Research article

Study on relationship and selection index in chickpea

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Abstract: Correlation, path coefficients and selection index were studied in eight irradiated chickpea lines for eleven quantitative characters to design the selection strategy towards higher yield. Genotypic correlation coefficients were higher than the phenotypic correlation coefficients. Seed weight per plant (SW/P) was positively correlated with days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant weight after fully dry (PWFD), pod weight per plant (PdW/P) and number of seeds per plant (NS/P) both at phenotypic and genotypic levels. PdW/P and NS/P exhibited high significant positive correlation on SW/P. NS/P had the highest positive direct effect of 1.077 and 1.334 on SW/P at both levels, respectively whereas PdW/P showed positive direct effect of 0.346 at genotypic levels. Regarding selection NPBMF and root weight after fully dry showed highest genetic gain among the combinations of selection indices.
Keywords: Correlation - Irradiation - Path Coefficients - Path Diagram - Yield.

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INTRODUCTION

Yield is the ultimate goal of a breeding program. Seed yield being most important trait, is governed by many physiological changes within the plant and influenced by many environmental factors. So, the breeder needs some index traits to select elite genotype for higher yield. Information on correlation, path-coefficients and selection index analyses is of much use to plant breeders for selection and breeding genotypes with increased yield potential. Correlation coefficients in general show associations among independent characteristics and the degree of linear relation between these characteristics. It is not sufficient to describe this relationship when the causal association among characteristics is needed (Toker & Cagirgan 2004). Correlation does not provide the adequate picture of the relationship among traits. In such cases, it is inevitable to study a method which takes into account the causal relationship between the variables in addition to the degree of such relationship. Path-coefficient analysis measures the direct influence of one variable upon the other and permits separation of correlation coefficients into components of direct and indirect effects. The plus point of this analysis is that it allows the partitioning of correlation coefficient into its components (Dewey & Lu 1959). In addition, selection index disclose about the primary yield components. The present study was undertaken to find out the association of different traits and their contribution to define seed yield.

MATERIAL AND METHODS

BARI (Bangladesh Agriculture Research Institute) Chola (*Cicer arietinum* L.) 1, 2, 3, 4, 5, 6, 7 and 8 were taken from Regional Agriculture Research Station, Ishourdi, Pabna, Bangladesh as materials. All the above varieties originated from ICRISAT line except BARI Chola 5 which is from local cultivar of Pabna, Bangladesh. Selected varieties of chickpea were irradiated with irradiation source of Co^{60} at the Institute of Food and Radiation Biology, Atomic Energy Research Establishment, Savar, Dhaka, Bangladesh. Layout of the experimental field and trial of the irradiated varieties as lines was conducted in the research field of the department of Botany, University of Rajshahi under randomized complete block design with 4 replications in two consecutive years namely 2007–2008 (Y_1) and 2008–2009 (Y_2). Each replication having 4 blocks and each block having 8 plots. Each plot contains 3 rows and per row there are 5 hills. In each hill, one plant was maintained for data. Gap between blocks and that between plots were 5 cm. The same between rows and that

between plants were 70 and 25 cm, respectively. The data of eleven quantitative traits viz., days to maximum flower (DMF), number of primary branches at maximum flower (NPBMF), number of secondary branches at maximum flower (NSBMF), plant height at maximum flower (PHMF), plant weight after fully dry (PWFD), root weight after fully dry (RWFD, number of pods per plant (NPd/P), pod weight per plant (PdW/P), number of seeds per plant (NS/P), seed weight per plant (SW/P) and 1000-seed weight were collected on individual plant basis following C.G.S system. The data were analyzed by Excel software.

Statistical Analysis

   i.   Correlation coefficient: The correlation coefficient at phenotypic (r_p) and genotypic (r_g) levels were calculated as follows:

$$r_p = (\sigma^2_{p12})/ (\sigma^2_{P11} \times \sigma^2_{P22})^{1/2}$$
$$r_g = (\sigma^2_{g12})/ (\sigma^2_{g11} \times \sigma^2_{g22})^{1/2}$$

   Where, σ^2_{P12} and σ^2_{g12} express phenotypic and genotypic co-variance of character 1 and 2 whereas, σ^2_{P11} and σ^2_{g11} represent phenotypic and genotypic variance of character 1 and σ^2_{p22} and σ^2_{g22} indicate variance at phenotypic and genotypic levels of character 2.

   ii. Path-coefficient: The path-coefficient analysis was carried out using the formula of Wright (1921 & 1923) as illustrated by Dewey & Lu (1959). The path-coefficient analysis was done at both phenotypic and genotypic levels by solving the simultaneous equations using matrix method. The form of equation is as follows:

$$r_{xy} = p_{xy} + r_{x2} P_{2y} ++ r_{x3}p_{xy} + ...r_{xn}Pny$$

   Where, r_{xy} = correlation between one components character and yield. P_{xy} = Path-coefficient between the same character and yield. r_{x2}, r_{x3}....r_{xn}= Represent correlation coefficient between that character and each of the other yield components in turn.

   iii. Selection index: The expected genetic advance from straight selection {GA(S)} and from discriminant function {GA(D)} was calculated as follows:

$$GA (S) = (Z/P) \times (g_{yy})/(t_{yy})^{1/2}$$
$$GA (D) = (Z/P) \times (b_{1g1y} + b_{2g2y})^{1/2}$$

   Where, Z/P = the selection differential in standard units, for the present study it was 2.06 at 5% level of selection. g_{yy} and t_{yy} = the genotypic and phenotypic variances of character. b_1, b_2, ...b_n = the relative weights for character. g_{1y}, g_{2y} . . . . . = the genotypic co-variances of independent character with y. The expected gain from the discriminant function over straight selection was calculated for all the functions as shown below:

$$\text{Expected gain (\%)} = [\{GA (D)/GA(S)\}-1] \times 100$$

RESULTS

Correlation coefficients

   In most of the cases the genotypic correlation coefficients were higher than the phenotypic correlation coefficients (Table 1). The results indicated that SW/P was positively correlated with DMF, NPBMF, NSBMF, PWFD, PdW/P and NS/P both at phenotypic and genotypic levels. On the other hand, RWFD, NPd/P and 1000-SW were negatively correlated with SW/P at phenotypic and genotypic level, while PHMF was correlated with SW/P at phenotypic and genotypic levels with positive and negative values, respectively. The genotypic correlation coefficient of SW/P with PdW/P and NS/P were high and greater than the phenotypic correlation coefficients of those characters and exhibited significant values. The genotypic correlation coefficients of NPBMF and NSBMF with SW/P were significant at 5% and 1% levels, whereas DMF with SW/P showed significant value at 5% level. The genotypic correlation coefficients of PHMF and RWFD with SW/P expressed significance with negative values at 5% level and 1000-SW had negative significant values at 5% and 1% levels.

   In this analysis, DMF was positively correlated with NSBMF, PHMF, NPd/P, PdW/P and NS/P both at phenotypic and genotypic levels. RWFD and 1000-SW correlated with DMF positively at both levels and NPBMF correlated negatively and positively with DMF at phenotypic and genotypic levels, respectively.The character, PWFD correlated with DMF positively and negatively at phonotypic and genotypic levels, respectively. In all the cases genotypic correlation coefficient was higher than the phenotypic correlation

coefficient excluding PWFD, RWFD and 1000-SW. The genotypic correlation coefficients of NPd/P, PDW/P and NS/P with DMF were significant at 5% level, whereas NPBMF with DMF showed significant values at both levels. RWFD had negative significant genotypic correlation coefficient value at 5% level.

Table 1. Phenotypic (r_p) (upper diagonal) and Genotypic (r_g) (lower diagonal) correlation coefficients between yield and yield contributing traits in chickpea.

Traits	DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPd/P	PdW/P	NS/P	1000-SW	SW/P
DMF		-0.036	0.149	0.139	0.069	-0.008	0.076	0.048	0.079	-0.055	0.059
NPBMF	0.844**		0.279	0.135	0.064	-0.175	0.294	0.244	0.299	-0.294	0.251
NSBMF	0.191	0.741*		0.228	0.088	-0.065	0.126	0.124	0.132	-0.009	0.121
PHMF	0.246	0.166	-1.314**		0.044	0.027	0.007	-0.008	0.033	-0.033	0.009
PWFD	-0.062	0.647	-0.158	0.405		0.100	0.169	0.165	0.159	-0.098	0.141
RWFD	-0.989**	-0.952**	-0.891**	0.220	-0.278		-0.187	-0.082	-0.185	0.222	-0.111
NPd/P	0.812*	1.200**	0.737*	-0.448	0.497	-0.855**		0.910**	-0.006	0.007	-0.003
PdW/P	0.789*	1.098**	0.585	-0.607	0.756*	-0.502	0.964**		0.882**	-0.022	0.936**
NS/P	0.766*	1.169**	0.769*	-0.295	0.411	-0.939**	-0.031	0.943**		-0.252	0.939**
1000-SW	-0.534	-1.156**	-0.832**	-0.512	-0.584	0.972**	0.0318	-1.213**	-1.218**		-0.011
SW/P	0.816*	1.139**	0.925**	-0.768*	0.423	-0.754*	-0.025	1.005**	0.969**	-1.260**	

Note: DMF- Days to maximum flower; NPBMF- Number of primary branches at maximum flower; NSBMF- Number of secondary branches at maximum flower; PHMF- Plant height at maximum flower; PWFD- Plant weight after fully dry; RWFD- Root weight after fully dry; NPd/P- Number of pods per plant; PdW/P- Pod weight per plant; NS/P- Number of seeds per plant; 1000-SW-Thousand seed weight ; SW/P- Seed weight per plant.
*& ** indicated significant at 5% and 1% levels respectively.

NPBMF showed positively correlation with NSBMF, PHMF, PWFD, NPd/P, PdW/P, NS/P at phonotypic and genotypic levels. RWFD and 1000-SW expressed negative correlation with NPBMF. The genotypic correlation coefficient was higher than the phenotypic correlation coefficient in all the cases except RWFD and 1000-SW. The genotypic correlation coefficients of NPd/P, PdW/P and NS/P with NPBMF were significant at 5% and 1% levels. NSBMF exhibited significant r_g value at 5% level. It is observed that RWFD and 1000-SW correlated with NPBMF significantly but in negative direction.NSBMF exhibited that this character correlated positively both at phenotypic and genotypic levels with NPd/P, PdW/P and NS/P. But this character correlated negatively with RWFD and 1000-SW at phenotypic and genotypic levels, respectively. In addition, PHMF and PWFD correlated positively with NSBMF at phenotypic level but negatively at genotypic level. It is noticed that NSBMF had significant r_g values at 5% level with NPd/P and NS/P in positive direction and PHMF, RWFD and 1000-SW showed negative significant r_g values. The character, PHMF correlated positively both at phenotypic and genotypic levels with PWFD and RWFD but negatively with PdW/P and 1000-SW. On the other hand, it showed positive and negative correlation at phenotypic and genotypic levels with NPd/P and NS/P, respectively.

PWFD correlated positively with NPd/P, PdW/P and NS/P both at phenotypic and genotypic levels and also indicated that the value of the genotypic correlation coefficient was higher than that of the phenotypic correlation coefficient. But PWFD positively and negatively correlated at phenotypic and genotypic levels with RWFD but 1000-SW had negative correlation at both levels. In addition, PdW/P showed significant r_g value at 5% level. RWFD had positive correlation both at phenotypic and genotypic levels with 1000-SW but negatively with NPd/P, PdW/P and NS/P. NPd/P and NS/P had significant r_g values in negative direction while, 1000-SW in positive direction.

NPd/P exhibited positive correlation both at phenotypic and genotypic levels with PdW/P and1000-SW and NS/P had negative correlation. Besides, PdW/P revealed significant correlation with NPd/P.The character, PdW/P was positively correlated both at phenotypic and genotypic levels with NS/P and negatively with 1000-SW. The value of r_g and $r_p$of NS/P with PdW/P had significant positive values while, 1000-SW with PdW/P had negative r_g value.NS/P correlated negatively with 1000-SW and the value of phenotypic correlation coefficient was lower than genotypic correlation coefficient. The genotypic correlation coefficient of NS/P with 1000-SW was significant at 5% and 1% levels but in negative direction.

Path-coefficient analysis at phenotypic level **(Fig. 1)**

It was observed from the table 2 that NS/P had the highest positive direct effect (1.077) on seed weight per plant (SW/P). DMF, NSBMF, PHMF, PWFD and PdW/P showed negative and NPBMF, RWFD, NPd/P and 1000-SW expressed least positive direct effect on seed weight per plant (SW/P). DMF had negative direct effect of -0.008 and indirect positive effect with NPd/P (0.006) and NS/P (0.085) on SW/P. The positive direct effect
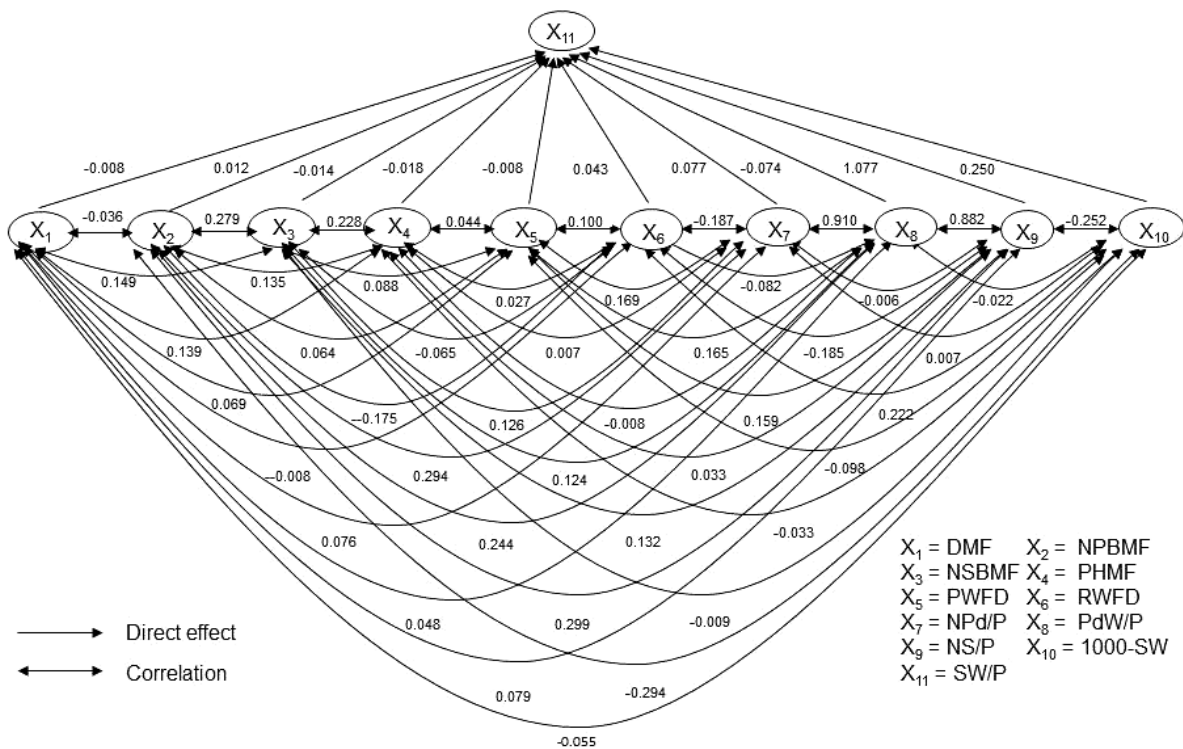
Figure 1. Path diagram of different yield contributing traits at phenotypic level.

of NPBMF on SW/P was 0.012. The character, NPBMF exhibited high indirect positive effect of 0.322 through NS/P. NSBMF had negative direct effect of -0.014 on SW/P. The high indirect positive effect of this character via NS/P was 0.142. The character, PHMF showed negative direct effect with a value of -0.018 on seed weight per plant. But it had indirect positive influence through NPBMF, RWFD, NPd/P, PdW/P and NS/P.

Table 2. Path-coefficient analysis showing direct (in bold) and indirect effects of yield components on yield of chickpea at phenotypic and genotypic levels.

Traits		DMF	NPBMF	NSBMF	PHMF	PWFD	RWFD	NPd/P	PdW/P	NS/P	1000-SW
DMF	P	**-0.008**	-0.0004	-0.002	-0.002	-0.0006	-0.0003	0.006	-0.004	0.085	-0.014
	G	**-0.099**	-0.011	-0.029	-0.043	0.008	-0.145	-0.008	0.273	1.023	-0.152
NPBMF	P	0.0003	**0.012**	-0.004	-0.002	-0.0005	-0.008	0.023	-0.018	0.322	-0.074
	G	-0.084	**-0.013**	-0.112	-0.029	-0.082	-0.140	-0.012	0.380	1.560	-0.330
NSBMF	P	-0.001	0.003	**-0.014**	-0.004	-0.0007	-0.003	0.010	-0.009	0.142	-0.002
	G	-0.019	-0.009	**-0.151**	0.231	0.020	-0.131	-0.007	0.203	1.026	-0.237
PHMF	P	-0.001	0.002	-0.003	**-0.018**	-0.0004	0.001	0.0005	0.0006	0.035	-0.008
	G	-0.024	-0.002	0.198	**-0.176**	-0.052	0.032	0.004	-0.210	-0.393	-0.146
PWFD	P	-0.0006	0.0008	-0.001	-0.0008	**-0.008**	0.004	0.013	-0.012	0.171	-0.024
	G	0.006	-0.008	0.024	-0.071	**-0.127**	-0.041	-0.005	0.262	0.550	-0.166
RWFD	P	0.00006	-0.002	0.0009	-0.0005	-0.0008	**0.043**	-0.014	0.006	-0.200	0.056
	G	0.098	0.012	0.134	-0.039	0.035	**0.147**	0.008	-0.174	-1.253	0.277
NPd/P	P	-0.0006	0.004	-0.001	-0.0001	-0.001	-0.008	**0.077**	-0.068	-0.006	0.002
	G	-0.081	-0.015	-0.111	0.079	-0.063	-0.126	**-0.010**	0.334	-0.041	0.009
PdW/P	P	-0.0004	0.003	-0.002	0.0001	-0.001	-0.004	0.070	**-0.074**	0.950	-0.006
	G	-0.078	-0.014	-0.088	0.107	-0.096	-0.074	-0.009	**0.346**	1.258	-0.346
NS/P	P	-0.0006	0.004	-0.002	-0.0006	-0.001	-0.008	-0.0004	-0.066	**1.077**	-0.063
	G	-0.076	-0.015	-0.116	0.052	-0.052	-0.138	0.0003	0.327	**1.334**	-0.347
1000-SW	P	0.0005	-0.004	0.0001	0.0006	0.0008	0.010	0.0005	0.002	-0.271	**0.250**
	G	0.053	0.015	0.126	0.090	0.074	0.143	-0.0003	-0.420	-1.625	**0.285**

Note: DMF- Days to maximum flower; NPBMF- Number of primary branches at maximum flower; NSBMF- Number of secondary branches at maximum flower; PHMF- Plant height at maximum flower; PWFD- Plant weight after fully dry; RWFD- Root weight after fully dry; NPd/P- Number of pods per plant; PdW/P- Pod weight per plant; NS/P- Number of seeds per plant; 1000-SW- Thousand seed weight; SW/P- Seed weight per plant.
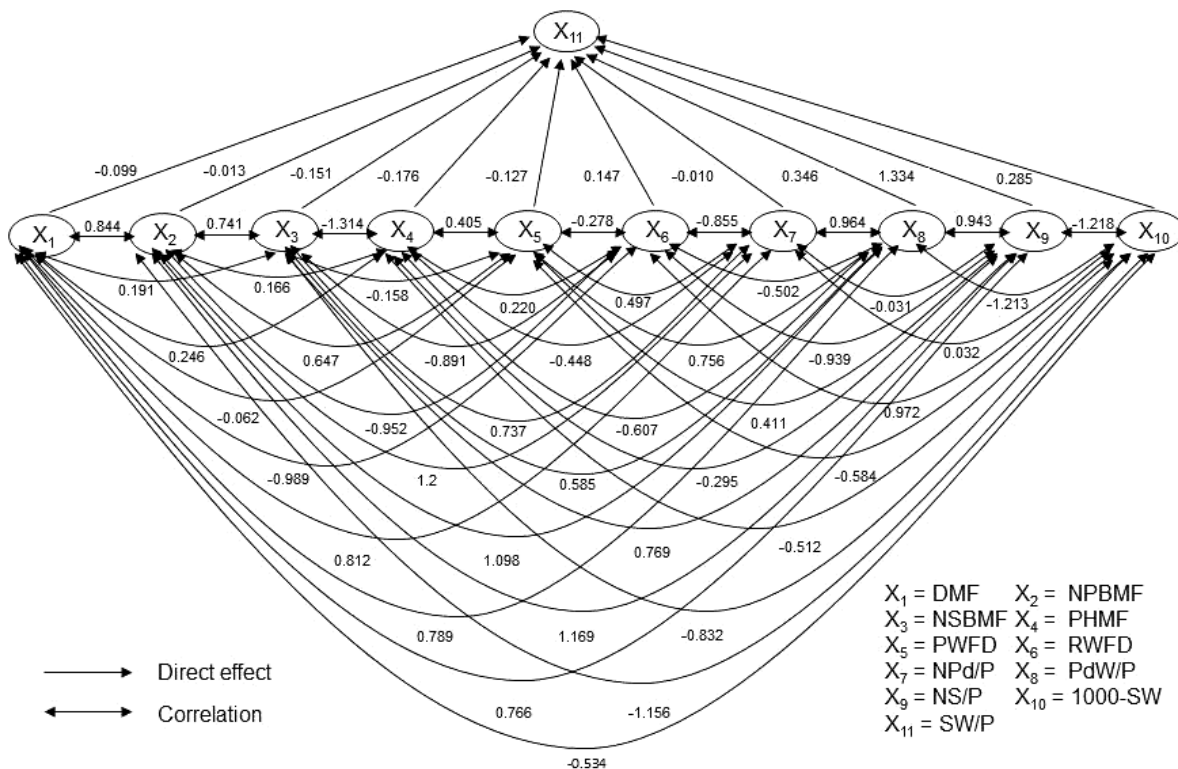
PWFD had direct negative effect (-0.008) on SW/P and showed high indirect positive effect (0.171) on SW/P via NS/P. RWFD had positive direct effect on SW/P and the value was 0.043. RWFD exhibited high

indirect positive effect (0.056) on SW/P via 1000-SW. Number of pods per plant (NPd/P) had positive direct effect (0.077) on SW/P and exhibited high positive indirect effect (0.004) on SW/P through NPBMF. The character, PdW/P showed the negative direct influence with a value of -0.074 on SW/P and expressed highest positive indirect effect (0.950) through NS/P. The total effect of NPd/P on SW/P was 0.936 (the second highest value).NS/P indicated positive direct effect (1.077) on SW/P. NS/P showed indirect positive influence (0.004) on SW/P via NPBMF. The total effect of NS/P on SW/P was 0.939 (highest value). 1000-SW indicated positive direct effect (0.250) on SW/P. It showed the highest indirect positive influence (0.010) on SW/P via RWFD. Although it exhibited indirect positive effect through all the characters except NPBMF and NS/P on SW/P, the values were least and negligible. The total effect of NS/P on SW/P was -0.011.

Path-coefficient analysis at genotypic level **(Fig. 2)**

   This table 2 exhibited that the highest positive direct effect was expressed by NS/P on SW/P and it was followed by PdW/P, 1000-SW and RWFD. The characters, DMF, NPBMF, NSBMF, PHMF, PWFD and NPd/P showed negative direct effect.

   DMF had negative direct effect (-0.099) on SW/P. But this character contributed to SW/P through positive indirect effects of PWFD, PdW/P and NS/P. NPBMF showed low direct negative influence on SW/P which was -0.013. This character also contributed to SW/P indirectly through NS/P and PdW/P. The total effect of NPBMF on SW/P was 1.139 (the highest value). NSBMF had direct negative effect with a value of **-**0.151on SW/P. This character expressed through positive indirect effect of NS/P, PdW/P, PWFD and PHMF. The maximum indirect effect was exhibited by NS/P (1.026). PHMF expressed negative direct effect on SW/P with a value of -0.176. This character showed positive indirect effect on SW/P through NSBMF, RWFD and NPd/P with the values of 0.198, 0.032 and 0.004, respectively.

Figure 2. Path diagram of different yield contributing traits at genotypic level.

   PWFD had negative direct effect on SW/P was -0.127 and the positive indirect influence through DMF, NSBMF, PdW/P and NS/P were 0.006, 0.024, 0.262 and 0.549, respectively. More or less, it contributed to SW/P in spite of having indirect negative effect through NPBMF, PHMF, RWFD, NPd/P and 1000-SW. RWFD had positive direct effect on SW/P and the value was 0.147. RWFD exhibited indirect positive effect on SW/P via most of the characters except PHMF, PdW/P and NS/P. Its total effect was -0.754 due to indirect negative effect on SW/P via NS/P (-1.253).

   NPd/P had negative direct effect of -0.010 on SW/P. The character, PdW/P showed the positve direct effect of 0.346 on SW/P. It contributed to SW/P greatly through NS/P (1.258) followed by PHMF. It showed negative indirect effect via DMF, NPBMF, NSBMF, PWFD, RWFD, NPd/P and 1000-SW. The total effect of this

character on SW/P was 1.005.NS/P had the highest positive direct effect (1.334). The character NS/P showed the positive indirect influence through PHMF, NPd/P and PdW/P and other characters expressed negative indirect effect on SW/P. The total effect of this character on SW/P was 0.969. The character, 1000-SW indicated positive direct effect (0.285) on SW/P. It exhibited indirect positive effect through all characters except NPd/P, PdW/P and NS/P on SW/P. The total effect of NS/P on SW/P was -1.260.

Selection index

The results obtained for different indices, containing SW/P and its components with expected gain in percentage over straight selection are shown in table 3. The maximum genetic gain of 570.49249% was exhibited when NPBMF (2) and RWFD (6) were included in the discriminant function. This value was followed

Table 3. Expected grain 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.

Selection Index	Expected Gain	Selection Index	Expected Gain	Selection Index	Expected Gain	Selection Index	Expected Gain
DMF(1)	53.967	8+11	104.337	4+6+11	180.105	3+4+6+11	138.833
NPBMF(2)	1118.189	1+2+3	128.757	4+8+11	79.100	3+4+8+11	59.964
NSBMF(3)	-397.918	1+2+4	123.037	6+8+11	93.099	3+6+8+11	70.155
PHMF(4)	272.021	1+2+6	148.169	1+2+3+4	95.050	4+6+8+11	71.394
PWFD(5)	-56.164	1+2+8	61.056	1+2+3+6	112.783	1+2+3+4+5	12.005
RWFD(6)	476.857	1+2+11	145.061	1+2+4+6	108.035	1+2+3+4+6	84.92
NPd/P(7)	-105.106	1+3+11	84.752	1+2+4+11	108.905	1+2+3+4+11	89.627
PdW/P(8)	13.305	1+4+6	61.467	1+2+6+11	126.603	1+2+3+6+11	103.632
NS/P(9)	-153.254	1+4+11	85.140	1+2+8+11	65.882	1+2+3+8+11	52.615
1000-SW(10)	-118.038	1+6+11	100.218	1+3+4+11	65.561	1+2+4+6+11	96.808
SW/P(11)	381.482	2+3+4	261.351	1+3+6+11	76.689	1+2+4+8+11	51.682
1+2	174.667	2+3+6	357.340	1+4+6+11	76.444	1+2+6+8+11	59.445
1+4	61.3769	2+3+8	118.126	2+3+4+6	210.381	1+3+4+6+11	59.625
1+6	69.980	2+3+11	284.938	2+3+4+8	88.167	2+3+4+5+11	52.314
1+11	113.285	2+4+5	61.008	2+3+4+11	190.200	2+3+4+6+8	79.254
2+3	531.598	2+4+6	284.288	2+3+5+6	51.659	2+3+4+6+11	162.82
2+4	375.941	2+4+11	238.974	2+3+5+11	66.902	2+3+4+8+11	85.761
2+5	77.667	2+5+6	71.495	2+3+6+8	104.540	2+3+5+6+11	60.457
2+6	570.492	2+5+11	84.216	2+3+6+11	231.595	2+3+6+8+11	99.261
2+8	162.569	2+6+8	138.978	2+3+8+11	112.169	2+4+5+6+11	59.030
2+11	384.049	2+6+11	298.668	2+4+5+6	56.053	2+4+6+8+11	93.208
3+4	141.311	2+8+11	139.454	2+4+5+11	65.418	3+4+6+8+11	54.910
3+6	175.808	3+4+6	133.333	2+4+6+8	101.879	1+2+3+4+5+6	11.548
3+11	252.579	3+4+11	162.111	2+4+6+11	200.379	1+2+3+4+6+11	80.227
4+6	214.057	3+6+11	202.553	2+4+8+11	104.758	1+2+3+6+8+11	47.666
4+11	217.258	3+8+11	76.636	2+5+6+11	75.493	2+3+4+6+8+11	76.849
6+11	282.698	4+6+8	50.494	2+6+8+11	121.88		

Note: DMF- Days to maximum flower; NPBMF- Number of primary branches at maximum flower; NSBMF- Number of secondary branches at maximum flower; PHMF- Plant height at maximum flower; PWFD- Plant weight after fully dry; RWFD- Root weight after fully dry; NPd/P- Number of pods per plant; PdW/P- Pod weight per plant; NS/P- Number of seeds per plant; 1000-SW- Thousand seed weight; SW/P- Seed weight per plant.

by 531.59816% genetic gain which was obtained when NPBMF (2) and NSBMF (3) were included in the discriminant function. The next high genetic gain of 384.04907% was obtained when NPBMF (2) and SW/P (11) were included in the discriminant function and followed by 282.6984% (6+11) and 252.57943% (3+11). The characters, DMF (1) NPBMF (2), PHMF (4), RWFD (6), PdW/P (8) and SW/P (11) showed positive expected gain and among them NPBMF (2) exhibited highest genetic gain.

In the discriminant function analysis, when selection indices contained three characters, the maximum genetic gain was recorded as 357.34037% for 2+3+6, followed by 298.66798% for 2+6+11, 284.93796% for 2+3+11, 284.28844% for 2+4+6, 261.35085% for 2+3+4, 238.97406% for 2+4+11, 202.55362% for 3+6+11 and 162.11135% for 3+4+11. In the same way, when four characters were included in the discriminant function viz., 2+3+6+11 gave the highest genetic gain of 231.595803 and followed by 210.381174%, 200.379694% and 190.200556% for 2+3+4+6, 2+4+6+11, and 2+3+4+11, respectively. Similarly, when five characters were

included in the discriminant function, the combination like 2+3+4+6+11 exhibited the highest genetic gain of 162.82608% followed by 103.63273% for 1+2+3+6+11. In case of six characters combination of discriminant function components like 1+2+3+4+6+11 had the highest genetic gain of 80.22788% followed by 76.849099% for 2+3+4+6+8+11.When the combinations of 7, 8, 9, 10 and 11 quantitative characters were considered the expected genetic gain was found to be low and negative in most of the cases in the present discriminant function analysis.

DISCUSSION

In the present study, SW/P was positively correlated with DMF, NPBMF, NSBMF, PWFD, PdW/P, and NS/P both at phenotypic and genotypic levels (Table 1). Seed yield per plant exhibited positive association with NPB/P as reported by Thakur & Sirohi (2009) in chickpea followed by Singh *et al*. (1990) in chickpea and Yucel *et al*. (2006) who obtained the positive correlation of PBN, SBN and SN with SY. Saleem *et al*. (2002) in chickpea observed the positive correlation of DTF and TWP with SY. Roy *et al*. (2006) in bush bean got positive correlation of DTF with SY/P followed by Singh *et al*. (1987) in chickpea and Singh (1985) in pea. On the other hand, RWFD, NPd/P and 1000-SW were negatively correlated with SW/P at phenotypic and genotypic levels. While PHMF positively and negatively correlated with SW/P at phenotypic and genotypic levels, respectively.

The genotypic correlation coefficient of SW/P with PdW/P and NS/P were high and greater than the phenotypic correlation coefficient of those traits and exhibited significant value. Thus, it can be inferred that selection based on any one of two traits either alone or in combination, would result in identifying high yielding genotypes. The genotypic correlation coefficient of DMF, NPBMF and NSBMF with SW/P were significant. PHMF, RWFD and 1000-SW with SW/P expressed significant but negative values. Ali *et al*. (2009) in chickpea reported the significant association of seeds per plant and primary branches per plant with grain yield per plant and negative correlation of PH with GY/P. Khan & Qureshi (2001) in chickpea also observed the significant association of PB/P and SB/P with GY followed by Sharma and Saini (2010) and Khan (1985) in mungbean.

In correlation analysis, DMF was positively correlated with NSBMF, PHMF, NPd/P, PdW/P and NS/P both at phenotypic and genotypic levels. Saleem *et al*. (2002) in chickpea observed the positive correlation of NSB, PH and NPP with DTF followed by Ali *et al*. (2009) regarding correlation of PH with DTF. NPBMF showed positive correlation coefficient with NSBMF, PHMF, PWFD, NPd/P, PdW/P and NS/P at phonotypic and genotypic levels. These results confirmed the findings of Khan & Qureshi (2001). NSBMF exhibited that this trait was positively correlated both at phenotypic and genotypic levels with NPd/P, PdW/P and NS/P. But this trait was negatively correlated with RWFD and 1000-SW at both levels, respectively. Qureshi *et al*. (2001) got the positive correlation of SB/P with GY and negative correlation of 100-GWT with SB/P reported by Ali *et al*. (2009). The trait, PHMF was positively correlated both at phenotypic and genotypic levels with PWFD and RWFD. PWFD was positively correlated with NPd/P, PdW/P and NS/P both at phenotypic and genotypic levels and also indicated that the value of the genotypic correlation coefficient was higher than that of the phenotypic correlation coefficient. RWFD had positive correlation both at phenotypic and genotypic levels with 1000-SW and NPd/P exhibited positive correlation both at phenotypic and genotypic levels with PdW/P and 1000-SW. In addition, PdW/P was positively correlated both at phenotypic and genotypic levels with NS/P. NS/P was positively correlated with 1000-SW and the value of phenotypic correlation coefficient was higher than genotypic correlation coefficient.

The path coefficient analysis based on SW/P as a dependent variable at phenotypic level revealed that all traits, except NPBMF, RWFD, NPd/P, NS/P and 1000-SW exhibited negative direct effects (Table 2). Among positive direct effects NS/P had the highest value of 1.077 on SW/P. It means a slight increase in any one of the above traits may directly contribute towards SW/P. For NPd/P (0.077), the direct effect was positive followed by RWFD and 1000-SW while, their association with SW/P were observed to be negative, indicating the importance of restricted selection model for exploitation of the direct effects noticed.

In path-coefficient, the highest positive direct effect was expressed by NS/P on SW/P and followed by PdW/P, 1000-SW and RWFD at genotypic level. Compared to the correlation analysis at genotypic level, path-coefficient of SW/P and its components indicated that NS/P and PdW/P exerted the highest direct influence, with values of 1.334 and 0.346, respectively. Though RWFD and 1000-SW on SW/P showed positive direct effects but regarding correlation the relationship was negative. Uddin *et al*. (1990) in chickpea and Yucel *et al*. (2006) reported that SN was the major contributor to SW/P. Ali & Shaikh (1986) in mungbean observed that

100-SW had a positive direct effect on SW/P, though a significant negative correlation was found and followed by Roy *et al*. (2006).

In selection study, the maximum genetic gain of 570.49249% was exhibited when NPBMF (2) and RWFD (6) were included in the discriminant function followed by 531.59816% (2+3). Table 3 also revealed that among the individual traits namely, DMF (1), NPBMF (2), PHMF (4), RWFD (6), PdW/P (8) and SW/P (11) showed positive expected gain and among them NPBMF (2) exhibited highest genetic gain, followed by RWFD (6), SW/P (11) and PHMF (4) and the remaining traits indicated negative genetic gain. The highest genetic gain of NPBMF (2) as showed individually might be due to environment as it is obvious that influence on individual trait is more than over multiple traits.

CONCLUSION

During selection emphasis should be given on PdW/P and NS/P as they exhibited high correlation and high positive direct effect on yield. Besides, NPBMF and RWFD may be considered as primary yield components because they showed highest genetic gain among the combinations of selection indices and also exhibited positive genetic correlation with yield and positive direct effect on phenotypic level.

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