Studies on Genetic Variability and Divergence in Sweet Gourd (*Momordica subangulata* ssp. *renigera* [(G. Don) W.J. de Wilde)] Accessions Collected from West Bengal

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Eleven genotypes were evaluated for 14 quantitative and two qualitative components during the rainy season of 2007–08 and 2008–09. The genotype × environment interactions were non-significant for all the characters, hence, the data were pooled over the years and discussed on the basis of mean of two years. Analysis of variance indicated significant differences for all the characters investigated. High GCV and PCV values were observed for characters like primary branches/vine followed by total fruit yield/vine, fruit weight and protein content. High heritability coupled with low genetic advance was observed for almost all the quantitative and qualitative characters. High heritability coupled with exceptional high genetic advance was found for total fruit yield/vine. Correlation studies in relation to various characters revealed that total fruit yield/vine was positively and significantly correlated to fruit weight, fruit length, fruit diameter, fruit girth and protein content. Days to first female flower appearance which reflects the earliness to fruiting was positively and significantly associated with days to first male flower appearance and pedicel length. Among the biochemical traits, protein content showed significant and positive correlation with fruit weight, fruit length, fruit diameter, fruit girth and total fruit yield/vine. Path analysis at phenotypic level revealed that total fruit yield/vine was positively dependent on characters like number of fruits/vine and fruit weight.

Key Words: Correlation, Genetic divergence, *Momordica subangulata,* Path Analysis, Variability

Introduction

Momordica subangulata ssp. renigera [(G.Don) W.J. de Wilde] belongs to the melon family (Cucurbitaceae) and is indigenous to South-East Asia. It is also known as baby jackfruit, spiny bitter gourd and sweet gourd. It's Latin name is *Momordica subangulata* ssp. *renigera* (G.Don) W.J. de Wilde, "Bhat karela" (Indian name), "spiny bitter gourd, sweet gourd (English), "*Kakrol* or *Kakur*" (Hindi). Different research workers in India and South-East Asia treat dioecious species in the genus *Momordica* differently. The cultivated '*bhat karela*' of East and North-East India is referred to as *Momordica dioica* Roxb. by botanists and herbarium curators whereas agricultural scientists in general designate it as *Momordica cochinchinensis*. A critical study of 266 herbarium sheets housed at CAL and BSISH and *in situ* field studies at specific pockets in the North East India followed by preliminary characterization revealed it's correct identity as *Momordica subangulata* ssp. *renigera* [(G. Don) de Wilde]. The species was found in wild as well as in homestead cultivation in North-East India and exemplify direct utilization of biodiversity by indigenous people. The vegetable is rich in calcium, phosphorous, iron, carotene, lycopene and protein. It is mostly dioecious and propagated vegetatively through tuberous roots/vine cuttings. They grow in warm and humid weather and tuberous roots are planted in pits. The vines are trained on bowers and 5 to 10 % of male parents are provided for good fruit setting. Plantation is done at the onset of summer with the first shower, flowering starts in April and fruiting ends in October-November. The plants remain dormant in winter. The tubers are left *in situ* and they over winter. It is an important summer vegetable crop in West Bengal. It has many advantages like high market price, good nutritional value and keeping quality is longer. Being a minor crop not much attention was focused on improvement of this crop in the past but with it's popularity gaining high among the masses, development programmes had been initiated on this crop. Collection and evaluation of the existing germplasm and selection of better parents are pre-requisite for commencing a breeding programme in any crop. Besides, knowledge of genetic diversity and relationship among the sets of

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germplasm is critical to plant improvement. Keeping the importance of this cucurbit and the lack of information on genetic architecture of the breeding population the present investigation was under taken to know the genetic divergence, correlation and path coefficient among yield and it's contributing characters.

Materials and Methods

The experimental material consisted of 11 genotypes of sweet gourd collected from different parts of West Bengal *viz*., Malda Selection-1, Malda Selection-2, Malda Selection-3, Malda Selection-4, Joynagar Selection-1, Joynagar Selection-2, Baruipur Selection-1, Barasat Selection-1, Bonga Selection-1, Bonga Selection-2 and Bonga Selection-3. The experiment was laid out in randomized block design (RBD) during the onset of rainy season during 2007–08 and 2008–09 having three replications of each genotype. The tuberous roots were sown on two ridges in each plot, having a spacing of 0.75 m between plant-plant and 1.0 m in between the ridges, ensuring 8 plants/plot. Manures like - FYM @ 20–25 t/ha as basal dose along with half dose of nitrogen @ 35kg/ha, full dose of P_2O_5 @ 25kg/ha and full dose of K_2O @ 25kg/ha were applied during field preparation. The remaining amount of nitrogen *i.e.* 35 kg was applied in two split doses, the first being applied one month after sowing and the second one at the initiation of flowering and fruit setting. Nitrogen in the form of urea and phosphorus in the form of single super phosphate and potash in the form of murate of potash were applied to the experimental plots. Essential intercultural operations such as weeding, staking, trailing and timely irrigation were carried out as and when required. Plant protection measures were carried out at regular intervals by application of pesticides to protect and prevent the incidence of pests like fruit fly, red pumpkin beetle, aphid and red spider mite.

Observations on various morphological, biochemical and other yield-contributing traits *viz.*, vine length (m), primary branches/vine, node to which first female flower appears, days to first male flower appearance, days to first female flower appearance, fruit length (cm), fruit girth (cm), fruit diameter (cm), pedicel length (cm), number of fruits/vine, average fruit weight (g), days taken from fruit set to edible maturity, total fruit yield/vine (g), number of seeds/fruit, protein (g/100 g) and calcium content (mg/100 g) were scored on five plants randomly selected from each plot of the designated replications, representing the genotypes of sweet gourd. The estimation of calcium and protein was done as per the method described by Rangana (1986) and Lowry (1951), respectively. Plot Means were used for standard analysis using the statistical package SPAR-2 developed by Indian Agricultural Statistical Research Institute (IASRI) and Genres (version 2.01) developed by Pascal International Software Solutions. The genotypic (GCV) and phenotypic coefficient of variation (PCV), heritability in broad sense and genetic advance were worked out as per the formula given by Johnson *et al*. (1955). The genotypic and phenotypic correlations were calculated as per the method of Al-Jibouri *et al*. (1958). Path coefficient analysis was done according to the method given by Dewey and Lu (1959). Mahalanobis (1936) D^2 statistics was used to assess genetic diversity. Genotypes were grouped on the basis of minimum generalized distance using Tocher's method as described by Rao (1952).

Results and Discussion

Analysis of variance for all the quantitative and qualitative characters revealed that mean squares were highly significant for all the characters. The interactions between genotype × environment were non-significant for all the traits, hence, the generated data were pooled and discussed on the basis of mean of two years. Substantial variability as evidenced from range, PCV and GCV was noted for all the quantitative and qualitative traits (Table 1). The PCV was slightly higher to more or less similar to the corresponding GCV for all the traits, justifying that variability is due to genetic constitution. Among the quantitative traits, the PCV and GCV values were higher for characters like primary branches/vine *i.e.* 33.56 and 34.11, respectively, followed by total fruit yield/vine (32.17 and 32.91) and fruit weight (30.90 and 31.17). Among qualitative traits PCV and GCV was high for protein content (22.53 and 22.91). Selection of these traits offers good opportunity for improvement of this crop and probability of getting high performance recombinant segregants will be more. Moderate GCV and PCV values were obtained for number of seeds/fruit, number of fruits/vine, pedicel length, node to which first female flower appears, vine length, fruit length and calcium content. The coefficient of variation under both GCV and PCV was low for days to first female flower appearance, days to first male flower appearance, fruit girth, fruit length and days taken from fruit set to edible maturity. Our findings are in accordance to those of Maharana *et al.* (1995), Rasul *et al.* (2002), Ram *et al*. (2004) and Bharathi *et al*. (2006).

Table 1. Grand mean, range, phenotypic and genotypic goefficient of variation, heritability (h^2), genetic advance and genetic advance as percent of mean for different quantitative and qualitative characters among 11 accessions of sweet gourd

Characters	Grand mean	Range	GCV	PCV	h^2 (%)	GA	GA as % of Mean
Vine length (m)	2.64	1.86–3.50	15.12	17.84	71.84	0.70	26.40
Primary branches/vine	4.32	1.35–7.80	33.56	34.11	96.78	2.94	68.01
Node to which first female flower appears	23.35	15.00–36.00	18.08	18.62	94.23	8.44	36.15
Days to first male flower appearance	53.18	46.00–62.00	11.05	11.52	91.96	11.61	21.83
Days to first female flower appearance	61.31	50.00–72.00	11.45	11.95	92.03	13.91	22.69
Fruit weight (g)	45.47	18.90–68.50	30.90	31.17	98.28	28.70	63.11
Fruit length (cm)	6.09	3.85–7.80	16.21	16.53	96.15	1.99	32.75
Fruit diameter (cm)	4.53	3.20–5.90	10.58	10.88	94.61	0.26	21.21
Fruit girth (cm)	13.59	9.90–15.80	10.91	11.18	95.32	2.98	21.95
Pedicel length (cm)	12.89	7.50–17.90	20.97	21.06	99.15	5.55	43.02
Days taken from fruit set to edible maturity	16.36	12.00–19.00	7.96	9.16	75.47	2.00	14.24
Number of fruits per vine	23.16	13.00–36.00	20.19	21.41	88.88	9.08	39.21
Protein content (g/100g)	0.48	0.30–0.72	22.53	22.91	96.61	0.22	45.61
Number of seeds per fruit	45.65	24.00–68.00	24.09	24.13	99.66	22.61	49.55
Calcium content (mg/100g)	60.35	32.60–72.56	15.56	15.90	95.61	18.91	31.34
Total fruit yield per vine (g)	1022.06	580.0–1490.0	32.17	32.91	95.53	661.89	64.76

The magnitude of heritability in broad sense was high for most of the traits under study except for vine length and days taken from fruit set to edible maturity (Table 1) thus, suggesting that the highly heritable traits were least affected by environmental variation and selection based on phenotypic performance would be reliable. Similar findings were also reported by Ram *et al*. (2004) and Bharathi *et al*. (2006). High heritability coupled with low genetic advance were observed for almost all the quantitative and qualitative characters like protein content, fruit diameter, fruit length, primary branches/vine, fruit girth, pedicel length, node to which first female flower appears and number of fruits/vine except for total fruit yield/vine indicating that these characters are mostly controlled by non-additive genes either dominant or epistasis and improvement can be made by intermating the superior genotypes of the segregating population to develop multiple crosses and the desirable genes can be accumulated in the lines. High heritability coupled with exceptional high genetic advance was found for total fruit yield/vine thus indicating that this trait was controlled by additive gene action and offers the more selective criteria for selection. High heritability coupled with moderate genetic advance were observed in traits like fruit weight, number of seeds/fruit and calcium content. High heritability coupled with extremely low genetic advance was observed for protein content. Moderate heritability coupled with low genetic advance was observed in vine length and days taken to first female flower appearance which might be attributed to non-additive gene action and thereby, simple selection would not be rewarding.

The genotypic correlation in general was higher in magnitude than corresponding phenotypic correlation (Table 2) thereby indicating that there was inherent association among various characters. Genotypic correlation studies in relation to various characters revealed that total fruit yield/vine was positively and significantly correlated to fruit weight, fruit length, fruit diameter, fruit girth and protein content. Phenotypic correlation to different characters revealed that total fruit yield/vine was significantly and positively associated with traits like fruit weight, fruit length, fruit diameter, fruit girth and protein content. Days taken from fruit set to edible maturity was significantly and positively associated with vine length and negatively associated with fruit diameter in a significant manner. Node to which first female flower appears was significantly and negatively correlated to primary branches/vine. Similar findings were observed by Bharathi *et al*. (2005). Days to first female flower appearance which reflects the earliness to fruiting was positively and significantly associated with days to first male flower appearance and pedicel length. Fruit weight showed positive and significant association with fruit length, fruit diameter, fruit girth, protein content and total fruit yield per vine. Among the biochemical traits protein content showed significant and positive correlation with fruit weight, fruit length, fruit diameter, fruit girth and total fruit yield/vine while calcium content showed significant and positive correlation only with number of fruits/vine at genotypic level. Bharathi *et al*. (2005) in their study observed that total yield/vine was negatively

Table 2. Correlation coefficients at phenotypic (P) and genotypic (G) levels among different traits

Characters		Vine length (m)	Primary branches per vine	Node to which first female flower appears	Days to first male flower appearance	Days to first female flower appearance	Fruit weight (g)	Fruit length (cm)	Fruit diameter (cm)	Fruit girth (cm)	Pedicel length (cm)	Days taken from fruit set to edible maturity	Number of fruits per vine	Protein content (g/100g)	Number of seeds per fruit	Calcium content (mg /100g)	Total fruit yield per vine (g)
Vine length (m)	P	**1.000**	0.258	–0.470	0.297	0.403	–0.439	–0.602*	–0.414	–0.610	0.561	0.545	0.122	–0.281	0.307	–0.253	–0.221
	G	**1.000**	0.323	–0.556	0.344	0.432	–0.531	–0.684*	–0.471	–0.705*	0.680*	0.785**	0.224	–0.351	0.357	–0.295	–0.230
Primary branches\vine	P		**1.000**	–0.635*	0.045	0.112	0.320	–0.005	0.288	0.013	0.429	0.152	0.148	0.583	0.276	0.098	0.240
	G		**1.000**	–0.663*	0.047	0.098	0.323	–0.017	0.284	–0.001	0.445	0.168	–0.122	0.601	0.287	0.088	0.271
Node to which first female flower appears	P			**1.000**	–0.337	–0.408	0.084	0.426	0.282	0.373	–0.565	–0.349	0.344	–0.018	–0.291	0.148	0.282
	G			**1.000**	–0.384	–0.389	0.093	0.432	0.320	0.418	–0.578	–0.413	0.377	–0.033	–0.302	0.144	0.295
Days to first male flower appearance	P				**1.000**	0.901**	–0.465	–0.354	–0.289	–0.342	0.801**	0.086	0.246	–0.364	0.154	0.352	–0.294
	G				**1.000**	0.967**	–0.485	–0.365	–0.320	–0.369	0.838**	0.165	0.313	–0.381	0.166	0.360	–0.292
Days to first female flower appearance	P					**1.000**	–0.369	–0.342	–0.286	–0.286	0.845**	0.229	0.258	–0.245	0.091	0.414	–0.190
	G					**1.000**	–0.391	–0.336	–0.333	–0.312	0.890**	0.298	0.326	–0.253	0.101	0.434	–0.181
Fruit weight (g)	P						**1.000**	0.865**	0.741**	0.762**	–0.312	–0.184	–0.272	0.870**	0.103	0.102	0.711*
	G						**1.000**	0.896**	0.766**	0.784**	–0.320	–0.237	–0.295	0.894**	0.102	0.166	0.735**
Fruit length (cm)	P							**1.000**	0.743	0.850**	–0.397	–0.296	0.003	0.706*	–0.015	0.261	0.768**
	G							**1.000**	0.764**	0.880**	–0.400	–0.346	0.019	0.737**	–0.013	0.248	0.811**
Fruit diameter (cm)	P								**1.000**	0.798**	–0.202	–0.562	0.001	0.610*	0.316	0.205	0.633*
	G								**1.000**	0.790**	–0.212	–0.670*	0.050	0.656*	0.333	0.182	0.698*
Fruit girth (cm)	P									**1.000**	–0.335	–0.484	0.030	0.575	0.050	0.275	0.656*
	G									**1.000**	–0.352	–0.569	0.064	0.615*	0.055	0.264	0.711*
Pedicel length (cm)	P										**1.000**	0.262	0.275	–0.098	0.441	0.276	–0.080
	G										**1.000**	0.298	0.279	–0.100	0.441	0.290	–0.087
Days taken from fruit set to edible maturity	P											**1.000**	–0.071	0.004	–0.255	–0.235	–0.131
	G											**1.000**	–0.069	–0.056	–0.292	–0.299	–0.129
Number of fruits/vine	P												**1.000**	–0.067	–0.002	0.598	0.457
	G												**1.000**	–0.073	–0.019	0.702*	0.423
Protein content (g/100 g)	P													**1.000**	–0.003	0.320	0.777**
	G													**1.000**	–0.006	0.331	0.807**
Number of seeds/fruit	P														**1.000**	–0.209	0.117
	G														**1.000**	–0.207	0.111
Calcium content (mg/100 g)	P															**1.000**	0.466
	G															**1.000**	0.520
Total fruit yield/vine (g)	P																**1.000**
	G																**1.000**

Note: *and **significant at 5% and 1% levels of significance, respectively

correlated with the number of days to flowering which is in agreement to our findings.

Path analysis at phenotypic level (Table 3) revealed that the largest direct effect on total fruit yield/vine was through traits like number of fruits/vine (0.631) and fruit weight (0.461). The phenotypic direct effect was positive but moderate for protein content, fruit length and vine length. Days to first female flower appearance, number of seeds/fruit and pedicel length contributed the least towards total fruit yield/vine. Rest of the characters exhibited negative direct effect towards total fruit yield/vine, the highest being contributed by days to first male flower appearance (–0.229) followed by fruit girth, calcium content, days taken from fruit set to edible maturity and fruit diameter. Thus, it can be ascertained that for selecting high yielding types emphasis should be laid on traits like number of fruits/vine and fruit weight. The residual effect was low suggesting the inclusion of maximum fruit yield influencing characters in analysis. Our findings could be related to those of Dey *et al.* (2007), Bhave *et al.* (2003) and Sharma and Bhutani (2001).

Multivariate analysis based on D^2 statistics indicated the presence of considerable amount of genetic diversity among the genotypes studied. The genotypes were grouped into three clusters with cluster I being the largest having five genotypes, followed by cluster III and II having four and two genotypes, respectively. Genotypes from different geographical regions were grouped in the same cluster indicating no relationship exists between geographical distribution and genetic divergence. The intra- and inter-cluster distance represented the index of genetic diversity among the clusters (Table 5). The data suggest that intra-cluster distance was high in Cluster I followed by Cluster III and Cluster II. Inter-cluster distances between II and III was maximum followed by I and III. Genotypes belonging to the cluster having maximum inter-cluster distance are genetically more divergent and hybridization between genotypes of divergent cluster is likely to produce wide variability. The cluster-wise mean values (Table 6) showed that the differences in cluster means were substantially high for characters like days to first male flower appearance, days to first female flower appearance, fruit weight, protein content, number of seeds/fruit and calcium content. Cluster I was having maximum number of genotypes and was not having any highest mean values for any of the traits under study. Cluster II had highest mean values for characters like node to which first female flower appears, fruit weight, fruit length, fruit diameter,

Table 3. Phenotypic path values among fifteen characters in sweet gourd (*Momordica subangulata* ssp. *renigera* (G.Don) W.J. de Wilde). (Dependent Variable – Total fruit yield/vine)

Trait	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
1	**0.155**	–0.046	0.068	–0.079	0.030	–0.245	–0.193	0.001	0.032	0.013	–0.012	0.141	–0.118	0.017	0.005
2	0.050	**–0.142**	0.081	–0.011	0.006	0.149	–0.005	–0.001	–0.001	0.008	–0.003	–0.077	0.202	0.014	–0.001
3	–0.086	0.094	**–0.123**	0.088	–0.027	0.043	0.119	–0.001	–0.019	–0.011	0.006	0.238	–0.011	–0.015	–0.002
4	0.053	–0.007	0.047	**–0.229**	0.067	–0.223	–0.103	0.001	0.017	0.015	–0.002	0.198	–0.128	0.008	–0.006
5	0.067	–0.013	0.048	–0.221	**0.069**	–0.181	–0.095	0.001	0.014	0.016	–0.004	0.203	–0.086	0.005	–0.007
6	–0.082	–0.046	–0.011	0.111	–0.027	**0.461**	0.252	–0.002	–0.035	–0.006	0.004	–0.186	0.300	0.005	–0.002
7	–0.106	0.002	–0.052	0.084	–0.023	0.413	**0.282**	–0.002	–0.040	–0.007	0.005	0.012	0.248	–0.001	–0.004
8	–0.073	–0.040	–0.039	0.073	–0.023	0.353	0.215	**–0.002**	–0.036	–0.004	0.010	0.031	0.220	0.016	–0.003
9	–0.109	–0.001	–0.051	0.084	–0.022	0.361	0.248	–0.002	**–0.046**	–0.007	0.008	0.040	0.207	0.003	–0.004
10	0.105	–0.063	0.071	–0.192	0.061	–0.147	–0.112	0.001	0.016	**0.018**	–0.004	0.176	–0.034	0.021	–0.005
11	0.122	–0.024	0.051	–0.038	0.021	–0.109	–0.097	0.001	0.026	0.006	**–0.015**	–0.044	–0.019	–0.014	0.005
12	0.035	0.017	–0.046	–0.072	0.022	–0.136	0.005	–0.001	–0.003	0.005	0.001	**0.631**	–0.025	–0.001	–0.011
13	–0.054	–0.085	0.004	0.087	–0.018	0.412	0.208	–0.001	–0.028	–0.002	0.001	–0.046	**0.336**	–0.001	–0.005
14	0.055	–0.041	0.037	–0.038	0.007	0.047	–0.004	–0.001	–0.003	0.008	0.004	–0.012	–0.002	**0.048**	0.003
15	–0.046	–0.012	–0.018	–0.082	0.030	0.054	0.070	–0.001	–0.012	0.005	0.004	0.443	0.111	–0.010	**–0.016**

Residual effect = 0.109

1. Vine length (m), 2. Primary branches/vine, 3. Node to which first female flower appears, 4. Days to first male flower appearance, 5. Days to first female flower appearance, 6. Fruit weight (g), 7. Fruit length (cm), 8. Fruit diameter (cm), 9. Fruit girth (cm), 10. Pedicel length (cm), 11. Days taken from fruit set to edible maturity, 12. Number of fruits/plant, 13. Protein content (g/100 g), 14. Number of seeds/fruit, 15. Calcium content (mg/100 g).

Table 4. Grouping of 11 genotypes of sweet gourd in clusters

Clusters	Number of genotypes	Name of genotypes
I	5	Malda Selection-1, Malda Selection-2, Malda Selection-3, Bonga Selection-2 and Bonga Selection-3.
II	2	Baruipur Selection-1 and Joynagar Selection-1.
III	4	Malda Selection-4, Joynagar Selection-2, Barasat Selection-1 and Bonga Selection-1.

Table 5. Average inter and intra-clusters D^2 values among three clusters in 11 sweet gourd genotypes

Clusters	I	II	III
I	16088.36	11892.57	30235.22
II		4845.04	30779.83
III			13532.11

Table 6. Clusters-wise mean values of 16 characters in sweet gourd

Characters	Cluster I	Cluster II	Cluster III
Vine length (m)	2.353	2.717	2.942
Primary branches/vine	3.153	4.600	5.600
Node to which first female flower appears	25.162	25.750	19.758
Days to first male flower appearance	52.653	46.833	56.850
Days to first female flower appearance	59.627	57.250	65.342
Fruit weight (g)	42.573	62.217	40.608
Fruit length (cm)	6.167	7.083	5.533
Fruit diameter (cm)	4.353	4.867	4.492
Fruit girth (cm)	13.847	14.450	12.775
Pedicel length (cm)	11.600	11.400	15.283
Days taken from fruit set to edible maturity	15.893	17.400	16.467
Number of fruits/vine	22.180	22.583	24.617
Protein content (g/100 g)	888.307	1410.933	1999.742
Number of seeds/fruit	46.680	41.683	50.942
Calcium content (mg/100 g)	58.560	58.983	63.050
Total Fruit yield/vine (g)	0.429	0.598	0.478

fruit girth, days taken from fruit set to edible maturity and total fruit yield per vine. Cluster III had highest mean values for characters like vine length, primary branches/vine, days to first male flower appearance, days to first female flower appearance, pedicel length, number of fruits/vine, calcium content, number of seeds/fruit and protein content. Hence, selection for divergent parents based on these characters will be useful for heterosis breeding in sweetgourd. In general, the pattern of distribution of genotypes from different region to different cluster was random. Similar observations were reported by Wahab and Gopalakrishnan (1993) in bittergourd. One of the possible reasons may be the difficulty in establishment of actual location of the origin of the genotype. Further, the free exchange of genetic material among the farmers in the country makes it very difficult for the breeders to recognize or maintain the real identity of the genotypes on the basis of morphological characters. The absence of relationship between genetic diversity and geographical distance indicates that forces other than geographic origin such as exchange of genetic stock, genetic drift, spontaneous variation, natural and artificial selection may be responsible for genetic diversity.

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