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RESEARCH ARTICLE

Assessment of Phenotypic Variations and Correlation among Yield Attributing and Biochemical Traits in Mutant Population of Grasspea (*Lathyrus sativus* L.)

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Abstract

The experiment was conducted during the winter season 2014-17 in West Bengal to assess the agro-morphological variation and to carry out association analysis among yield related traits, including biochemical parameters in the gamma rays and EMS derived a total of 51 mutant lines of grasspea. A wide range of variation among the mutant line was observed for 11 agronomic and maturity characters, including yield and three nutritional quality parameters (β-ODAP, protein and TIA). Significant reduction in β-ODAP content as compared to their respective parent was recorded in 5 mutant lines of Nirmal (0.293% β-ODAP), 6 lines selected from Biol-212 (0.107% β-ODAP) and 7 lines isolated from Berhampur Local (0.533% β-ODAP). An association study revealed that seed yield/ plant exhibited positive and significant ($p < 0.01$) correlation with plant height, primary branches/plant, secondary branches/plant, number of pods/plant, seeds/plant, 100 seed weight, fresh weight/ plant and seed protein content while, it showed highly negative correlation with anti-nutritional parameters like β-ODAP (-0.374) and TIA (-0.395). Meanwhile, the number of seeds/pod, days to 50% flowering and days to maturity did not exhibited any significant association with plant yield. On the contrary, maturity traits showed a strong positive association with β-ODAP and TIA and a strong negative correlation with seed protein content, which stipulates that a high yielding and early flowering mutants might have low β-ODAP content, which leads to the simultaneous improvement of yield, β-ODAP and protein content of the grasspea mutants under study.

Keywords: Biochemical parameters, Correlation, Grasspea, Mutant, Variation.

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Introduction

Grasspea is an important crop of economic significance in India, China, Bangladesh, Pakistan, Nepal and Ethiopia. India is the leading country of grasspea cultivation in area and production, ranking second in productivity after Bangladesh. Currently, in India, about 3.62 lakh ha area of land is under grasspea cultivation (Department of Agriculture and Farmers Welfare, 2021). It is one of the important pulse crop of West Bengal cultivated in Murshidabad, East Midnapur, South 24 Porgonas, Nadia, Malda, Coochbehar and Jalpaiguri districts etc. The area, production and productivity of grasspea in West Bengal during the period 2011-12 is 33.5 thousand hectares, 26.93 thousand tons and 804 kg/ha, respectively.

Grasspea is an underutilized and neglected food, feed and a pharmaceutically important versatile crop shows resistance to harsh environmental conditions (Kumar *et al.*, 2020 and Tripathi *et al.*, 2021). The crop known for its several unique properties like tolerance to various abiotic stress, very hardy and penetrating root system, low fertilizer and water responsiveness, crop residue acting as source of good green manure, grain sturdiness, and a good source of protein which make this otherwise neglected crop tolerant and adaptable to a wide range of agro-climatic conditions.

On contrary, the presence of anti-nutritional substances (β-ODAP and Trypsin Inhibitor) in seeds and other plant parts render the crop unsuitable for human consumption leads to banned the crop production in some Indian states under the Prevention of Food Adulteration Act 1961 (Arora *et al*., 1995). This has resulted in reduction of its cultivation areas from 1.3 million hectares to less than 850,000 ha in a decade (Kumar *et al*., 2020). Presently, in South Asia, low β-ODAP varieties disseminating to the farmers in the grasspea growing regions reduced the incidence of neurolathyrism considerably (Ramya *et al*., 2022). Hence, identifying genotypes with high yield, high protein content and low anti-nutritional factors are the prime focus of any grass pea breeders and researchers worldwide that could help in achieving long lasting and dependable solution in efforts to face the threat of lathyrism.

Inadequate genetic variation in grasspea due to the predominant presence of self-pollination behavior and inter specific incompatibility hinders its improvement through conventional breeding which might be outbreak through induced mutagenesis (Singh and Sadhukhan, 2019). Mutagenesis and mutation breeding can be a valuable supplement to conventional breeding methods that can be introduced deliberately by employing ionizing radiation (γ-rays) as well as chemical mutagens like EMS (Singh *et al*., 2019) to create additional genetic variability in the existing gene pool. Furthermore, to complement genetically engineered crops mutation breeding offers the benefit of not introducing foreign DNA as a form of genetic diversity, preventing the restriction and utilization of mutant plants (Thapa *et al*., 2016).

Various metrical attributes like yield, number of branches, number of pods and seeds, leaf area, fresh weight etc. and biochemical traits are very complex as polygenes govern it and are greatly influenced by environmental factors. Further, an increase in yield is not the direct action of mutagen alone rather it also depends on other yield attributing interrelated characters hence direct selection for yield as such can be misleading. Intrinsically assessing variability through induced mutagenesis among various mutants for morphological and biochemical characters is highly important. The correlation of a particular trait with others contributes to the indiect selection of potential genotypes, which is important to understand the performance of mutants in comparison to the existing parent genotypes for desirable traits (Kadam *et al*., 2014). So, indirect selection can use character associations between yield components as the best guide for successful yield improvement. Singh *et. al.* (2017) reported the association of various traits with seed yield in the mutagenic population of grasspea. Moreover, earlier finding concerning correlation study among yield and yield attributing characters including biochemical traits through induce mutagenesis, have also been reported by several researchers in chickpea (Hassan *et al.,* 2005), black gram (Baisakh *et al.,* 2014), moong bean (Ahmad *et al.,* 2012), soybean (Singh and Singh, 1999) *etc*. However, limited information is available regarding this aspect in grasspea. Considering the above fact and to contribute towards genotypic improvement of grasspea, the present investigation was carried out to assess the agro-morphological variation and the mode of association for various yield attributing traits, including biochemical parameters in the putative mutants of grasspea.

Materials and Methods

The present investigation was conducted at District Seed Farm, Bidhan Chandra Krishi Viswavidyalaya, West Bengal, India during the winter season 2014-17. The experimental site comes under the Gangetic plains of West Bengal, India at latitude 22°58´ N and longitude 88°32´ E with an average altitude of 9.75 m above mean sea level (AMSL). The experimental material consisted of three diverse genotypes of grasspea viz. Nirmal (V_1) selected from germplasm, Biol-212 (V_2) a Somaclone of cv. Pusa-24 (Report of All India Coordinated Research Project on Mungbean, Urdbean, Lentil, Lathyrus, Rajmash, and Pea, 2009) and Berhampur Local (V_3) locally collected from Berhampur (W.B.). Dry and healthy seeds (2500 for each variety) were subjected to different treatments of physical (400, 500 and 600 Gy gamma rays) and chemical (0.5 and 1% ethyl methane sulphonate) mutagens individually and in the combination of both (400 Gy of gamma rays followed by 0.5 and 1% EMS concentrations). So, a total of eight treatment combinations, including control (untreated seeds) were developed in each variety to raise the mutagenic population.

The mutagen-treated seeds were sown immediately in the main field along with their respective controls in a randomized block design (RBD) with three replications (total 300 seeds of each treatment) to raise the M_1 generation during 2014-15. In M_2 generation, a total of 900 seeds (in RBD 300 seeds for each treatment in 3 replication and 600 seeds in simple line method for each treatment) were grown during 2015-16, to maximize the mutagenic population for the selection of desirable mutants. Viable mutations were scored based on various morphological changes like plant habit, leaf morphology, flower color, seed morphology and color and maturity. Collectively from three varieties of grasspea, a total of 51 mutant families were isolated in M_2 generation (Table 1). These mutant families isolated from various mutagenic treatment comprising a different concentration of EMS (9 from 0.5% and 6 from 1% treatment), various irradiation doses of gamma rays (9 from 400Gy, 7 from 500Gy and 8 from 600Gy) and combination treatment of physical and chemical mutagens (4 from 400 Gy+0.5% EMS and 8 from 400 Gy+ 1% EMS).

All the 51 mutant lines selected in M2 were evaluated in M_3 generation (2016-17) in RBD with three replications and

Table 1: List of viable mutants lines of grasspea selected from different mutagenic doses and their characteristic features

S. No.	*Mutant line*	*Mutant type*	*Treatment detail*
Parent: Nirmal			
1.	*Nm1*	High yielding	600 Gy
2.	*Nm2*	Flower color	400 Gy
3.	*Nm3*	Flower and leaf	400 Gy+1% EMS
4.	*Nm4*	Flower and seed	400 Gy
5.	*Nm5*	Flower color	1% EMS
6.	*Nm6*	Plant habit and seed color	400 Gy+1% EMS
7.	*Nm7*	Early maturity	1% EMS
8.	*Nm8*	Seed size	400 Gy+1% EMS
9.	*Nm9*	Seed size	0.5% EMS
10.	*Nm10*	Early maturity	1% EMS
11.	*Nm11*	Early maturity	1% EMS
12.	*Nm12*	Plant hight	0.5% EMS
Parent: Biol-212			
13.	*Biom1*	High yielding	400 Gy+0.5% EMS
14.	*Biom2*	Chlorophyll	600 Gy
15.	*Biom3*	Plant habit	600 Gy
16.	*Biom4*	Chlorophyll with late maturity	0.5% EMS
17.	*Biom5*	Seed size with early maturity	0.5% EMS
18.	*Biom6*	Leaf shape	500 Gy
19.	*Biom7*	High yielding	400 Gy+ 1% EMS
20.	*Biom8*	Leaf size	500 Gy
21.	*Biom9*	Plant habit	400 Gy+ 1% EMS
22.	*Biom10*	Plant habit and early maturity	400 Gy+ 1% EMS
23.	*Biom11*	Plant habit	400 Gy
24.	*Biom12*	Flower color	400 Gy
25.	*Biom13*	High yielding	0.5% EMS
26.	*Biom14*	Flower color	400 Gy
27.	*Biom15*	Seed size and color	400 Gy
28.	*Biom16*	Plant habit and seed size	400 Gy
29.	*Biom17*	Seed size and Early maturity	400 Gy
30.	*Biom18*	Plant habit	500 Gy
31.	*Biom19*	Seed color	600 Gy
32.	*Biom20*	Seed size	500 Gy
33.	*Biom21*	Seed color	500 Gy
34.	*Biom22*	Seed size	600 Gy
35.	*Biom23*	Seed size	1% EMS
36.	*Biom24*	Plant habit	0.5% EMS
37.	*Biom25*	Plant height	0.5% EMS
38.	*Biom26*	Leaf shape	600 Gy
39.	*Biom27*	Leaf shape	400 Gy+ 1% EMS
40.	*Biom28*	Leaf shape	400 Gy+0.5% EMS
41.	*Biom29*	Seed color	500 Gy
Parent: Berhampur Local			
42.	*Blm1*	High yielding	400 Gy+0.5% EMS
43.	*Blm2*	Seed size	0.5% EMS
44.	*Blm3*	High yielding	400 Gy+0.5% EMS
45.	*Blm4*	Seed color	600 Gy
46.	*Blm5*	Chlorophyll with high yielding	0.5% EMS
47.	*Blm6*	Flower color and plant habit	1% EMS
48.	*Blm7*	Seed size	500 Gy
49.	*Blm8*	Seed size and color	400 Gy+1% EMS
50.	*Blm9*	Plant hight	400 Gy
51.	*Blm10*	Leaf shape	600 Gy

"Nm" denotes the Nirmal mutant, *"Biom"* denotes the Biol-212 mutant *"Blm"* denotes the Berhampur local mutant.

yield attributing data and quality parameters were recorded. Eleven agronomic and maturity characters namely plant height (cm), number of primary branches/ plant, number of secondary branches/plants, number of pods/plant, number of seeds/pod, number of seeds/plant, 100 seed weight (g), fresh weight/plant (g), days to 50% flowering, days to physiological maturity and seed yield/plant (g) along with three nutritional quality parameters (β-ODAP, protein and TIA) were accessed in selected mutant lines.

The nutritional parameters were only estimated from the seed (powder) part. The protein content, using bovine serum albumin (BSA) as a standard protein was analyzed using Lowry's method (Lowry *et al*., 1951). The trypsin inhibitor activity is measured indirectly by inhibiting the activity of trypsin. The subsequent analysis of trypsin inhibitor activity was done following the method of Kakade *et al.* (1974) using N-α-benzoate-DL-arginine-paranitroanilide (BAPNA) hydrochloride as substrate solution. Estimation of β-N-oxalylamino-L-alanine (BOAA) is also known as β-N-oxalyl-L-α-β-diamino propionic acid (β -ODAP) in *Lathyrus* seeds was assessed as per the method given by Rao (1978).

Five random plants of all the putative mutants were tagged in each replication to record 11 quantitative traits and estimate 3 biochemical parameters and mean data used for statistical analysis. The mean value of all the characters that showed significant variations were used to determine the simple correlation coefficients according to Khan and Khanum (1994).

Results and Discussion

Variability studies among the selected mutant showed highly significant differences for all the yield attributing and quality traits except for number of days required to physiological maturity in mutant lines of variety Berhampur Local (Table 2). This indicates the presence of considerable variability among the selected mutants of grasspea. The chronicled mean values for different agro-morphological and nutritional parameters have been displayed comparatively (Figure 1). A subset of 29, 12 and 10 M_3 lines from the variety Biol-212, Nirmal and Berhampur local, respectively were assessed to measure the yield attributes and seed composition traits like protein, β-ODAP and trypsin inhibitor activity. The putative mutant lines showed a broad range of variability for these yield attributing, maturity and biochemical traits (Figure 2).

Wide range of variation among the mutant line was observed for the yield attributing traits like plant height (53.45 to 118.45 cm in V_1, 29.65 to121.15 cm in V_2 and 46.95 to 91.45 cm in V_3), primary branches/plant (4.47 to 9.17 in V_1, 5.38 to 12.50 in V_2 and 3.95 to 8.77 in V_3), secondary branches/plant (8.67 to 17.85 in V_1, 10.38 to 26.67 in V_2 and 12.67 to 23.75 in V_3), fresh weight/plant (41.30 to 92.55 g in V_1, 47.75 to 105.45 g in V_2 and 38.15 to 82.75g in V_3), number of seeds/pod (3.33 to 4.67 in V_1, 2.83 to 4.33 in V_2 and 3 to 4.47 in V_3), number of seeds/plant (289.85 to 411.92 in V_1, 212.92 to 533.57 in V_2 and 316.92 to 473.27 in V_3), 100 seed weight (6.85 to 9.05 g in V_1, 6.78 to 12.15 g in V_2 and 5.65 to 8.43 g in V_3) and yield/ plant (21.58 to 34.20 g in V_1, 18.47 to 47.25 g in V_2 and 20.09 to 31.65 g in V_3).

Among the mutant lines extensive variability was also noticed for maturity indices. Days to 50% flowering ranged from 58 to 75 days in V_1, 64 to 78 days in V_2 and 78 to 89 days in V_3 whereas days to physiological maturity varied from 107 to 128 days in V_1, 112 to 130 days in V_2 and 122 to 134 days in V_3. Similarly, β-ODAP content ranged from 0.2 to 0.34%, 0.08 to 0.14% and 0.16 to 0.52% in the mutant lines of variety V_1, V_2 and V_3 respectively. Protein content varied between 22.75 to 31.07% in V_1, 23.97 to 30.47% in V_2 and 20.52 to 26.20 in V_3 while, the trypsin inhibitor activity ranged from 15.15 to 21.25 TIU mg^{-1} of dry matter in V_1, 14.16 to 17.88 TIU mg^{-1} of dry matter in V_2 and 23.69 to 27.83 TIU mg^{-1} of dry matter in V_3.

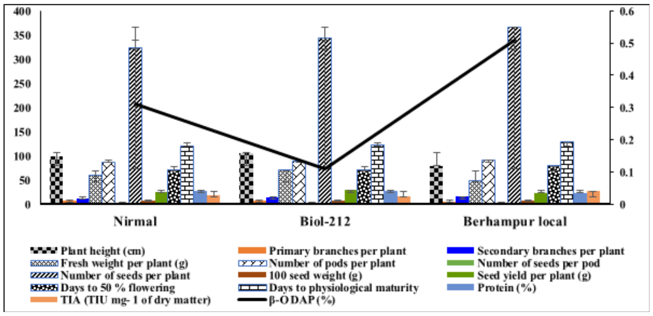

Figure 1: Mean performance of 51 putative mutants of three varieties for different yield attributing and biochemical traits in M_3 generation

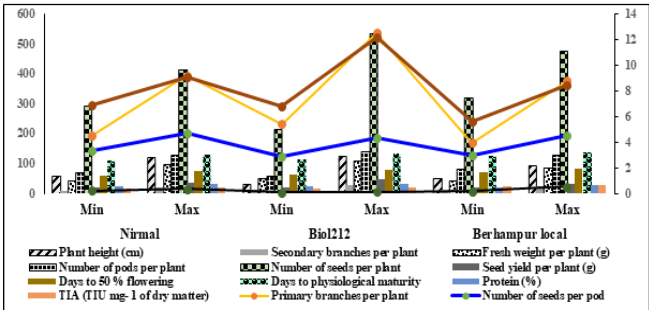

Figure 2: Range of 14 yield attributing and biochemical characters of 51 putative mutants selected from the variety Nirmal, Biol-212 and Berhampur Local

Table 2: Range value and mean performance for different yield attributing and biochemical traits in M_3 generation of 51 putative mutants isolated from three varieties

Characters	*Nirmal (V_1)*			*Biol212 (V_2)*			*Berhampur Local (V_3)*		
	Min	*Max*	*Mean*	*Min*	*Max*	*Mean*	*Min*	*Max*	*Mean*
Plant height (cm)	53.45	118.45	99.32	29.65	121.15	104.10	46.95	91.45	77.78
Primary branches per plant	4.47	9.17	6.25	5.38	12.50	7.31	3.95	8.77	4.52
Secondary branches per plant	8.67	17.85	11.19	10.38	26.67	13.99	12.67	23.75	15.52
Fresh weight per plant (g)	41.30	92.55	58.98	47.75	105.45	69.40	38.15	82.75	47.11
Number of pods per plant	67.73	125.81	85.93	54.87	138.63	89.24	77.67	124.33	91.22
Number of seeds per pod	3.33	4.67	3.69	2.83	4.33	3.72	3.0	4.47	3.71
Number of seeds per plant	289.85	411.92	322.17	212.92	533.57	343.39	316.92	473.27	365.28
100 seed weight (g)	6.85	9.05	7.42	6.78	12.15	7.86	5.65	8.43	6.16
Seed yield per plant (g)	21.58	34.20	25.24	18.15	47.25	28.54	20.09	31.65	23.33
Days to 50 % flowering	58.00	75.00	70.05	64.00	78.00	71.23	71.00	83.00	78.89
Days to physiological maturity	107.00	128.00	119.93	112.00	130.00	121.95	122.00	134.00	127.60
β-ODAP (%)	0.20	0.34	0.31	0.08	0.14	0.11	0.16	0.52	0.51
Protein (%)	22.75	31.07	28.16	23.97	30.47	27.47	20.52	26.20	23.51
TIA (TIU mg^{-1} of dry matter)	15.15	21.25	19.28	14.16	17.88	16.80	23.69	27.83	26.34

The mutational change in each quantitative trait can be large or small. Such changes in both macro and micro mutation are of significance in breeding programme depending on the characters involved. In the present investigation, isolated mutant lines exhibited variation in both positive and negative direction for all the traits under study. Meanwhile, in comparison to parents few lines showed significant reduction in mean value for maturity and anti-nutritional characters (β-ODAP and TIA) while few had substantial increase value of protein and other yield attributing traits over the control. Significant reduction in β-ODAP content as compared to their respective parent was recorded in *Nm5, Nm6, Nm7, Nm8, Nm11,*lines of Nirmal (0.293%), *Biom10, Biom17, Biom19, Biom20, Biom21* and *Biom22* lines selected from Biol-212 (0.107%) and *Blm1, Blm3, Blm4, Blm6, Blm7, Blm8* and *Blm9* lines isolated from Berhampur Local (0.533%). Isolation of such putative mutants will lead to the genetic improvement of grasspea and also enrich the germplasm. Various macro mutants were earlier reported in grasspea and other leguminous crops are in accordance with the present findings. Early maturity mutants have been reported by Bawankar and Patil (2001); Makeen *et al*. (2013) and Auti (2012) in grasspea, black gram and greengram, respectively. Similarly, plant habit mutants like dwarf (Talukdar, 2009a), reduction of lateral branches and biomass (Rybinski *et al*., 2004) were isolated in grasspea. High yielding macro-mutants were earlier isolated by Tripathy and Lenka (2010) in grasspea, Makeen *et al.* (2009) in urdbean and Tripathy (2009) in mungbean are in agreement of few high yielding line isolated in present study. Biochemically significant (low β-ODAP, low TIA and high protein) mutant lines were also selected during present investigation are supported by similar findings reported earlier by Das and Kundagrami (2005) and Tripathy and Lenka (2010) in *Lathyrus* for low β-ODAP, Kaveri (2009) in groundnut, Yathaputanon *et al* (2009) in soybean and Kamble and Patil (2014) in chickpea for higher protein mutants.

Association analysis for all the characters was worked out in all possible combinations at phenotypic levels (Table 3).

Traits like plant height, primary and secondary branches, pods, seeds, 100 seed weight, fresh weight and seed protein content exhibited significant ($p < 0.01$) positive association with yield/plant. Seed β-ODAP content (-0.374) and TIA (-0.395) had highly negative correlation with yield. Positive association of seed yield with most of the yield attributing traits except seed β-ODAP content exhibited independent genetic behavior in grasspea (Pandey *et al*., 2000). Sharma *et al.* (2000) reported significant negative correlation between seed yield/plant and days to flowering, days to maturity, pod length and its positive association with pods/plant in grasspea. Strong positive correlation of seed yield with protein content in grasspea was earlier reported by Basaran *et el*. (2016) which is in strong agreement of present finding. Talukdar (2009) in grasspea recorded positive and statistically significant correlation between seed yield and plant height, number of primary branches, number of pods and 100 seeds weight.

In general, correlations between β -ODAP and other traits were either negative or nonsignificant. Conversely, β-ODAP exhibited strong positive association with TIA and significant positive correlation with days to 50% flowering and days to physiological maturity. Similarly, negative correlation of β-ODAP with seed yield, protein content and days to flowering were observed earlier by Basaran *et el*. (2016) and Talukdar (2009) in grasspea. Likewise, a negative correlation between β-ODAP and seed yield was reported earlier by Tadesse and Bekele (2003) and Basaran *et al*. (2013). However, Cocks *et al.* (2000) reported a negative relationship between ODAP concentration and the total amount of ODAP in the plant (total seed weight x ODAP concentration) and proposed that low toxin concentration in plant with high seed yielding were caused by toxin dilution. So, the negative and significant correlation between β-ODAP and yield should be taken into consideration for simultaneous improvement of these traits.

Seed protein content had highly significant positive correlation with plant height and 100 seed weight and positive significant association with Seed yield/plant. on contrary, showed highly negative and significant association with days to 50% flowering, days to physiological maturity and seed β-ODAP content. The above finding suggests that protein content and yield can be improved simultaneously. Similar findings have also been reported by Roy *et al*. (2001) in grasspea.

Trypsin Inhibitor Activity (TIA) showed highly significant positive correlation with days to 50% flowering, days to physiological maturity and β-ODAP. While, it exhibited strong negative relationship with most of the traits, including yield/plant. A negative correlation between TIA and seed yield and seed protein was earlier observed in field pea and grass pea (Wang *et al*., 1998). Whereas, no correlation of TIA with maturity, oil content, seed protein content and seed yield was reported by Manjaya *et al.* (2007) in soybean. Strong positive relation between TIA and days to physiological maturity and highly negative association with seed yield in the present study indicates that a high yielding and early flowering mutants might also have low TIA content which may leads to concurrent improvement of seed yield and TIA in grasspea.

Plant height showed highly positive significant correlation with number of primary branches, number of pods, number of seeds plant, 100 seed weight, fresh weight, seed protein content and seed yield. While, negative and significant relationship recorded with number of seeds/pod and seed β-ODAP content and strong negative association with TIA. Basaran *et al*. (2013) reported that plant

Table 3: Simple correlation coefficient among different yield attributes protein, β-ODAP content and trypsin inhibitor activity (TIA) in control and 51 putative mutants of grasspea in M_3 generation

Characters	*PH*	*PB*	*SB*	*PP*	*SP*	*SPP*	*SW*	*FWP*	*DFF*	*DPM*	*ODAP*	*SP*	*TIA*
PB	0.561**												
SB	0.254	0.736**											
PP	0.489**	0.626**	0.779**										
SP	-0.285*	-0.249	-0.289*	-0.357**									
SPP	0.391**	0.545**	0.666**	0.843**	0.190								
SW	0.390**	0.230	0.070	0.043	-0.466**	-0.213							
FWP	0.674**	0.706**	0.543**	0.548**	-0.276*	0.436**	0.448**						
DFF	-0.086	0.081	0.448**	0.428**	-0.109	0.393**	-0.216	0.047					
DPM	-0.006	0.131	0.481**	0.461**	-0.143	0.410**	-0.120	0.157	0.934**				
ODAP	-0.318*	-0.274*	-0.065	0.083	0.044	0.076	-0.545**	-0.414**	0.276*	0.288*			
SP	0.412**	0.200	-0.210	-0.130	-0.037	-0.153	0.544**	0.177	-0.438**	-0.370*	-0.417**		
TIA	-0.485**	-0.296*	0.072	0.096	0.022	0.101	-0.577**	-0.443**	0.481**	0.441**	0.717**	-0.661**	
SYP	0.637**	0.626**	0.580**	0.709**	-0.201	0.636**	0.609**	0.716**	0.127	0.220	-0.374**	0.328*	-0.395**

*Significant at 5%; ** Significant at 1%

PH = Plant height (cm), PB = No. of primary branches, SB =No. of secondary branches, PP =No. of pods / plant, SP =No. of seeds / pod, SPP =No. of seeds / plant, SW= 100 seed weight (g), FWP= Fresh weight / plant (g), DFF= Days to 50% flowering, DPM= Days to physiological maturity, ODAP= Seed β-ODAP content (%), SP= Seed protein (%), TIA= Trypsin Inhibitor Activity (TIU mg-1 of dry matter), SYP= Seed yield / plant (g)

height exhibited strong correlation with seed yield and a nonsignificant positive and negative association with seed protein content and β-ODAP, respectively, which supports the present finding. Furthermore, a dwarf mutant line can be taken in consideration for the simultaneous enhancement of yield and quality parameters in *Lathyrus*. The number of primary branches plant had strong positive associations with secondary branches, number of pods, seed plant, fresh weight and seed yield whereas, it showed significant negative correlation with seed β-ODAP content and TIA. The number of secondary branches exhibited a highly positive correlation with plant height, number of pods, number of seeds plant, fresh weight, days to 50% flowering, days to physiological maturity and seed yield. However, it had significantly negative relationship with number of seeds pod.

Number of pods plant exhibited positive and highly significant correlation with plant height, number of primary and secondary branches, number of seeds, fresh weight, and days to 50% flowering, days to physiological maturity and seed yield plant while it had strong negative association with number of seeds pod. Similarly, seeds pod showed significant negative correlation with most of the traits but did not have significant positive association with any of the character. Strong positive association was recorded between number of seeds plant with plant height, primary and secondary branches, pods plant, fresh weight, days to 50% flowering, days to physiological maturity and seed yield plant whereas, there was no negative correlation observed with any other characters. 100 seed weight showed highly positive and significant correlations with plant height, fresh weight, seed protein content and seed yield/plant while, it had strong negative association with number of seeds/pod, seed β-ODAP and TIA.

Fresh weight/plant exhibited strong positive correlation with plant height, number of primary and secondary branches, number of pods, seeds plant, 100 seed weight and seed yield while it showed highly negative association with β-ODAP and TIA. So, a bushy type mutant with high fresh weight might have low β-ODAP and TIA can be selected for fodder purposes and utilized in future breeding programs. Days to 50% flowering and days to physiological maturity were positively associated with number of secondary branches, pods plant, seeds plant, TIA and β-ODAP content. On other hand, it had highly negative correlation with seed protein and nonsignificant relation with seed yield. Kumar and Dubey (2001) reported significant negative correlation between days to flowering and yield which is in agreement of present finding.

Conclusion

Consequently, in the present study few mutant lines exhibited lower concentrations of anti-nutritional factors while others had high value of protein content and grain yield than their respective control parent. Isolation of such lines would be beneficial for genetic improvement of grasspea. Further, important yield contributing characters like plant height, number branches, number of pods, number of seeds, 100 seed weight, fresh weight and protein content exhibited strong positive and significant correlation with yield. Henceforth, based on character association selection of these traits will be helpful to improve the grain yield. On contrary, TIA and β-ODAP exhibited strong negative association with plant yield and a significant negative correlation with most of the important yield attributing traits along with protein but they were very strongly and positively associated with each other and also, they had positive association with maturity traits. Therefore, the result obtained in the present study indicates that a high yielding, early flowering and early maturing mutants may also have low β-ODAP and TIA content, leading to the concurrent improvement of yield in consort with anti-nutritional and protein of the grasspea mutants under study.

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