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Assessment of genetic variability, heritability, character association and selection indexes in chickpea (*Cicer arietinum* L.)

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Abstract

An experiment was carried out to assess the nature and extent of genetic variability, heritability, genetic advance, correlation coefficient, path coefficient and construct the selection index in the material. The experiment was set up during the four consecutive robi seasons of 2009-2010, to 2012-2013 at the Botanical Research Field, University of Rajshahi, Rajshahi-6205, Bangladesh and thirteen yield and yield components of eight genotypes of chickpea have been considered. The analysis of variance showed significant differences among genotypes for all the studied characters. The highest phenotypic variation was observed for NPd/P followed by NS/P and PWH. The highest GCV with high PCV were found for NS/P and NPd/P. The heritability (h^2_b), genetic advance (GA) and genetic advance as percentage of mean (GA %) were found to be low for most of the characters. Yield per plant exhibited positive association with NPBFF, NPBMF, NPd/P, PdW/P and NS/P both at genotypic and phenotypic levels. In the analysis of descriminant function, NPBFF and NPBMF gave the highest expected genetic gain. Since these two traits exhibited highest genetic gain in the combination of selection index and showed positive correlation with SW/P both at both levels hence considered as primary yield component.

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Introduction

Food legumes are the important source of good quality protein in the diets of people and are valuable as animal feed. Legumes also increase and sustain the productivity of the soil by reducing chance of build-up of diseases, insect pests and obnoxious weeds in rotation with cereals (Zali *et al.*, 2011). Pulse crops (food legumes) are the second most planted crops in Bangladesh after rice, reflecting the importance of pulses as a source of protein in Bangladeshi diets. Among the cultivated winter pulses in Bangladesh, chickpea with 17-24% protein, 41-50.8% carbohydrates and high percentage of other mineral nutrients and unsaturated linloeic and oliec acid is one of the most important crops for human consumption. Unfortunately despite its nutritional values, the average yield of chickpea is relatively low in Bangladesh. To improve the yield of this crop, plant breeders are continuously engaged to meet up the demands of an ever increasing population.

The magnitude of genetic variability is a precondition for chickpea breeding program, which provides opportunity to a plant breeder or researcher for selecting high yielding genotypes. The estimates of genotypic and phenotypic variances as well as coefficient of variation provide information on the extent of variability.

Several researchers such as Sarker *et al.* (2013) and Zeeshan *et al.* (2013) have emphasized the utility of the estimates of genetic variability in chickpea. But genetic variability is uninformative for heritable portion of this variation. Knowledge on the heritability together with genetic advance is important to a plant breeder since it indicates the possibility and extent to which improvement is possible through selection. it is recognized that the yield is affected by many genetic as well as environmental factors. Under such situation, the path coefficient analysis is more helpful than simple correlation to determine the direct contribution of these characters and their indirect contribution via other characters (Singh *et al.*, 1990). Correlation coefficient and path coefficient analysis of various characters on yield and yield components have been reported by several researchers such as Jivani *et al.* (2013), Mushtaq *et al.* (2013) and Zeeshan *et al.* (2013).

However, the information on the nature and extent of genetic variability present in a population for desirable character, their association and relative contribution to yield comprise the basic requirement of selection desirable genotypes but the discriminant function provides an efficient method for simultaneous selection (Smith, 1936). Thus construction of selection indices will be very helpful to differentiate desirable genotypes. This method has been successfully followed by various scientists in different crops such as Deb and Khaleque (2007) in chickpea, Sarker and Deb (2009) in blackgram and Sarker *et al.* (2013) in chickpea.

The present investigation was therefore, undertaken to assess the magnitude of genetic variability, heritability and genetic advance to determine the nature and magnitude of correlations among different traits and their direct and indirect effect on seed yield and construction of selection indices in chickpea. Therefore, the available information will be helpful for an efficient selection criterion in selecting the most desirable and high yielding genotype of chickpea.

Materials and methods

A. Materials

The materials for the present study comprised eight genotypes of chickpea viz., BARI chola-1, BARI chola-2 BARI chola-3 BARI chola-4 BARI chola-5 BARI chola-6 BARI chola-7and BARI chola-8. The materials were collected from Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh.

B. Methods

(i) Experimental field: The experiment was set in the botanical research field behind the third science building, University of Rajshahi, during the consecutive four *rabi* crop seasons of 2009-2010, 2010-2011, 2011-2012 and 2012-2013. Lay-out of the experimental field considering randomized complete block design with three replications. Each replication having eight plots.

Each plot contains five rows and per row having five hills. In each hill, single plant was maintained. Gap between replications, plots, rows and hills were 120 cm, 80 cm, 45cm and 45cm, respectively.

Collection of data:

Thirteen yield and yield contributing characters viz., date of first flower (DFF), plant height at first flower (PHFF), number of primary branches at first flower (NPBFF), number of secondary branches at first flower (NSBFF), date of maximum flower (DMF), plant height at maximum flower (PHMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight at harvest (PWH), number of pods per plant (NPd/P), pod weight per plant (PdW/P), number of seeds per plant (NS/P) and seed weight per plant (SW/P) were considered for the present investigation.

Techniqus of analysis of data:

Data were recorded on individual plant basis and analyzed following the biometrical techniques of analysis as developed by Mather (1949a) based on the mathematical models of Fisher *et al.* (1932). Heritability (in broad sense) estimates was computed as suggested by Warner (1952), genetic advance was calculated by the following formula as suggested by Lush (1949), the path coefficient analysis was done by using Wright's (1921 and 1923) formula as was extended by Dewey and Lu (1959).

The coefficients b_1, b_2,............b_n used in the discriminant function technique were obtained from the genotypic and phenotypic variances and covariances by solving the following equations of an index simultaneously. Similar equations were set up for each index and the values obtained for b_1, b_2, ...b_n were used in the discriminant function selection technique.

$$b_1P_{11} + b_2P_{12} + \ldots\ldots\ldots\ldots\ldots\ldots + b_nP_{1n} = G_{1y}$$
$$b_1P_{12} + b_2P_{22} + \ldots\ldots\ldots\ldots\ldots\ldots + b_nP_{2n} = G_{2y}$$
$$b_1P_{1n} + b_2P_{2n} + \ldots\ldots\ldots\ldots\ldots\ldots + b_nP_{nn} = G_{ny}$$

Where,

P_{11} = an estimate of the phenotypic variance of character 1

P_{12} = an estimate of phenotypic covariance of characters 1 and 2

G_{1y}, G_{2y}, G_{3y}......ny = an estimate of genotypic covariance of character 1 and yield (seed weight per plant), etc.

The phenotypic and genotypic variances and covariances as obtained were used for constructing discriminant functions using different character combinations according to the method developed by Fisher (1936) and Smith (1936). Later on, Hazel (1943) developed a simultaneous selection model following path analysis approach. Since then, the theory of selection index has been extended and modified in various ways by various authors to suit the requirements of practical breeders (Robinson *et al.*, 1951; Singh, 1972). The expected genetic advance from strait selection [GA (S)] and from the dicriminant function [GA (D)] was calculated as follows:

$$GA(S) = \frac{Z}{P}\left(\frac{g_{yy}}{\sqrt{t_{yy}}}\right) \text{ and}$$

$$GA(D) = \frac{Z}{P}\sqrt{\left(b_1 g_{1y} + b_2 g_{2y} + \ldots\ldots + b_n g_{ny}\right)}$$

Where,

$\frac{Z}{P}$ = selection differential in standard units, for the present study it was 2.06 at 5% level of selection (Lush, 1949)

G_{yy} and t_{yy} = genotypic and phenotypic variances of the character y

b_1, b_2,..........b_n = relative weight for each character

G_{1y}, G_{2y}...G_{ny} = genetic covariances of independent characters with y.

The expected gain from the discriminant function over strait selection was calculated for all the functions and studied as follows:

Expected gain (%) = [{GA (D)/ GA(S)}-1] × 100

Results

Variability

The results of the analysis of variance for all the quantitative characters were presented in Table 1. For this investigation a mixed model was followed for testing the main items and their interaction. Item genotype was highly significant for all the traits and item year found to be highly significant for all the traits except DMF. Components of variation, Coefficient of variability, Heritability in broad sense (h^2_b), genetic advance and genetic advance as percentage of mean were estimates for all the traits and presented in Table 2. Phenotypic variation was greater than those of σ^2_G, $\sigma^2_{G\times Y}$ and σ^2_E components of variation for all the characters as expected. The highest phenotypic variation was found for NPd/P with a value of 1413.361 while the lowest recorded for NPBFF with a value of 0.290.

The highest σ^2_G recorded for NS/P with a value of 499.591 while the lowest noted for NPBFF with a value of 0.047. Phenotypic coefficient of variability was found greater than genotypic and error coefficient of variability which was expected for all the traits. The height PCV was found for the trait NPd/P with a value of 1163.243 while the lowest was found for DMF with a value of 5.844. The values of 389.340 and 1.148 noted as the highest and the lowest genotypic coefficient of variability for NS/P and NSBMF, respectively. Perusal the Table 2, the highest h^2_b was found for DMF with a value of 71.237 followed by PHFF (62.799) and DFF (60.685) while, the lowest was found for PdW/P (6.152). Again, genetic advance of the trait NS/P was found to be the highest with a value of 28.294 while the lowest was found for NSBMF with a value of 0.163.

The traits NS/P and NSBMF showed the highest and the lowest GA % of 22.050 and 2.190, respectively.

Table 1. Analysis of variances among genotypes and its interaction with year for thirteen characters in chickpea.

Source	df	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
Replication (R)	2	14.238	12.500	0.124	0.034	4.714	18.155	0.130	1.906	129.011	771.246	6.008	503.006	12.372
Genotype (G)	7	273.860	195.487	0.961	1.545	52.306	77.222	1.020	2.897	663.597	7221.873	98.581	7528.231	82.480
Year (Y)	3	228.868	39.520	34.275	23.027	1.296	76.777	33.343	14.230	1553.936	23498.795	744.696	17090.423	463.828
G×Y	21	24.473	15.235	0.403	0.607	2.829	18.175	0.362	1.870	369.985	1676.033	67.262	1533.145	41.540
Within Error	62	7.959	5.730	0.163	0.227	1.083	9.342	0.289	0.685	190.287	588.795	26.094	468.543	15.875

* = significant at 5% level, ** = significant at 1% level and ^{NS} = non-significant

Table 2. Phenotypic (σ^2_P), genotypic (σ^2_G), interaction ($\sigma^2_{G\times Y}$), within error (σ^2_E) components of variation, phenotypic (PCV), genotypic (GCV) coefficient of variability, heritability in broad sense (h^2_b), genetic advance (GA) and genetic advance as percent of mean (GA%) for thirteen characters in chickpea.

Character	σ^2_P	σ^2_G	$\sigma^2_{G\times Y}$	σ^2_E	PCV	GCV	h^2_b in%	GA	GA%
DFF	34.246	20.782	5.504	7.959	42.723	25.926	60.685	7.316	9.126
PHFF	23.919	15.021	3.168	5.730	66.871	41.994	62.799	6.327	17.688
NPBFF	0.290	0.047	0.080	0.163	9.903	1.591	16.062	0.178	6.088
NSBFF	0.432	0.078	0.127	0.227	14.980	2.711	18.099	0.245	8.500
DMF	5.788	4.123	0.582	1.083	5.844	4.163	71.237	3.530	3.565
PHMF	17.207	4.921	2.944	9.342	34.665	9.913	28.596	2.444	4.923
NPBMF	0.368	0.055	0.024	0.289	8.677	1.292	14.893	0.186	4.387
NSBMF	1.165	0.086	0.395	0.685	15.631	1.148	7.343	0.163	2.190
PWH	274.654	24.468	59.899	190.287	303.414	27.030	8.909	3.041	3.360
NPd/P	1413.361	462.153	362.413	588.795	1163.243	380.368	32.699	25.324	20.842
PdW/P	42.426	2.610	13.723	26.094	131.690	8.101	6.152	0.825	2.562
NS/P	1323.001	499.591	354.867	468.543	1031.038	389.340	37.762	28.294	22.050
SW/P	27.842	3.412	8.555	15.875	114.588	14.041	12.254	1.332	5.482

Correlation coefficient

The correlation coefficient between pairs of characters was computed both at phenotypic and genotypic levels and are presented in Table 3 and 4 respectively. In the present investigation, correlation study showed that the most of character pairs both of genotypic and phenotypic associations were in same direction and genotypic correlation value was greater than respective phenotypic ones. NPd/P, PdW/P and NS/P exhibited significant correlation with SW/P at both levels. Traits viz., NPBFF and NPBMF showed significant positive association with SW/P at genotypic level only.

Among the yield contributing traits, DFF showed positive correlation with PHFF, DMF, PHMF, PWH, NPd/P and NS/P both at genotypic and phenotypic levels. Positive correlation of PHFF was observed with DFF, NPBFF, DMF, PHMF, PWH, NPd/P and NS/P at both levels. Character NPBFF showed positive and significant correlation with PHFF, DMF, PWH, NPd/P, PdW/P and NS/P at genotypic level while, with PHFF, NSBFF and DMF at phenotypic level. The trait NSBFF exhibited significant and positive correlation with NSBMF and NS/P at genotypic level while with NPBFF and NSBMF at phenotypic level. On the other hand, negative genotypic correlation with this trait was exhibited by DFF, PHFF, NPBFF, PHMF, NPBMF and PdW/P. Again, at phenotypic level, NSBFF exhibited negative correlation with DFF, PHFF, PHMF, PWH and PdW/P. Ttraits DMF had positive and significant association with DFF, PHFF, NPBFF, PHMF and NS/P at both levels. The trait PHMF exhibited positive and significant correlation with DFF, PHFF, DMF and PWH at genotypic level while, with DFF, PHFF and DMF at phenotypic level. Character NPBMF had significant and positive genotypic correlation with NSBMF, NPd/P, PdW/P and NS/P while, it had positive but non-significant association with NPBFF at genotypic level. NSBMF had positive and significant correlation with NSBFF and NPBMF at genotypic level while, with NSBFF at phenotypic level. Positive and significant correlation showed by PWH with DFF, PHFF, NPBFF, DMF and PHMF at genotypic level while, with DFF at phenotypic level. PWH negatively associated with NPBMF, NSBMF, NPd/P, PdW/P and NS/P at genotypic level. The trait NPd/P showed positive and significant association with DFF, PHFF, NPBFF, DMF, NPBMF and NS/P at genotypic level. Positive and significant correlation was exhibited by PdW/P with NPBFF and NPBMF at genotypic level and with NPd/P and NS/P at phenotypic level. NS/P had positive and significant association with DFF, PHFF, NPBFF, NSBFF, DMF, NPBMF and NPd/P at genotypic level while, with DMF, NPd/P and PdW/P at phenotypic level.

Table 3. Genotypic (r_g) correlation coefficients between yield and yield contributing characters in chickpea.

Character	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
DFF	0.9111^{**}	-0.3692^{**}	-0.7813^{**}	0.9074^{**}	0.7414^{**}	-0.3692^{**}	-0.7813^{**}	1.0193^{**}	0.5371^{**}	-0.2118^{*}	0.5278^{**}	-0.3065^{**}
PHFF		0.2801^{**}	-0.2150^{*}	1.0041^{**}	1.0104^{**}	-0.4643^{**}	-0.4883^{**}	0.8286^{**}	0.3374^{**}	-0.7886^{**}	0.3257^{**}	-0.6565^{**}
NPBFF			-0.0857^{NS}	0.4015^{**}	0.0840^{NS}	0.1303^{NS}	-0.7447^{**}	1.3917^{**}	0.8545^{**}	0.7067^{**}	0.8974^{**}	0.5483^{**}
NSBFF				0.0867^{NS}	-0.1005^{NS}	-0.4626^{**}	0.6856^{**}	0.1026^{NS}	0.4024^{NS}	-0.9067^{**}	0.2864^{**}	-0.4632^{**}
DMF					0.9779^{**}	-0.3947^{**}	-0.3909^{**}	0.9489^{**}	0.4963^{**}	-0.9980^{**}	0.4590^{**}	-0.7263^{**}
PHMF						-0.5860^{**}	-0.6910^{**}	0.7430^{**}	0.0042^{NS}	-1.2284^{**}	-0.0020^{NS}	-1.0915^{**}
NPBMF							1.0867^{**}	-0.4930^{**}	0.7977^{**}	1.1047^{**}	0.8119^{**}	1.0673^{**}
NSBMF								-0.3638^{**}	0.1469^{NS}	-1.2831^{**}	0.1281^{NS}	-0.3862^{**}
PWH									-0.4089^{**}	-1.3810^{**}	-0.3438^{**}	-0.9923^{**}
NPd/P										-0.1796^{NS}	0.9941^{**}	0.2047^{*}
PdW/P											-0.0302^{NS}	0.9406^{**}
NS/P												0.3373^{**}

* = Significant at 5% level

** = Significant at 1% level

^{NS} = Non-significant.

Table 4. Phenotypic (r_p) correlation coefficients between yield and yield contributing characters in chickpea.

Character	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P	SW/P
DFF	0.6143^{**}	-0.0170^{NS}	-0.2466^{*}	0.5984^{**}	0.3375^{**}	-0.0170^{NS}	-0.2466^{*}	0.2485^{*}	0.1653^{NS}	-0.1475^{NS}	0.1871^{NS}	-0.1572^{NS}
PHFF		0.2488^{*}	-0.0332^{NS}	0.7396^{**}	0.5252^{**}	-0.0957^{NS}	-0.1474^{NS}	0.1320^{NS}	0.1284^{NS}	-0.1018^{NS}	0.1594^{NS}	-0.1239^{NS}
NPBFF			0.3248^{**}	0.2844^{**}	0.1715^{NS}	0.0482^{NS}	-0.0089^{NS}	-0.0036^{NS}	0.1510^{NS}	0.0060^{NS}	0.1742^{NS}	0.1145^{NS}
NSBFF				0.0353^{NS}	-0.1229^{NS}	0.1552^{NS}	0.2404^{*}	-0.1921^{NS}	0.0591^{NS}	-0.2418^{*}	0.0324^{NS}	-0.1562^{NS}
DMF					0.4774^{**}	-0.1655^{NS}	-0.0627^{NS}	0.1265^{NS}	0.1861^{NS}	-0.2033^{*}	0.2015^{*}	-0.1842^{NS}
PHMF						-0.1735^{NS}	-0.1753^{NS}	0.1339^{NS}	0.0964^{NS}	-0.0728^{NS}	0.0523^{NS}	-0.1252^{NS}
NPBMF							0.1996^{NS}	0.0046^{NS}	0.0309^{NS}	0.0435^{NS}	0.0831^{NS}	0.0314^{NS}
NSBMF								-0.0508^{NS}	0.1532^{NS}	0.0828^{NS}	0.1520^{NS}	0.1718^{NS}
PWH									0.0812^{NS}	0.1374^{NS}	0.0949^{NS}	0.0806^{NS}
NPd/P										0.3417^{**}	0.9758^{**}	0.3753^{**}
PdW/P											0.3829^{**}	0.8538^{**}
NS/P												0.4369^{**}

* = Significant at 5% level

** = Significant at 1% level

^{NS} = Non-significant.

Path coefficient

The path coefficients were estimated both at genotypic and phenotypic levels and results are presented in Table 5 and 6. In the present experiment, characters DFF, NSBFF, PHMF, NSBMF, PdW/P and NS/P had positive direct effect on seed yield (SW/P) and among them NS/P had the highest positive direct effect with a value of 13.1562. While, negative direct effect showed by PHFF, NPBFF, DMF, NPBMF, PWH and NPd/P.

The indirect effects of DFF on seed yield via NPBFF, PHMF, NPBMF and NS/P were positive and it had positive direct effect on seed yield (0.5425) which was nullified mainly due to DMF and NPd/P. The total effect of PHFF was negative (-0.6565) due to mainly via NPBFF, NSBFF, DMF, NSBMF, PWH, NPd/P and PdW/P. The direct effect of NPBFF was -0.3699 which was compensated by high positive indirect effect via NS/P (11.8063) and the total effect was 0.5483. NSBFF had second highest positive direct effect on seed yield (0.6365). The indirect effects of NSBFF on seed yield via DFF, DMF, PHMF, PWH, NPd/P and PdW/P were negative thus the total effect of this trait was negative (-0.4632). DMF had second highest negative direct effect on seed yield and it had negative indirect effect via PHFF, NPBFF, NSBMF, PWH, NPd/P and PdW/P. The trait PHMF had positive direct effect on seed yield (0.2840) which was turn into negative total effect via negative indirect effect of all the traits except DFF and NPBMF. NPBMF had negative direct effect which turns into positive via PHFF, DMF, NSBMF, PWH, PdW/P and NS/P and among them NS/P had a great role (10.6815) to reverse negative direct effect into positive total effect. Rest of the trait had negligible negative indirect effect on seed yield except NPd/P. The trait NSBMF had positive but small direct effect on seed yield which turns into negative via DFF, PHMF, NPBMF, NPd/P and PdW/P. In this case, NPBMF (-0.9368) and NPd/P (-1.7156) had a great role to reverse its positive direct effect into negative total effect. Rest of the trait had small positive indirect effect on seed yield except NS/P. The indirect effect of PWH were positive on seed yield via DFF, NSBFF, PHMF, NPBMF and NPd/P and the total effect of PWH was -0.9923. The trait NPd/P had the highest negative direct effect (-11.6785) on seed yield but this high value nullified by high indirect effect of NS/P (13.0785) and other positive indirect effect via DFF, NSBFF, PHMF, NSBMF and PWH. PdW/P had positive and small direct effect of 0.3203 on seed yield. It exhibited positive indirect effect via PHFF, DMF, PWH and NPd/P. The highest positive direct effect (13.1562) on seed yield was exhibited by NS/P.

But this high value reduces by high negative indirect effect of NPd/P (-11.6096) and other small negative indirect effect via PHFF, NPBFF, DMF, PHMF, NPBMF and PdW/P. The residual effect at genotypic level was -0.6876.

Table 5. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at genotypic level.

Character	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P
DFF	0.5425	-0.3213	0.1366	-0.4973	-1.0997	0.2106	0.3183	-0.1987	-0.0051	-6.2725	-0.0678	6.9438
PHFF	0.4943	-0.3526	-0.1036	-0.1369	-1.2168	0.2870	0.4002	-0.1242	-0.0042	-3.9403	-0.2526	4.2850
NPBFF	-0.2003	-0.0988	-0.3699	-0.0546	-0.4866	0.0239	-0.1123	-0.1894	-0.0070	-9.9792	0.2264	11.8063
NSBFF	-0.4239	0.0758	0.0317	0.6365	-0.1051	-0.0285	0.3988	0.1743	-0.0005	-4.6994	-0.2905	3.7679
DMF	0.4923	-0.3541	-0.1485	0.0552	-1.2119	0.2778	0.3402	-0.0994	-0.0048	-5.7960	-0.3197	6.0387
PHMF	0.4022	-0.3563	-0.0311	-0.0640	-1.1851	0.2840	0.5051	-0.1757	-0.0037	-0.0490	-0.3935	-0.0263
NPBMF	-0.2003	0.1637	-0.0482	-0.2945	0.4783	-0.1664	-0.8620	0.2763	0.0025	-9.3159	0.3539	10.6815
NSBMF	-0.4239	0.1722	0.2754	0.4364	0.4737	-0.1963	-0.9368	0.2543	0.0018	-1.7156	-0.4110	1.6853
PWH	0.5530	-0.2922	-0.5147	0.0653	-1.1500	0.2110	0.4250	-0.0925	-0.0050	4.7753	-0.4424	-4.5231
NPd/P	0.2914	-0.1190	-0.3160	0.2561	-0.6015	0.0012	-0.6876	0.0374	0.0021	-11.6785	-0.0575	13.0785
PdW/P	-0.1149	0.2781	-0.2614	-0.5771	1.2095	-0.3489	-0.9523	-0.3263	0.0070	2.0975	0.3203	-0.3973
NS/P	0.2863	-0.1149	-0.3319	0.1823	-0.5563	-0.0006	-0.6999	0.0326	0.0017	-11.6096	-0.0097	13.1562

Residual effect = -0.6876

Table 6. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at phenotype level.

Character	DFF	PHFF	NPBFF	NSBFF	DMF	PHMF	NPBMF	NSBMF	PWH	NPd/P	PdW/P	NS/P
DFF	**0.0402**	-0.0502	-0.0020	0.0008	-0.0397	0.0002	0.0015	-0.0254	-0.0075	-0.1120	-0.1123	0.1496
PHFF	0.0247	**-0.0818**	0.0296	0.0001	-0.0491	0.0002	0.0087	-0.0152	-0.0040	-0.0870	-0.0775	0.1274
NPBFF	-0.0007	-0.0203	**0.1191**	-0.0010	-0.0189	0.0001	-0.0044	-0.0009	0.0001	-0.1023	0.0046	0.1393
NSBFF	-0.0099	0.0027	0.0387	**-0.0031**	-0.0023	-0.0001	-0.0140	0.0247	0.0058	-0.0400	-0.1841	0.0259
DMF	0.0240	-0.0605	0.0339	-0.0001	**-0.0664**	0.0002	0.0150	-0.0065	-0.0038	-0.1261	-0.1548	0.1611
PHMF	0.0136	-0.0429	0.0204	0.0004	-0.0317	**0.0005**	0.0157	-0.0180	-0.0040	-0.0653	-0.0554	0.0418
NPBMF	-0.0007	0.0078	0.0057	-0.0005	0.0110	-0.0001	**-0.0904**	0.0205	-0.0001	-0.0209	0.0331	0.0664
NSBMF	-0.0099	0.0121	-0.0011	-0.0007	0.0042	-0.0001	-0.0181	**0.1029**	0.0015	-0.1038	0.0630	0.1215
PWH	0.0100	-0.0108	-0.0004	0.0006	-0.0084	0.0001	-0.0004	-0.0052	**-0.0301**	-0.0550	0.1046	0.0759
NPd/P	0.0066	-0.0105	0.0180	-0.0002	-0.0124	0.0001	-0.0028	0.0158	-0.0024	**-0.6776**	0.2602	0.7801
PdW/P	-0.0059	0.0083	0.0007	0.0007	0.0135	0.0001	-0.0039	0.0085	-0.0041	-0.2315	**0.7615**	0.3061
NS/P	0.0075	-0.0130	0.0207	-0.0001	-0.0134	0.0001	-0.0075	0.0156	-0.0029	-0.6612	0.2916	**0.7995**

Residual effect = 0.4608

At the phenotypic levels the highest direct effect showed by NS/P (0.7995) followed by PdW/P (0.7615) while, the highest negative direct effect exhibited by NPd/P (-0.6776) followed by NPBMF (-0.0904). The trait DFF had positive direct effect on seed yield with a value of 0.0402 however, it become negative due to negative indirect effect via PHFF, NPBFF, DMF, NSBMF, PWH, NPd/P and PdW/P. PHFF had positive indirect effect of on seed yield via DFF, NPBFF, NSBFF, PHMF, NPBMF and NS/P. Positive indirect effect via NS/P was comparatively high among the positive indirect effect showing traits. The direct and total effect for this trait was recorded as 0.1191 and 0.1145, respectively. NSBFF had negative and negligible direct effect (-0.0031) on seed yield. The direct effect of DMF on the seed yield was negative and small (-0.0664).

The trait PHMF had positive but vary small direct effect (0.0005) on seed yield which turns into negative total effect via PHFF, DMF, NSBMF, PWH, NPd/P and PdW/P. NPBMF had negative direct effect (-0.0904) which was turn into positive total effect (0.0314) via positive indirect effect of PHFF, NPBFF, DMF, NSBMF, PdW/P and NS/P specially PdW/P and NS/P. Trait NSBMF had positive direct effect of 0.1029 on yield. It had positive indirect effect on seed yield via PHFF, DMF, PWH, PdW/P and NS/P and the total effect was 0.1718. The direct effect of PWH had negative and small (-0.0301) on yield.

The trait NPd/P had the highest negative direct effect (-0.6776) on seed yield but it become positive total effect due to the positive indirect effect specially via PdW/P and NS/P which were higher than negative indirect effect via rest of the traits. In the present experiment, the second highest positive direct effect of 0.7615 on seed yield was exhibited by PdW/P. PdW/P had positive indirect effect on seed yield via all the traits except DFF, NPBMF, PWH and NPd/P. The total effect was 0.9406. The highest positive direct effect on seed yield (0.7995) exhibited by NS/P. It had negative indirect effect which reduced its amount of total effect on seed yield via PHFF, NSBFF, DMF, NPBMF, PWH and NPd/P. The total effect was 0.4369. The residual effect at phenotypic level was 0.4608.

Selection index

Selection index for yield were constructed for each set of data and different combinations were studied to identify the character which might be useful during selection program. For construct the selection indices, all the thirteen agronomical character were considered. Here, SW/P was use as dependent character. The selection indices and the expected genetic gain in percentage over straight selection for yield and its components are presented in Table 7. In this study, 8750 different combinations were calculated and only high value showing combinations are presented in Table 7.

Table 7. Expected gain in percentage in seed weight per plant over straight selection from the use of various selection indices in chickpea genotypes (Index which, showed high value is presented only).

Combination	Gain %
13	157.20
1	-173.88
2	19.16
3	2143.01
4	-2757.46
5	-376.81
6	147.08
7	3286.72
8	942.67
9	43.08
10	-109.27
11	-675.86
12	-74.40
1+4	-211.958
1+5	-202.973
2+3	67.1229
2+4	-264.773
2+5	-238.136
2+7	124.7193
3+4	-1322.4
3+5	-340.819
3+6	175.8112
3+7	1949.522
3+8	1171.211
3+9	83.11538
3+11	-360.659
3+13	247.5535
4+5	-411.069
4+7	-503.165
4+8	-1642.03
4+9	-247.575
4+11	-853.026
4+13	-451.063
5+6	-228.671
5+7	-301.551
5+8	-360.598
5+9	-233.186
5+11	-349.489
5+13	-288.191
6+7	231.3657
6+8	140.6306
6+13	83.84756
7+8	1768.277
7+9	136.794
7+11	305.1981
7+13	371.1951
8+11	-549.435
8+13	155.7536
11+13	-252.77
1+4+5	-216.576
1+4+8	-207.374
1+4+11	-215.777
1+5+8	-200.273
1+5+11	-204.003
2+3+4	-206.185
2+3+5	-220.937
2+3+7	142.924
2+3+8	66.808
2+4+5	-263.912
2+4+8	-249.087
2+4+11	-275.276
2+4+13	-217.223
2+5+8	-232.421
2+5+11	-238.539
2+5+13	-214.843
2+6+7	66.404
2+7+8	119.709
2+7+13	59.019
3+4+5	-379.609
3+4+6	-209.21
3+4+7	-688.211
3+4+8	-933.333
3+4+11	-662.317
3+4+13	-319.910
3+5+6	-206.971
3+5+7	-263.075
3+5+8	-326.491
3+5+9	-215.552
3+5+11	-323.147
3+5+13	-263.572
3+6+7	241.223
3+6+8	166.744
3+6+11	57.87166
3+6+13	102.343
3+7+8	1350.986
3+7+9	153.0216
3+7+11	380.2664
3+7+13	382.6844
3+8+9	81.38379
3+8+11	-270.648
3+8+13	229.732
4+5+6	-262.015
4+5+7	-350.589
4+5+8	-395.088
4+5+9	-260.059
4+5+11	-375.369
4+5+13	-319.906
4+6+7	-301.194
4+6+11	-252.242
4+7+11	-502.972
4+7+13	-267.635
4+8+9	-231.72
4+8+11	-739.085
4+8+13	-402.945
4+9+11	-265.201
4+11+13	-403.733
5+6+8	-222.168
5+6+11	-232.935
5+7+8	-288.075
5+7+11	-295.342
5+7+13	-231.899
5+8+9	-227.501
5+8+11	-337.557
5+8+13	-278.941
5+9+11	-234.660
5+9+13	-201.882
5+11+13	-281.297
6+7+8	217.912

Combination	Gain %
6+7+9	71.740
6+7+11	111.208
6+7+13	136.292
6+8+13	81.440
7+8+9	130.9166
7+8+11	277.7719
7+8+13	337.385
7+9+13	83.66271
7+11+13	127.9177
8+11+13	-221.817
1+3+4+5	-209.189
1+3+4+11	-203.451
1+4+5+7	-200.231
1+4+5+8	-213.896
1+4+5+11	-215.605
1+4+5+13	-200.345
1+4+8+11	-211.825
1+5+8+11	-201.566
2+3+4+5	-249.315
2+3+4+7	-239.51
2+3+4+11	-240.185
2+3+5+8	-215.508
2+3+5+11	-224.714
2+3+6+7	75.09319
2+3+7+8	136.6712
2+3+7+11	59.87234
2+3+7+13	88.97106
2+4+5+6	-201.537
2+4+5+7	-231.991
2+4+5+8	-258.233
2+4+5+9	-204.405
2+4+5+11	-258.894
2+4+5+13	-230.492
2+4+8+11	-263.863
2+4+11+13	-216.436
2+5+7+11	-206.814
2+5+8+11	-233.686
2+5+8+13	-202.049
2+5+11+13	-210.627
2+6+7+8	64.35695
2+7+8+13	73.59978
3+4+5+6	-244.76
3+4+5+7	-319.805
3+4+5+8	-365.37
3+4+5+9	-245.29
3+4+5+11	-351.788
3+4+5+13	-298.797
3+4+6+7	129.9546
3+4+6+8	-217.555
3+4+6+13	-210.558
3+4+7+8	-613.585
3+4+7+9	54.3383
3+4+7+11	-318.91
3+4+7+13	-355.221
3+4+8+11	-582.713
3+4+8+13	-280.758
3+4+9+11	-228.449
3+4+11+13	-337.327
3+5+6+8	-200.689
3+5+6+11	-216.37
3+5+7+8	-250.838
3+5+7+11	-268.102
3+5+7+13	-202.258
3+5+8+9	-210.128
3+5+8+11	-312.364
3+5+11+13	-262.253
3+6+7+8	227.543
3+6+7+9	79.87321
3+6+7+11	128.7677
3+6+7+13	145.7141
3+6+8+11	57.91431
3+6+8+13	98.66718
3+7+8+9	146.1181
3+7+8+11	340.6964
3+7+8+13	349.7776
3+7+9+11	69.71017
3+7+9+13	95.69281
3+7+11+13	164.0836
3+8+11+13	-211.712
4+5+6+7	-223.043
4+5+6+8	-255.629
4+5+6+11	-258.156
4+5+6+13	-225.463
4+5+7+8	-337.158
4+5+7+9	-227.431
4+5+7+11	-329.928
4+5+7+13	-275.968
4+5+8+9	-254.425
4+5+8+11	-363.569
4+5+8+13	-310.672
4+5+9+11	-255.738
4+5+9+13	-227.102
4+5+11+13	-305.568
4+6+7+8	98.44165
4+6+7+13	-259.789
4+6+8+11	-237.993
4+7+8+11	-436.141
4+7+8+13	-276.959
4+7+11+13	-243.932
4+8+9+11	-253.873
4+8+11+13	-376.687
4+9+11+13	-207.708
5+6+8+11	-227.52
5+6+11+13	-202.847
5+7+8+11	-285.105
5+7+8+13	-223.563
5+7+9+11	-201.984
5+7+11+13	-239.301
5+8+9+11	-229.835
5+8+11+13	-273.855
5+9+11+13	-207.133
6+7+8+9	69.4649
6+7+8+11	107.0889

Combination	Gain %
6+7+8+13	130.667
6+7+11+13	68.39016
7+8+9+13	80.93732
7+8+11+13	123.6122
1+3+4+5+8	-206.606
1+3+4+5+11	-209.07
1+4+5+7+11	-201.324
1+4+5+8+11	-213.179
1+4+5+11+13	-200.706
2+3+4+5+7	-216.227
2+3+4+5+8	-243.98
2+3+4+5+11	-246.744
2+3+4+5+13	-218.464
2+3+4+7+8	-240.779
2+3+4+7+13	-223.195
2+3+4+8+11	-229.57
2+3+5+8+11	-220.105
2+3+6+7+8	72.67581
2+3+6+7+13	50.36936
2+3+7+8+11	58.72243
2+3+7+8+13	85.948
2+4+5+6+11	-204.473
2+4+5+7+8	-226.8
2+4+5+7+11	-232.784
2+4+5+7+13	-202.974
2+4+5+8+9	-201.304
2+4+5+8+11	-254.054
2+4+5+8+13	-226.298
2+4+5+9+11	-206.126
2+4+5+11+13	-229.796
2+4+7+8+13	-200.156
2+4+8+11+13	-208.931
2+5+7+8+11	-202.249
2+5+8+11+13	-206.913
3+4+5+6+7	-203.394
3+4+5+6+8	-238.778
3+4+5+7+8	-307.777
3+4+5+7+9	-211.281
3+4+5+7+11	-306.772
3+4+5+7+13	-254.004
3+4+5+8+9	-239.992
3+4+5+8+11	-341.064
3+4+5+8+13	-290.328
3+4+5+9+11	-243.476
3+4+5+9+13	-214.879
3+4+5+11+13	-288.724
3+4+6+7+8	124.6043
3+4+6+7+11	-233.006
3+4+6+7+13	78.12196
3+4+6+8+13	-213.322
3+4+7+8+9	54.31083
3+4+7+8+11	-265.388
3+4+7+8+13	-348.911
3+4+8+9+11	-217.737

Combination	Gain %
3+4+8+11+13	-314.515
3+5+6+8+11	-211.207
3+5+7+8+11	-258.738
3+5+7+11+13	-218.214
3+5+8+9+11	-216.002
3+5+8+11+13	-255.345
3+6+7+8+9	77.2654
3+6+7+8+11	123.4761
3+6+7+8+13	139.6862
3+6+7+9+13	54.06544
3+6+7+11+13	81.03654
3+7+8+9+11	67.92662
3+7+8+9+13	92.33651
3+7+8+11+13	156.0004
4+5+6+7+8	-217.179
4+5+6+7+11	-227.303
4+5+6+8+11	-252.782
4+5+6+8+13	-220.831
4+5+6+9+11	-201.708
4+5+6+11+13	-226.546
4+5+7+8+9	-222.264
4+5+7+8+11	-319.712
4+5+7+8+13	-267.864
4+5+7+9+11	-229.171
4+5+7+11+13	-270.913
4+5+8+9+11	-250.933
4+5+8+9+13	-222.93
4+5+8+11+13	-298.137
4+5+9+11+13	-226.993
4+6+7+8+13	58.66331
4+7+8+11+13	-220.572
4+8+9+11+13	-200.108
5+7+8+11+13	-232.601
5+8+9+11+13	-203.427
6+7+8+11+13	66.4227
1+3+4+5+8+11	-206.728
2+3+4+5+7+8	-211.275
2+3+4+5+7+11	-219.982
2+3+4+5+8+11	-242.172
2+3+4+5+8+13	-214.461
2+3+4+5+11+13	-219.65
2+3+4+7+8+13	-223.774
2+4+5+7+8+11	-228.334
2+4+5+7+11+13	-207.117
2+4+5+8+9+11	-203.356
2+4+5+8+11+13	-226.125
3+4+5+6+7+11	-212.083
3+4+5+6+8+11	-239.071
3+4+5+7+8+11	-297.455
3+4+5+7+8+13	-246.492
3+4+5+7+9+11	-216.149
3+4+5+7+11+13	-253.653
3+4+5+8+9+11	-238.935
3+4+5+8+9+13	-210.89

Combination	Gain %
3+4+5+8+11+13	-281.83
3+4+5+9+11+13	-216.721
3+4+6+7+8+11	-234.382
3+4+6+7+8+13	75.75462
3+4+6+7+11+13	-218.854
3+5+7+8+11+13	-211.835
3+6+7+8+9+13	52.41296
3+6+7+8+11+13	78.38716
4+5+6+7+8+11	-222.367
4+5+6+8+11+13	-222.534
4+5+7+8+9+11	-224.746
4+5+7+8+11+13	-264.281
4+5+8+9+11+13	-223.341
2+3+4+5+7+8+11	-215.742
2+3+4+5+8+11+13	-216.14
2+4+5+7+8+11+13	-203.662
3+4+5+6+7+8+11	-207.359
3+4+5+6+8+11+13	-211.054
3+4+5+7+8+9+11	-211.924
3+4+5+7+8+11+13	-247.461
3+4+5+8+9+11+13	-213.226
3+4+6+7+8+11+13	-219.503
4+5+7+8+9+11+13	-200.392

N.B. Numerical sign viz., 1, 2, 3 etc indicated different characters as follows:

1 = DFF, 2 = PHFF, 3 = NPBFF, 4 = NSBFF,
5 = DMF, 6 = PHMF, 7 = NPBMF, 8 = NSBMF,
9 = PWH, 10 = NPd/P, 11 = PdW/P, 12 = NS/P,
13 = SW/P,
Gain % = Expected Genetic ga

In the present investigation, the result showed that the character NPBMF had the highest (3286.72%) positive expected gain followed by NPBFF (2143.01%) and NSBMF (942.67%) when individual traits were considered separately. In the discriminante function analysis, high value of expected gain exhibited by two characters in a combination with value of 1949.52% (NPBFF + NPBMF) followed by 1768.27% (NPBMF + NSBMF) and 1171.21% (NPBFF + NSBMF). Included three characters, the maximum genetic gain was recorded as 1350.99% for NPBFF + NPBMF + NSBMF followed by 382.68% for NPBFF + NPBMF + SW/P and 380.27% for NPBFF + NPBMF + PdW/P. When included four characters, the maximum genetic gain was recorded as 349.78% for NPBFF + NPBMF + NSBMF + SW/P followed by 340.70% for NPBFF + NPBMF + NSBMF + PdW/P and 227.54% for NPBFF + PHMF + NPBMF + NSBMF. The maximum genetic gain was recorded in a combination of five characters as 156% for NPBFF + NPBMF + NSBMF + PdW/P + SW/P followed by 139.69% for NPBFF + PHMF + NPBMF + NSBMF + SW/P and 124.6% for NPBFF + NSBFF + PHMF + NPBMF + NSBMF. Similarly, inoculation of six and more traits in a combination, the value of expected gain become lower than 100. On the other hand, when included eight and more traits in a combination the value of expected gain become negative. While included all the traits under studied in a combination, the expected genetic gain was noted as -102.79%. In an overall basis the highest expected genetic gain was noted as 1949.5222 for the combination of NPBFF + NSBMF followed by 1768.277 for NSBMF + PWH and 1350.986 for NSBFF + NSBMF + PWH.

Discussion

In plant breeding research quantitative characters were no doubt important and most of quantitative characters are economically important. In the present investigation, analysis of variance revealed highly significant difference (P<0.01) among the chickpea genotypes for all the characters under investigation thereby indicating the presence of a considerable magnitude of genetic variability among the experimental material and advocated that enough scope was present for the selection of good performing genotypes in relation to seed yield. Similar results were reported by Jivani *et al.* (2013), Sarker *et al.* (2013) and Zeeshan *et al.* (2013). The year item was also highly significant (P<0.01) for all the characters except DMF, which indicated that year was also significantly different. This result was in agreement with the findings of Sarker *et al.* (2013). The interaction between year and genotypes was significant all the characters except NPBMF.

Significant interaction item indicated that year interacted with genotypes significantly.

Variability is the prerequisite for the initiation of any breeding program for any crop (Ali and Khan, 2007).

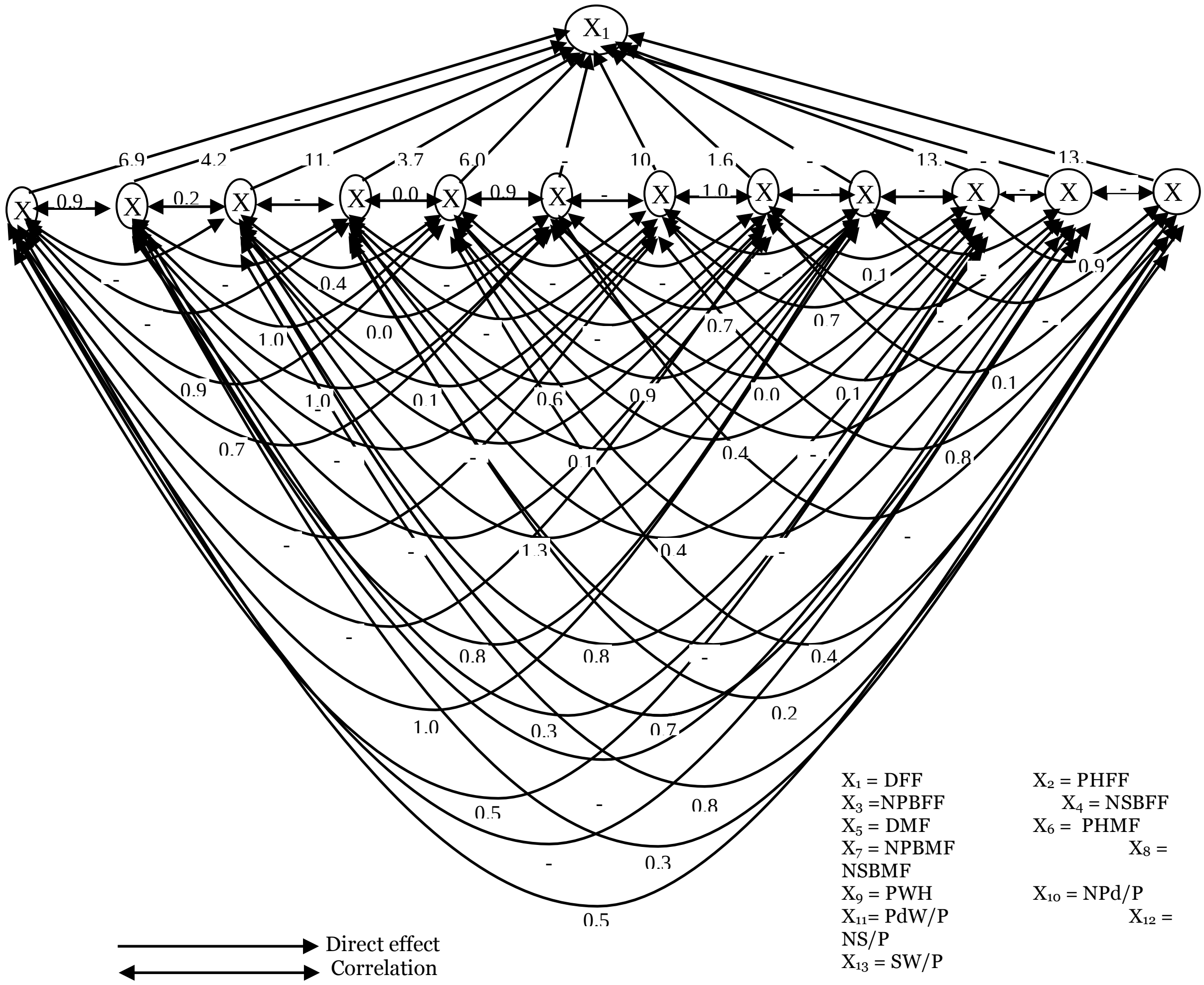

Fig. 1. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at phenotype level.

High magnitude of genetic variability gives free hand to plant breeder for selection and rejection of any character or genotypes have that specific character. In the present study, different components of variation varied differently in different characters. Phenotypic component of variation (σ^2_P) was the higher than other component of variation. In the present materials, high phenotypic value causes high genotypic value. The highest genotypic variation along with high phenotypic variation was recorded for NS/P flowed by NPd/P and PWH. Larger genotype value for any character is always helpful for effective selection. The highest value for $\sigma^2_{G\times Y}$ and σ^2_E component of variation also indicated better scope for the improvement of NPd/P, NS/P and PWH through selection, while rest of the traits exhibited low value for σ^2_P, σ^2_G, $\sigma^2_{G\times Y}$ and σ^2_E which indicating difficulties regarding improvement of these traits through selection. Hasan (2001) and Sarker (2012) reported similar results in chickpea. The differences between phenotypic and genotypic component of variation were grater in magnitude was recorded for NPd/P, NS/P and PWH, which indicated that environment has considerable effect on these characters. This is accordance with Sarker *et al.* (2013). Wide difference between PCV and GCV indicated that susceptibility to environmental fluctuation and narrow different between phenotypic and genotypic coefficient of variation in traits implied relative resistance to environmental alteration (Singh *et al.*, 2010). Relatively higher value of PCV and GCV are indicative of variability ensuring wide scope for improvement through selection and vice-versa (Gupta *et al.*, 2009).

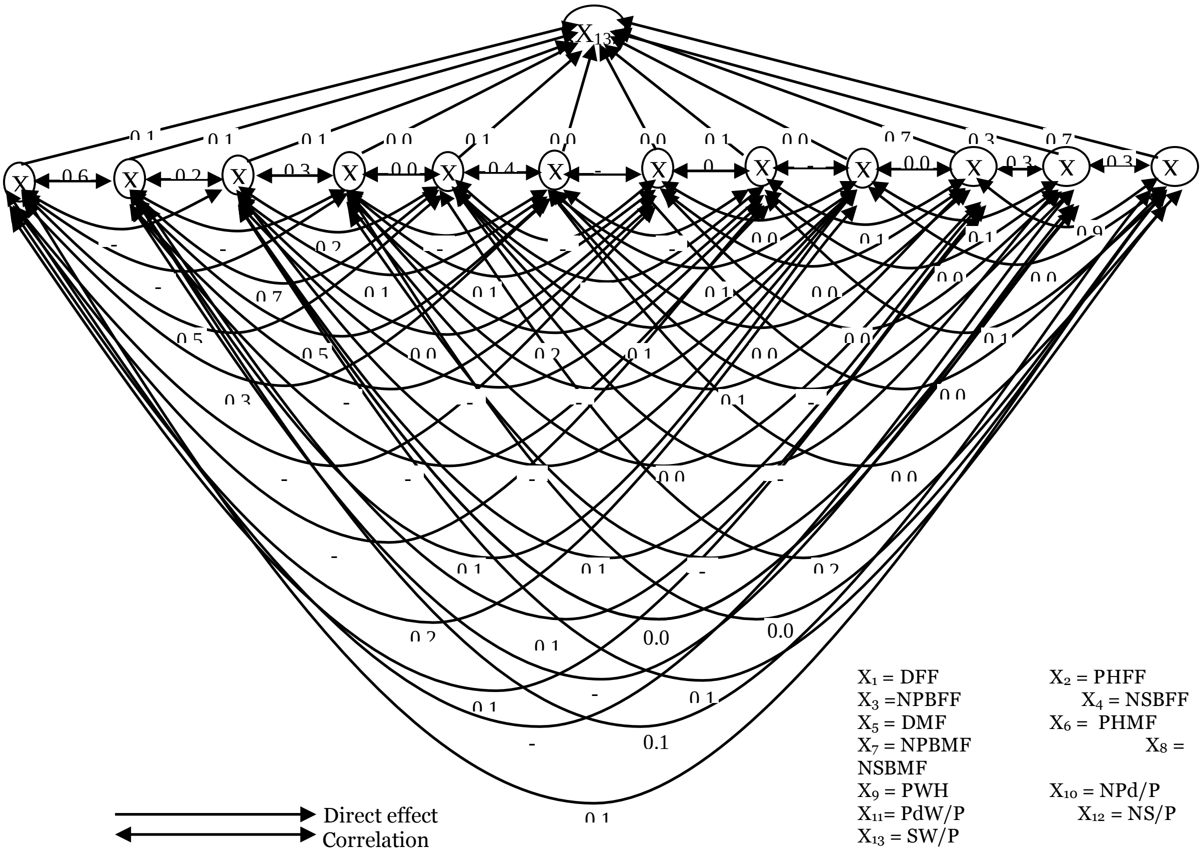

Fig. 2. Path coefficient analysis showing direct (bold) and indirect effects of yield components on yield of chickpea at genotype level.

However, in the present investigation PCV was higher than the GCV for all the traits indicating environmental factors influenced their expression. The results are in agreement with the findings of Hasan and Deb (2013), Sarker *et al.* (2013) and Zeeshan *et al.* (2013). The highest GCV as well as high PCV was recorded for NS/P followed by NPd/P, PHFF, PWH and DFF. Thus, the major portion of variation for these traits was contributed by genotypic component, indicating the possibility of improving these traits by adopting proper selection method. This observation is conformity with the findings of earlier workers viz., Pratap *et al.* (2004), Jeena *et al.* (2005), Tomar *et al.* (2009). Sharma and Saini (2010) had also found high magnitude of GCV as well as PCV for number of pods per plant, plant height and days to flowering. Difference between PCV and GCV were greater in magnitude for PWH, NPd/P, PdW/P and NS/P which indicated that environment also had considerable effects on these characters. Similar findings have been reported by Hasan and Deb (2013) and Sarker *et al.* (2013).

The coefficient of variability indicates only the extent of variability present for different characters but do not indicates the heritable portion. The efficiency of selection not only depends on the magnitude of genetic variability but also the heritability of that character. Heritability alone is not very useful but this statistic alone with genetic advance is valuable (Johanson *et al.*, 1955). In the present investigation, moderate to high heritability was recorded for DFF, PHFF, DMF, NPd/P and NS/P but rest of the trait had comparatively low heritability (<30%).

Here, low values of heritability indicate that there is predominance of non-additive gene action and recombinant breeding may thus be useful (Arshad *et al.*, 2003a). As per Johanson *et al.* (1955), the heritability value alone provides no indication in selecting the best individual and heritability should be considered along with genetic advance as percentage of mean, however it is not necessary that character showing high heritability will also exhibit high genetic advance. High genetic advance as percentage of mean (GA%>20%) with considerable amount of heritability (h^2_b) and high magnitude of GCV were observed for NS/P and NPd/P suggesting that these traits were genetically controlled by additive gene action and can be improved through mass selection, family selection or other modified selection.

These results are very close to findings of Pratap *et al.* (2004), Jeena *et al.* (2005), Sharma *et al.* (2005) and Tomar *et al.* (2009). Date of first flower (DFF) and date of maximum flower (DMF) exhibited high heritability accompanied by low genetic advance as percentage of mean indicting the influence of dominant and epistatic genes for these traits and the high heritability may be due to the influence of environmental condition. Arshad *et al.* (2003a) observed similar results for days to flowering, days to maturity and 100-seed weight. Low heritability accompanied with low genetic advance as percentage of mean (GA%) observed for most of the traits which offers less scope for selection, as they were more influenced by the environment and accounted for non-additive gene effect (Srivastava *et al.*, 2012). Low heritability and low genetic advance were also observed byYucel *et al.* (2006), Sharma and Saini (2010) and Sarker *et al.* (2013) in chickpea.

Grain yield is a complex character that is outcome of interaction between many plant traits, which are in turn influenced by their genetic makeup and environment where plant is grown. Thus it is very important to analyses the data for relative contribution of various components to yield performance. The simple correlation analysis is an important tool for this purpose.

It was observed in correlation analysis that most of the character pairs both at genotypic and phenotypic levels were in same direction and genotypic estimates were higher than that of phenotypic ones indicating strong inherent association between the traits under studied and little role of environment in the expression of genetic relationship on the phenotypes (Singh *et al.*, 2010).

Similar results in chickpea were reported by Tomar *et al.* (2009) and Sharma and Saini (2010). However, seed weight per plant (SW/P) that is yield per plant which is the most important economic trait exhibited positive association with NPBFF, NPBMF, NPd/P, PdW/P and NS/P both at genotypic and phenotypic levels, in addition with NSBMF and PWH at phenotypic level.

Among them NPd/P, PdW/P and NS/P exhibited significant positive association with SW/P both at genotypic and phenotypic levels while, NPBFF and NPBMF with SW/P only at genotypic level. Above information indicates that these characters are genetically related with SW/P more than those of the other yield related components (Deb and Khaleque, 2005) and suggested that any positive increase in such traits will improve the seed yield in chickpea. Thus it can be inferred that selection based on these traits in combination, will results in identifying high yielding genotypes.

Similar findings for most of the traits have also been reported by Zali *et al.* (2011), Ali *et al.* (2012) and Jivani *et al.* (2013). Bakhsh *et al.* (2006) also reported primary branches and number of pods per plant in chickpea were positively correlated with grain yield. Significant and positive correlation of NS/P with seed yield has also reported by Yucel and Anlarsal (2010). Significant and positive correlation of NPd/P with seed yield were reported by Shahid *et al.* (2010), Akhtar *et al.* (2011) and Zeeshan *et al.* (2013). The characters viz., DFF, PHFF, NSBFF, DMF and PHMF exhibited negative association with SW/P both at genotypic and phenotypic levels while, SW/P with NSBMF and PWH only at genotypic level. In this investigation, negatively correlated traits were all significant at genotypic level indicating a weak association. Khan *et al.* (2006) reported plant height was negatively correlated with seed yield, Sharma and Saini (2010) reported that 100-seed weight, days to maturity and plant height were negatively correlated with seed yield. Due to negative and significant genotypic association of DFF, PHFF, NSBFF, DMF, PHMF, NSBMF and PWH with seed weight per plant, it may suggested that early flowering, short plant stature, less number of secondary branches both at first and maximum flowering stage and less vegetative growth of a chickpea plant gave more seed weight per plant.

Among the yield contributing traits, genotypic correlation of DFF was highly significant and positive with PHFF, DMF, PHMF, PWH, NPd/P and NS/P indicating that the increasing of DFF would increase plant height, date of maximum flower, plant weight at harvest, number of pods as well as number of seeds per plant. PHFF had positive and highly significant association with PWH, NPd/P and NS/P but negative and highly significant association with PdW/P which indicated that taller plant at first flower gave more vegetative weight at harvest and more number of pods as well as seeds but pod or seed weight may be reduced while taller plant at maximum flower only gave more vegetative weight at harvest due to highly significant association with PWH. Almost similar result was reported by Zeeshan *et al.* (2013). Number of primary branches both at first flower and maximum flower had positive and highly significant association with NPd/P, PdW/P and NS/P reviled that more number of primary branches produce more large pods as well as seeds while, more number of secondary branches both at first flower and at maximum flower may be produce more pods as well as seeds but pod weight as well as seed weight may be reduced due to negative association with PdW/P. These findings are similar with Sharma and Saini (2010). PWH had significant and negative correlation with NPd/P, PdW/P and NS/P which indicated increase of PWH, yield may be significantly hampered. Trait NPd/P showed non-significant and negative correlation with PdW/P while highly significant and positive correlation with NS/P at genotypic level which indicated that if the number of pods increased, the number of seeds will also increased significantly but weight of seed slightly reduced.

Path coefficient analysis both at genotypic and phenotypic levels are worked out to partition the correlation coefficient into direct and indirect effects considering seed weight per plant as a dependent variable. A combination of direct and indirect selection will be effective to get a high selection response.

In the present study, highest positive direct effect of NS/P on seed yield coupled with a relatively high value of correlation both at genotypic and phenotypic levels suggested that improvement of grain yield in chickpea in linked with this traits and selection of this character might have good impact on seed yield per plants. Ali *et al.* (2009), Yucel and Anlarsal (2010) and Zali *et al.* (2011) reported the same result. On the other hand, the highest negative direct effect on seed yield per plant was recorded for NPd/P both at genotypic and phenotypic levels but highest positive indirect effect of NS/P nullified its negative effect and finally it turn into positive. It demands a good compromise between NPd/P and NS/P. This was an agreement with the findings of Deb and Khaleque (2005). Results of the path analysis revealed that most of the traits had great positive indirect effect on seed yield through NS/P. Thus improving of these traits may increase seed yield. It also indicated that NS/P exerted the greatest direct effect. This trait major contributes to seed yield could therefore be used to improve seed yield in chickpea breeding program. Similar reports have been noticed by Ali *et al.* (2009) and Zali *et al.* (2011) however these finding are contrary with Renukadevi and Subbalakshmi (2006). They found NPd/P as positive and NS/P as negative direct effect on seed yield. Sharma and Saini (2010) and Ali *et al.* (2011) found NPd/P as the highest positive direct effect on yield. Vaghela *et al.* (2009) found NPd/P and NS/P as positive direct effect on seed yield while, Mushtaq *et al.* (2013) found both NPd/P and NS/P as negative direct effect on seed yield.

Among the yield contributing traits at genotypic level, the trait DFF had positive direct effect on seed yield which was nullified mainly due to high negative indirect values of DMF and NPd/P, thus the total effect was negative but indirect effect of NS/P was high so, indirect selection for this trait to improve seed yield will be desirable. The direct effect of NPBFF and NPBMF had negative but total effect was positive mainly due to high positive indirect effect on seed yield via NS/P indicating that indirect selection through this trait might be helpful in yield improvement but since the direct effect was negative, so direct selection for these traits to improve yield will not be desirable. This result is in line with the findings of Saleem *et al.* (1999). On the other hand, NSBFF, PHMF and NSBMF had positive direct effect on seed yield but low and the indirect effect of most of the traits also low and negative so, direct or indirect selection for these traits to improve yield will not be effective. At the phenotypic level, the results were almost same as genotypic level, though their direct and indirect values were very low. The residual effect permits precise explanation about the interaction of yield components. The results exhibited medium residual effect both at genotypic and phenotypic levels, which indicated that the variability in the seed yield was contributed by the character with environment included in the present study. Sharma and Saini (2010) also observed medium residual effect at genotypic level.

It is recognized that the yield is a complex character which depends upon the action and interaction of a number of factors and highly influenced by many genetic factors as well as environmental fluctuation. Therefore, it may be misleading to direct selections for yield. The methods of discriminant function are more helpful to estimates reliable effectiveness of the character and character combinations. This method has been successfully followed by various researchers in various crops such as Deb and Khaleque (2007) and Sarker *et al.* (2013) in chickpea and Sarker and Deb (2009) in blackgram. In the present study, characters such as PHFF, NPBFF, PHMF, NPBMF, NSBMF, PWH and SW/P exhibited positive expected genetic gain while rest of the characters show negative genetic gain alone. Deb and Khaleque (2007) in chickpea and Nahar (1997) in sugarcane also observed negative value of expected genetic gain. The highest positive genetic gain (3286.72%) was observed for the character NPBMF followed by NPBFF (2143.01%) and NSBMF (942.67%).

The highest genetic gain over straight selection (1949.52%) was recorded when two character viz., NPBFF and NPBMF comprised the selection index and this was followed by 1768.28% when NPBMF and NSBMF included in a combinations. Further, the obtained results showed that with the inclusion of NPBFF and NPBMF in an index, the value of expected genetic gain was greatly increased, confirm, that these two traits are more important component for yield. Again, increases in the genetic gain with the addition of more traits were negligible. The results also revealed that, when the characters viz., NPBFF and NPBMF are common in different combination with SW/P gave the maximum expected gain. Therefore, these two yield components viz., NPBFF and NPBMF may be considered as the primary yield component and SW/P will increased by the improvement of the character NPBFF and NPBMF. It also revealed that the studied characters are quantitative in nature and are under polygenic control as they showed slightly under moderate heritability and genetic advance as percentage of mean. The genotypic correlation also indicates that NPBFF and NPBMF had highly significant and positive correlation with seed yield. Hence, those traits having significant correlation alone may be included to formulate selection indices for the improvement of seed yield. Inclusion of more traits may not be necessarily increasing the expected genetic gain and sometimes it may reduce the genetic gain. Moreover, selection of limited characters is more efficient and practical approach in breeding program than the inclusion of more character. Hence, in the present study the selection index based on seed yield, NPBFF and NPBMF may be considered as appropriate selection index for seed yield improvement in chickpea genotypes. Character viz., NPBMF, NSBMF and RWFD considered as the primary yield components in chickpea by Sarker *et al.* (2013).

In the present study, moderate heritability and high genetic advance as percentage of mean were observed for NPd/P and NS/P which implies that these characters were under the control of additive type of gene action.

Again, these two traits showed significant positive correlation with SW/P. Therefore, selection of these traits would better scope for improvement of seed yield in chickpea. Correlation and path analysis also indicated PdW/P as good yield component for chickpea improvement program due to its high positive correlation value and positive direct effect on seed yield.

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