Available online at http://www.journalcra.com

International Journal of Current Research
Vol. 16, Issue, 05, pp.28407-28413, May, 2024
DOI: https://doi.org/10.24941/ijcr.47226.05.2024

ISSN: 0975-833X

INTERNATIONAL JOURNAL OF CURRENT RESEARCH

RESEARCH ARTICLE

RELATIONSHIP BETWEEN FLOWER COLOUR, SEED COAT COLOUR, SEED INDEX, SEED YIELD AND PROTEIN CONTENT IN DESI CHICKPEA (*CICER ARIETINUM* L.)

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ARTICLE INFO

Article History:
Received 20th February, 2024
Received in revised form
25th March, 2024
Accepted 14th April, 2024
Published online 30th May, 2024

Key words:
Flower Colour, Seed Coat Colour, Seed Index, Protein and Desi Chickpea.

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ABSTRACT

This study investigated the relationship between flower colour, seed coat colour, seed index, seed yield, and protein content in desi chickpea (*Cicer arietinum*). The objective was to understand the potential impact of these traits on the productivity and nutritional quality of the crop. Forty two desi chickpea accessions were evaluate. Seed yield, measured in kilograms per hectare, was recorded from field trials. Protein content, representing the nutritional quality of the seeds, was determined through laboratory analysis. The results revealed significant variability in flower colour, seed coat colour, seed index, seed yield, and protein content among the desi chickpea accessions. Flower colour was found to be diverse, with pink being the most prevalent, followed by blue. Seed coat colour exhibited variations, with dark brown and brown being the most common, while yellow and green were comparatively less frequent. Seed index varied across the accessions, indicating differences in seed size and weight. Seed yield ranged from moderate to high, highlighting the potential for improved productivity. Protein content also showed considerable variability, with accessions exhibiting a wide range of nutritional quality ranging from 13.87 to 26.85 % in seed and 21.70 to 48.50% in leaves of desi chickpea. Correlation analysis demonstrated a positive relationship between plant height, number of secondary branches, pods per plant, seed index, biological yield, harvest index and seed yield, suggesting that larger seeds may contribute to higher yield potential. However, no significant correlation was found between protein content and seed index, although, it showed significant association with days to 50% flowering, plant height, pods per plant and plot yield. Plant height exhibited significant positive correlation with height of first pod.

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Citation: Shalu Kumari, Ritu R Saxena, Kanushree Nandedkar, Luchika Rana1, Suman Rawte, Ravi R Saxena and Mangla Parikh. 2024. "Relationship between flower colour, seed coat colour, seed index, seed yield and protein content in desi chickpea (*Cicer arietinum* L.)*". International Journal of Current Research*, 16, (05), 28407-28413.

INTRODUCTION

Chickpea (*Cicer arietinum* L.) is a winter annual crop belonging to the family Leguminosae/ Fabaceae. In India, chickpea is known by different names like *Chana* or *Gram* or *Bengal gram* or *Chani* in Haryana, Rajasthan, Uttarakhand, Uttar Pradesh, Madhya Pradesh, Chhattisgarh, Bihar, Jharkhand, etc.; *Chhole* in Punjab, Jammu and Kashmir and Delhi; *Chola* in West Bengal; *Harbara* in Maharashtra*; Boot* in Orissa; *Sanagulu* in Andhra Pradesh; *Kadale* in Karnataka; *Kadalai* in Tamil Nadu; and *Kadala* in Kerala, indicating its wide spread cultivation and knowledge of utilization. Chromosome number in *Cicer* species can be generalized as 2n=2x= 16, although varying numbers both for chickpea (2n= 2x= 14, 16, 24, 32) and other wild *Cicer* species (2n=14, 16, 24) have been reported, but could not be confirmed by other workers. It is the third most important legume in the world after dry beans and dry peas. South West Asia and Mediterranean region are the primary center of origin while, Ethiopia as the secondary center of origin. It is an annual herb which grows maximum 1.0 m in height. Its growth habit is indeterminate type. Based on the angle formed by the branches with respect to the ground, the plants can be divided into semi erect, erect, semi spreading, spreading and prostrate. The leaves are oval or elliptical in shape and are compound imparipinnate. Chickpea is categorized into two major types based on distinct botanical or morphological traits as well as molecular diversity analysis: desi type and kabuli type (Jadhav *et al.*, 2015). The desi (microsperma) chickpea is distinguished by its small seeds, pods, leaflets, and plantlets. Despite this, considerable differences in flower and seed coat colour, as well as seed morphology, are typical. The flower colour ranges from white to red, purple, and blue, with a variety of brown seed coats.

The seed coat ranges in texture from smooth to wrinkled, reflecting genetic variation. The kabuli kind of "macrosperma" chickpea is notable for its ram's head shaped seeds. The kabuli type, in contrast to the desi type, has huge seeds, pods, leaflets, and plantlets. The colour of the flower and seed coat is usually white or cream. The kabuli type's seed coat is thinner and less wrinkled than the desi type's. ICRISAT's chickpea germplasm collection contains roughly 3.8 percent of a rare chickpea variety known as "pea shaped." They have morphologies that are halfway between desi and kabuli: small seeds and pods smooth seed coats, spherical seed shapes that resemble pea seeds, and a variety of seed coat colour. Madhya Pradesh, Rajasthan, Maharashtra, Uttar Pradesh, Andhra Pradesh, Karnataka, Chhattisgarh, Bihar, and Jharkhand are the primary chickpea-growing states, accounting for more than 95 percent of the country's total chickpea production (AICRP, 2020, 2019). Chickpea has played a major role in realization of 'Pulse Revolution' in India making the country near self-sufficient in Pulses. There has been remarkable increase in chickpea production and productivity in the country during 2014-15 to 2020-21.

From a level of 7.59 million tonnes in 2014-15, chickpea production rose to an all-time high of 12.61 million tons during 2020-21. This represented an increase of nearly 66% during six years (Iruela *et al.*, 2002). Chickpeas are high in protein, minerals (iron, and zinc), and vitamins (B vitamins) (riboflavin, niacin, thiamin, folate and the vitamin A precursor beta-carotene). Chickpeas are commonly eaten with cereals (wheat, rice, and maize), and this combination diet offers all of the essential amino acids by complementing each other for limiting amino acids (lysine in cereals and sulphur-containing amino acids in chickpea (Kishor, 2018). Chickpeas are in high demand due to their nutritious content. Despite their nutritious value, chickpeas include anti-nutrients such as tannin and phytic acid. Tannins inhibit the digestibility of protein and starch; whereas, phytic acid decreases the bioavailability of some essential minerals like iron, zinc etc (Kumar, 1982). Protein is a necessary component of life. Pulses have two to three times the protein content of cereals. It is a significant source of protein in the Indian diet. However, potentiality of the protein has not been fully exploited as a source of protein in human diets. The protein content of currently available chickpea cultivars ranges between 20 and 22 percent, with a large range of variance in chickpea germplasm, ranging from 12 to 30 percent (Jadhav, 2014). As a result, it seems feasible to develop cultivars with 20–25 percent higher protein content than present cultivars. However, there have been limited breeding efforts on further improving chickpea protein content. The development of high-protein variants can aid in the alleviation of this problem. Protein deficit can be alleviated through the production of high-protein cultivars.

Crop improvement is determined by the amount of genetic variability in the base population. The effectiveness of the selection criteria determines progress in breeding of any crop. Correlation is a valuable statistical approach for detecting useful features that influence yield as well as unfavorable associations between component characters. The linkage has been reported between the flower colour, protein content and seed size (Miller *et al.*, 1958). In chickpea, there are three distinct flower colours namely, pink, blue, and white. The blue flower colour, high protein content, and small seed size were linked. But the linkage was not tight (Miller *et al.*, 1958). To recover segregating plants combining high seed protein percentage with large seeds, genetic studies on flower colour and seed protein content become important. Information on protein content inheritance patterns and connections with other traits could aid in the development of chickpea cultivars with increased protein content, high yield, market-preferred grain qualities (size, shape, and colour), and other desired agronomic traits. Thus, an attempt was made to find out desi chickpea genotypes possessing high yield with high protein content and also to understand the relationship among the flower colour, seed size and protein content.

MATERIALS AND METHODS

The present research work was conducted at Research cum Instructional farm Department of Genetics and Plant Breeding, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, during the *Rabi* season of 2021-22. Chhattisgarh is situated between 17°14'N and 24°45'N latitudes and 79°16' E and 84°15' E longitudes. Raipur (C.G.) is lies at 21°16'N latitude and 81°36' E longitude with an altitude of (289.60 m) above mean sea level. The maximum monthly mean temperature was 36.52°C during March, 2022 and minimum monthly mean temperature was 12.80°C during January, 2022. The total rainfall during crop growing period was (156.20 mm). Forty-two genotypes of desi chickpea along with checks were taken for this research (Table 1). These genotypes were selected from a chickpea germplasm procured from NBPGR on the basis of protein content (more than 20%). The material was grown in the *Rabi* season of 2021-22. The chickpea seeds were sown in the field, in RBD with 2 replications on 7th December, 2021. Each plot comprised of 4 rows of 4m length in each replication. The row x row and plant x plant distance of 30 cm and 10 cm and net plot area was 4.8m^2. The seeds were pre-treated with Bavistin, Trichoderma, Rhizobium and PSB cultures. Fertilizer dose @ of 20:40:20 kg per hectare (NPK) was applied. Two irrigations were given to the trial after one month of sowing and after 45 days of first irrigation.

Thirteen yield and yield attributing traits and one quality trait that is protein content were taken to fulfil the purpose of the study. Random five plants were selected from each of the plot and replications for collecting data of different traits at optimal plant growth period. For statistical analysis, average data from the sampled plants were taken on days to 50 % flowering (DF), days to maturity (DM), height of the first pod (cm) (HOFP), plant height (cm) (PH), primary branches (PB), secondary branches (SB), seeds per pod (SPP), pods per plant (PPP), 100 grain weight (g) (HSW), biological yield per plant (g) (BY), harvest- index (%) (HI), plot yield in grams (g) (PYLG), seed yield per plant (g) (SYP) and protein content (PROT) (Jukanti, 2022; Thakur *et al.*, 2018). Protein content was obtained by multiplying the total nitrogen content in the seeds by the multiple factor 6.25 (Jukanti, 2012). These mean data were utilized to calculate variability parameters using SPSSv17.0. The coefficient of variation (Burton, 1953) and its magnitude was given as higher (> 20%), moderate (between 10-20 %) and low (< 10%) (Wright, 1921); broad sense heritability were classified as low (< 30 %), moderate (31-60 %) and high (> 60 %) and expected genetic advance (>20 % = High; 10 – 20 % = Moderate and < 10 % = Low) (Jones, 1941). Association analysis among yield traits was worked out (Sahrawat, 2002). Path analysis was first used for plant selection (Deepika., 2021). It measures the direct and indirect contribution of independent variables on dependent variable using the scale (Robinson, 1951).

RESULTS AND DISCUSSION

The occurrence of significant level of variation in the observed traits implies the presence of variability. The relatively large and significant percentage of total variation attributable to G x E interaction implies that genotypes responded differently to environment of chickpea. This variability can be exploited and utilised to improve genotype development. Individual genetic traits in a population are said to have genetic variability when they have a proclivity to differ from one another. This is the foundation upon which any breeding effort must be built. DF ranged from 46 days to 70.5 days with a mean of 60.81 days. JG-24 flowered early while GP-181 and GP-160 recorded late flowering. DM ranged from 97 (JG-315) to 114 (GP-152) days with an average of 107.46 days. JG 315 and JG24 showed medium duration maturity (90-100 days) and rest of the entries matured late (>100 days). The tallest genotype recorded is 42.92 cm (JG-24) while the shortest genotype recorded a height of 31.50 cm (GP-16) with mean height of 36.98 cm. GP19, GP 29 and GP 54 fell into medium stature of height (45-65 cm) and rest of the entries exhibited short stature (<45 cm). GP-19 (33.92 cm) recorded high score for HOFP. GP-181 and GP-16 recorded more number of primary and secondary branches, respectively. GP-54 and GP-91 had more number of pods and seeds per pod, respectively. The HSW ranged from 8.88 g to 35.78 g with an average of 14.22 g. T39-1 (Blue flower) had the least weight i.e. 8.88 g; while GP-54 recorded the highest HSW of 35.78 g. BY observed is 4.17g for GP-181 whereas, the highest value was observed in (14.75g) for T39-1(B), with the mean of 8.25 g. HI ranged from a minimum of 13.28% for to a highest of 53.40% with an average of 48.16 %. The PYLG ranged from 139.50g to 652.50g with the mean of 398.83g. GP-54 recorded high PYLG and SYP. GP-15 (26.85%) recorded high protein content. Six genotypes showed protein content ranging from 13.87% (T 39-1 pink) to 19.77% (GP 165) falling in low classification of protein (10-20%); thirty-two genotypes exhibited medium category (20-25%) of protein whereas, GP 10, GP 94, GP 2 and GP 15 were the four genotypes which reported high values for protein content ranging from 25.33 to 26.85 % (table 2).

Phenotypic (PCV) and genotypic coefficient of variation (GCV) (%): The study of variation is based on the division of variation into components attributed to various sources (phenotypic, genetic and environmental). The relative amounts of these elements can have an impact on a population's genetic makeup. Statistics has provided a number of analytical approaches for evaluating genetic variability. GCV and PCV are two of the most common methods for determining the amount of heritable and non-heritable variation. The magnitudes of PCV were greater than GCV magnitudes; this demonstrated the influence of the environment on the genotypic effect, which in turn reflected the phenotypic effect. Seven characters, SB, PPP, HSW, BY, HI, PYLG, and SYP showed high PCV coupled with high GCV. Four characters, namely, PH, HOFP, SPP and PROT showed moderate values of PCV along with moderate values of GCV. For all the characters under study, magnitude of PCV was more than magnitude of GCV (Table 2). From this, one can infer that the variation is not only due to the genes but also due to the influence of environment on the character expression. Similar conclusion for respective characters concluded by (4, 6, 20, 17, 10).

Heritability (h^2_{bs}) (%) and Genetic advance as percent of mean (GAM) (%): Heritability is the heritable portion of phenotypic variance. It is good index for the transmission of character from parents to their offspring. The estimation of heritability helps the plant breeder in selection of elite genotype from diverse genetic population. Genetic advance refers to an increase in the mean genotypic value of selected plants compared to the parental population. It's a measure for how far genetic progress has been made due to selection. In estimating the gain under selection, heritability estimates combined with genetic advance are usually more useful than heritability estimates alone. Genetic diversity, heritability, and selection intensity all influence genetic progress under selection. High heritability along with high genetic advance indicates that the heritability is due to additive gene effect and selection will be effective. The characters which showed high heritability and genetic advance were, PH, HOFP, SB, SYP, BY, HSW, PYLG and PROT (Table 2). High heritability with low genetic advance indicates that character is governed by non-additive genes action. The high heritability being exhibited due to favourable influence of environment rather than genotype and selection may not reward for such traits. Low heritability along with high genetic advance indicates that character is governed by additive gene action and due to high environmental effect heritability is low. In this case selection may be effective. Low heritability accompanied with low genetic advance reveals that character is highly influenced by environmental effect and selection would be ineffective. In case of GA as % of mean, plot yield (74.98%) had maximum value.

Traits exhibiting high values of PCV, GCV, heritability and GAM were SB, HSW, BY, PYLG and SYP. This indicates the additive gene effects of the trait and the effect of the environment on heritability.

Correlation studies: In a breeding programme, association analysis is a critical step. It determines the component characters on which selection can be based for genetic improvement in grain yield and gives an idea of the relationship between the various characters (Dewey, 1959). The effectiveness of the selection process is also influenced by the degree of association. Simple correlation, total correlation, or zero order correlation coefficient refers to the relationship between two variables. Correlation studies aid in the comprehension of yield components and the effects of other characters on the same (Subramanian, 1973; Jones, 1941). The correlation coefficient analysis is a measure of how closely two variables are related. The relationship was studied and found that the genotypic correlation values were high in magnitude as compared to the phenotypic correlation values, indicating the less influence of environment. SYP showed positive and highly significant correlation with PH, SB, PPP, HSW, BY, HI and PYLG (Fig 2) at phenotypic level. The positive association between two traits indicates that the change in two variables are in same direction that means, high value of one variable is associated with other and *vice versa.*

Table 1. List of chickpea genotypes with checks

GP No.	Accession No.	Source	GP No.	Accession No.	Source	GP No.	Accession No.	Source
GP2	NC33367	unknown	GP52	IC468839	Raj	GP152	IC272459	Bihar
GP5	IC272496	AP	GP54	IC551991	unknown	GP154	IC328117	MP
GP6	IC272212	MP	GP58	IC468756	MP	GP156	IC552190	unknown
GP8	IC027282	unknown	GP60	ICC3498	unknown	GP159	IC275626	MP
GP10	IC275853	Raj	GP79	IC468727	MP	GP160	IC468600	UP
GP11	IC468840	Raj	GP80	IC486991	MH	GP161	IC327655	UP
GP12	IC468742	MP	GP81	IC770	unknown	GP164	IC327527	MP
GP13	IC327362	TN	GP82	IC512075	Delhi	GP165	IC84017	Delhi
GP15	IC267309	unknown	GP87	IC116340	unknown	GP181	IC305441	Punjab
GP16	IC272401	Bihar	GP91	IC506784	unknown	T39-1 ((P)	Check	Landrace
GP17	IC208294	MP	GP94	EC441751	unknown	T39-1 (B)	Check	Landrace
GP19	IC272196	MP	GP96	IC487505	MP	JG24	Check	MP
GP29	IC348552	MP	GP97	ICC5980	unknown	JG315	Check	MP
GP51	IC268874	UP	GP127	ICC4425	unknown	CG Chana 2	Check	CG

Table 2. Variability parameters for yield attributing traits and protein content in chickpea genotypes

Parameter/ traits	DF	DM	PH	HOFP	PB	SB	PPP	SPP	HSW	BY	HI	PLYG	PROT	SYP
GM	60.81	107.46	36.98	22.32	2.21	7.87	19.82	1.33	14.22	8.25	32.42	398.83	22.41	2.56
S.E.	0.77	0.66	0.81	0.65	0.08	0.47	1.28	0.04	0.69	0.39	1.51	23.61	0.43	0.15
CV (%)	8.19	3.96	14.21	18.91	24.36	38.62	42.02	17.35	31.64	30.59	30.10	38.37	12.45	38.94
Min.	46.00	97.00	31.50	16.34	1.15	3.40	6.50	1.05	8.88	4.18	13.28	139.50	13.87	1.30
Max.	70.50	114.50	53.50	33.92	3.75	16.92	53.00	2.10	35.79	14.75	53.40	652.50	26.86	6.85
PCV (%)	8.54	4.20	14.88	19.79	29.84	40.27	47.16	19.28	32.07	31.85	33.12	39.03	13.40	39.86
GCV (%)	7.83	3.70	13.51	17.99	17.22	36.90	36.15	15.17	31.21	29.28	26.74	37.69	11.43	38.00
h^2 ($_{bs}$) (%)	83.97	77.26	82.48	82.58	33.30	83.94	58.77	61.94	94.71	84.55	65.19	93.26	72.74	90.88
GAM (%)	14.77	6.69	25.28	33.67	20.47	69.64	57.10	24.60	62.57	55.47	44.48	74.98	20.08	74.62
MSG	**	**	**	**	*	**	**	**	**	**	**	**	**	**

DF = Days to flowering; DM = Days to maturity; PH = Plant height (cm); HOFP = Height of first pod (cm); PB = Primary branches; SB = Secondary branches; PPP = Pods per plant; SPP = Seeds per pod; HSW = Hundred seed weight (g); BY = Biological yield (g); HI = Harvest index (%); PLYG = Plot yield (g); Protein = protein content (%); SYP = Seed yield per plant (g); MSG = Mean sum of square due to genotype

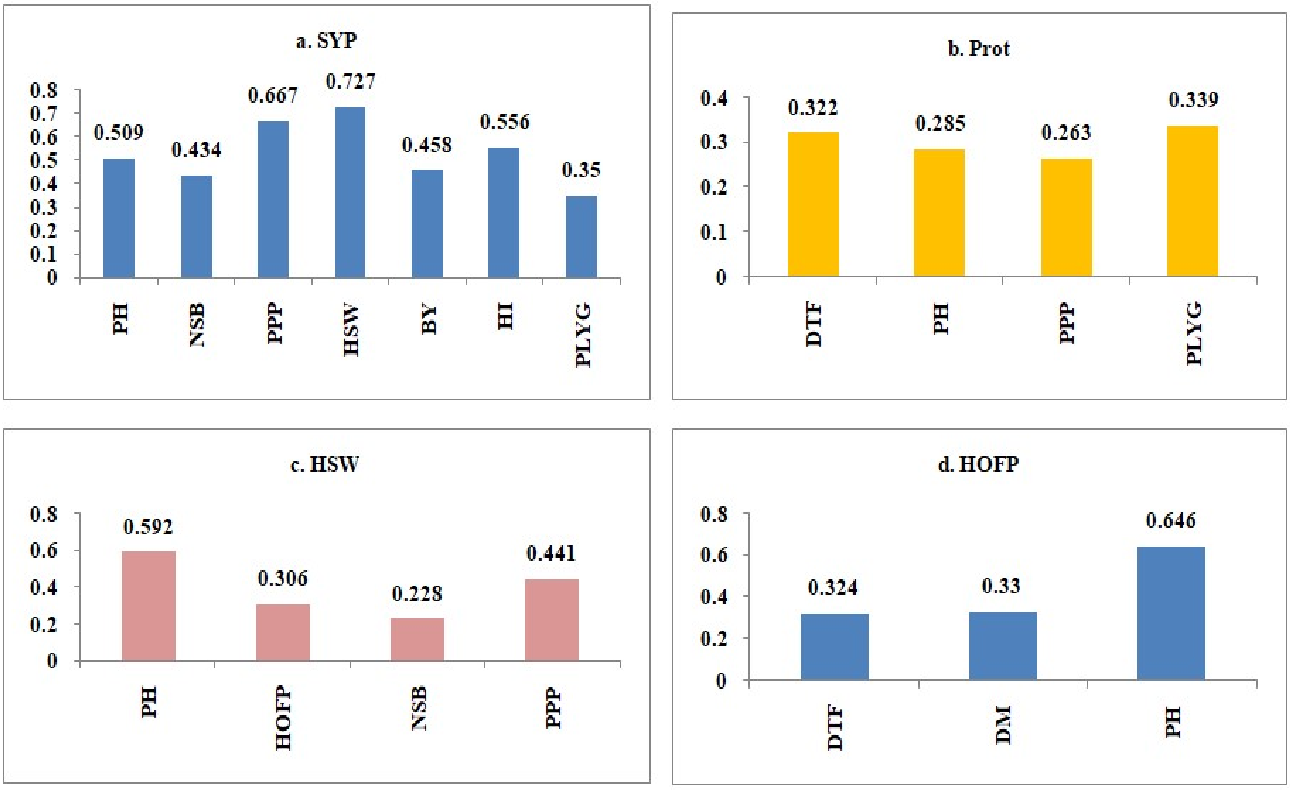

Fig. 2. Phenotypic relationship of SYP; Prot; HSW and HOFP with other yield traits

Table 3. Phenotypic direct effects of yield attributing traits on SYP as dependent variable

Traits	SYP	P corr
HSW	0.26	0.727**
BY	0.57	0.458**
HI	0.70	0.556**

Residual Effect= 0.044

Likewise, a negative association tells that increase in one trait leads to decrease in other traits. PROT showed positive significant correlation with DF, PH, PPP and PYLG, at phenotypic level while association with number of primary branches was negative at phenotypic level. PYLG showed positive correlation with DM, SB and PPP whereas, negative significant correlation with PB. HI exhibited positive relationship with PPP and HSW. BY showed negative correlation with HI. HSW showed positive association with PH, HOFP, SB and PPP. From the above observations, we can infer that the improvement of seed yield per plant could be brought about through selection for improvement in number of secondary branches, pods per plant, hundred seed weight, harvest index, and plot yield. Equivalent findings were reported by (4, 5, 1, 14) for different traits studied.

Path analysis: Path analysis reveals how a component trait influences the dependent trait, both directly and indirectly, through other characters. This indicates whether the association with the dependent trait is due to a direct effect of the component trait or an indirect effect via other component traits. The path coefficient analysis was performed by calculating the correlation coefficient between different quantitative characters in order to determine the direct and indirect effects of different characters on seed yield per plant. The residual effect sheds light on other important traits that were not investigated in this study, as well as their effects on the dependent variable. The correlation coefficient between seed yield per plant and other yield attributing character are partitioned into direct and indirect effect. The study was carried out by considering the grain yield as dependent variable and rest of the traits as the independent variables. Moderate to high positive direct effect on SYP was exhibited by HSW, BY and HI (table 3). These traits also exhibited significant phenotypic correlation coefficient with seed yield per plant. In this case, direct selection and improvement of these traits can achieve the improvement of the dependant trait. Residual effect was recorded very negligible. It indicates that besides the character studied, there are only few other attributes for yield.

Table 4. Relationship of chickpea genotypes with flower colour, seed coat colour, seed size, seed yield and protein content (seed and leaf)

GP NO.	Acc. No.	Flower colour	Seed coat colour	HSW (g)	SYP (g)	PLYG (g)	Protein (seed)	Protein (leaf)
GP2	NC33367	Pink	Brown	12.98	2.90	565.00	25.84	35.0
GP5	IC272496	Pink	Brown	12.84	2.14	634.00	24.11	31.1
GP6	IC272212	Pink	Brown	10.23	2.15	437.50	22.24	37.0
GP8	IC027282	Pink	Brown	15.66	4.00	546.00	24.81	30.2
GP10	IC275853	Pink	Dark Brown	12.91	3.45	571.50	25.33	32.2
GP11	IC468840	Pink	Brown	11.18	2.40	617.00	23.65	29.5
GP12	IC468742	Pink	Yellow	16.08	4.15	584.00	21.80	28.7
GP13	IC327362	Pink	Yellow	14.46	3.35	588.50	23.55	27.7
GP15	IC267309	Pink	Brown	18.13	2.30	453.00	26.85	26.6
GP16	IC272401	Pink	Brown	12.18	2.50	594.50	22.03	28.5
GP17	IC208294	Pink	Green	12.51	2.65	450.50	21.95	23.5
GP19	IC272196	Pink	Dark Brown	20.23	2.60	183.50	22.84	28.6
GP29	IC348552	Pink	Brown	13.23	2.65	436.00	24.47	24.6
GP51	IC268874	Pink	Brown	11.98	2.25	553.00	23.21	25.0
GP52	IC468839	Pink	Brown	13.08	2.45	512.50	24.43	28.0
GP54	IC551991	Pink	Brown	35.78	6.85	652.50	24.60	26.0
GP58	IC468756	Pink	Dark Brown	13.73	2.55	267.00	23.11	26.8
GP60	ICC3498	Pink	Brown	17.01	4.05	458.00	20.83	24.2
GP79	IC468727	Pink	Brown	12.54	2.70	455.00	22.70	25.5
GP80	IC486991	Pink	Yellow	13.94	1.55	415.50	23.79	22.8
GP81	IC770	Pink	Yellow	13.41	2.00	589.00	21.91	21.7
GP82	IC512075	Pink	Brown	12.49	1.60	388.50	21.51	25.0
GP87	IC116340	Pink	Brown	13.46	1.75	345.50	22.24	23.3
GP91	IC506784	Pink	Brown	10.46	1.45	149.00	23.88	26.0
GP94	EC441751	Pink	Dark Brown	25.14	4.00	163.00	25.45	27.8
GP96	IC487505	Pink	Brown	12.74	1.50	360.00	24.13	24.3
GP97	ICC5980	Blue	Yellow	10.09	1.85	372.50	23.18	47.8
GP127	ICC4425	Pink	Green	11.44	1.65	453.00	19.20	27.7
GP152	IC272459	Pink	Brown	11.16	2.00	258.00	23.45	23.5
GP154	IC328117	Pink	Brown	12.88	1.30	425.00	23.38	48.5
GP156	IC552190	Pink	Yellow	13.58	3.15	364.50	21.21	48.0
GP159	IC275626	Pink	Yellow	11.78	3.35	449.50	24.52	43.2
GP160	IC468600	Pink	Brown	13.41	2.05	160.00	21.76	44.6
GP161	IC327655	Pink	Brown	13.63	2.45	328.50	22.15	38.3
GP164	IC327527	Pink	Brown	15.13	2.15	438.00	23.08	44.0
GP165	IC84017	Pink	Brown	13.46	2.40	224.00	19.77	48.1
GP181	IC305441	Pink	Dark Brown	11.01	1.90	139.50	22.25	47.8
T39-1 (P)	Check	Pink	-	12.00	2.25	203.50	13.87	-
T39-1 (B)	Check	Blue	-	8.88	1.95	190.50	24.46	-

Table 5. Summarized data of promising chickpea genotypes with flower colour, seed coat colour, seed size, seed yield and protein content (seed and leaf)

GP NO.	Acc. No.	Flower colour	Seed coat colour	HSW (g)	SYP (g)	PLYG (g)	Protein (seed)	Protein (leaf)
GP2	NC33367	Pink	Brown	12.98	2.90	565.00	25.84	35.0
GP5	IC272496	Pink	Brown	12.84	2.14	634.00	24.11	31.1
GP8	IC027282	Pink	Brown	15.66	4.00	546.00	24.81	30.2
GP10	IC275853	Pink	Dark Brown	12.91	3.45	571.50	25.33	32.2
GP15	IC267309	Pink	Brown	18.13	2.30	453.00	26.85	26.6
GP29	IC348552	Pink	Brown	13.23	2.65	436.00	24.47	24.6
GP52	IC468839	Pink	Brown	13.08	2.45	512.50	24.43	28.0
GP54	IC551991	Pink	Brown	35.78	6.85	652.50	24.60	26.0
GP94	EC441751	Pink	Dark Brown	25.14	4.00	163.00	25.45	27.8
GP96	IC487505	Pink	Brown	12.74	1.50	360.00	24.13	24.3
GP159	IC275626	Pink	Yellow	11.78	3.35	449.50	24.52	43.2
T39-1 (P)	Check	Pink	-	12.00	2.25	203.50	13.87	-
T39-1 (B)	Check	Blue	-	8.88	1.95	190.50	24.46	-

Relationship of chickpea genotypes with flower colour, seed coat colour, seed size, seed yield and protein content (seed and leaf): The summarized data in the table 4 and 5 depicts about the relationship between the flower colour, seed coat colour, hundred seed weight, seed yield per plant and protein content both from seeds and as well as from leaves of chickpea genotypes. In our study, the high protein content in seeds were recorded by GP2 (NC 33367) which had pink flower along with brown seed coat and possessed very small seed size (12.98g); however the protein content in leaves was high and its translocation to sink was found to be less. GP2, GP5, GP8, GP 10, GP 15, GP 29, GP52, GP 96, GP 159 and T39-1(P) beard pink flower colour and all these entries also possessed very small seed size ranging from 12.00g to 18.13g. The seed coat colour also ranged from brown to dark brown colour except GP 159 showed yellow seed coat colour. On contrary to these results, T39-1 (B) exhibited blue colour flower with 8.88g seed size with the seed protein content of 24.46g. There are different reports on inheritance of seed size in chickpea, and the main reason of difference is about the parents used in the crossing program. The flower colour, seed coat colour showed varying colour intensities.

This suggests the pleiotropic effects of gene(s) on these traits. T 39-1 with blue flower had on an average small seed (8.88g 100 seed^{-1}) and higher protein content (24.46%) than the pink flowered (T39-1) with 12g 100 seed^{-1}; 13.87% protein content. The high protein content in blue flower could be because of their reduced seed size compared to pink flower. (Kumar, 1982) also found that blue flowered plants with small seeds had higher protein content compared to pink flowered with larger seeds.

They suggested linkages between genes for flower colour, protein content and seed weight. It was also reported by (Atta *et al*., 2003) suggested that breeding lines combining high protein content with medium size can be successfully developed. A significant association of protein content with flower colour, seed coat colour and seed shape suggests the development of chickpea cultivars with high protein content and desired seed traits (size, shape and colour) would require large segregating populations and the selection of desired recombinants. Thus, it would be important to search for other high protein lines in the germplasm and use diverse sources of high protein content in breeding programs or development of high protein chickpea cultivars with desired seed traits (size, shape and colour).

CONCLUSION

From the above studies, it can be conclude that desi chickpea genotypes have immense potential as they serve the poor people of the nation who can afford good quality nutritious food. The chickpea genotypes namely, GP 10, GP 94, GP 2 and GP 15 reported high values for protein content ranging from 25.33 to 26.85%. These can be used in breeding program as donors to enhance the protein content as well as can be released and distributed under PDS (Public distribution System) for upliftment of nutritional status malnourished and/or undernourished community.

Author contributions: RRS and MP planned the study; SK, KN and LR raised the material under in the field; SR analyzed the seed samples for seed nutrient concentrations in quality lab; RRS analyzed the data; SK and RRS prepared the manuscript; RRS, MP and SR provided their inputs. All the authors reviewed and approved the final manuscript.

Conflict of Interest: All the authors have no conflict of interest.

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