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SESAME GERMPLASM EVALUATION FOR REPRODUCTIVE PERIOD AND HARVEST INDEX

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In sesame, reproductive period is a component of crop maturity and harvest index is a component of seed yield. Both are important traits in applied plant breeding and associated with seed filling process, which helps optimizing crop duration and maximizing sesame yield. The study was focused on genetic control of these traits and to identify potential genotypes to use as parents in breeding programme. Seventy sesame germplasm lines were evaluated in randomized block design replicated thrice. Great variability for reproductive period and harvest index was observed. High heritability accompanied by high genetic gain for reproductive period, harvest index, biological yield and seed yield. Reproductive period was associated positively with days to maturity. Harvest index was associated positively with seed yield and biological yield but negatively with days to maturity. These circumstances suggest that increasing seed yield in sesame is possible through breeding for reproductive period and harvest index. However, performance data of selected genotypes demonstrate that it is wise to select for yield in conjunction with high biological yield and greater proportion of photosynthate partitioning together with optimum length of reproductive period. Use of present genetic variation like MARGO-TALL in manipulating both reproductive period and harvest index may be beneficial in sesame breeding programme.

Keywords: *Sesamum indicum*, germplasm, physiological traits, character association, yield

INTRODUCTION

Sesame (*Sesamum indicum* L.) is an annual, indeterminate plant with a diploid chromosome number of 2n=2x= 26 and belonging to family *pedaliacea*. It is a plant breeder's dream crop because it presents great genetic variability (LANGHAM and WIEMERS, 2002). In addition to a good valued oilseed crop, main challenges associated with sesame cultivation are drought and heat

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stress at certain periods of the growing season (BAYDAR, 2005; GROVER and SINGH, 2007) as well as pathogen attacks (JYOTHI *et al.*, 2011; KAPADIYA *et al.*, 2015). Due to epipetalous nature of stamens, this crop offers good scope for the exploitation of heterosis through manual emasculation and crossing. In practice, however, these techniques have not contributed much to the current oil seed scenario. Further, relevant information about the inheritance of various traits is helpful in deciding proper selection strategies besides to generating variability. India is world leader sesame producing country.

Sesame has a great potential of production for domestic and export markets but comparatively low seed yield is one of the most important reasons that sesame needs breeding to produce more yield (FURAT and UZUN, 2010). The low average yield is due to low standards of husbandry, poor soils and low yielding varieties. The average productivity of sesame in India (430 kg/ ha) is far below as compared to that of China (1,222 kg/ ha) and Egypt (1,250 kg/ ha). So the challenge of the sesame breeder is to step up yield through ideotype breeding (BAYDAR, 2005).However, it is essential to know the genetic architecture of traits related to yield for breeding ideotypes with special emphasis on certain characters. Trait-based approaches rather than yield alone may be more beneficial in sesame breeding, if such yield related traits have been well documented (RANGANATHA *et al.,* 2012).

BORRAS *et al.* (2009) suggested that importance of phenological traits may not only concern with adaptability to particular environments but also influence crop yield improvement through increasing yield potential. The yield potential of earlier-maturing sesame might be improved by selecting lines that combine early flowering with earlier maturity. Combine selection of both these traits should not affect the length of reproductive period, is time period from initiation of flowering to physiological maturity. Earlier report indicated that there is a significant contribution of days from flowering to maturity to sesame oil yield (BANERJEE and KOLE, 2006).

Improvement in harvest index is the another approach to increase seed yield in sesame. Higher yields can be obtained, if photosynthate translocation toward seeds becomes more efficient (JAMIE *et al.*, 2002). ARAÚJO and TEIXEIRA (2008) proposed that assimilate partitioning, days to maturity and rate of biomass accumulation are the three important physiological genetic components of the process of accumulating crop yield. MENZIR (2012) found that seed and biomass yields, capsule filling period and days to maturity are the principal components of variation in sesame. MONPARA *et al.* (2008) observed that higher yields in sesame are likely to be associated with higher primary branches per plant, capsules per plant and seeds per capsule. There is a positive association between seed yield and harvest index (KUMARESAN and NADARAJAN, 2002; ANURADHA and REDDY, 2006). Inheritance of physiological traits is observed to be the predominant involvement of non-additive gene actions (BANERJEE and KOLE, 2009) in sesame.

The purpose of this study was to understand the nature and magnitude of variability for reproductive period and harvest index, and their relationships with other agronomic traits. Attempt was also made based on available data to identify potentially useful genotypes to be utilized as parents in future breeding programmes.

MATERIALS AND METHODS

Experimental site

This study was conducted during rainy season of 2011 at the Agricultural Research Station, Junagadh Agricultural University, Amreli, Gujarat, India. The location receives low annual rainfall. Moreover, erratic rainfall makes the area vulnerable either to water lodge condition or to terminal moisture stress. Average annual rainfall varies from 500 to 800 mm. The soil of experimental area was medium black, fertilized at the rate of 25 kg N ha^{-1} and 25 kg P ha^{-1} as basal dose. The same quantity of nitrogen, i.e., 25 kg N ha^{-1} was applied as topdressing at 30 to 35 days after sowing.

Experimental material

Seventy sesame germplasm lines (30 landraces + 25 indigenous cultures + 15 exotic cultures) were used for this study. All these lines were chosen from the available sesame germplasm to maximize the diversity of the material studied with respect to growth habit, yield, reproductive period, harvest index and maturity. All the genotypes were arranged in a randomized block design with three replications. A plot consisted of single row of 4 meter length. The seeds were drilled in the rows of 60 cm apart. Before sowing, the seeds were treated with a fungicide to prevent soil and seed born diseases. Plants within the row were thinned on 15 to 20 days of germination at the distance of 10 cm. All recommended cultural practices were followed to raise the good crop.

Data collection

Plant architecture and biomass measurements were collected in randomly selected five plants tagged before starting of flower initiation. At harvesting, 1000-seed weight (SW), biological yield per plant (BY) and seed yield per plant (SY) in grams (g) were measured. Oil content (OC) in per cent was determined through NMR technique in the seeds of selected plants. Phenological measurements were recorded on a plot basis: days to flower initiation (DI) is the days from sowing to first flower opening, days to anthesis (DA) is the days from sowing to 50% of plants flowering and days to physiological maturity (DM) is the days from sowing to 50% capsules turned yellow in the plot. The plants were harvested at maturity, then combined and air-dried. Reproductive period (RP) was measured as days from DI to DM and harvest index (HI) in per cent was calculated as: SY/BY x 100.

Statistical analysis: Analysis of variance (ANOVA) was carried out for each character using the computer system SAS/STAT software (SAS INSTITUTE, 2008).Based on the analysis of variance, variance components were estimated as under.

$$Environmental\ varience\,(\sigma_e^2) = MSE$$

$$Genotypic\ variance\,(\sigma_g^2) = \frac{MSG - MSE}{r}$$

$$Phenotypic\ variance\,(\sigma_p^2) = \sigma_g^2 + \sigma_e^2$$

Where, MSE is mean square due to error, MSG is mean square due to genotypes and r is number of replication

Phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were computed as the formulae described below.

$$PCV(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{X}}\ X\ 100$$

$$GCV(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{X}}\ \mathrm{X}\ 100$$

Where, σ^2_p=Phenotypic variance, σ^2_g = Genotypic variance and $\bar{X}$ =General mean of the character

Heritability in broad sense **(h^2)** was worked out as under.

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} x\, 100$$

The expected genetic advance at 5% selection intensity was estimated by using following formula.

$$Gs = k \ x \ \sigma_p \ x \ h^2$$

Where, Gs = Expected genetic advance under selection, k = Selection differential (value of k at 5% selection intensity is 2.06), σ_p = Phenotypic standard deviation andh^2 = Heritability value of the character

The genetic advance **(GA)** expressed as percentage of mean was computed as under.

$$\text{GA as (\%)of mean} = \frac{Gs}{\bar{X}} X\, 100$$

Phenotypic correlation (rp) and genotypic correlation (rg) coefficients were calculated as per the following formula.

$$rp = \frac{\text{cov}_{(xy)p}}{\sqrt{\sigma_{px}^2 \cdot \sigma_{py}^2}}$$

and

$$rg = \frac{\text{cov}_{(xy)g}}{\sqrt{\sigma_{gx}^2 \cdot \sigma_{gy}^2}}$$

Where, Cov(xy)p and Cov(xy)g is phenotypic or genotypic covariance between two characters x and y, respectively. The σ^2_p and σ^2_g represents the phenotypic and genotypic variance for character x and y, respectively.

The coefficients of correlation were tested using 'r' tabulated value at n-2 degrees of freedom at $P<0.05$ and $P< 0.01$ probability level, where n denote as number of genotypes studied.

RESULTS

Variation among the genotypes for reproductive period (RP), harvest index (HI) and other characters was found significant (Table 1). Substantial ranges of observations occurred among the genotypes for all the traits considered. For example, RP ranged from 36.7-66.7 days and HI ranged from 19.5-55.4%. It is evident that range of RP was larger than that of days to anthesis (DA) and days to maturity (DM). Indeed, variability can be better judged through estimation of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV). Close estimates of GCV and PCV indicated less influence of environment on the expression of all the characters. Both these parameters were moderate (10 to 20%) for RP and high (>20%) for HI, biological yield per plant (BY) and seed yield per plant (SY). The magnitude for other characters was low. Estimates of broad sense heritability were high (>80%) for all the characters, except DA, for which it was moderate. However, genetic gain as percentage of mean was high (>20%) for RP, HI, BY and SY, moderate (10 to 20%) for DM and 1000-seed weight (SW) and low (<10%) for DA and oil content (OC).

Table 1. Mean, range and variability parameters for eight characters in sesame

Characters§	Mean± SEm	Range	GCV (%)	PCV (%)	h^2 (%)	GA as % of mean
RP	49.1± 0.9	36.7 - 66.7	15.4	15.7	0.96	31.1
DA	39.7± 0.7	35.3 - 44.0	5.0	5.8	0.75	8.9
DM	85.6± 1.6	76.3 - 101.0	8.1	8.7	0.86	15.5
SW	3.1± 0.1	2.4 - 3.7	8.8	9.4	0.87	16.9
OC	49.3± 0.4	45.3 - 54.4	3.4	3.7	0.85	6.5
BY	12.2± 0.8	4.6 - 23.5	34.7	36.7	0.89	67.5
HI	29.5± 1.6	19.5 - 55.4	24.7	26.4	0.87	47.6
SY	3.4± 0.2	1.4 - 6.2	31.5	32.6	0.93	62.7

§RP= Reproductive period, DA= Days to anthesis, DM= Days to maturity, SW=1000-seed wt (g), OC= Oil content (%), BY= Biological yield plant^{-1} (g), HI= Harvest index (%), SY= Seed yield plant^{-1} (g), GCV=Genotypic coefficient of Variation, PCV= Phenotypic Coefficient of Variation, h^2=Heritability in broad sense, GA=Genetic Advance

Phenotypic and genotypic correlation values (Table 2) indicated that RP was negatively associated with DA, i.e. early start of anthesis was associated with longer reproductive period. In contrast, association between RP and DM was positive. Negative association between RP and BY was significant at phenotypic level and non-significant at genotypic level. The association of HI was significantly positive with BY and SY but was significantly negative with DM. The values of correlation between HI and other characters were non-significant.

Table 2. Phenotypic (rp) and genotypic (rg) correlation coefficient of reproductive period and harvest index with other yield attributing traits in sesame

Attributing traits§	RP		HI	
	rg	rp	rg	rp
DA	-0.24**	-0.21**	-0.01	0.02
DM	0.80**	0.74**	-0.14*	-0.14*
SW	0.00	0.00	0.08	-0.07
OC	0.06	0.06	-0.03	-0.03
BY	-0.13*	-0.12	0.43**	0.44**
SY	-0.10	-0.10	0.22**	0.18**

§RP= Reproductive period, DA= Days to anthesis, DM= Days to maturity, SW=1000-seed wt (g), OC= Oil content (%), BY= Biological yield plant^{-1} (g), HI= Harvest index (%), SY= Seed yield plant^{-1} (g)

Mean values of short, intermediate and long RP (Table 3) indicated that there were substantial differences for reproductive period, days to maturity, 1000-seed weight, harvest index and seed yield per plant. Length of reproductive period of long RP genotypes averaged 14 and 24 days longer than those of intermediate and short RP genotypes, respectively. While time to maturity averaged 8 and 20 days greater in long RP genotypes than for intermediate and short RP genotypes. Similarly, long RP genotypes expressed, on an average, 0.11g and 0.15 g higher 1000-seed weight than intermediate and short RP genotypes. On the other hand, seed yield per plant was higher in intermediate RP genotypes (4.24 g), which was 0.46 g higher than that of long RP genotypes.

Table 3. Mean performance of five genotypes with short, intermediate and long reproductive period in sesame

	Genotypes	RP[§]	DA	DM	SW	OC	BY	HI	SY
Short RP									
1.	DTV-620	36.67	43.00	76.33	2.86	50.43	17.83	25.23	4.46
2.	VIJPADI-1	38.34	44.00	80.00	3.56	51.47	15.99	33.90	5.40
3.	IC-56196	40.33	38.00	80.33	3.07	53.90	19.66	31.60	6.20
4.	KERIYA-9	40.99	40.33	78.66	3.16	52.04	12.62	24.33	3.06
5.	SP-1168	41.33	41.33	79.33	2.93	47.41	5.87	31.36	1.83
	Mean	39.53	41.33	78.93	3.12	51.05	14.39	29.28	4.19
Intermediate RP									
1.	KHAMBA-14	48.33	39.33	84.66	3.12	51.53	8.16	22.43	1.83
2.	KMR-36	48.66	42.67	89.33	2.69	47.34	12.64	40.03	5.03
3.	NAVAGAM-4	49.00	38.33	84.00	3.49	47.66	13.80	39.53	5.40
4.	MARGO-TALL	49.33	40.66	86.33	3.41	48.37	20.18	28.86	5.80
5.	KADKALA-3	49.67	42.00	88.00	3.07	48.32	9.96	32.26	3.16
	Mean	49.00	40.60	86.46	3.16	48.64	12.95	32.62	4.24
Long RP									
1.	KMR-52	62.33	38.67	97.33	3.04	49.41	17.38	26.43	4.60
2.	IC-131499	63.67	36.67	98.00	3.09	50.29	7.93	31.50	2.50
3.	IC-209165	64.00	39.33	100.00	3.74	48.34	14.38	22.03	3.16
4.	VIJPADI-6	64.67	37.33	99.33	3.43	47.89	16.35	25.40	4.06
5.	SPS-19	66.67	35.33	99.00	3.07	54.36	11.83	39.30	4.60
	Mean	64.27	37.47	98.73	3.27	50.06	13.57	28.93	3.78

[§] RP= Reproductive period, DA= Days to anthesis, DM= Days to maturity, SW=1000-seed wt (g), OC= Oil content (%), BY= Biological yield plant^{-1} (g), HI= Harvest index (%), SY= Seed yield plant^{-1} (g)

The genotypes within high HI gave better seed yield (4.55g) than medium (4.27g) and low HI (3.43g) genotypes (Table 4). Mean harvest index and biological yield per plant differed greatly among the HI groups. However, very little difference in mean of high, medium and low HI genotypes was observed for days to anthesis, days to maturity and oil content. High HI genotypes tended to have shorter reproductive period.

Table 4. Mean performance of five genotypes with low, medium and high harvest index in sesame

Genotypes	RP§	DA	DM	SW	OC	BY	HI	SY
Low HI								
1. IC-132181	62.00	37.33	97.00	3.38	48.91	16.38	19.53	3.20
2. SONAGADH	42.33	44.00	83.33	2.89	50.68	13.51	19.93	2.66
3. HADIDA-11	47.00	37.00	82.33	3.39	48.68	11.87	20.50	2.43
4. KALYANPUR-3	43.33	38.66	79.33	2.88	48.53	20.38	20.73	4.23
5. KMR-83	46.00	38.33	81.33	2.58	49.51	21.67	21.33	4.63
Mean	48.13	39.06	84.66	3.02	49.26	16.76	20.40	3.43
Medium HI								
1. MARGO-TALL	49.33	40.66	86.33	3.41	48.37	20.18	28.86	5.80
2. SG-830	42.33	37.66	77.66	3.36	51.57	12.36	29.06	3.60
3. ES-48-28	48.33	38.66	83.33	3.18	48.18	14.46	29.73	4.33
4. KERIYA-5	38.34	43.33	78.67	2.77	51.90	14.12	30.36	4.26
5. NAVAGAM-14	55.67	40.33	92.00	3.16	48.88	10.91	30.93	3.36
Mean	46.80	40.13	83.60	3.18	49.78	14.41	29.79	4.27
High HI								
1. NAVAGAM-4	49.00	38.33	84.00	3.49	47.66	13.80	39.53	5.40
2. KMR-36	48.66	42.67	89.33	2.69	47.34	12.64	40.03	5.03
3. NIC-7819	45.33	38.00	80.00	3.25	47.94	10.31	46.53	4.76
4. BORDA-3	40.00	43.33	80.33	3.37	49.83	6.06	54.70	3.23
5. LALAVADAR-6	46.67	39.33	84.00	2.71	48.52	8.03	55.40	4.33
Mean	45.93	40.33	83.53	3.10	48.26	10.17	47.24	4.55

§RP= Reproductive period, DA= Days to anthesis, DM= Days to maturity, SW=1000-seed wt (g), OC= Oil content (%), BY= Biological yield plant^{-1} (g), HI= Harvest index (%), SY= Seed yield plant^{-1} (g)

DISCUSSION

Sesame breeders always does focus on enhancing yield potential either by direct selection for seed yield itself or indirect selection through component traits. Some physiological traits related to crop yield being relatively simple and may allow the crop to improve the overall efficiency of use of resources and thereby yield. Such potential physiological traits like reproductive period and harvest index are expected to be responsible to describe seed yield in sesame. If sizeable heritable differences occur within a species for these characters, an opportunity is existed to improve yield by altering them in a breeding programme. The present study generated heritability estimates from analysis of variance method using stable and diverse germplasm lines of sesame (Table 1). It is evident that heritability estimates were high (>80%) for RP, DA and DM but the genetic gain as percentage of mean obtained high (>20%) only for RP. However, magnitude of GCV (15.4%) and PCV (15.7%) for RP was moderate. Thus, results suggest that improvement in RP may be possible through selection. TABATABAEI *et al.* (2011) demonstrated wide range of variation for reproductive period among Iranian sesame genotypes. In fact, strong positive association between DM and RP and significant negative association between DA and RP (Table 2) indicate that vegetative duration together with maturity period determines the length of RP. The RP can be reliably used in discriminating between early and late genotypes, where evaluation for DM is untenable due to forced maturation. The RP was not associated with SY. Thus, selection for long RP would show minimal correlated response in SY. Longer RP specifically in indeterminate sesame type growing in India is of great importance for overcoming many environmental conditions that reduce yields substantially in the short flowering period crops (LANGHAM, 2007). Earlier report indicated that flowering period and maturity period are the important contributors to the total variation in sesame (TABATABAEI *et al.,* 2011). KHAIRNAR and MONPARA (2013) observed reproductive period as a potent contributor for seed yield improvement in sesame.

In case of HI and its component traits like BY and SY, the values of GCV and PCV were magnitudinally high (Table 1) and also registered high estimates of heritability and genetic advance, indicating involvement of additive gene action for these traits. PAWAR and MONPARA (2016), while studying with combining ability in sesame, reported that both additive and nonadditive gene action are importance for the inheritance of HI, BY and SY. It was also seemed that association of HI was highly significant and positive with BY and SY (Table 2). There was a weak but significant negative correlation estimated between HI and DM. Thus earliness always tends to improved HI. Occurrence of favorable association between the yield components as observed in the present study would be less complex from breeding point of view because selection for one trait may bring the favorable changes for improvement of other traits. These circumstances indicate that due consideration should be focused on selection for harvest index to recover high yielding sesame archetypes (GANESHAN, 2005).

Five genotypes for high, five for intermediate (surrounding the general mean) and five for low expression in respect of RP and HI were isolated to identify potentially useful genotypes for enhancing sesame yield. The mean differences were wider for reproductive period among short, intermediate and long RP genotypes (Table 3). Reproductive period was found longer in long RP genotypes and shorter in short RP genotypes. Similarly, long RP genotypes showed long duration of crop maturity than intermediate and short RP genotypes. Reverse was the trend for days to anthesis, but the differences in mean values for this character was small as compared to that of DM and RP. This reveals that variation in DM rather than DA determines the length of RP.

The short, intermediate and long RP genotypes had the seed size of 3.12, 3.16 and 3.27 g/1000 seed and their yields were 4.19, 4.24 and 3.78 g/plant, respectively. Obviously, intermediate RP was important for higher yield and long RP was important for larger seed size, but there was no relation between seed size and yield (Table 3). Such results may be expected because of intermediate nature of sesame plants. If a genotype had long RP, then a longer period is available for sound seed filling to early formed capsules and late formed capsules at the top of the plant suffered severely to allow seed filling. Consequently, shriveled seed produced in late formed capsules may account largely for biological yield rather than economic yield. Thus, opportunity exists for improving yield through developing genotypes with optimum lengths of reproductive periods in a breeding programme.

The HI mean values displayed in Table 4 indicated that selection of low, medium and high HI genotypes showed larger effects on the harvest index, biological yield per plant, seed yield per plant and reproductive period. Mean values indicate that as HI increases, reproductive period decreases. Thus, harvest index and reproductive period are negatively correlated to each other. High HI genotypes showed the average harvest index of 47.24%, which was about 17% and 27% higher than the medium and low HI genotypes. In contrast, biological yield was high in low HI genotypes and decreased with medium and high HI genotypes. However, seed yield per plant was higher by 0.84g in medium HI and 1.12g in high HI genotypes over the average yield of 3.43g in short HI genotypes. It is interesting to not that high HI genotypes have not always produced higher seed yield. For example, MARGO-TALL gave the highest seed yield (5.80g) and higher production of biomass (20.18g) but it comes under the category of medium HI. Thus, it is important to select for yield in conjunction with high biological yield and greater proportion of dry matter partitioning to the seed (JAMIE *et al.*, 2002).

CONCLUSION

In conclusion, the present study added upon the existing knowledge of the genetic control of RP, HI, BY and SY. Selection for these traits in breeding programme would be more effective. Significant positive association of HI with BY and SY, and RP with DM reveals less complex relationships among yield and its components. Selected genotypes could be more precisely evaluated for HI and RP. This study demonstrated that HI together with RP could reliably be used in discriminating early maturing high yielding sesame genotypes.

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EVALUACIJA GERMPLAZME SUSAMA ZA REPRODUKTIVNI PERIOD I ŽETVENI INDEKS

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Izvod

Istraživanja su fokusirana na genetičku kontrolu reproduktivnog perioda i žetvenog indeksa u cilju identifikacije potencijalnih genotipova koji bi se koristili. Ocenjivano je 77 linija u slučajnom blok sistemu sa tri ponavljanja. Utvrđen je visok stepen varijabilnosti obe ispitivane osobine. Utvrđen je visok stepen naslednosti praćen visokom genetičkom dobiti za reproduktivni period, žetveni indeks, biološki prinos i prinos semena. Reproduktivni period je pozitivno udružen sa brojem dana do zrelosti. Utvrđena je pozitivna asocijacija žetvenog indeksa sa prinosom semena i i biološkim prinosom ali negativna sa brojem dana do zrelosti. Ovi rezultati sugerišu da povećanje prinosa semena susama je moguće u programima oplemenjivanja na reproduktivni period i žetveni indeks. Osobine odabranih genotipova pokazuju da je mudro vršiti selekciju na prinos vezano sa biološkim prinosom, većoj proporciji učešća produkata fotosinteze zajedno sa optimalnom dužinom reproduktivnog perioda. Korišćenje postojećeg genetičkog variranja kao MARGO-TALL u manipulacijama sa reproduktivnim periodom i žetvenim indeksom mogu da budu korisne u programima oplemenjivanja susama.

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