correlation

($r = 0.840^{**}$) with seed yield (Table 5). Less number of pods plant⁻¹ and less competition for assimilates may be the one of the reasons for high 100 seed weight in chickpea genotypes (Fallah, 2008). Toker and Cagirgan (1998) also reported a positive correlation of 100 seeds weight and biological yield with seed yield under rain-fed conditions in chickpea.

The study concluded that chickpea genotypes which are varying for terminal drought stress could be useful resources for development of superior progeny lines. Under drought stress condition, a reduction was found in all the yield related traits but the reduction was less in drought tolerant genotype/progeny lines. Yield-related traits showed highly significant positive correlation with seed yield. The progeny lines viz. P9, P15, P17 and P18 of cross HC-1 × RSG 931 had higher seed yield per plant than drought tolerant parental chickpea genotype, RSG 931 and these can be incorporated in chickpea breeding program to increase yield under terminal drought stress.

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Table 1. Phenological traits of parental chickpea genotypes of cross HC-1 × RSG 931 under irrigated and terminal drought stress conditions

Phenological traits	Irrigated		Drought		Percent reduction under drought stress	
	HC-1	RSG 931	HC-1	RSG 931	HC-1	RSG 931
Days to 50% flowering	92	96	81	88	11.96	8.33
Days to 50% podding	113	119	102	108	9.73	9.24
Days to physiological maturity	135	151	121	139	10.37	7.95

Table 2. Phenological traits of 18 F₃ progeny lines of cross HC-1 × RSG 931 under terminal drought stress conditions

F ₃ progeny line	Days to 50% flowering	Days to 50% podding	Days to physiological maturity
P1	88	110	140
P2	90	109	142
P3	86	106	136
P4	88	108	136
P5	85	103	126
P6	82	100	120
P7	85	104	130
P8	84	105	126
P9	86	102	124
P10	87	107	130
P11	91	106	138
P12	80	99	132
P13	83	104	128
P14	83	111	136
P15	85	106	136
P16	84	102	123
P17	81	105	138
P18	92	113	144
Mean	85.86±1.92	105.56±2.15	132.5±4.02
Range	80-92	99-113	120-144

Table 3. Yield and yield-related traits of parental chickpea genotypes of cross HC-1 × RSG 931 under irrigated and terminal drought stress conditions

Yield and yield-related traits	Irrigated		Drought		Percent reduction under drought stress	
	HC-1	RSG 931	HC-1	RSG 931	HC-1	RSG 931
No. of branches plant ⁻¹	3.66±0.33	5.66±0.33	3.33±0.33	5.33±.33	9.02	5.83
No. of pods plant ⁻¹	57±1.52	59.66±0.88	49.33±1.2	55.33±0.88	13.46	7.26
No. of seeds pod ⁻¹	1.63±0.03	1.67±0.01	1.32±0.02	1.60±0.02	20.25	4.19
100 seeds weight (g)	14.62±0.27	15.22±0.52	11.05±0.3	12.72±0.61	24.42	16.43
Seed yield (g plant ⁻¹)	13.57±0.28	15.20±0.63	7.19±0.23	11.27±0.51	47.02	25.86
Biological yield (g plant ⁻¹)	25.26±0.41	23.42±0.28	18.53±0.53	20.03±0.76	26.64	14.47

Table 4. Yield and yield-related traits of 18 F₃ progeny lines of cross HC-1 × RSG 931 under terminal drought stress conditions

F ₃ progeny line	No. of branches plant ⁻¹	No. of pods plant ⁻¹	No. of seeds pod ⁻¹	100 seeds weight (g plant ⁻¹)	Seed yield (g plant ⁻¹)	Biological yield (g plant ⁻¹)
P1	3.0±0.00	53.33±2.40	1.30±0.03	8.84±0.48	6.07±0.34	16.32±0.25
P2	5.0±0.58	54.67±1.76	1.24±0.01	12.42±0.46	8.62±0.46	19.04±0.81
P3	5.7±0.67	55.33±0.88	1.33±0.02	8.98±0.42	6.76±0.11	15.35±0.18
P4	5.3±0.33	54.33±1.86	1.56±0.03	11.26±0.56	10.11±0.63	20.98±0.84
P5	5.3±0.33	51.67±2.40	1.51±0.02	11.03±0.65	9.16±0.36	19.67±0.77
P6	5.0±0.58	51.00±1.73	1.26±0.03	12.12±0.62	8.26±0.53	18.90±0.31
P7	4.0±0.00	54.33±0.88	1.63±0.01	10.87±0.36	9.89±0.52	19.47±0.48
P8	5.0±1.00	50.67±2.33	1.39±0.01	12.79±0.40	9.31±0.47	19.83±0.42
P9	7.0±0.58	58.00±2.52	1.58±0.03	13.45±0.36	11.93±0.41	22.66±0.58
P10	5.0±1.00	61.33±2.03	1.52±0.01	11.46±0.39	10.42±0.42	22.13±0.21
P11	5.3±0.33	58.67±2.33	1.49±0.01	12.44±0.35	10.50±0.42	21.70±0.63
P12	6.0±1.00	60.00±2.08	1.38±0.01	11.32±0.53	9.25±0.66	20.46±0.45
P13	7.7±0.33	58.33±1.45	1.58±0.01	12.17±0.73	10.85±0.55	21.13±0.40
P14	4.7±0.33	55.00±1.00	1.55±0.02	12.10±0.36	9.97±0.05	20.25±0.69
P15	8.3±0.88	60.33±1.86	1.59±0.02	13.40±0.46	13.33±0.42	22.31±0.45
P16	7.0±1.53	60.00±2.08	1.38±0.02	9.52±0.25	7.70±0.26	19.22±0.18
P17	6.0±0.58	63.33±2.19	1.59±0.01	13.74±0.66	14.09±0.80	21.98±1.01
P18	5.3±0.33	62.33±1.45	1.53±0.04	12.31±0.46	11.39±0.47	19.74±0.61
Mean	5.63±0.70	56.81±2.28	1.47±0.07	11.68±0.83	9.87±1.19	21.86±0.76
Range	3.0- 8.3	43.33-63.33	1.24-1.63	8.84-13.74	6.07-14.09	15.35-22.31

Table 5. Correlation matrix among yield and yield-related traits in F₃ progeny lines of cross HC-1 × RSG 931

	SY	NB	NP	NS/P	100SW	BY
SY	1					
NB	0.496*	1				
NP	0.598**	0.503*	1			
NS/P	0.770**	0.313	0.420	1		
100SW	0.840**	0.362	0.277	0.429	1	
BY	0.826**	0.410	0.496*	0.707**	0.755**	1

* significant at 0.05, ** significant at 0.01

SY- seed yield plant⁻¹, NB- number of branches plant⁻¹, NP- Number of pods plant⁻¹, NS/P- number of seeds pod⁻¹, 100SW- 100 seed weight, BY- biological yield plant⁻¹,