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Manish Kumar
Department of Genetics and Plant Breeding, COA, CAU, Imphal, Manipur, India

MS Jeberson
Plant Breeding AICRP on MULL ARP, CAU, Imphal, India Imphal, Manipur, India

NB Singh
Department of Genetics and Plant Breeding, COA, CAU, Imphal, Manipur, India

Ranjit Sharma
Department of Genetics and Plant Breeding, COA, CAU, Imphal, Manipur, India

Raviraj Singh Patel
Department of Genetics and Plant Breeding, COA, CAU, Imphal, Manipur, India

Correspondence
Manish Kumar
Department of Genetics and Plant Breeding, COA, CAU, Imphal, Manipur, India

Analysis of trait association and principal component of variability in field pea (*Pisum sativum* L.) genotypes

Manish Kumar, MS Jeberson, NB Singh, Ranjit Sharma and Raviraj Singh Patel

Abstract
Existing genetic variability and strong trait association among cultivars/germplasm offer great help in enhancing the genetic gain/breeding value in crop plants. The objective of this study was to analyze the traits association and principal components causing genetic variability present in twenty-eight genotypes (Parents + Hybrids) using 12 agro-morphological traits. The experiment was consisted 28 genetically diverse pea genotypes (7 parents and 21 F_1 crosses, developed in half diallel fashion) were evaluated under Randomized Block Design (RBD) under recommended agro-practices. The ANOVA analysis revealed that parentage and crosses has genetic variability (among parentage and F1s) for all the traits studied. The no. of pod per plant ($r = 0.685$ and 0.670, respectively at $P \leq 0.01$) has substantial genotypic and phenotypic correlation with seed yield/plant followed by pod length (0.639), no. of nodes to first flowering (0.576) etc. Existence of great genetic variability with comparative value of PCV and GCV reflects that the genotypes have played substantial role rather least environmental effects on these traits suggest selection suitability of these traits. Hence, information generated in the study has immense value in formulation of further breeding strategies and exploitation of maximum genetic gain in field pea

Keywords: Genetic diversity, PCA, GCV, PCV, correlation coefficient, agro-morphological traits, field pea, *Pisum sativum* L

1. Introduction
Pea (*Pisum sativum* L) is known to be one of the oldest culture along with cereals and lens in the world (Zohary *et al*., 2012) [27]. Field pea is mainly used for human consumption as well as feeding livestock. Being a rich source of proteins (21 to 25%) used as a potential alternative to soybean in European countries (Barac *et al*., 2010) [3]. In India, pulses are the major source of protein for vegetarian. Moreover, field pea is also a good source of carbohydrates and total digestible nutrients (86 to 87%), makes it an excellent livestock feed (Enderes *et al*., 2016) [6]. Through symbiosis association, pea can fix atmospheric nitrogen and hence does not need nitrogenous fertilizer (Janzen *et al*. 2014) [15]. It can sustain under drought hence useful in enhancement of cropping intensity and livelihood *per se* in prone area (Janzen *et al*., 2014) [15]. Pea is second most important pulse after common bean, widely cultivated worldwide (Esposito *et al*., 2007) [7] in an area of 68, 68, 131 ha with global production of 1, 13, 32, 772 tons (Faostat, 2014) [9]. Canada is the leading producer with approximately 3 million metric tons in 2012 (Janzen *et al*., 2014) [15] followed by France, Russian federation, China mainland and Ukraine.

In India, pea is found to be grown since ancient and utilized for various purpose, however, owing to introduction of exotic collections and adoption of improved cultivars, this heritage was greatly eroded. The landraces had greater extent of tolerance to biotic and abiotic stresses were replaced by new varieties (Cupic *et al*., 2009; Arbouche *et al*., 2011) [5, 2]. Only least portion of those could preserved in gene banks (Hagenblad *et al*., 2014) [14] or among farmers occupying marginal lands (FAO, 2011) [8] who practicing family farming. Genetic diversity in crop plants is the prerequisite in formulation of breeding strategies for further invigoration in genetic pool.

Pea landraces however can play a very important role in improvement works and selection, offering interesting characteristics for farming. However, the description and knowledge of these genotypes is a prerequisite for their use (Marchenay and Lagarde, 1987) [18]. So, several studies of pea germplasm using different approaches have been published in the world (Ali *et al*., 2007, Sarikamis *et al*., 2010, Ghixari *et al*., 2014) [1, 19, 12]. In Manipur, landraces are still neglected in favor of imported varieties of peas and then the number of local genotypes is much reduced.

Traditionally, germplasm diversity is assessed by morphological descriptors, which remain the only legitimate marker type accepted by the International Union for protection of New varieties of plants (UPOV, 2009) [23] (Ghixari *et al*., 2014) [12].

The objective of this research was to assess the trait association and principal genetic components among pea genotypes (Parents + Hybrids) which found to be contributing substantially toward maximization of genetic gain.

2. Materials and Methods

Owing to adoption of improved varieties/cultivars in cultivation, genetic diversity in field pea genotypes, used to be reservoir for many important traits of sustainability (natural landrace, wild relatives) is ruthlessly eroded. threatened, Search pea landraces from farmers was very difficult to do because of the priority given to the introduced varieties and thus, the number of cultivars collected was limited to twelve (Table 1).

Plant materials

The experiment was consisted 7 genetically diverse pea varieties obtained from the department of Plant Breeding and Genetics, CAU, Imphal, Manipur. The parentages were sown in crossing blocks and F1s were generated in diallel fashion (half diallel) during *Rabi* 2013-14. The F1s along with parents (7 parents + 21 F_1 crosses) were evaluated under Randomized Block Design (RBD) with three replications during *Rabi* 2014-15. Seeding was done with a spacing of 30cm × 10 cm, each treatment had one line with 4 m length. All recommended agro-practices were applied to raise good crop. The observations were recorded for 12 agro-morphological characters which were analyzed by SPAR.2.0 software developed at IASRI, New Delhi. The analysis of variance (ANOVA) was performed by Fisher's least significant difference (LSD) method to test the significance difference between means. Correlation analysis was performed based on twelve quantitative characters (DFsF, NNFF, DFF, DM, PHt, NPP, PL, NSP, SYP, BYP, SW, HI,). The principal component analysis and the cluster analysis were done using twelve characters (DFsF, NNFF, DFF, DM, Pht, NPP, PL, NSP, SYP, BYP, SW, HI,).The cluster analysis was adopted with the Ward's method as a clustering algorithm (Ward, 1963) [25].

3. Results and Discussion

Existing genetic variability among germplasm offer great help in enhancing the genetic gain/breeding value in crop plants. Landraces, found to have broad adaptability, sustainability in their habitat, hence, are known to be reservoir for all desirable genes which might change the crop scenario in several directions. The experimental genotypes reported to have great genetic variability (among parentage and F1s) for all the traits studied (Table 2) which are also found in concordance with the works of Gixhari *et al*. (2014) [12], Wani *et al*. (2013) [24], Khan *et al*. (2013) [16] and Gatti *et al*. (2011) [10]. Resultant hybrids were reported to have substantial heterotic over parental value indicates, good combing ability among parentage involved, which is good for heterosis breeding in field pea. The existing genetic diversity among parents and crosses might be useful for making strategies for further invigoration of field pea breeding programs (Cupic *et al*., 2009) [5] by selecting well combining parental lines among accessions (Gatti *et al*., 2011) [10]. Also, the differences were significant for all treatments (seven parents + twenty-one hybrids). These findings showed that enough genetic variability available in the materials studied. Esposito *et al.*, (2007) [7] had also observed significant differences among the genotypes for different characters viz., days to first flowering, nodes to first flowering, days to 50% flowering, days to maturity, plant height, number of pods/plant, pod length, number of seeds/pod, seed yield/plant, biological yield/plant, 100 seed weight and harvest index.

The genotypes involved in the study had substantial level of genetic diversity for morphological traits (table 3) which is prerequisite for maximizing genetic gain in more efficient way. The plant height is a positive yield correlated trait in field pea, reported to have vast variability among parents (132.7 cm in Pant P 217 to 58.73 in Prakash) and crosses (139.00 cm in Prakash x Pant P 217 to 109.0 cm in Rachna x VL-58). Researchers obtained lengths varying between 65.67 and 132 cm (Ceyhan and Avci, 2015), 51.20 and 111.30 cm (Georgieva *et al*., 2016), 65.67 and 126 cm (Khan *et al*., 2013) [16]. On the other hand, the average (63.64 cm) reported by Habtamu and Million (2013) is lower than that obtained in the present work (90.05 cm). Differences in plant height might be due to genetic characteristic of genotypes and adaptability to a particular environment (Khan *et al*., 2013) [16], especially that this character is dependent on the environment (Solberg *et al*., 2015) [21].

Principal component analysis

Principal component analysis (PCA) was performed to identify association between traits, responsible traits for yield and grouping pattern of field pea genotypes on the basis of the traits. The first three PCs accounted for about 75% of the total variability with >1.0 Eigen value. The first three principal components (PC) accounted for 75.0% of the variation (41.0, 25.0 and 9.0 for PC1, PC2 and PC3 respectively, table 4, Fig. 1 and 2). The first component was showed positive relation for almost all 9 traits except days to first flowering, days to fifty percent flowering and days to maturity which showed negative correlation. However, PC2 explained 25% of total variation where all traits except plant height, No. of pods/plant and number of seed per pod, rest are shown positive relation to yield contributing traits. Besides, number of seeds per pod and pod length recorded positive relation with yield contributing traits in PC3 shown positive relation with yield contributing traits in field pea. These results showed close association with work of Gixhari *et al*. (2014) [12] who studied PCA on pea and noted that some of these characters as leaflet length and width, number of seed per pod, weight of 100-seeds and yield per genotype contributed to a great part of variability. In the work of Esposito *et al*. (2007) [7] on pea genotypes, the two first components explained 67.7% of variability in the first season of experiment and 69.8% in the second one. According to the same author, length and width of stipule, length and width of leaflet, length and width of pod, number of days to flowering explained most of the variability. The study conducted by Umar *et al*. (2014) [22] on pea genotypes from different origins showed that the two parameters: Pod length and width are related to the first component which explained 40.29% of variation.

Table 1: List of genotypes and their origins.

S. No.	Genotypes/crosses	Developing institute
1	Makyatmubi	CAU, Imphal
2	Makuchabi	CAU, Imphal
3	KPMR851	CSAUAT, Kanpur
4	Prakash	IIPR, Kanpur
5	Pant P 217	GBPUAT, Pantnagar
6	Rachana	CSAUAT, Kanpur
7	VL 58	VPKAS, Almorah
8	21 F1s developed in half diallel fashion at CAU, Imphal	

Table 2: Analysis of variance for different characters of field pea

Source of variation	d.f.	Mean sum of squares											
		Days to first flowering	Nodes to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of pods/plant	Pod length(cm)	No. of seeds/pod	seed yield/plant (g)	biological yield/plant (g)	100 seed wt. (g)	Harvest index (%)
Replication	2	21.893	0.940	19.393	6.655	59.465	0.155	0.040	0.464	9.27	58.333	9.79*	74.33**
Genotypes	27	25.344**	3.302**	23.275**	7.458**	709.920**	9.815**	0.520**	0.876**	24.10**	96.64**	21.33**	47.08**
Error	54	9.485	1.015	7.936	3.260	66.566	2.599	0.124	0.403	4.057	19.56	2.27	10.55

Table 3: Mean *per se* performance of parents and crosses for days to first flowering, nodes to first flowering, days to 50% flowering, days to maturity, plant height, No. of pods/plant, pod length, No. of seeds/pod, seed yield/plant, biological yield/plant, 100 seed weight and harvest index in a half-diallel cross of pea

Parent/Cross	Days to first flowering	Nodes to first flowering	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of pods per plant	Pod length (cm)	Number of seeds per pod	Seed yield per plant (g)	Biological yield perplant (g)	100 seed wt. (g)	Harvest index (%)
Makyatmubi x Makuchabi	64.67	16.33	68.33	109.33	118.07	10.00	7.04	6.33	13.80	30.52	25.08	45.12
Makyatmubi x KPMR851	60.67	16.00	67.00	109.00	120.67	13.00	7.13	5.33	15.49	37.02	22.61	41.52
Makyatmubi x Prakash	67.00	16.33	71.00	111.00	128.80	9.00	7.31	5.67	12.02	32.29	25.90	37.45
Makyatmubi x Pant P 217	62.67	15.67	66.67	109.00	134.47	10.00	7.27	6.33	13.77	31.73	22.08	43.31
Makyatmubi x Rachna	68.67	15.00	73.00	112.00	112.67	8.00	6.33	5.33	12.20	31.53	21.21	38.92
Makyatmubi x VL 58	61.33	14.67	67.33	109.67	111.53	9.00	6.56	5.67	11.79	28.80	24.83	46.87
Makuchabi x KPMR851	60.00	16.33	65.67	109.00	116.47	10.67	6.75	6.00	13.42	27.88	19.72	47.81
Makuchabi x Prakash	62.67	16.00	67.00	109.00	120.40	10.33	7.11	6.33	13.91	29.02	23.15	47.92
Makuchabi x Pant P 217	63.00	16.00	67.67	110.00	115.97	8.33	6.92	6.33	12.60	27.06	20.41	46.87
Makuchabi x Rachna	66.33	15.67	71.33	111.00	118.40	9.33	6.96	6.33	10.62	25.23	19.86	42.18
Makuchabi x VL 58	62.00	13.67	67.00	108.00	118.83	13.00	7.19	6.67	15.36	34.13	20.71	45.17
KPMR851 x Prakash	58.33	15.00	65.00	108.33	132.13	10.00	6.43	5.00	11.73	25.43	21.07	46.19
KPMR851 x Pant P217	58.00	14.33	65.00	108.00	130.40	12.67	6.17	5.67	11.43	25.80	18.42	44.47
KPMR851 x Rachna	62.33	13.33	64.67	107.67	114.33	11.67	6.49	5.67	8.49	22.00	18.01	38.93
KPMR851 x VL 58	61.33	13.33	63.67	108.33	116.80	8.33	6.33	5.33	9.76	22.87	19.15	43.27
Prakash x Pant P 217	60.00	16.00	64.00	108.33	139.00	8.00	6.57	6.33	11.40	25.26	19.99	45.11
Prakash x Rachna	63.33	15.67	67.33	109.00	130.47	8.67	6.43	5.33	9.10	21.07	20.03	43.03
Prakash x VL 58	63.67	15.00	68.00	109.33	136.07	10.00	5.76	5.00	11.99	27.08	19.04	44.22
Pant P 217 x Rachna	62.00	14.33	65.67	109.33	125.73	8.67	6.35	6.67	11.81	26.98	17.81	43.88
Pant P 217 x VL 58	59.33	13.33	64.33	107.67	134.57	8.00	6.10	6.33	10.41	24.70	15.75	45.18
Rachna x VL-58	63.00	14.00	66.33	109.33	109.27	8.67	6.51	5.67	7.53	19.80	17.22	38.24
Makyatmubi	63.00	15.33	69.00	110.33	111.27	6.67	7.27	5.00	8.70	21.47	23.51	40.43
Makuchabi	63.67	15.67	69.33	110.67	105.53	7.33	6.82	6.33	6.60	16.46	18.43	40.11
KPMR851	62.33	15.33	67.00	110.00	109.27	8.67	6.37	5.67	7.73	20.96	18.46	36.76
Prakash	70.33	15.33	74.67	114.00	58.73	6.00	6.37	5.00	6.77	15.78	20.93	43.17
Pant P 217	61.67	14.33	68.67	110.00	132.07	7.67	6.61	6.33	7.70	18.14	17.42	42.42
Rachna	67.00	13.00	71.67	112.67	111.53	7.67	5.99	5.33	5.29	15.72	15.76	33.44
VL 58	61.67	13.67	70.67	112.33	104.33	7.33	6.49	6.00	6.21	18.48	18.25	33.50

Table 4: Matrix of eigenvalues and eigenvectors of principal components for different traits in pea.

	Eigen vectors											
	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11	PC12
Eigen values variances	4.930	3.050	1.080	0.890	0.650	0.600	0.330	0.190	0.150	0.110	0.020	0.000
% contribution	0.410	0.250	0.090	0.070	0.050	0.050	0.030	0.020	0.010	0.010	0.000	0.000
% cumulative	0.410	0.660	0.750	0.820	0.870	0.920	0.950	0.970	0.980	0.990	0.990	0.990
Days to first flowering	-0.290	0.345	-0.045	0.184	0.261	0.226	-0.105	0.761	-0.110	0.020	0.199	0.000
No. of nodes to first flowering	0.133	0.414	0.113	-0.407	-0.202	0.248	0.693	0.048	-0.191	0.076	-0.073	0.000
Days to fifty % flowering	-0.317	0.352	-0.019	0.188	0.170	0.182	0.048	-0.199	0.504	-0.105	-0.605	-0.070
Days to maturity	-0.376	0.267	0.033	0.067	0.113	0.127	0.072	-0.509	0.087	-0.045	0.680	0.120
Plant height	0.306	-0.181	0.023	0.105	-0.369	0.719	-0.131	0.082	0.391	-0.051	0.173	0.020
No. of pods/plant	0.334	-0.022	-0.317	0.427	0.149	-0.292	0.495	0.121	0.390	0.216	0.189	0.050
Pod length	0.172	0.386	0.346	0.148	-0.410	-0.408	-0.101	0.133	0.167	-0.527	0.108	0.020
No seed/pod	0.173	-0.016	0.818	0.281	0.258	0.054	0.010	-0.057	-0.043	0.382	-0.033	0.000
Seed yield/plant	0.348	0.255	-0.206	0.318	0.123	0.178	-0.124	-0.192	-0.412	-0.149	-0.182	0.580
Biological yield/plant	0.153	0.468	-0.169	-0.177	-0.238	-0.143	-0.430	-0.059	0.136	-0.643	0.021	0.000
100 seed weight (g)	0.309	0.038	0.079	-0.571	0.550	-0.031	-0.131	0.080	0.361	-0.196	0.089	0.260
Harvest Index	0.390	0.216	-0.131	0.093	0.093	0.120	-0.105	-0.176	-0.191	-0.185	0.091	-0.740

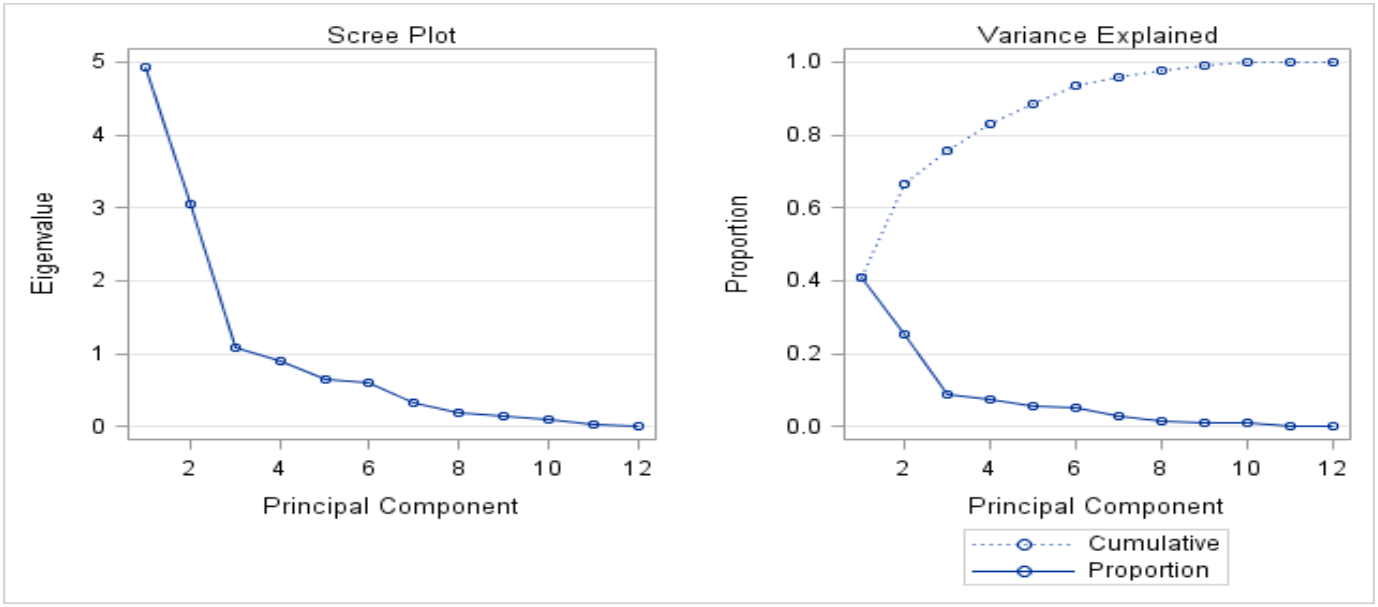

Fig 1: Screen plot of PCA components

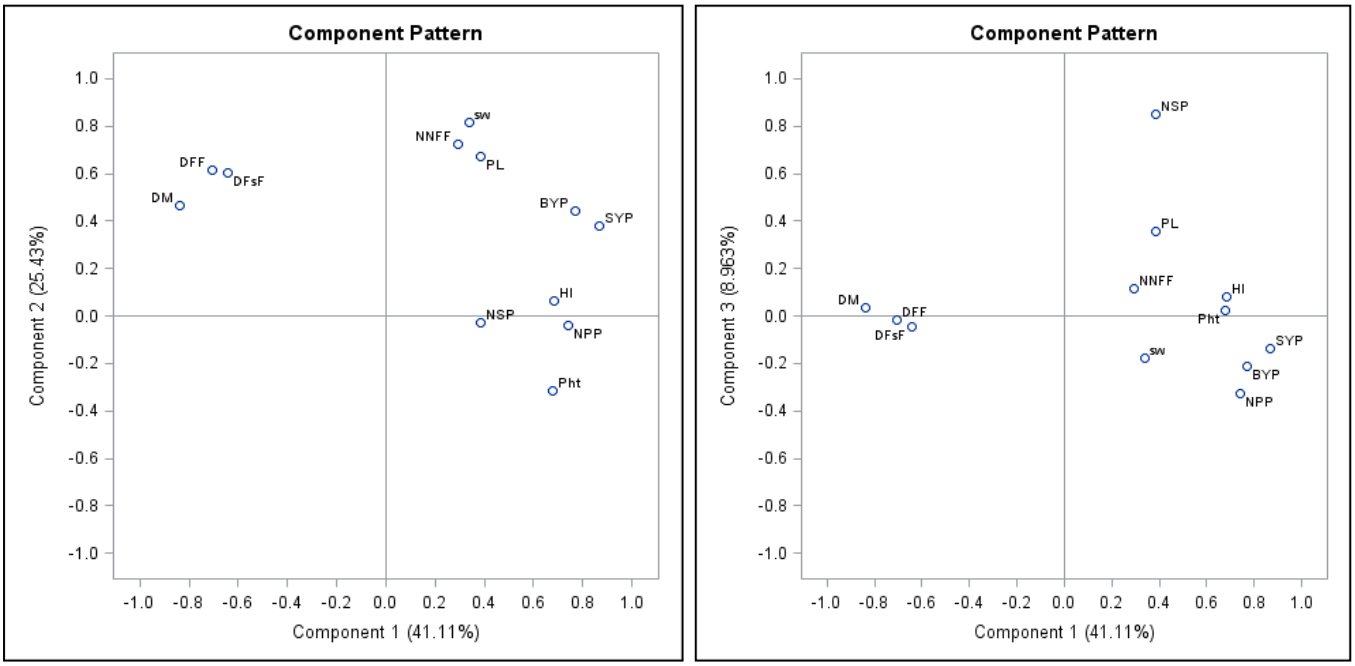

Fig 2: Patterns of PCA components

4. Conclusion

The traits associations and principal genetic components contributing substantially toward enhancing in genetic gain in field pea revealed the existence of a great variability within the studied genotypes of pea. This variability can be used in the work of selection and improvement is observed on the level of precocity to flowering but also for other qualitative and quantitative traits. On the other hand, expression of characteristics is highly influenced by the environment. Two groups were noted. The first group (Makyatmubi) was characterized by a seed yield highest biological yield per plant; the other group also comprised genotypes with substantial yield potential (Makyatmubi, Makuchabi, KPMR851, Rachna and VL 58) may be utilized for further breeding invigoration and genetic gain in field pea.

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Conflict of Interests

The authors have not declared any conflict of interests.

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