

Research Article

Evaluation of Fieldpea (*Pisum sativum* L.) Genotypes based on Genetic Variation and association among Yield and Yield Related Traits under High Ganges River Floodplain

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Abstract

The analysis of genetic variability and divergence was carried out for nine field peas genotype in the Pulses Research Center, Ishurdi under Bangladesh Agricultural Research Institute (BARI), Bangladesh. The experiment was conducted randomly in complete block design (RCBD), with 3 replicas. Observations were recorded on different yield and yield contributing characters. All cultivars showed considerable differences in their performance, indicating the presence of extensive changes in genotypes for most parameters. The highest yield of pods was BFP 11015, followed by Bagha local and Jhikargachha local. The PCV for all the characters was uninterrupted from their respective GCVs. High GCV as well as PCV were observed for the number of pods per plant, 100 seed weight, powdery mildew severity and pod yield, indicating the existence of a broad genetic basis. The High values of heritability with high genetic advance over percent mean were observed for all traits except days to maturity. Plant height and maturity days showed a positive correlation and a significant correlation for seed yield and a negative correlation with a character yield of 100 seed weight. By using principal component analysis first 3PCs were presented variance for 92.37% of the total variation. First, two PC's were used to build the biplot in which the genotypes such as, 1-IPSA motorsuti-3, 2-Jhikorgachha local, 4-Faridpur local, 7-BFP 11016 are scattered in four quadrants representing the most genetic divergence. Considering the yield, BFP 11015 and Bagha local genotypes are recommended for releasing as a variety and Jhikargachha local, Faridpur local & BFP 11016 are using crossing materials for advanced genetic material.

INTRODUCTION

Field pea (*Pisum sativum* L.), a legume crop, belongs to the Leguminosae family and contains a high amount of protein including amino acids, especially lysine [1]. Beans are considered to be the most nutritious part of the human diet because they contain 42.65% carbohydrates, 27.8% protein and iron (Fe), sodium (No), phosphorus (P), potassium (K), and some other important elements [2]. Field pea has multifaceted uses as food, feed and fodder. The residues provide nutritious food for cattle and dairy cows and thus provide an additional benefit to poor farming families. Field peas are cultivated mainly for green beans and seeds are used as vegetables. Mature seeds can be used to make 'dal' or 'chatapati' and other value-added goods such as 'fried dal'. As a legume, the field has a unique ability to fix atmospheric nitrogen through pea symbiosis.

It may have originated in South Asia but it is one of the most important herbaceous vegetables in Bangladesh. Field peas

with an annual production of 13534166 tons [3] are one of the most produced pulses crops in the world. Major pea producing countries include Canada, the Russian Federation, China, Ukraine, India, USA, France, Australia, Ethiopia and Germany [3]. In Bangladesh, the annual production of field pea is around 14550 mt from an area of 11753 ha with a productivity level of 1240 kg/ha [4].

The success of the breeding program depends on the amount of genetic variability available for absorption and the extent to which the desirable characters are heritable [5]. Collection, preservation and evaluation of germplasm are key information for any breeder to initiate a breeding program for crop improvement. Heritability act as a predictive tool in expressing the reliability of phenotypic traits and thus high heritability traits can aid in the effective selection of specific characters and create future breeding programs [6]. The analysis of the relationship helps in evaluating the existing relationship between

the yield and its components. The study of genetic variability and interrelationships is of great value in the selection of the preferred characters of field pea genotypes to increase seed yield and quality.

Genetic diversity is available in multivariate analysis, multiple statistical tools such as Euclidean clustering and principal component analysis (PCA). Multivariate analysis is an important tool for estimating genetic divergence in the populations of several workers, such as [7-12]. The principal component analysis is an adaptive data analysis technique that is used to effectively visualize similarities and differences between genotypes and to identify the quantitative characters that contribute the highest towards genetic divergence [13,14].

Pea productivity is too low to fulfill the required demand and this may be mainly due to the lack of high yielding varieties and resistance to biotic and abiotic stress [15]. To meet the present demand, there is an essential germplasm evaluation for the genetic improvement of pea to develop desired high yielding genotypes. Thus, the present study was conducted to identify higher genotypes based on genetic variability and association between yield and yield-related traits and to identify genetically different genotypes using PCA for further different breeding programs in the development of high yielding field pea varieties.

MATERIALS AND METHODS

The field test was conducted at the Breeding Research Field of Pulses Research Center, Ishurdi, Pabna under Bangladesh Agricultural Research Institute (BARI), Bangladesh. The geographical coordinates of the research site are 24.07° north latitude and 89.03° east longitude and 11.58 m above sea level. The experimental component consisted of 7 indigenous (Jhikorgacha local, Bagha local, Faridpur local, BD 4142, BFP 11016, BD 9047 and BFP 11015), and 1 exotic (Sikkim local) and 1 check variety (IPSA Motorshuti-3). The size of the plot is 4 meters x 3 meters. The initial soils characteristics of the experimental site are given in Table 1 with a soil depth of 0-15 cm belong to agro-ecological zone-11 (High Ganges River Flood Plains). The average annual rainfall is reported as 1200 ± 300 mm. The experiment was placed in a randomized complete block design (RCBD) with three replications. Proposed nutrients such as nitrogen, phosphorus and potassium @ 20-40-20 kg/ha were applied as basal dose in the final preparation of the land. Recommended agro-based practices and plant protection measures were followed to maintain optimal plant position. One hand weeding was performed for control weed at 25 days after sowing. Observations were plot basis measurements of days to 50% flowering, days to maturity, plant height, the number of pods per plant, 100 seed weight (g) from five competing plants randomly selected from each plot in every replication for the traits and seed yield per hectare was measure plot basis. The severity of powdery

mildew disease (PMS) in different lines was recorded on the whole plot basis based on the 0-5 scale described by Ghufranal et al. [16], is given below in Table 2. The data were averaged and statistically analyzed for analysis of variance in favor of each trait as per the method suggested by Panse and sukhatme [17], using STAR software. The genotypic and phenotypic correlation coefficients were calculated from the genotypic and phenotypic covariances and variances as described by Singh and Choudhary [18], and as per the formula given by Johnson et al. [19], and categorized as described by Sivasubramanian and Menon [20]. The data were averaged and statistically analyzed for variant analysis for each feature according to the method proposed by Panse and sukhatme [17], using STAR software. Coefficients of genotypic and phenotypic levels were calculated from genotypic and phenotypic covariances and variances as described by Singh and Choudhary [18], and classified by Johnson et al. [19], and Sivasubramanian and Menon [20], as described. The broad-sense heritability and genetic advance in percent of means were calculated as suggested and categorized in three types as low, moderate and high as suggested by Johnson et al. [19]. Normal Pearson's correlation and principal component analysis were carried out through STAR 2.0.1 software packages to find the pattern of variation in the data. The collected characteristics were evaluated for the genotypic and phenotypic variance by the formulae given by Lush [21], and Choudhary and Prasad [22].

RESULT AND DISCUSSION

Descriptive statistics for all the traits are summarized among nine field pea genotypes (Table 3). The highest variation was found in yield (kg/ha), followed by plant height (cm) and days to flower. Moderate variation was observed for days to maturity and 100 seed weight. Powdery mildew severity showed lower variability among the genotypes. The mean values of various genotypes have also shown a wide range of variability for various characters, which were studied in the present investigation (Table 3). The range record for days to 50 % flowering (37-65), days to maturity (80-110), plant height (79.80-112), number of pods per plant (8-26), the score of powdery mildew diseases (0-4), weight of 100 seeds (6.11-29.54) and pod yield kg per hectares (654-1632). Similar results were also observed by Kumar et al. [23].

Analysis of variance

An analysis of variance for randomized complete block design accommodating nine germplasm in three replications carried out for each of the seven characters. The mean sum squares due to replications, germplasm, and errors for all the characters are presented in Table 4. The variation due to replication was significant for days to maturity, number of pods per plant, hundred seed weight and seed yield. However, it was non-significant for remaining all the characters under study. Singh et al. [24], were also recorded similar observations in their study.

Table 1: Initial soil properties at 0-15 cm soil depth.

Particle size distribution			Textural class	Bulk density (g/cm ³)	pH	SOM (g/kg)	Total N (g/kg)	Exchangeable (meq 100 g/soil)	Other nutrients (mg/kg)			
Sand (%)	Silt (%)	Clay (%)							P	S	Zn	B
56	18	26	Sandy loam	1.42	7.3	1.25	0.065	0.17	12	14	0.57	0.17

Table 2: Disease scoring scale.

Disease grade	Percent leaf area infected	Disease reaction
0	No infection	Immune
1	0-10	Resistant
2	10.1-30	Moderately resistant
3	30.1-70	Moderately susceptible
4	70.1-80	Susceptible
5	80.1-100	Highly Susceptible

Table 3: Descriptive statistics for seven quantitative traits of nine field pea genotypes.

Characters	Range		Mean	StdDev (σ)	Variance (σ^2)
	Minimum	Maximum			
Days to flower (No.)	37	65	50.15	8.76	76.74
Days to maturity (No.)	80	110	97.37	7.75	60.06
Plant height (cm)	79.80	112	96.74	10.96	120.12
Pods per plant (No.)	8	26	14.78	4.95	24.50
Powdery mildew severity (0-5)	0	4	1.56	1.53	2.34
100 seed weight (g)	6.11	29.54	13.44	7.32	53.58
Yield (kg/ha)	654	1632	1155	290.12	84169.61

Table 4: Analysis of variance (mean sum of squares) of seven important characters in respect of nine fieldpea genotypes.

Sources of variation	DF	Mean sum of squares						
		DF	DM	PH	PPP	PMS	100 Wt	YLD
Replication	2	8.26	32.26**	5.15	6.78**	0.11	5.99**	1002.78*
Genotype	8	241.34**	181.95**	386.09**	76.00**	7.17**	171.87**	272920.83**
Error	16	2.88	2.51	1.58	0.94	0.19	0.34	189.99

* - Significant at $p = 0.05$ and ** - Significant at $p = 0.01$; DF= Degrees of freedom, DF = Days to 50% flowering, DM = Days to maturity, PH = Plant height (cm), PPP = Pods per plant, PMS = Powdery mildew severity, 100Wt = Hundred seed wt. (g) and YLD = Yield (Kg/ha)

The variation due to genotypes was highly significant for all majorities of the traits. This indicated the presence of sufficient genetic variability for the traits in order to select diverse parental lines for effective breeding programs.

Mean performance of genotypes

The average performance of the pea genotypes in the 9 field pea revealed significant differences for all traits (Table 5). The days to 50 percent flowering varied from 37 to 65 days with a grand mean of 50 days. The released variety, IPSA maturshuti-3 (38 days), had the earliest days to 50% flowering and Sekim local (62 days), was the longest in this regard followed by Faridpur local (60 days), and BD 9047 (58 days). The differences between field pea cultivation in terms of day maturity were significant ($p > 0.05$) which was found to be between 82 and 106 days. The minimum days to maturity were observed under the genotype IPSA Maturshuti-3, followed by Jhikargach local, BD-4442 and Bagha local. Although the most days of maturity has been taken under the Faridpur local genotype. Possible factors of early flowering and maturation in certain species indicate their adaptability to a particular environment, better and more efficient use of nutrients in relatively hostile environments may lead to early completion of plant stages and relatively early reproductive stage [25]. Similar results were previously published in Garden pea by Hussein et al. [26], Singh et al. [27], and Javaid et al. [28].

Plant height data indicated significant differences among the cultivars (Table 5). Comparison of cultivar means, it is known that the maximum plant height (111.37 cm), was attained by the plants of Jhikargacha local followed by Sekim local (110.17 cm), while the minimum was recorded in BFP 11016 (81.93 cm) Table 3. The number of nodes is primarily dependent on the cultivar used [29]. As the height of plants varies between different species, it can be said that height is a genetic trait. Similar results have been published in previous staff [26,30,31]. The number of pods per plant revealed significant differences between all genotypes. The highest number of pods per plant was found in Jhikargachha local (24), followed by BD-1142 (20), and BD-9047 (16). The genotype BFP 11016 remained at the bottom (9). More number of pods per plant may be due to small pod size as less nutrient are required for small pods compared with larger pods [32]. Some researchers observed the number of pods per plant as the most useful yield component [28].

Significant differences in genotypes for 100-seed weight were also observed (Table 5). Sekim local (27.87 g), gave the maximum 100 seed weights followed by BPF 110116 (21.35 g), and IPSA Maturshuti-3 (20.30 g). The results suggest a strong correlation between the maximum translocation of plant material from plant to reproductive part for better environmental conditions which increases seed weight [33]. Data on seed yields indicate a significant difference among the cultivars. The lowest yield

Table 5: Performance of fieldpea genotypes for yield and yield contributing characters.

S.N.	Name of entry	Days to flower	Days to maturity	Plant height (cm)	Pods/plant	100 Seed weight (g)	Yield (kg/ha)	PM score (0-5)
1	IPSA Motorshuti-3	38	82	87.03	10	20.33	859	0
2	Jhikorgacha local	45	96	111.37	24	11.42	1340	0
3	Bagha Local	49	98	85.33	15	7.49	1403	2
4	Faridpur Local	60	106	89.23	10	6.99	938	4
5	BD 4142	45	97	98.7	20	7.11	1004	0
6	Sekim Local	62	104	110.17	15	27.87	1275	2
7	BFP 11016	39	89	81.93	9	20.33	671	0
8	BD 9047	58	102	98.93	16	7.96	1297	3
9	BFP 11015	54	102	108	14	11.45	1608	2
Level of Significance		**	**	**	**	**	**	**
CV (%)		3.39	1.63	1.31	6.58	4.35	1.19	28.35
LSD (0.05)		2.93	2.74	2.18	1.68	1.01	23.86	0.76
**:		Significant at 1%						

Table 6: Genetic variability components for different quantitative traits in fieldpea.

Characters	σ^2g	σ^2p	Coefficient of variation (%)			h_b^2 (%)	GA	GAM
			GCV (%)	PCV (%)	CV			
Days to flower (No.)	79.48	82.36	17.77	18.09	3.39	96.50	18.04	35.98
Days to maturity (No.)	59.81	62.32	7.94	8.11	1.63	95.97	15.61	16.03
Plant height (cm)	128.17	129.75	11.70	11.77	1.31	98.78	23.18	23.96
Pods per plant (No.)	25.02	25.96	33.84	34.47	6.58	96.37	10.12	68.44
PMS (0-5)	2.32	2.51	97.77	101.69	28.35	92.45	3.02	193.67
100 seed weight (g)	57.17	57.51	56.26	56.42	4.35	99.41	15.53	115.56
Yield (kg/ha)	90910.28	91100.27	26.11	26.13	1.19	99.79	620.47	53.72

PMS: Powdery Mildew severity, σ^2g : Genotypic variance, σ^2p : Phenotypic variance, GCV: Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, CV= Coefficient of variation (%), h_b^2 = Broad sense heritability, GA= Genetic advance and GAM= Genetic advance as percent of mean

Table 7: Pearson's correlation coefficients between different traits in fieldpea.

Traits	DF	DM	PH	PPP	HSW	PM.score	YLD
DF	1						
DM	0.923**	1					
PH	0.439	0.477	1				
PPP	0.028	0.231	0.688*	1			
HSW	-0.100	-0.338	0.094	-0.325	1		
PM.score	0.870**	0.785*	0.022	-0.271	-0.320	1	
YLD	0.495	0.674*	0.668*	0.511	-0.264	0.330	1

was recorded at BFP 110116 (671 kg/ha), followed by IPSA Maturshuti-3 (859 kg/ha), and Faridpur local (938 kg/ha), where the maximum yield of field pea seeds was in BFP 11015 (1608 Kg/ha.) Followed by Bagha local (1403 kg/ha), and Jhikargachha local (1340 kg/ha). Substantial differences among the pea lines can be observed in terms of disease incidence. IPSA Motorsuti-3, Jhikurgachha local, BD 4142 and BFP 11016 showed the immune response with a disease score of 0 while the 3 genotypes (Bagha local, Sekim local and BFP 11015) showed moderate resistance to powdery mildew. BD 9047 displayed the moderately susceptible action with grade 3. Faridpur local exhibited the maximum disease development (S) with rating 4 towards the powdery mildew (Table 1 & Table 5).

Genetic Variability

The genetic variability present in the germplasm provides, the raw material of any plant breeding program based on which selection works to develop superior genotypes. Thus, the greater amount of variation for character in breeding materials, the greater the chance of its improvement through selection.

The phenotypic coefficient of variation (PCV) for all the characters studied in the present investigation (Table 6), was greater than the genotypic coefficient (GCV), of the variant, indicating variability presented in the genetic material, which was not only due to genotypic effects but also due to environmental

influences. Iqbal et al. [34], Gudadini et al. [35], Pandey et al. [36], Barcchiya et al. [37], Katoch et al. [38], Bashir et al. [39], and Meena et al. [40], was observed that relative magnitude of phenotypic coefficients of variation was higher than genotypic coefficients of variation for all the characters under study indicating environmental influence on the traits. In the present study, high GCV and PCV were observed for pods per plant, powdery mildew severity, 100 seed weight and pod yield. It indicates the existence of broad genetic base, which would be amenable for further selection. Similar searches have been previously reported by Pandey et al. [36], Saxesena et al. [41], Gudadini et al. [35], Kumar et al. [15], and Katoch et al. [38]. Medium GCV and PCV plant height and days to flowering were observed. This implied the equal importance of additive and non-additive gene action in these characters. These results are consistent with previous reports from Barcchiya et al. [37], Gudadini et al. [35], Thakur et al. [42]. Low GCV and PCV were observed for a days to mature. This indicates the existence of a narrow genetic base. These results were consistent with the results of the Yumkhaibam et al. [43], Katoch et al. [38]. The coefficient of variation indicates the degree of variability present in the genotypes for different traits but the predictions of response to selection heritability estimates are useful. High broad sense heritability (> 60%) was observed for all traits indicated that these traits could be improved through selection based on their phenotype. Similar results were obtained by Georgieva et al. [44], Katoch et al. [38], Thakur et al. [42], and Barcchiya et al. [37].

High genetic advance only occurs due to additive gene action [45]. Thus the heritability combined with genetic advance will be more effective than the heritability alone. Very high estimates of heritability with high values of genetic advance by over percent mean were observed for all traits except maturity days that these characters are largely controlled by additive gene action, which indicates that improvement in these characters is possible through mass selection and progeny selection. These results are in accordance with the findings of Pandey et al. [36], Gudadini et al. [35], Georgieva et al. [44], and Thakur et al. [42]. Pods per plant, powdery mildew severity, 100 seed weight and pod yield exhibited high degree of additive components like high estimates of heritability coupled with high GAM and presence of high GCV and PCV, it indicates in fieldpea genetic improvement can be achieved through selection by using the existing germplasm for above characters.

Correlation coefficients

Estimates of Pearson's correlation coefficient among the seven characters of the fieldpea genotypes are presented in Table 7. Seed yield showed significant and positive correlation with plant height (0.668), and days to maturity (0.647); positive association with days to flower (0.495), pods per plant (0.511), powdery mildew severity (0.330) and 100 seed weight (-0.264), characters showed negative with non significant. Positive association between yield and pods per plant was also reported earlier by Tyagi and Shrivastava [46], Sharma et al. [47], and Patel et al. [48]. Plant height was positive and significantly related to grain yield for each plant and pods per plant. Days 50% of flowering were positively and significantly associated with days of maturity and powdery mildew intensity and

negatively correlated with 100 seed weight. The days of maturity had a significant positive connection with the powdery mildew intensity. Chaudhary and Sharma [49], Sureja and Sharma [50], Choudhary et al. [51], Singh and Singh [52], Nawab et al. [1] and Sonali et al. (2009) got the same result.

Genetic divergence

Genetic diversity is important for the use of any genotype in any crop improvement program. According to the principal component analysis, three principal components have eigen values more than unity and the variance accounted for 92.37% of the total variance amongst nine fieldpea genotypes evaluated for seven quantitative traits (Table 8). Among the three principal components, the PC1 shares a high proportion of total variation of 49.85% and the rest of the two principal components viz., PC2 and PC3 contributed 26.71% and 15.81% of the total variance respectively [54].

The screen plot explains the percentage of different variables related to each principal component obtained by drawing a graph between the eigen values and the number of principal component (Figure 1). From the graph, it is clear that most variations were observed in PC1 compared to the other 4 PCs. Thus, the line selection from this PC1 will be effective (Figure 1). Those principal components having more than one eigen value that showed more variation among the fieldpea genotypes for the selection of the diverse parents.

Extend of variation and relation among the quantitative characters is represented in Figure 2. First, two PC's were used to construct the biplot in which nine genotypes are scattering apart (Figure 2). Genotypes which are closer to the origin and closer to each other are said to have more similarity and genotypes apart from each other are more divergent [55]. In the present study, genotypes viz., 1-IPSA Motorshuti-3, 2-Jhikorgacha local, 4-Faridpur local, 7-BFP 11016 are scattered apart in all the four

Table 8: Eigen values, % variance and cumulative of fieldpea germplasm.

Parameters	PC1	PC2	PC3
Proportion of variance (%)	49.85	26.71	15.81
Cumulative proportion (%)	49.85	76.56	92.37
Eigen values	3.49	1.87	1.11

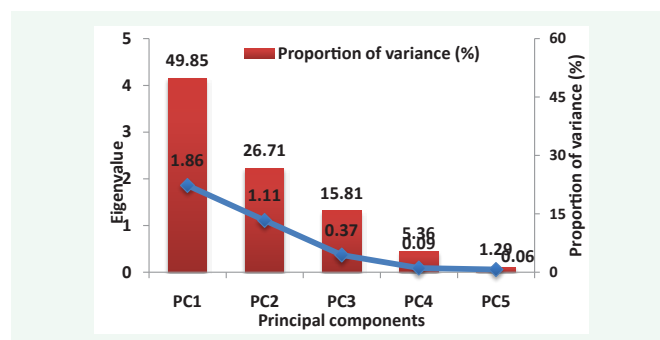


Figure 1 Scree plot between eigen values and number of principal components.

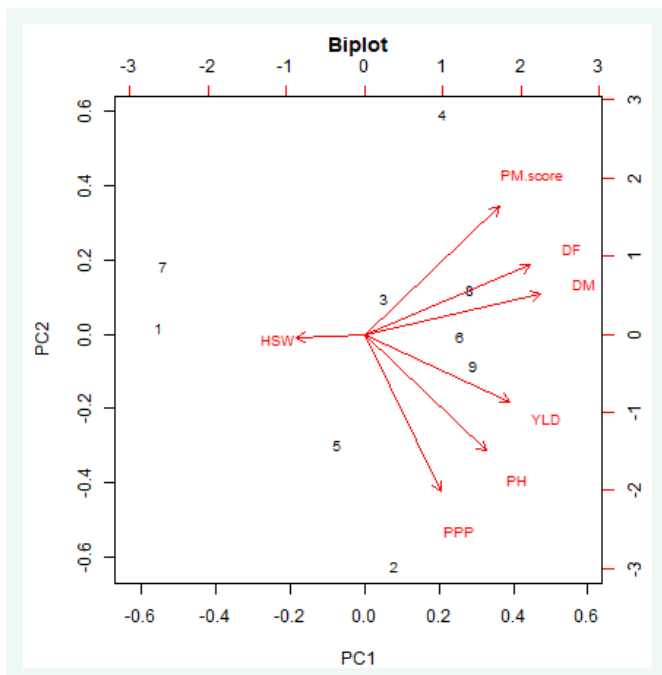


Figure 1 Scree plot between eigen values and number of principal components.

quadrates of the biplot representing maximum genetic divergence among the genotypes. Genotypes like 3-Bagha local, and 6-Sekim local were closer to the origin and closer to each other indicates that low genetic divergence among them. A character like 100 seed weight is closer to the origin considered to have lower loading score with least contribution towards divergence and the rest of the characters away from origin are considered to have the highest loading score with a maximum contribution towards the divergence.

Extend of variation and relation among the quantitative characters is represented in figure 2. The first two PCs were used to construct biplot where nine genotypes are scattered (Figure 2). Genotypes that are close to the origin and close to each other are said to have more similarities and genotypes apart from each other are more divergent [55]. In the present study, genotypes viz., 1-IPSA Motorshuti-3, 2-Jhikorgacha local, 4-Faridpur Local, 7-BFP 11016 are scattered apart in all the four quadrates of the biplot representing the highest genetic variation among the genotypes. Genotypes such as 3-Bagha local and 6-Sikkim local were close to the origin and close to each other indicating low genetic differentiation between them. A character 100 seed weight is closer to the origin considered to be the lowest loading score and other characters away from the origin are considered the highest loading score with the greatest contribution to the divergence.

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