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APPRAISAL OF INTERACTION AMONG NIPPING AND CHICKPEA (CICER ARIETINUM L.) GENOTYPES AND THEIR CORRELATED RESPONSE FOR GRAIN YIELD

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ABSTRACT

Nipping is considered to be the cause of increase in seed yield of chickpea. Whether, either morphs of chickpea (Desi & Kabuli) verify this statement or not, an experiment was carried out using twenty chickpea genotypes (11 Desi & 9 Kabuli) and two treatments (nipped, control). Two nippings were carried out with 20-25 days interval. Data analysis revealed highly significant differences among genotypes, treatments and genotype by nipping interaction for yield and yield attributing traits. Eight genotypes viz, NDC-4-20-3, NIFA-2005, Karak-2, SL-3-15, NKC-5-S-12, Karak-1, NDC-15-1 and SL-3-64 revealed positive response to nipping, which also provides green forage. Whereas, twelve genotypes including 3 Desi and 9 Kabuli genotypes showed disincline to nipping. It is concluded that nipping should not be practised without prior testing of its effect on genotypes. Moreover, Desi chickpea respond positively as compare to Kabuli chickpea. Seed yield plant^{-1} showed highly significant and positive genotypic and phenotypic correlation with secondary branches plant^{-1} (r_g = 0.54,r_p = 0.46), pods plant^{-1} (r_g = 0.89,r_p = 0.83), seeds pod^{-1} (r_g = 0.58,r_p = 54), biological yield plant^{-1} (r_g = 0.97,r_p = 0.92), 100-seed weight (r_g = 0.52,r_p = 0.53), suggesting these traits to be used as selection criteria for yield improvement.

Keywords: Chickpea, genotypes, nipping, correlation, yield.

INTRODUCTION

Chickpea (*Cicer arietinum L.*) belongs to family Leguminosae, sub family Papilionaceae and tribe Cicereae. It is one of the major pulse crops of South East Asia, having diploid chromosome number of 2n = 16 (Nazir, 1994). It is grown in more than 50 countries. The largest producing country is India, which accounts for 64% of the global chickpea production and others include Pakistan, Iran, Myanmar, Australia, Ethiopia, Canada, Mexico and Iraq (Gaure *et al*., 2010). Chickpea is a cheap source of protein for vegetarians and its grain is having 19.5 % protein, 57-60 % carbohydrates, 1.4 % fats, 4.8 % ashes and 4.9-15.59 % moisture content (Hasan *et al*., 2008). It also provides livestock feed and increases soil fertility. People use green leaves and pods of gram as vegetables (Khalil and Jan, 2002).

The presence of genetic variation among genotypes is the base of selection for all plant breeders in every plant breeding programme (Hasan *et al.*, 2008). Removal of 4 cm of the growing tip of every branch plant^{-1} is called nipping. Nipping results in an increase of productive branches, pods plant^{-1} and grain yield. The plant hormones auxins are triggered to lateral shoot buds which results in more branches. Better plant canopies are also obtained through nipping. Nipping was done after complete emergence of a variety and must be before flowering stage avoiding extreme nipping (Khan *et al.*, 2006).

The eventual objectives of plant breeders are the development of high yielding cultivars or varieties, which can be adapted to an extensive range of diversified environments. Moreover, information on association between yield and its various components provides basis for selecting improved varieties (Kown and Torrie, 1964). Genetically correlated traits are used by plant breeders as indirect selection criterion for many traits (Biabani *et al.*, 2011). In most of the chickpea producing areas like D. I. KHAN people use animal grazing at seedling stage and consider it to be the cause of profused plant growth (Khattak *et al.*, 2007). The present study was planned to appraise the interaction between nipping and genotypes of chickpea as well as to evaluate genotypic and phenotypic association among yield and other traits to be considered as yield contributing traits.

Similarly, chickpea nipping has been reported to an innovative and profitable venture in D.I.Khan by using crop for grazing goats and sheep at seedling stage resulting profuse growth of the plants

MATERIALS AND METHODS

Location and Experimental Design: This experiment was conducted at The University of Agriculture, Peshawar during cropping season of 2013-14. Randomized complete block design with split-plot arrangements (genotypes in main plots and treatments in sub-plots) including three replications, was used. The

experimental material comprised twenty chickpea genotypes enlisted in Table 1. Sowing was done on 23th October 2013. Main plot for each genotype had 8 rows while sub-plot consisted of 4 rows. Row length was 4 m with 30 cm row-row, 10 cm plant-plant and 60 cm plot-plot distance. Two treatments i.e. control (without nipping) and nipped were evaluated. Nipping was done after complete emergence of a variety before flowering stage avoiding extreme nipping. In this experiment nipping was done two times. Number of nipping and interval between two nipping usually depend on crop growth. Under Peshawar condition, two nippings were possible, first at three node stage of the plants and second with 20-25 days interval just before flowering i.e. in the start of February. Insecticide (emamectine) was sprayed two times for control of pod borer at the time of pod formation phase. Standard cultural practices were applied from sowing to the time of harvesting.

Data Collection and Statistical analysis: Data were recorded on ten randomly selected plants from each plot of both treatments (un-nipped and nipped) replication^{-1}. The studied traits included number of secondary branches plant^{-1}, number of pods plant^{-1}, seeds pod^{-1}, hundred seed weight and seed yield plant^{-1}. The recorded data for all traits were analysed through (Statistix version 8.1). Genetic and phenotypic relationship among different traits and their contribution to define seed yield was determined by following procedure of Singh and Chaudhary (1997).

RESULTS AND DISCUSSION

Nipping exhibited highly significant differences for all the studied parameters including secondary branches plant^{-1}, pods plant^{-1}, seeds pod^{-1}, 100-seed weight, biological yield plant^{-1} and seed yield plant^{-1}.

Secondary branches per plant: Data presented for secondary branches plant^{-1} showed highly significant differences for genotypes, treatments (nipped & un-nipped) and genotype by nipping interaction (Table 2). Mean secondary branches plant^{-1} among genotypes ranged from 5.95 to 13.32. Maximum number of secondary branches plant^{-1} was recorded for genotype NKC-5-S-20 (13.40) under un-nipped and Karak-1 (19.03) under nipped treatment, While NDC-15-1 obtained minimum secondary branches under both treatments (Table 4). Nipping resulted in more (10.96) secondary branches as compared to un-nipped (9.93) treatment. According to the findings of Khan et al. (2006) number of secondary branches was increased because the hormone auxins are triggered to lateral shoots which results in more branches. Percent change in secondary branches plant^{-1} revealed positive effect in most of the genotypes except seven (six Kabuli and only one Desi) which showed negative response to nipping (Fig. 1).

Pods per plant: Analysis of variance for pods plant^{-1} revealed highly significant differences for genotypes, treatments and genotype by nipping interaction (Table 2). Highly significant genotype by nipping interaction confirmed that the performance of genotypes for pods plant^{-1} was different under both conditions. Genotypes mean values ranged from 35.13 to 79.83 pods plant^{-1}. Un-nipped treatment revealed maximum (81.87) pods plant^{-1} for SL-5-53, while nipped treatment exhibited maximum pods plant^{-1} for Karak-3 (86.67) followed by Karak-1 (86.00) (Table 4). Overall means of treatments showed more (61.03) pods plant^{-1} for nipped and less (57.03) for un-nipped treatment. Sharma *et al.* (2003) also observed increase in number of pods by the removal of apical meristems (nipping) in pigeon pea. Percent change in pods plant^{-1} among genotypes was strewn, 50% genotypes (7 Kabuli & 3 Desi) revealed negative response while remaining 10 genotypes showed positive response of different intensities to nipping (Fig. 1).

Seeds per pod: Data regarding seeds pod^{-1} manifested highly significant differences for genotypes and nipping, whereas non-significant genotype by nipping interaction (Table 2). Small number of seeds pod^{-1} (1.25) was recorded under nipping while more number (1.41) of seeds pod^{-1} under un-nipped system. Genotype NDC-15-1 and Karak-1 achieved lowest (1.07) and highest (1.82) mean number of seeds pod^{-1}, respectively (Table 4). Yaqoob et al. (2010) also registered significant differences among chickpea genotypes whereas non-significant differences between chickpea genotypes for seeds pod^{-1} was found by Khan et al. (2006). Baloach and Zubair (2010) observed highly significant genotype by treatment interaction while non-significant differences were recorded for treatments in chickpea. Percent change for seeds pod^{-1} indicated that only NKC-5-S-17 revealed (2.78 %) increase, while rest of the genotypes exhibited percent decrease due to the removal of foliage. Percent change analysis showed that 99.9% studied genotypes respond negatively to nipping (Fig. 2). Our results are in agreement with Khan et al. (2006); Baloach and Zubair (2010) who also observed decrease in number of seeds pod^{-1} under nipping as compared to control.

Hundred seed weight: Mean squares data for hundred seed weight indicated highly significant differences for genotypes, significant differences for treatments while non-significant for genotype by nipping interaction (Table 3). This demonstrated that 100-seed weight is not affected by interactive effect of chickpea genotypes and nipping. In the both treatment, genotype NKC-5-S-17 demonstrated maximum 100-seed weight (35.33 and 35.00 g, respectively). Genotype across nipping means, showed that among genotypes 100-seed weight ranged from 19.67 (Karak 2) to 34.17 g (NKC-5-S-17) (Table 5). Among treatments nipping revealed more (26.14 g) 100-seed weight whereas, un-nipped field exhibited less

(25.54 g) 100-seed weight. Percent change in genotypes for 100-seed weight due to nipping was low; five genotypes showed slightly decrease while remaining revealed either no or very little increase in the studied parameters (Fig. 2).

Biological yield per plant: Biological yield plant^{-1} also exhibited highly significant differences for genotypes, nipping and genotype by nipping interaction (Table 3). Mean biological yield plant^{-1} among genotypes ranged from 23.15 g to 71.47 g (Table 5). Genotype NDC-4-20-3 obtained minimum biological yield under both conditions. Maximum (74.33 g) biological yield plant^{-1} was recorded for NKC-5-S-15 under un-nipped condition, while nipping revealed maximum biological yield for SL-5-53 (70.44 g) (Table 5). In general, biological yield plant^{-1} produced by un-nipped treatment was higher (49.70 g) than that of nipped (46.31 g). Generally, the percent change was positive only in eight genotypes (NIFA-2005, Karak-2, SL-3-15, SL-3-64, NDC-15-1, NDC-4-20-3, Karak-1 and NKC-5-S-12) while on eleven the impact of nipping was negative (Fig. 3). Increase in biological yield of eight genotypes might be due to the increase in productive branches. Just like other studied parameters biological yield plant^{-1} also showed positive response to nipping in Desi genotypes while response of Kabuli genotypes is not only negligible but greatly negative. Aslam et al. (2010) also reported increase of biological yield when nipping was done 15 cm above ground level.

Seed yield per plant: Analysis of variance for seed yield plant^{-1} manifested highly significant differences for genotypes, nipping and genotype by nipping interaction (Table 3). Average seed yield plant^{-1} among genotypes ranged from 8.59 g to 34.26 g. Un-nipped treatment exhibited maximum (35.18 g) seed yield plant^{-1} for NKC-5-S-15 and minimum (7.29 g) for NDC-4-20-3. Maximum seed yield plant^{-1} under nipped treatment was recorded for SL-5-53 (33.62 g) followed by Karak 1 (32.47 g) and minimum (9.38 g) for genotype NDC-5-1 (Table 5). Yield is the result of many contributing traits like secondary branches, pods plant^{-1}, 100-seed weight, etc. Overall, the yield of un-nipped treatment was higher (21.56 g) than the nipped treatment (20.19 g). Percent change showed increase in yield of eight chickpea genotypes (NIFA-2005, Karak-2, SL-3-15, SL-3-64, NDC-15-1, NDC-4-20-3, Karak-1 and NKC-5-S-12) among twenty (Fig. 3). It indicated that the lateral dominance is triggered by decapitating the shoot apical meristem or artificially decreasing the concentration of auxin in plant tissues which results in an increase of secondary branches and pods plant^{-1} (Elizabeth et al., 2006). Our results are supported by Gul et al. (2014) who observed highly significant differences among chickpea genotypes. Moreover, Khan et al. (1997) reported increase in yield as a result of grazing in chickpea.

Correlation: Information on association between yield and its various components provides basis for selecting improved varieties. Secondary branches plant^{-1} showed highly significant and positive phenotypic and genotypic correlation with pods plant^{-1} (r_g = 0.56, r_p = 57), biological yield plant^{-1}(r_g = 0.51, r_p = 0.42) and seed yield plant^{-1} (r_g = 54, r_p = 0.46). Highly significant positive phenotypic and significant positive genotypic correlation of secondary branches plant^{-1} was recorded with seeds pod^{-1} (r_g = 0.35, r_p = 0.28), while its positive genotypic and non-significant but positive phenotypic correlation was recorded with 100-seed weight (r_g = 0.34, r_p = 0.17) (Table 6). Habibpour *et al*. (2012) also reported non-significant correlation of secondary branches plant^{-1} with 100-seed weight in chickpea. Pods plant^{-1} showed highly significant and positive genotypic as well as phenotypic correlation with seeds pod^{-1} (r_g = 0.46, r_p = 0.38), biological yield plant^{-1} (r_g = 0.86, r_p = 0.77) and seed yield plant^{-1} (r_g = 0.89, r_p = 0.83). Seeds pod^{-1} showed negative but non-significant phenotypic and genotypic correlation with 100-seed weight (r_g = -0.15, r_p = -0.09), whereas its correlation with biological yield plant^{-1} (r_g = 0.60, r_p = 0.52) and seed yield plant^{-1} (r_g = 0.58, r_p = 0.54) was highly significant and positive at both genotypic as well as phenotypic levels. Biological yield plant^{-1} revealed highly significant positive genotypic and phenotypic correlation with seed yield plant^{-1} (r_g = 0.97, r_p = 92) and 100-seed weight (r_g = 0.44, r_p = 0.50) (Table 13). Qureshi *et al*. (2004) also reported positive and highly significant correlation of biological yield plant^{-1} with 100-seed weight in chickpea. 100-seed weight showed highly significant positive genotypic and phenotypic correlation with seed yield plant^{-1} (r_g = 0.52, r_p = 0.53). Noor *et al*. (2003) also reported similar results, and observed significant correlation of 100-seed weight with seed yield and biological yield plant^{-1}.

Strong positive genotypic as well as phenotypic correlation of the studied traits with seed yield suggested that enhancement of seed yield in chickpea is primarily associated with these characters and selection of these traits could have good impact on grain yield plant^{-1} of chickpea. Anita *et al*. (2012) also found highly significant positive correlation of seed yield with pods plant^{-1}, seeds plant^{-1}, biological yield plant^{-1} and 100-seed weight in chickpea, while Bakhsh *et al*. (1998) found significant correlation of seed yield with pods plant^{-1} and 100-seed weight. Majid *et al*. (1982) also recorded highly significant correlation of seed yield with pods plant^{-1} in chickpea.

Table 1. List of 20 chickpea genotypes along with their group and source.

Genotypes	Group	Source	Genotypes	Group	Source
NKC-10-99	Kabuli	ICARDA/Syria	NDC-15-1	Desi	NIFA/Pakistan
NKC-5-S-12	Kabuli	ICARDA/Syria	NDC-4-20-3	Desi	NIFA/Pakistan
NKC-5-S-14	Kabuli	ICARDA/Syria	NDC-4-20-4	Desi	NIFA/Pakistan
NKC-5-S-24	Kabuli	ICARDA/Syria	NIFA-2005	Desi	NIFA/Pakistan
NKC-5-S-20	Kabuli	ICARDA/Syria	SL-3-15	Desi	Karak/Pakistan
NKC-5-S-17	Kabuli	ICARDA/Syria	Karak-1	Desi	Karak/Pakistan
NKC-5-S-16	Kabuli	ICARDA/Syria	Karak-2	Desi	Karak/Pakistan
NKC-5-S-15	Kabuli	ICARDA/Syria	Karak-3	Desi	Karak/Pakistan
ICC-19183	Kabuli	ICRISAT/India	SL-3-64	Desi	Karak/Pakistan
NDC-4-20-2	Desi	NIFA/Pakistan	SL-5-53	Desi	Karak/Pakistan

Table 2. Mean squares of Secondary branches plant^{-1}, pods plant^{-1} and seeds pod^{-1}of 20 chickpea genotypes evaluated under un-nipped and nipped treatment.

Source	Degree of Freedom	Sec. Br. Plant^{-1}	Pods plant^{-1}	Seeds Pod^{-1}
Replication	2	0.20	3.18	0.08
Genotypes	19	24.04**	1073.62**	0.23**
Error-A	38	2.64	20.36	0.02
Treatments	1	31.98**	480.40**	0.76**
G × T	19	15.36**	248.84**	0.03^{ns}
Error-B	40	1.87	12.45	0.02

NS = non-significant; *, ** = Significant at 5 and 1% level of probability, respectively

Table 3. Mean squares of biological yield plant^{-1}, 100-seed weight, and seed yield plant^{-1} of 20 chickpea genotypes evaluated under un-nipped and nipped treatment.

Source	Degree of Freedom	Bio. yield Plant^{-1}	100 seed weight^{-1}	Seeds yield Plant^{-1}
Replication	2	0.36	7.55	0.25
Genotypes	19	1201.96**	93.26**	373.59**
Error-A	38	11.81	6.97	4.40
Treatments	1	339.47**	15.40*	47.63**
G× T	19	102.29**	2.86^{ns}	25.30**
Error-B	40	13.13	3.16	4.29

NS = non-significant; *, ** = Significant at 5 and 1% level of probability, respectively

Table 4. Mean values for secondary branches plant^{-1}, pods plant^{-1} and number of Seed pod^{-1} of 20 chickpea genotypes evaluated under nipped and control environment.

Genotypes	Secondary branches plant^{-1}			Number of Pods plant^{1}			Number of Seed pod^{-1}		
Kabuli Genotype	Control	Nipping	Mean	Control	Nipping	Mean	Control	Nipping	Mean
NKC-10-99 (K)	9.17	7.83	8.50	65.00	64.33	64.67	1.33	1.30	1.32
NKC-5-S-14 (K)	9.23	10.07	9.65	57.33	60.00	58.67	1.63	1.40	1.52
ICC-19183 (K)	10.10	7.83	8.97	74.53	55.23	64.88	1.30	1.20	1.25
NKC-5-S-20 (K)	13.40	10.67	12.03	67.87	61.57	64.72	1.43	1.30	1.37
NKC-5-S-16 (K)	12.60	10.40	11.50	59.00	51.67	55.33	1.60	1.47	1.53
NKC-5-S-15 (K)	11.47	10.60	11.03	65.00	60.50	62.75	1.60	1.27	1.43
NKC-5-S-17 (K)	10.07	9.00	9.53	72.87	67.00	69.93	1.20	1.23	1.22
NKC-5-S-24 (K)	12.13	12.93	12.53	61.80	60.67	61.23	1.37	1.23	1.30
NKC-5-S-12 (K)	12.00	13.67	12.83	54.33	73.00	63.67	1.30	1.23	1.27
Desi Genotype	Control	Nipping	Mean	Control	Nipping	Mean	Control	Nipping	Mean
NIFA-2005 (D)	10.47	13.67	12.07	41.57	74.33	57.95	1.23	1.07	1.15
Karak-2 (D)	7.93	13.48	10.71	50.07	65.67	57.87	1.30	1.20	1.25
SL-3-15 (D)	11.07	10.33	10.70	35.85	45.80	40.83	1.23	1.03	1.13

NDC-4-20-4 (D)	8.33	9.73	9.03	64.73	52.00	58.37	1.27	1.10	1.18
SL-3-64 (D)	9.40	11.53	10.47	39.47	59.33	49.40	1.87	1.13	1.50
NDC-15-1 (D)	5.80	6.10	5.95	32.37	38.47	35.42	1.10	1.03	1.07
NDC-4-20-3 (D)	7.93	8.53	8.23	28.58	41.67	35.13	1.17	1.03	1.10
NDC-4-20-2 (D)	7.33	7.40	7.37	43.20	39.40	41.30	1.17	1.03	1.10
SL-5-53 (D)	11.53	12.07	11.80	81.87	77.33	79.60	1.57	1.40	1.48
Karak-1 (D)	7.60	19.03	13.32	72.17	86.00	79.08	1.87	1.77	1.82
Karak-3 (D)	11.07	14.40	12.73	73.00	86.67	79.83	1.67	1.57	1.62
Overall Mean	9.93	10.96		57.03	61.03		1.41	1.25	
LSD (0.05) for G = 1.90		LSD (0.05) for G = 5.27			LSD (0.05) for G = 0.18				
LSD (0.05) for T = 0.50		LSD (0.05) for T = 1.30			LSD (0.05) for T = 0.05				
LSD (0.05) for G x T = 2.48		LSD (0.05) for G x T = 6.69			LSD (0.05) for G x T = 3.44				

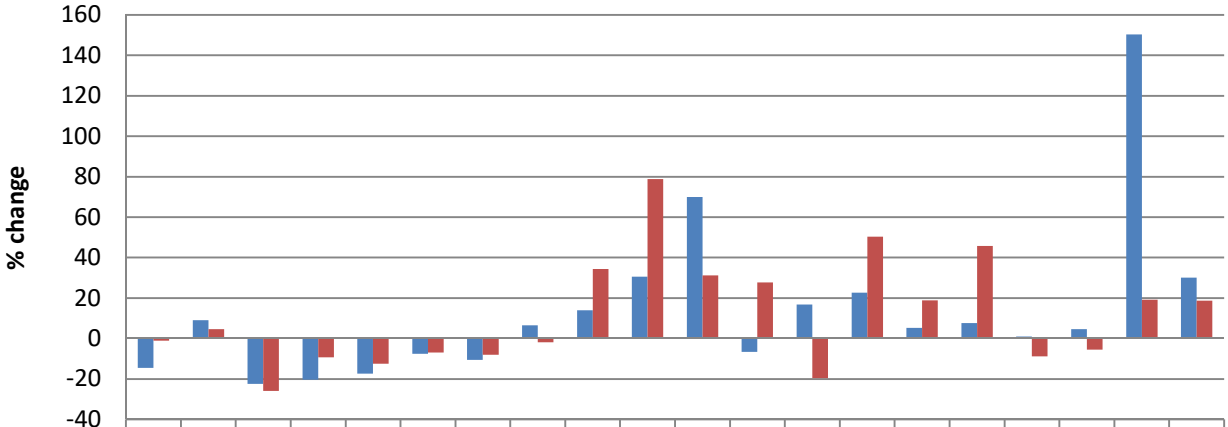
Table 5. Mean values for 100-seed weight, biological yield plant^{-1}, and seed yield plant^{-1} of 20 chickpea genotypes evaluated under un-nipped and nipped treatment.

Genotypes	**100-seed weight (g)**			**Biological yield plant^{1} (g)**			**Seed yield plant (g)**		
Desi Genotype	**Control**	**Nipping**	**Mean**	**Control**	**Nipping**	**Mean**	**Control**	**Nipping**	**Mean**
NKC-10-99 (K)	25.33	25.33	25.33	57	45.67	51.33	25.12	22.22	23.67
NKC-5-S-14 (K)	25.33	27.67	26.50	56.67	57.31	56.99	26.67	23.14	24.90
ICC-19183 (K)	24.33	24.00	24.17	45.67	38.46	42.06	23.68	15.78	19.73
NKC-5-S-20 (K)	28.33	28.33	28.33	66.67	51.52	59.10	27.36	22.30	24.83
NKC-5-S-16 (K)	24.33	25.00	24.67	52.33	51.25	51.79	22.81	18.69	20.75
NKC-5-S-15 (K)	32.33	33.33	32.83	74.33	53.67	64.00	35.18	25.53	30.35
NKC-5-S-17 (K)	28.33	29.33	28.83	52.35	45.01	48.68	23.72	20.81	22.26
NKC-5-S-24 (K)	30.67	31.00	30.83	54.67	56.67	55.67	23.03	27.00	25.02
NKC-5-S-12 (K)	35.33	35.00	34.17	71.77	53.33	62.55	30.67	29.08	29.87
Kabuli Genotype	Control	Nipping	Mean	Control	Nipping	Mean	Control	Nipping	Mean
NIFA-2005 (D)	23.33	22.67	23.00	29.04	34.89	31.96	11.99	16.00	14.00
Karak-2 (D)	19.67	19.67	19.67	37.34	45.62	41.48	12.72	15.53	14.12
SL-3-15 (D)	27.33	29.67	28.50	32.21	40.95	36.58	12.01	14.18	13.09
NDC-4-20-4 (D)	24.33	24.67	24.50	47.90	42.67	45.28	19.98	13.97	16.98
SL-3-64 (D)	18.67	22.00	20.33	39.47	40.82	40.14	14.00	14.60	14.30
NDC-15-1 (D)	24.00	23.33	23.67	22.21	24.40	23.30	8.64	9.38	9.01
NDC-4-20-3 (D)	21.67	22.33	22.00	22.12	24.18	23.15	7.29	9.89	8.59
NDC-4-20-2 (D)	25.33	23.67	24.50	33.34	25.70	29.52	12.80	9.83	11.32
SL-5-53 (D)	27.33	29.33	28.33	72.49	70.44	71.47	34.89	33.62	34.26
Karak-1 (D)	20.33	23.33	21.83	61.47	65.33	63.53	27.74	32.47	30.10
Karak-3 (D)	24.67	23.33	24.00	65.00	58.33	61.67	31.07	29.97	30.52
Overall Mean	25.54	26.14		49.70	46.31		21.56	20.19	
LSD (0.05) for G = 3.08		LSD (0.05) for G = 4.01			LSD (0.05) for G = 2.45				
LSD (0.05) for T = 0.65		LSD (0.05) for T = 0.76			LSD (0.05) for T = 1.33				
LSD (0.05) for G x T = ns		LSD (0.05) for G x T = 3.44			LSD (0.05) for G x T = 5.83				

Table 6. Genotypic (above diagonal) and phenotypic (below diagonal) correlation among various traits of 20 chickpea genotypes

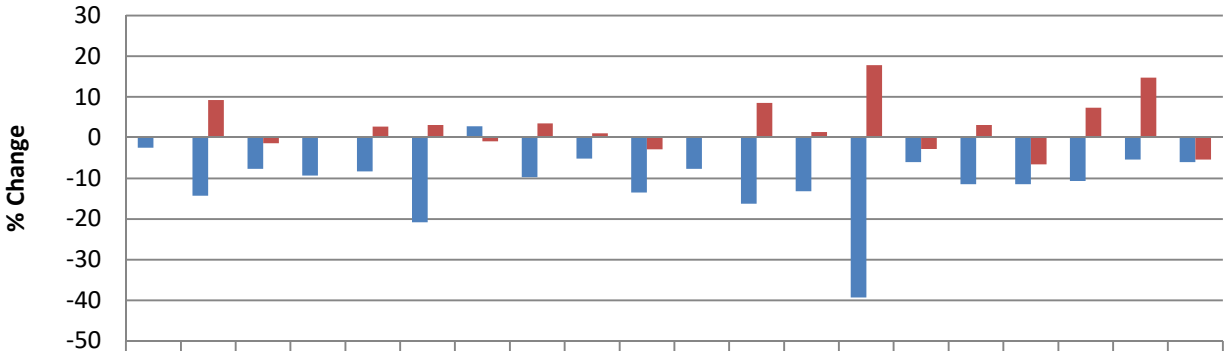
Traits	**Sec. Br. plant^{-1}**	**Pods plant^{-1}**	**Seeds pod^{-1}**	**100-seed wt**	**Bio. Yield pl^{-1}**	**Seed yield pl^{-1}**
Sec. Br. plant^{-1}	-	0.56**	0.35**	0.34**	0.51**	0.54**
Pods plant^{-1}	0.57**	-	0.46**	0.31	0.86**	0.89**
Seeds pod^{-1}	0.28**	0.38**	-	-0.15	0.60**	0.58**
100-seed wt	0.17	0.25**	-0.09	-	0.50**	0.53**
Bio.Yield pl^{-1}	0.42**	0.77**	0.52**	0.44**	-	0.97**
Seed yield pl^{-1}	0.46**	0.83**	0.54**	0.52**	0.92**	-

Fig. 1: % change in Secondry branches per plant (series 1) and pods per plant (series 2)

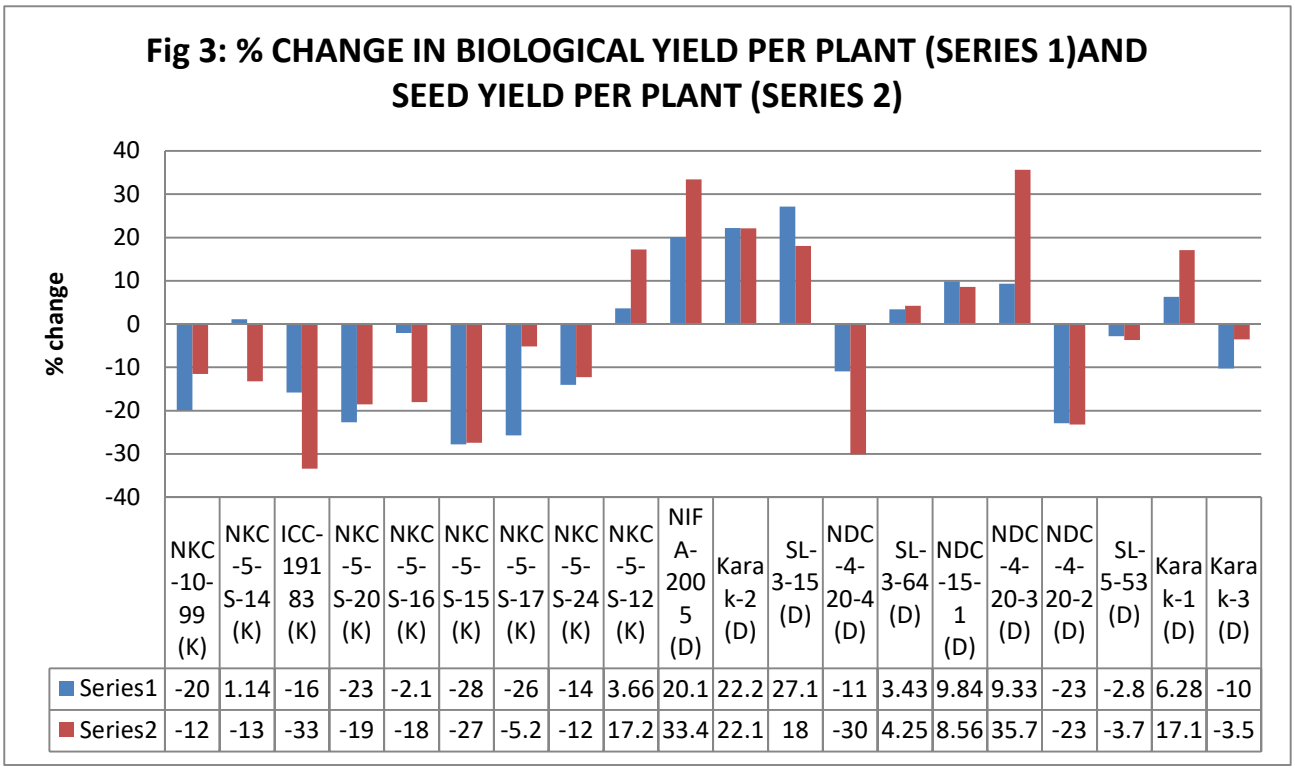


	NKC-10-99 (K)	NKC-5-S-14 (K)	ICC-19183 (K)	NKC-5-S-20 (K)	NKC-5-S-16 (K)	NKC-5-S-15 (K)	NKC-5-S-17 (K)	NKC-5-S-24 (K)	NKC-5-S-12 (K)	NIFA-2005 (D)	Karak-2 (D)	SL-3-15 (D)	NDC-4-20-4 (D)	SL-3-64 (D)	NDC-15-1 (D)	NDC-4-20-3 (D)	NDC-4-20-2 (D)	SL-5-53 (D)	Karak-1 (D)	Karak-3 (D)
Series1	-15	9.03	-22	-20	-17	-7.6	-11	6.59	13.9	30.6	70	-6.6	16.8	22.7	5.17	7.56	0.91	4.62	150	30.1
Series2	-1	4.65	-26	-9.3	-12	-6.9	-8.1	-1.8	34.4	78.8	31.2	27.8	-20	50.3	18.9	45.8	-8.8	-5.5	19.2	18.7

Fig 2: % change in seeds per pod (series 1) and 100 seed weight (series 2)



	NKC-10-99 (K)	NKC-5-S-14 (K)	ICC-19183 (K)	NKC-5-S-20 (K)	NKC-5-S-16 (K)	NKC-5-S-15 (K)	NKC-5-S-17 (K)	NKC-5-S-24 (K)	NKC-5-S-12 (K)	NIFA-2005 (D)	Karak-2 (D)	SL-3-15 (D)	NDC-4-20-4 (D)	SL-3-64 (D)	NDC-15-1 (D)	NDC-4-20-3 (D)	NDC-4-20-2 (D)	SL-5-53 (D)	Karak-1 (D)	Karak-3 (D)
Series1	-2.5	-14	-7.7	-9.3	-8.3	-21	2.78	-9.8	-5.1	-14	-7.7	-16	-13	-39	-6.1	-11	-11	-11	-5.4	-6
Series2	-0	9.21	-1.4	0	2.74	3.09	-0.9	3.53	1.09	-2.9	0	8.54	1.37	17.9	-2.8	3.08	-6.6	7.32	14.8	-5.4



	NKC-10-99 (K)	NKC-5-S-14 (K)	ICC-19183 (K)	NKC-5-S-20 (K)	NKC-5-S-16 (K)	NKC-5-S-15 (K)	NKC-5-S-17 (K)	NKC-5-S-24 (K)	NKC-5-S-12 (K)	NIFA-2005 (D)	Karak-2 (D)	SL-3-15 (D)	NDC-4-20-4 (D)	SL-3-64 (D)	NDC-15-1 (D)	NDC-4-20-3 (D)	NDC-4-20-2 (D)	SL-5-53 (D)	Karak-1 (D)	Karak-3 (D)
Series1	-20	1.14	-16	-23	-2.1	-28	-26	-14	3.66	20.1	22.2	27.1	-11	3.43	9.84	9.33	-23	-2.8	6.28	-10
Series2	-12	-13	-33	-19	-18	-27	-5.2	-12	17.2	33.4	22.1	18	-30	4.25	8.56	35.7	-23	-3.7	17.1	-3.5

Conclusions: The present investigations concluded that there is highly significant interaction between chickpea genotypes and nipping which indicated that, different genotypes of chickpea reacted in a different way to nipping. The interaction of most of the studied genotypes, specifically the Kabuli types of chickpea either showed no response or affected negatively by nipping. Therefore, nipping should only be practiced in tested genotypes/verities which showed positive response to nipping, while it should be avoided in those genotypes which reveal negative response to nipping. In the present study yield of only eight genotypes viz. NIFA-2005, Karak-2, SL-3-15, SL-3-64, NDC-15-1, NDC-4-20-3, Karak-1 and NKC-5-S-12 was increased with nipping which provide green forage at same time when there is scarcity of forage in the months of winter. So these genotypes could be recommended for growing in areas where there is shortage of fodder, furthermore these genotypes might also play imperative role in chickpea improvement. Highly significant and positive genotypic correlation between yield related traits showed that these parameters can be used as selection criteria in future chickpea breeding program.

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