Research Article

Genetic variability, heritability, genetic advance and correlation studies among F₇ populations of chickpea (*Cicer arietinum* L.)

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Abstract

Genetic variability is the main basis of improvement in crops. The experiment was conducted at The University of Agriculture Peshawar to estimate genetic variability, heritability, genetic advance and correlation studies among F₇ populations of chickpea. The experimental material comprised 35 chickpea genotypes Viz. 33 F₆ populations of chickpea and two check varieties i.e., NIFA-2005 and Karak-1. The genotypes were sown in RCB design with two replications. Data were collected on eight yield contributing traits viz. Secondary branches plant⁻¹, pods plant⁻¹, seed pod⁻¹, 100-grain weight, grain yield plant⁻¹ and harvest index. The analysis of variance showed significant differences ($p \leq 0.01$) among F₆ populations of chickpea for all the traits studied. Maximum number of secondary branches plant⁻¹ (23.50), seeds pod⁻¹ (1.80) and seed yield plant⁻¹ (22.76 g) revealed by C1-P2-1-2. Maximum pods plant⁻¹ (58.60), 100-seed weight (30.64 g) and harvest index (42.55%) were recorded for C1-P1-1-1, C1-P1-6-4 and karak-1, respectively. Pods plant⁻¹ exhibited high heritability (0.93) followed by seed yield plant⁻¹ (0.86), secondary branches plant⁻¹ (0.85), 100-seed weight (0.75), plant height (0.73) and harvest index (0.68). High genetic advance was noticed for seed yield plant⁻¹ (33.21), pods plant⁻¹ (29.61%) and secondary branches plant⁻¹ (22.73%). The genotypic and phenotypic correlation of seed yield plant⁻¹ was positive and highly significant with secondary branches plant⁻¹, pods plant⁻¹ and harvest index. Chickpea genotypes C1-P2-1-1, C1-P1-6-2, C1-P2-1-2, C1-P1-6-4, C1-P2-3-3 and C1-P2-3-1 showed best performance than local checks Karak-1 and NIFA-2005 for pods plant⁻¹ and seed yield plant⁻¹ and should be further tested at multi-location for possible release as a new cultivars.

Keywords: F₇ populations of Chickpea; Heritability; Genetic advance; Correlation

Introduction

Chickpea is the third most important pulse crop in the world after dry bean and dry peas

[1]. It contribution to world pulses production is 12%. The Asian region contributes 70% to the total world's chickpea production [2]. It

is probably originated in the area of present day Southeastern Turkey and adjoining Syria. Chickpea is an important food legume providing protein in human diet. It has the ability to fix atmospheric nitrogen and improve soil fertility with low added cost of production [3].

Chickpea is an important annual rabi season crop. On the basis of photoperiod and photosynthesis it is C_3 (inefficient) and long days crop respectively. It is a deep tap rooted crop and adapted to water stress condition. The crop is sensitive to excess of water and yield best on sandy loam soils [4]. Nutritionally, the importance of chickpea in human food from the high protein contents of its seeds, a better protein digestibility than several other pulses, no hemagglutinating activity and low antitryptic activity. It contain protein (23%), carbohydrates (64.5%), starch (47%) and fats (5%), crude fiber (6%) [5].

On the basis of area and production India, Pakistan and Turkey are the major chickpea growing countries. Among these, India is leading the world in chickpea production, producing 5980 thousand tons annually followed by Pakistan 845 thousand tons and then Turkey 525 thousand tons. In Pakistan, the area under chickpea cultivation is about 1054 thousand hectares with an average yield of 472 kg ha⁻¹. In Khyber Pakhtunkhwa chickpea is growing on an area of 39.7 thousand hectares, production of 22.9 thousand tons with an average of 577.0 kg ha⁻¹ [6]. Chickpea is cultivated on approximately 75% rain fed area of Khyber Pakhtunkhwa i.e. Karak, Bannu, Lakki Marwat, Dera Ismail Khan and Tank [7].

Genetic variation is important in breeding programs for traits and for picking desirable genotypes. Analysis of the correlation among parameters is essential for determining selection criteria [8]. Plant breeders are continuously trying to improve

yield of chickpea to feed an ever-increasing population. For this purpose improvement in chickpea production need information on nature and extent of genetic variation in quantitative traits and their interrelationship in population including diverse genotypes, which are pre-requisites for efficient breeding program [9]. As genetic variability and correlation are essential in breeding programs, therefore the present study was aimed to study genetic variability, heritability, genetic advance and genotypic and phenotypic correlation in F_6 populations of chickpea for yield attributing traits.

Materials and methods

The contemporary investigations were carried out at The University of Agriculture Peshawar with aims to explore genetic variability, heritability, genetic advance and correlation coefficient among F_7 populations of chickpea. 35 chickpea genotypes including 33 crosses derived from the cross of parents ICC-19181 $\times$ NDC-4-20-4 and 2 check varieties (Table 1) were evaluated in RCB design with two replications during rabi season 2016-17. Row length was 2 m, row to row distance was 30 cm and plant spacing was 10 cm. Standard cultural practices were followed throughout the growing season including hand weeding, irrigation and at the time of pods formation insecticide (Emamectin benzoate) was sprayed.

The biometrical data were recorded from randomly selected five plants on Secondary branches Plant⁻¹, Pods plant⁻¹, seed pod⁻¹, 100-Grain Weight, Grain yield plant⁻¹ and harvest index.

Statistical analysis

Data recorded on each traits were analyzed using Statistix 8.1 software. The genotype means of each traits were compared using least significant differences test at 5% level. Heritability (h^2_{BS}) was worked out according to [10].

Table 1. List of 33 F₆ populations and 2 check varieties along with their parentage

S. No.	GENOTYPE	PARENTAGE	ORIGIN
1	C1-P1-1-2	ICC-19181 × NDC-4-20-4	UAP/Pakistan
2	C1-P1-2-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
3	C1-P1-2-3	ICC-19181 × NDC-4-20-4	UAP/Pakistan
4	C1-P1-2-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
5	C1-P1-2-5	ICC-19181 × NDC-4-20-4	UAP/Pakistan
6	C1-P1-2-7	ICC-19181 × NDC-4-20-4	UAP/Pakistan
7	C1-P1-3-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
8	C1-P1-3-6	ICC-19181 × NDC-4-20-4	UAP/Pakistan
9	C1-P1-4-2	ICC-19181 × NDC-4-20-4	UAP/Pakistan
10	C1-P1-4-3	ICC-19181 × NDC-4-20-4	UAP/Pakistan
11	C1-P1-4-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
12	C1-P1-4-5	ICC-19181 × NDC-4-20-4	UAP/Pakistan
13	C1-P1-5-3	ICC-19181 × NDC-4-20-4	UAP/Pakistan
14	C1-P1-5-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
15	C1-P1-6-2	ICC-19181 × NDC-4-20-4	UAP/Pakistan
16	C1-P1-6-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
17	C1-P1-6-5	ICC-19181 × NDC-4-20-4	UAP/Pakistan
18	C1-P2-1-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
19	C1-P2-1-2	ICC-19181 × NDC-4-20-4	UAP/Pakistan
20	C1-P2-2-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
21	CI-P2-3-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
22	CI-P2-3-3	ICC-19181 × NDC-4-20-4	UAP/Pakistan
23	CI-P2-3-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
24	CI-P2-4-2	ICC-19181 × NDC-4-20-4	UAP/Pakistan
25	CI-P4-3-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
26	CI-P4-4-1	ICC-19181 × NDC-4-20-4	UAP/Pakistan
27	CI-P4-4-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
28	C1-P4-6-3	ICC-19181 × NDC-4-20-4	UAP/Pakistan
29	C1-P4-6-4	ICC-19181 × NDC-4-20-4	UAP/Pakistan
30	C1-P4-6-6	ICC-19181 × NDC-4-20-4	UAP/Pakistan
31	C1-P4-6-8	ICC-19181 × NDC-4-20-4	UAP/Pakistan
32	C1-P4-6-9	ICC-19181 × NDC-4-20-4	UAP/Pakistan
33	C1-P4-6-10	ICC-19181 × NDC-4-20-4	UAP/Pakistan
34	KARAK-1	Local selection	KARAK/Pakistan
35	NIFA-2005	Local selection	NIFA/Pakistan

$$h^2 = \frac{V_g}{V_p}$$

Whereas

h^2 = heritability, V_g , V_p = Genetic and phenotypic variances respectively.

Expected genetic advance (GA) was predicted according to [11].

$$\text{Genetic advance (GA)} = k \times \sqrt{V_p} \times h$$

$$\text{Genetic advance (as percentage of mean)} = \frac{GA}{\bar{X}} \times 100$$

Whereas

K = selection intensity at 20%, V_p = Phenotypic variance of trait,

h^2 = Heritability of trait, $\bar{X}$ = Grand mean of trait

Genetic and phenotypic correlation among yield attributing traits was determined by the following procedure of [10].

$$\text{Genetic correlation} = r_{g(X1X2)} = \frac{\text{COV}_{g(X1X2)}}{\sqrt{V_{g(X1)} \cdot V_{g(X2)}}}$$

$$\text{Phenotypic correlation} = r_{p(X1X2)} = \frac{\text{COV}_{p(X1X2)}}{\sqrt{V_{p(X1)} \cdot V_{p(X2)}}}$$

Results and discussion

Secondary branches plant⁻¹

The mean square showed significant ($p \leq 0.01$) differences among F_7 populations for secondary branches plant⁻¹ (Table 2). It mean values ranged from 10.10 to 23.50 with an average value of 15.33. Maximum secondary branches plant⁻¹ 23.50 was recorded for C1-P2-1-2 followed by C1-P2-1-1 (4.20) and minimum 10.10 for C1-P2-2-4 (Table 3). [2, 12] also reported significant results in chickpea for secondary branches plant⁻¹. The genetic, environmental and phenotypic variances for secondary branches plant⁻¹ was 7.32, 1.33 and 8.65 respectively. Broad sense heritability for the said trait was

0.85 and genetic advance was 22.73% (Table 4). Our results are in line with [13, 14]. Correlation analysis revealed highly significant and positive association of number of secondary branches plant⁻¹ with pods plant⁻¹ ($r_g = 0.888^{**}$, $r_p = 0.781^{**}$) and seed yield plant⁻¹ ($r_g = 0.835^{**}$, $r_p = 0.770^{**}$) at both genotypic and phenotypic levels. There was a significant and positive relation of secondary branches plant⁻¹ with seeds pod⁻¹ ($r_g = 0.288^*$) at genotypic level only. While with remaining traits it had non-significant correlation. (Table 5) [15, 16] also came up with the same results.

Table 2. Mean squares of yield attributing traits of F_6 populations of chickpea

Source of variance	df	Secondary branches plant ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	100-grain weight	Seed yield plant ⁻¹	Harvest Index
Replication	1	2.88	11.69	0.10	3.47	29.23	51.21
Genotypes	34	15.97**	124.3**	0.02**	9.29**	20.84**	30.58**
Error	34	1.33	4.61	0.01	1.31	1.53	5.76
CV (%)	-	7.53	6.06	4.77	5.46	10.18	6.86

*, ** = Significant at 5% and 1% probability level, respectively

Pods plant⁻¹

Mean squares values declared significant ($p \leq 0.01$) differences among F_7 populations of chickpea for pods plant⁻¹ (Table 2). Pods plant⁻¹ varied from 18.70 to 58.60 with an average of 35.43. Maximum pods plant⁻¹ 58.60 was noted for C1-P2-1-1 followed by C1-P1-1-2 (58.40) and minimum 18.70 for C1-P2-2-4 (Table 3). [17, 18] also observed significant difference for pods plant⁻¹. The genetic, environmental and phenotypic variances for secondary branches plant⁻¹ was 59.86, 4.61 and 64.47 respectively. Broad sense heritability for the said trait was 0.93

and genetic advance was 29.46% (Table 4). High heritability for pods plant⁻¹ are supported by the results of [2, 19]. Pods plant⁻¹ showed highly significant and positive association with secondary branches plant⁻¹ ($r_g = 0.888^{**}$, $r_p = 0.781^{**}$), seed yield plant⁻¹ ($r_g = 0.959^{**}$, $r_p = 0.857^{**}$) and harvest index ($r_g = 0.427^{**}$, $r_p = 0.386^{**}$) at both genetic and phenotypic levels, whereas the said trait had non-significant association with rest of traits. (Table 5). [8, 20] also noted positive relationship between pods plant⁻¹ and grain yield.

Table 3. Mean values of yield attributing traits of F₆ populations of chickpea

Genotypes	Secondary branches Plant ⁻¹ (No.)	Pods Plant ⁻¹ (No.)	Seeds pod ⁻¹ (No.)	100-seed weight (g)	Seed yield Plant ⁻¹ (g)	Biological yield Plant ⁻¹ (g)	Harvest Index (%)
C1-P1-1-2	17.20	41.30	1.59	21.18	13.58	37.30	36.19
C1-P1-2-1	15.20	37.30	1.46	20.26	11.15	33.10	32.81
C1-P1-2-3	14.80	36.90	1.59	21.91	12.66	34.20	36.89
C1-P1-2-4	15.90	39.00	1.58	21.27	13.38	36.80	35.71
C1-P1-2-5	16.90	36.00	1.43	22.01	11.20	28.90	35.46
C1-P1-2-7	14.50	32.90	1.54	20.97	10.72	32.20	31.80
C1-P1-3-1	16.70	41.70	1.59	21.91	14.43	35.20	39.33
C1-P1-3-6	17.50	39.00	1.52	21.01	12.44	33.90	34.07
C1-P1-4-2	17.10	39.40	1.62	19.57	13.76	36.70	36.39
C1-P1-4-3	14.90	37.70	1.61	21.74	12.61	32.60	38.36
C1-P1-4-4	12.10	30.20	1.30	22.55	9.02	30.30	29.66
C1-P1-4-5	12.80	32.10	1.63	22.09	10.52	31.50	34.01
C1-P1-5-3	12.70	28.70	1.70	19.94	9.56	26.30	35.61
C1-P1-5-4	13.50	29.70	1.63	20.70	10.10	28.90	34.43
C1-P1-6-2	13.40	38.80	1.75	20.65	13.75	34.20	40.25
C1-P1-6-4	13.50	30.80	1.72	30.64	15.40	37.40	41.11
C1-P1-6-5	13.30	40.50	1.69	16.81	11.22	29.30	38.29
C1-P2-1-1	22.30	58.60	1.73	21.48	22.04	60.70	35.96
C1-P2-1-2	23.50	58.40	1.80	21.63	22.76	64.30	35.14
C1-P2-2-4	10.10	18.70	1.63	21.15	6.55	22.00	29.05
CI-P2-3-1	15.65	37.20	1.71	18.53	13.04	42.78	31.44
CI-P2-3-3	17.90	40.90	1.64	20.23	13.89	33.40	41.12
CI-P2-3-4	17.70	37.00	1.57	20.54	12.30	40.40	27.04
CI-P2-4-2	14.50	33.50	1.57	20.64	11.15	30.90	35.24
CI-P4-3-1	15.20	33.10	1.64	20.02	11.09	37.90	29.24
CI-P4-4-1	10.60	20.20	1.64	20.54	6.89	26.20	27.21
CI-P4-4-4	14.30	33.90	1.65	23.17	12.83	34.10	37.25
C1-P4-6-3	13.80	31.60	1.70	18.87	10.46	29.50	34.99
C1-P4-6-4	13.70	32.20	1.75	21.30	12.04	32.20	37.03
C1-P4-6-6	13.50	32.50	1.77	21.65	12.65	32.10	38.77
C1-P4-6-8	16.90	31.50	1.73	21.51	11.33	31.10	34.80
C1-P4-6-9	20.20	33.30	1.71	20.82	12.28	35.60	34.19
C1-P4-6-10	13.80	24.30	1.69	20.95	8.85	29.50	29.14
KARAK-1	15.30	37.15	1.57	19.22	11.02	25.90	42.55
NIFA 2005	15.45	33.95	1.58	17.20	9.12	28.40	34.00
Mean	15.33	35.43	1.63	20.99	12.17	34.17	34.99
LSD (5%)	2.35	4.36	0.16	2.33	2.52	9.55	4.88

Seeds pod⁻¹

The mean square revealed significant ($p \leq 0.01$) differences among F₇ populations of chickpea for seeds pod⁻¹ (Table 2). Means of seeds pod⁻¹ varied from 1.30 to 1.80 with an overall mean of 1.63. The maximum seeds pod⁻¹ 1.80 was perceived by C1-P2-1-2 while minimum 1.30 was noticed for C1-P1-4-4 (Table 3). Genetic, environmental, phenotypic variances for seeds pod⁻¹ was

0.01, 0.01 and 0.02 respectively. The heritability (bs) estimated for the same trait was 0.55 with a genetic advance of 5.43% (Table 4). [21, 22] observed moderate heritability for said trait. Seeds pod⁻¹ was significantly positive correlated with seed yield plant⁻¹ ($r_g = 0.537^{**}$, $r_p = 0.271^{**}$) at both level. Seeds pod⁻¹ and secondary branches plant⁻¹ ($r_g = 0.288^{**}$, $r_p = 0.090^{ns}$) was positive correlated. Similarly seeds pod⁻¹

¹ and harvest index ($r_g = 0.268$, $r_p = 0.266$) was significantly positive correlated at both levels. (Table 5). [23] also observed positive

association between grain yield and seeds pod⁻¹.

Table 4. Variance component, heritability (bs) and Genetic advance for yield attributing traits of F₆ populations of chickpea

TRAITS	Vg	Ve	Vp	h ² (bs)	GA	GA (%)
Secondary branches plant ⁻¹	7.32	1.33	8.65	0.85	3.48	22.73
Pods plant ⁻¹	59.86	4.61	64.47	0.93	10.44	29.61
Seeds pod ⁻¹	0.01	0.01	0.02	0.55	0.09	5.43
100-seed weight	3.99	1.31	5.30	0.75	2.42	11.55
Seed yield plant ⁻¹	9.65	1.53	11.19	0.86	4.04	33.21
Harvest Index	12.41	5.76	18.17	0.68	4.08	11.65

Table 5. Genotypic correlation (above diagonal) and phenotypic correlation (below diagonal) among yield attributing traits of F₆ populations of chickpea

Traits	Secondary branches plant ⁻¹	Pods plant ⁻¹	Seeds pod ⁻¹	100-seed weight	Seed yield plant ⁻¹	Harvest Index
Secondary branches plant ⁻¹	--	0.888**	0.288*	-0.043 ^{NS}	0.835**	0.231 ^{NS}
Pods plant ⁻¹	0.781**	--	0.121 ^{NS}	-0.085 ^{NS}	0.959**	0.427**
Seeds pod ⁻¹	0.090 ^{NS}	0.171 ^{NS}	--	-0.001 ^{NS}	0.537**	0.268*
100-seed weight	-0.030 ^{NS}	-0.051 ^{NS}	0.029 ^{NS}	--	0.295*	0.217 ^{NS}
Seed yield plant ⁻¹	0.770**	0.857**	0.271*	0.234 ^{NS}	--	0.484**
Harvest index	0.131 ^{NS}	0.386**	0.266*	0.189 ^{NS}	0.375**	--

*, ** = Significant at 5% and 1% probability level respectively whereas NS = Non-significant

100-Seed weight (g)

Mean squares displayed significant ($p \leq 0.01$) differences among F₇ populations for 100-Seeds weight (Table 2). The said trait ranged from 16.81 to 30.64 g among all the F₆ populations. The mean values indicated that maximum 100-Seeds weight 30.64 g was noticed for CI-P1-6-4 and minimum 16.81 g was recorded for C1-P1-6-5 (Table 3). Genotypic, environmental and phenotypic variances for 100-Seeds weight was 3.99, 1.31 and 5.30 respectively. Heritability and genetic advance for the said trait was 0.75 and 11.55% (Table 4). Our heritability estimates for the mention trait are in accordance with [1, 24, 25]. The correlation of 100-seed weight and seed yield plant⁻¹ ($r_g = 0.295^*$, $r_p = 0.234^{NS}$) was positive and significant at genotypic level but positive and non-significant at phenotypic level, while with rest of traits 100 seed weight had non-significant association (Table 5). [14, 26, 27] also noted positive correlation between grain yield and 100-Seeds weight.

Seed yield plant⁻¹ (g)

Mean squares evinced highly significantly ($p \leq 0.01$) difference among F₇ populations of chickpea for seed yield plant⁻¹ (Table 2). Means ranged from 6.25 to 22.76 g with an overall mean of 12.17 g. The highest seed yield plant⁻¹ 22.76 g was noticed for C1-P2-1-2 followed by C1-P2-1-1 (22.04) while lowest seed yield plant⁻¹ 6.55 g was noted for C1-P2-2-4 (6.55 g) (Table 3). The genetic, environmental and phenotypic variances for number of seed yield plant⁻¹ was 9.65, 1.53 and 11.19 respectively. Broad sense heritability for the said trait was 0.86 and genetic advance was 33.21% (Table 4). [28, 29, 30] also noted high heritability for seed yield in chickpea. Seed yield plant⁻¹ was highly significantly positive correlated with secondary branches plant⁻¹ ($r_g = 0.835^{**}$, $r_p = 0.770^{**}$), pods plant⁻¹ ($r_g = 0.959^{**}$, $r_p = 0.857^{**}$), seeds pod⁻¹ ($r_g = 0.537^{**}$, $r_p = 0.271^{**}$) and harvest index ($r_g = 0.484^{**}$, $r_p = 0.375^{**}$) at both genotypic and phenotypic level. Significant positive correlation was

noticed between the mention trait and 100-seed weight ($r_g = 0.295^*$, $r_p = 0.234^*$) at genotypic level but positive and non-significant at phenotypic level. (Table 5). Similar findings were observed by [31, 32].

Harvest index (%)

Mean square revealed significant ($p \leq 0.01$) difference among F_7 populations of chickpea for harvest index (Table 2). Means ranged from 27.04 to 42.55% with an average of 39.99%. The maximum harvest index 42.55% was recorded for KARAK-1 and minimum 27.04% for C1-P2-3-4 (Table 3). The genetic, environmental and phenotypic variances for harvest index was 12.41, 5.76 and 18.17 respectively. Broad sense heritability for the said character was 0.68 and genetic advance was 11.65% (Table 4). [33] also observed high heritability for harvest index in chickpea. Harvest index showed high significantly and positive correlation with pods plant^{-1} ($r_g = 0.427^{**}$, $r_p = 0.386^{**}$) and seed yield plant^{-1} ($r_g = 0.484^{**}$, $r_p = 0.375^{**}$) at both genotypic and phenotypic levels. The said trait revealed positive and significant correlation with seeds pod^{-1} ($r_g = 0.268^*$, $r_p = 0.266^*$) at both genetic and phenotypic levels. The mention trait showed non-significant positive relationship with remaining traits. (Table 5). [34] also observed positive association between grain yield and harvest index.

Conclusions and recommendations

The genotypes used in present studies were of diverse nature and produced more yield. High heritability and genetic advance were recorded for most of the traits which is the room for improvement. The genotype C1-P2-1-2 followed by C1-P2-1-1 exhibited better performance than local checks Karak-1 and NIFA-2005 in terms of seed yield plant^{-1} and should be further tested at multi-location for possible release as a new cultivars. Seed yield plant^{-1} showed highly significant positive genotypic and phenotypic correlation with primary branches plant^{-1} , secondary branches

plant^{-1} , pods plant^{-1} , seeds pod^{-1} , seeds plant^{-1} , biological yield plant^{-1} and harvest index showed that these traits are important for selection in chickpea.

Authors' contributions

Conceived and designed the experiments: H Rahman & A Sohail, Performed the experiments: S Ahmad, Analyzed the data: A Sohail, Contributed reagents/ materials/ analysis tools: T. Burni, S M A Shah, S Ali, & Q Hussain, Wrote the paper: A Sohail.

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