

## Genetic Evaluation of different Genotypes of Pea (*Pisum sativum* L.) for Yield and its Contributing Traits

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**ABSTRACT:** An experiment was carried out to investigate genetic assessment for yield and yield related attributes in twenty eight pea (*Pisum sativum* L.) genotypes during the cropping season 2021-22. Analysis of variance revealed significant differences among all the genotypes with respect to the character studied. For the trait pod weight, the estimates of phenotypic and genotypic coefficient of variation were higher reflecting presence of high variability among all the genotypes for this trait and offered better scope for improvement. In node at which the first flower appears, pod length, pod weight, plant height, number of pods per plant, and number of seeds per pod strong heritability and high genetic advance were observed indicating that selection would be effective for these traits. Minimum disease index of rust was reported in eight genotypes showing moderate disease reaction which can be a good option with reduced number of fungicidal sprays to obtain maximum yield with minimal rust severity. Among the tested genotypes Pusa Pragati, LC-P-1 and LC-P-2 performed better in yield and other important yield contributing traits therefore, these may be used in further breeding programme or can be used for cultivation under sub-tropical conditions of Himachal Pradesh.

**Keywords:** Genotypes, Evaluation, Heritability, Peas and Genetic advance.

### INTRODUCTION

The pea (*Pisum sativum*) is the world second most significant legume crop after the common bean (*Phaseolus vulgaris*) (Esposito *et al.*, 2007; Jaiswal *et al.*, 2013) and has recently been evaluated as an attractive protein source for animal and human nutrition. It thrives in cool, moist climates with moderate temperature ranging from 7 to 30 °C. Peas are grown for many purposes, including fresh consumption or canning. It is a biological nitrogen fixing legume crop, its significance for maintaining and recovering soil fertility, conservation and enhancement of soil physical qualities has long been recognized (Chakraborty *et al.*, 2003, Janzen *et al.*, 2014). The growing need for protein and mineral rich foods has increased interest in the crop as a protein source (Santalla *et al.*, 2001). Being a low-cost source of protein, it is known as 'poor man's meat' in the developing world (Saeed *et al.*, 2009), particularly in India, where the majority of the population is vegetarian. In the central and northern plains of India, it is cultivated as a winter season vegetable, whereas in the mountainous region, it is cultivated in the summer and as an autumn-winter crop. Pea produced in hills is also a high-priced crop due to its delicacy, sweetness, taste and excellent nutritious properties (Sharma *et al.*,

2020). Although there is considerable genetic variation in this crop with respect to yield and yield-related characteristics, still not much work has been done to improve the crop through the selection of superior kinds with high yield. The goal of the current study was to compare the effectiveness of several germplasms in terms of plant growth and production of pea. In order to select the elite genotypes, it is crucial to evaluate the phenotypic and genotypic variations for different traits, as well as their heritability. Estimates of variability parameters specially, heritability and genetic gain are good indicators of character improvement in a specific genetic material through selection (Kumari *et al.*, 2012). Keeping these in view, the current study was conducted to evaluate the pea genotypes in the sub-tropical conditions of Himachal Pradesh.

### MATERIALS AND METHODS

The experiment was carried out in the Department of Vegetable Science, College of Horticulture and Forestry, Neri, Hamirpur, during the Rabi season 2021-2022. The experimental site is located between 31°41'47.6"N latitude and 72°28'6.3"E longitude, at an elevation of 650 meters above mean sea level. The experimental materials included twenty-eight genotypes of pea that were obtained from various sources. These genotypes were evaluated in a randomized complete

block design with three replications, and data on pod yield and other component traits were recorded. The seed was sown in a well-prepared bed during the last week of October, with a row to row and plant to plant spacing of 60 cm × 10 cm. A healthy crop stand was maintained throughout the growing season by following the all standard agronomic practices. The data was collected on ten randomly chosen plants for the pod yield and other component traits, such as the node at which first flower appear, pod length (cm), pod weight (g), plant height (cm), number of pods per plant, number of seeds per pod, shelling percentage (%), pod yield (kg/plot) and disease index of rust (%) etc. The data were statistically analyzed using standard statistical procedures for randomized block design (Gomez and Gomez 1983). The genotypic, phenotypic, and environmental coefficients of variation were evaluated as method provided by Burton and De Vane (1953). The formula given by Burton and De Vane (1953); Johnson *et al.* (1955), the heritability in a broad sense and expected genetic advance were calculated.

## RESULTS AND DISCUSSION

Most of the traits showed significant variation for the twenty eight genotypes of pea. An experiment was conducted to evaluate genetic variability, heritability and genetic advance among different genotypes of pea (*Pisum sativum* L.).

**1. Node at which first flower appear:** Mean performance demonstrated highly significant differences for node at which first flower appear between genotypes, showing the existence of significant variation in the investigated material (Table 1). Mean value ranged from 7.47 to 15.67 with an overall mean of 12.02. The node at which first flower appear were earlier in twelve genotypes along with check as compared to the general mean. The least number of node at which first flower appear recorded in the Pusa Pragati (7.47), while the highest number of

node at which first flower appear reported in IC-356203 (15.67). However, the genotypes Pusa Pragati, LC-P-1 and LC-P-2 recorded the lower nodes at which first flower appear than check variety, Punjab-89. The results revealing considerable variability concerning this trait were reported by Devi *et al.* (2017); Bhardwaj *et al.* (2020); Kumar *et al.* (2021).

Among pea genotypes, phenotypic coefficient of variation (15.59) for node at which first flower appear was more than genotypic coefficient of variation (14.83) indicating that apparent variation is not only due to genotypes but also due to the influence of environment (Table 3). High broad sense heritability along with high genetic advance (90.58, 29.08) among pea genotypes was reported. The present findings are in agreement with the results of Kumar *et al.* (2015) (Fig. 1).

**2. Pod length (cm):** Different genotypes were found to have statistically significant divergence changes with regard to the pod length. The mean value range varied from 6.55 to 11.07 cm with an overall mean of 7.83 cm (Table 1). Seven genotypes along with check, were observed to have more pod length than the general mean. The maximum pod length was recorded in the genotype Pusa Pragati (11.07 cm). The minimum pod length was recorded in IC-356301 (6.55 cm) which was statistically identical to IC-107452 (6.73 cm). Out of all the genotypes investigated, comparatively greater pod length was observed in two genotypes Pusa Pragati and LC-P-1 than the best check Punjab-89 (10.43 cm). Tremendous variability with respect to pod length was also reported by Pandey *et al.* (2015); Gautam *et al.* (2017).

In pod length phenotypic variation (16.15) was larger than genotypic variation (16.07) (Table 3). The genotypic and phenotypic coefficients of variation were close to each other, indicating that the environment had little influence on this feature.

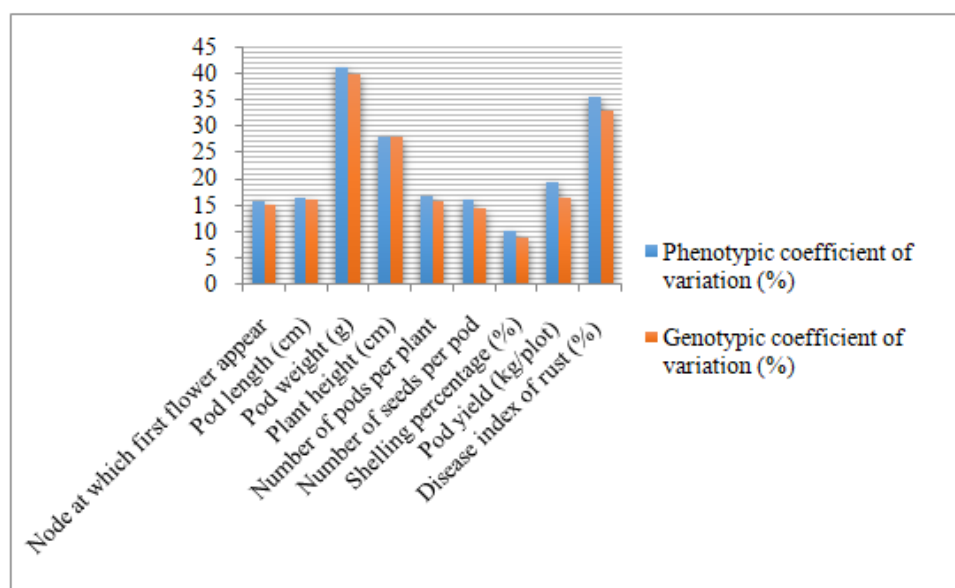
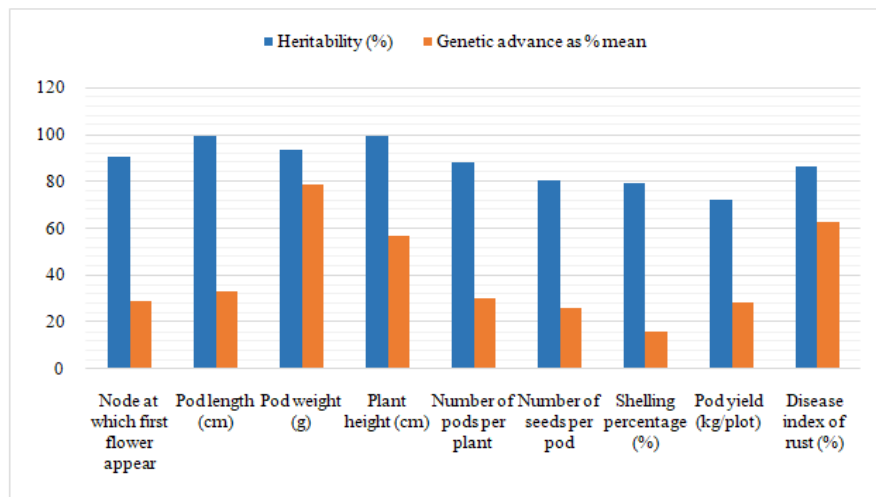


Fig. 1. Phenotypic and Genotypic coefficient of variation.



**Fig. 2.** Heritability and Genetic advance as percent of mean.

The estimations of heritability in general and genetic advance for pod length were high (99.03, 32.95, respectively), indicating that genetic influence dominated environmental influence in pod length. The results are in accordance with the findings of Devi *et al.* (2018); Singh *et al.* (2019).

**3. Pod weight (g):** The mean results recorded for pod weight show greater variability among all the genotypes as evident from the data presented in the Table 1. Based on the observations of the genotypes, the range varied from 3.12 to 9.77 g with the population overall mean of 4.67 g. The seven genotypes had more pod weight than the population mean including check. In the genotype Pusa Pragati (9.77 g) highest pod weight was reported, whereas, the lowest pod weight was recorded in IC-356301 (3.12 g) which was statistically identical to twelve genotypes. The results revealed that the genotypes *viz.*, Pusa Pragati, LC-P-1 and LC-P-2 were statistically found superior in terms of pod weight as compared to the check, Punjab-89. Genetic differences for pod weight among pea genotypes have also been reported by Gautam *et al.* (2017); Devi *et al.* (2018).

High phenotypic (40.96) and genotypic coefficient of variation (39.59), and high heritability (93.39) along with high genetic advance (78.81) was reported for this attribute (Table 3). These results are in agreement with the findings of Jeberson *et al.* (2016); Devi *et al.* (2018).

**4. Plant height (cm):** A significant variation between all the genotypes was recorded for plant height as revealed from Table 1. The mean and range values for this trait were recorded as 175.24 cm, 90.08 to 223.33 cm, respectively. The eighteen genotypes had more plant height than the populations mean. The maximum plant height was recorded in IC-107446 (223.33 cm) which was statistically equivalent to IC-374697, IC-107454, IC-49689, IC-98608 and IC-107498. While, the minimum plant height was reported in the genotype IC-374690 (90.08 cm) which was statistically different from other genotypes. The findings of the current assessment are trustworthy with the observations recorded by Basaiwala *et al.* (2013); Sharma and Sharma (2013); Kumar *et al.* (2021).

The phenotypic coefficient of variation for plant height was larger (27.89) than the genotypic coefficient of variation (27.77), and both values are near to one another, suggesting that the environment had little effect on this feature. The trait had high broad sense heritability (99.13) as well as a strong genetic advance as a percentage of mean (56.96) (Table 3). The results recorded in the current studies were consistent with the observations reported by Pandey *et al.* (2015).

**5. Number of pods per plant:** Analysis of variance indicated significant variations among pea genotypes for number of pods per plant (Table 1). The overall mean performance value for the attribute is 32.72 and range varied from 25.50 to 45.83. The seven genotypes had more number of pods per plant than the population mean. In IC-107446 largest number of pods per plant were recorded which was statistically similar to IC-374697. The lowest number of pods per plant was reported in IC-356203 which was statistically identical with IC-356301, IC-219023, IC-374690 and LC-P-3. Nine genotypes under study produced significantly more number of pods per plant than the check, Punjab-89. Sufficient range of variability for this trait was recorded by Pal and Singh (2013); Khan *et al.* (2017).

Moderate value of phenotypic (16.50) and genotypic (15.49) coefficient of variation for the number of pods per plant was observed. High broad sense heritability (88.06) along with the high genetic advance (29.94) was recorded (Table 3). Our results are also similar to the findings of Kumar *et al.* (2015); Devi *et al.* (2018).

**6. Number of seeds per pod:** In the current study, mean performance revealed significant differences in the number of seeds per pod among pea genotypes (Table 1). The evaluation of the genotypes for number of seeds per pod, the mean value was recorded as 6.49 and the range for this trait was observed as 5.00-9.00. Among all the genotypes studied, nine genotypes had more number of seeds per pod than the population mean. Check variety, Punjab-89 (9.00) exhibited maximum number of seeds per pod which was statistically equivalent to Pusa Pragati and LC-P-3. Whereas, minimum number of seeds per pod was recorded in IC-98609 (5.00) which was statistically equal with IC-374690 and IC-361877.

**Table 1: Mean performance of pea genotypes for different horticultural traits.**

Genotypes	Node at which first flower appear	Pod length (cm)	Pod weight (g)	Plant height (cm)	Number of pods per plant	Number of seeds per pod	Shelling percentage (%)	Pod yield (kg/plot)
IC-49689	13.27	7.19	3.87	220.92	41.25	5.83	52.89	2.50
IC-98608	12.87	7.03	3.50	219.66	40.83	5.83	53.07	2.48
IC-98609	13.33	7.36	3.98	209.59	31.83	5.00	55.65	2.23
IC-106905	12.13	7.16	3.93	204.00	29.75	6.08	51.57	2.11
IC-107446	12.07	7.09	3.50	223.33	45.83	6.50	55.03	2.70
IC-107452	11.67	6.73	3.45	210.67	32.08	6.08	41.16	2.31
IC-107454	12.33	7.13	3.55	221.67	41.00	6.67	53.53	2.52
IC-107498	12.47	7.18	3.81	217.08	33.42	7.25	45.46	2.33
IC-107510	11.47	7.13	3.51	211.00	28.92	6.08	47.24	2.08
IC-109810	12.13	6.89	3.38	215.00	33.83	6.17	57.12	2.30
IC-219023	14.66	7.07	3.66	198.17	28.18	6.42	47.18	1.80
IC-354439	12.73	7.52	4.11	208.00	31.08	6.17	52.84	2.18
IC-356203	15.67	7.73	3.81	181.33	25.50	6.25	48.33	1.49
IC-356267	13.80	6.79	3.27	204.42	30.05	6.00	51.74	2.13
IC-356301	13.73	6.55	3.12	193.92	28.00	6.58	45.45	1.65
IC-361173	12.53	7.18	4.04	207.92	30.08	6.08	54.64	2.15
IC-361877	11.93	7.58	4.01	212.91	32.17	5.67	52.98	2.32
IC-372703	14.33	6.97	3.14	105.25	31.83	5.83	52.48	1.89
IC-374690	11.93	7.43	4.06	90.08	28.25	5.25	52.26	1.60
IC-374697	11.93	7.63	4.62	222.50	44.00	5.92	54.90	2.53
Lincoln	10.73	8.44	5.31	115.25	30.58	6.33	49.99	2.16
Azad P-1	11.53	8.46	4.96	110.50	30.25	6.33	50.22	2.02
Pusa Pragati	7.47	11.07	9.77	121.08	35.92	8.83	60.30	3.23
LC-P-1	8.53	10.81	8.46	121.00	32.50	7.08	59.85	2.91
LC-P-2	9.00	9.66	8.78	118.00	30.67	7.67	59.76	2.86
LC-P-3	10.10	9.29	7.77	114.08	28.50	8.33	44.40	2.52
LC-P-4	12.27	7.76	4.25	112.42	30.58	6.33	56.35	2.36
Punjab-89 (Check)	10.03	10.43	7.15	116.92	29.27	9.00	56.53	2.71
Mean	12.02	7.83	4.67	175.24	32.72	6.49	52.25	2.29
Range	7.47-15.67	6.55-11.07	3.12-9.77	90.08-223.33	25.50-45.83	5.00-9.00	41.16-60.30	1.49-3.23
CD <sub>0.05</sub>	0.94	0.20	0.80	7.49	3.06	0.75	3.86	0.39

**Table 2: Mean performance of pea genotypes for rust disease.**

Genotypes	Disease index of rust (%)	Disease Reaction
IC-49689	19.35 (26.08)	Moderately Susceptible (MS)
IC-98608	19.13 (25.90)	Moderately Susceptible (MS)
IC-98609	9.92 (18.32)	Moderately Resistant (MR)
IC-106905	14.98 (22.75)	Moderately Susceptible (MS)
IC-107446	9.52 (17.95)	Moderately Resistant (MR)
IC-107452	12.86 (20.98)	Moderately Susceptible (MS)
IC-107454	15.97 (23.53)	Moderately Susceptible (MS)
IC-107498	17.72 (24.86)	Moderately Susceptible (MS)
IC-107510	18.27 (25.12)	Moderately Susceptible (MS)
IC-109810	15.30 (22.99)	Moderately Susceptible (MS)
IC-219023	17.28 (24.52)	Moderately Susceptible (MS)
IC-354439	20.98 (27.17)	Moderately Susceptible (MS)
IC-356203	20.98 (27.16)	Moderately Susceptible (MS)
IC-356267	16.04 (23.54)	Moderately Susceptible (MS)
IC-356301	22.96 (28.61)	Moderately Susceptible (MS)
IC-361173	9.96 (18.37)	Moderately Resistant (MR)
IC-361877	18.51 (25.45)	Moderately Susceptible (MS)
IC-372703	28.42 (32.20)	Susceptible (S)
IC-374690	27.13 (31.37)	Susceptible (S)
IC-374697	14.07 (22.01)	Moderately Susceptible (MS)
Lincoln	12.18 (20.41)	Moderately Susceptible (MS)
Azad P-1	9.44 (17.86)	Moderately Resistant (MR)
Pusa Pragati	9.65 (18.06)	Moderately Resistant (MR)
LC-P-1	9.82 (18.24)	Moderately Resistant (MR)
LC-P-2	9.64 (18.06)	Moderately Resistant (MR)
LC-P-3	20.05 (26.55)	Moderately Susceptible (MS)
LC-P-4	20.60 (26.97)	Moderately Susceptible (MS)
Punjab-89 (Check)	9.77 (18.20)	Moderately Resistant (MR)
Mean	16.09	
Range	9.44-28.42	
CD <sub>0.05</sub>	2.66	

Significant variation was also reported by Devi *et al.* (2018); Bhardwaj *et al.* (2020) for this trait. An estimated genotypic and phenotypic coefficient of variation was recorded for the attribute 14.22 and 15.87, respectively. Heritability in the broad sense was recorded 80.26 with high genetic advance 26.25 for number of seeds per pod (Table 3). High heritability coupled with high genetic advance for number of seeds per pod suggested that effective selection may be possible for this trait. Similar results were also estimated by Singh *et al.* (2019).

**7. Shelling percentage (%):** It is a beneficial trait as the pods with high shelling percentage are preferred by the consumers. The results observed for shelling percentage show large variability between all the genotypes (Table 1). The attribute mean performance value was 52.25 % and range varied from 41.16 to 60.30 %. Seventeen genotypes among the study have higher shelling percentage than the population mean. The highest proportion of shelling percentage was discovered in Pusa Pragati (60.30 %) which was statistically comparable to four genotypes along with check. While, the lowest shelling percentage was recorded in IC-107452 (41.16 %) which was statistically equivalent to LC-P-3. Ample amount of variation for shelling percentage was also reported by Singh *et al.* (2017); Devi *et al.* (2018); Kumar *et al.* (2021).

Among pea genotypes phenotypic and genotypic coefficient of variation was recorded 9.93 and 8.84, respectively. There was moderate broad sense heritability with moderate genetic advance (79.41, 16.24) for shelling percentage among pea genotypes (Table 3). Present findings are in agreement with the results of Kumar *et al.* (2015).

**8. Pod yield (kg/plot):** It is an important horticultural trait which determines the potential of any variety. Highly significant variations were observed for pod yield among the genotypes and it ranged from 1.49 to 3.23 kg with an overall mean of 2.29 kg. Fifteen genotypes had higher pod yield than the population

mean including check. The highest pod yield was reported in the genotype Pusa Pragati (3.23 kg) which was statistically at par with LC-P-1 and LC-P-2. The lowest pod yield was assessed in IC-356203 (1.49 kg) which was statistically equivalent to IC-374690, IC-356301 and IC-219023. However, the genotype Pusa Pragati was statistically found superior in pod yield than the check, Punjab-89. Sufficient range of variability for the trait was also reported by Kumar *et al.* (2015); Devi *et al.* (2017).

Pod yield had a higher phenotypic coefficient of variation (19.22) than the genotypic coefficient of variation (16.29). Broad sense heritability and genetic advance as percent of mean was reported for the trait 71.91 and 28.46, respectively (Table 3). The recent results are further in support to the findings of Devi *et al.* (2018); Singh *et al.* (2019).

**9. Disease index of rust:** The analysis of twenty-eight genotypes revealed significant variation for the rust disease. Disease index of rust ranged from 9.44 to 28.42 % with a mean value of 16.09 % (Table 2). The minimum disease index of rust was found in Azad P-1 (9.44 %) which was statistically at par with IC-107446, LC-P-2, Pusa Pragati, Punjab-89, LC-P-1, IC-98609, IC-361173 and Lincoln whereas maximum incidence was observed in IC-372703 (28.42 %) which was statistically equivalent to IC-374690. None of the genotypes were found resistant to the disease. Eight genotypes showed moderate reaction with 1 to 10 % disease index (IC-98609, IC-107446, IC-361173, Azad P-1, Pusa Pragati, LC-P-1, LC-P-2 and Punjab-89). Eighteen genotypes fall under moderately susceptible (11-25 %) category. Two genotypes showed susceptible (26-50%) reaction (IC-372703 and IC-374690). Thus, eight genotypes showing moderately resistant reaction can be a good option to integrate it with reduced number of fungicidal sprays to obtain maximum yield with minimal rust severity. Significant variation for rust disease among different genotypes was also reported by Upadhyay *et al.* (2017).

**Table 3: Estimates of different genetic parameters for various traits in pea (*Pisum sativum* L.).**

Sr. No.	Characters	Mean	Range	Coefficient of variation (%)		Heritability (%)	Genetic Advance as % mean
				Phenotypic	Genotypic		
1.	Node at which first flower appear	12.02	7.47-15.67	15.59	14.83	90.58	29.08
2.	Pod length (cm)	7.83	6.55-11.07	16.15	16.07	99.03	32.95
3.	Pod weight (g)	4.67	3.12-9.77	40.96	39.59	93.39	78.81
4.	Plant height (cm)	175.24	90.08-223.33	27.89	27.77	99.13	56.96
5.	Number of pods per plant	32.72	25.50-45.83	16.50	15.49	88.06	29.94
6.	Number of seeds per pod	6.49	5.00-9.00	15.87	14.22	80.26	26.25
7.	Shelling percentage (%)	52.25	41.16-60.30	9.93	8.84	79.41	16.24
8.	Pod yield (kg/plot)	2.29	1.49-3.23	19.22	16.29	71.91	28.46
9.	Disease index of rust (%)	16.09	9.44-28.42	35.44	32.87	86.11	62.87

## CONCLUSIONS

So, based on the overall mean performance of genotypes in the present investigation, it is concluded that the genotypes Pusa Pragati, LC-P-1 and LC-P-2 were recorded superior in terms of pod yield and other important horticultural traits. Thus, these genotypes can

be recommended for further breeding programme for their superior traits or for cultivation under the sub-tropical conditions of Himachal Pradesh.

## FUTURE SCOPE

The genotypes identified as superior can be exploited in

future breeding programme.

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**Conflict of Interest.** None.

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