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Phenotypic multicarter selection approach to predict genetics applied in the segregating generations F_2, F_3 and F_4 of common black beans

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Abstract

The objective of this work was to apply the phenotypic multicarter selection and predictive genetic for the attributes of the yield of common black bean seeds in the segregating generations F_2, F_3 and F_4.The experimental design was augmented blocks, where the BRS Esplendor (BE), BRS Supremo (BS) and IPR Tiziu (IT) genotypes were used as controls arranged in four replicates, the other treatments were organized in a unique way in the experiment, the F_2 segregating generation being represented by 36 common black bean populations, F_3 segregating generation composed of 72 families and the F_4 segregating generation formed by 44 families. The multicarter phenotypic index provided the simultaneous selection for the number and mass of seeds per plant, independent of the segregating generation of common black bean.Multicarter genetic variation is superior for the F_3 segregating generation, with pronounced environmental effects on the F_4 generation.The F_4 segregating families express superiority to the genetic gain and magnitude of superior genotypes in relation to the commercial controls, where high genetic increase is exposed between the F_3 to F_4selection.The use of the phenotypic index expresses applicability to the selection of common black bean genotypes to increase seed yield.

Keywords: *Phaseolus vulgaris* L., index selection, yield components, seed production.

Abbreviations: NS_number of seeds per plant;SM_seed mass per plant; V_G_genetic variance; V_E_residual variance; V_P_phenotypic variance; H^2_heritability; A_C_selection accuracy; G_ genetic value; U + G_predicted genetic value; G (%)_percentage of predicted genetic gain; NM_ new mean predicted; BE_BRS Supreme control; BS_BRS Supreme control; IT_IPR Tiziu control; REML_restricted maximum likelihood; BLUP_Best linear unbiased prediction;

Introduction

Common black common bean (*Phaseolus vulgaris* L.) is the second most consumed type of bean in Brazil, corresponding to 35% of the total bean consumed, being preferred mainly in the Southern Region of the country (Demariet al., 2015; Borémet al., 2015; Carneiro, 2015). It is considered one of the most important foods that constitute the Brazilian diet, because it is an excellent source of protein and provides the body with various sources of energy such as carbohydrates, vitamins, fibers, iron and zinc (Carvalhoet al., 2016).

Early selection of segregating generations is a crucial step because it maximizes the use of human and financial resources in a breeding program (Resendeet al., 2015; Szareski et al., 2017). Currently breeding programs have indicated superior genotypes for more than one trait, since selection based on just one character is not interesting. The correlation between characters can overcome the difficulties in breeding of characters of agronomic interest that suffer from pronounced effects of the growing environment and of low heritability, these may present genetic association caused by pleiotropic effects and linked genes (Bernardo, 2002).

In this context, multicarter selection and the simultaneous selection of these contribute positively to the improved, this makes possible simultaneous genetic gains (Teixeira, 2011). Even with the availability of advanced biometric methodologies to obtain reliable estimates, these can be influenced by biases intrinsic to the statistical model.Therefore, an approach that minimizes these effects is the estimation of the variance components (REML) that makes it possible to understand the determinant genetic fraction for phenotypic expression, where later these parameters will be used to predict the genetic value of each segregating generation analyzed (Pimentel et al., 2014). These inferences will make possible the general selections and directed in breeding program, which advocate developing common black bean genotypes with high seed production. In this context, the objective of this work was to apply the phenotypic multicarter selection and predictive genetic for the attributes of the yield of common black bean seeds in the segregating generations F_2, F_3 and F_4.

Results and discussion

Variance components variance and genetic parameters

Deviance analysis (LRT) revealed significance at 5% probability using the chi-square test (X^2) for the variance components and genetic parameters (REML) estimated for the NS x SM phenotypic index obtained for the segregating generations F_2, F_3 and F_4 of common black bean (Table 1). Obtaining superior genotypes is based on the superiority of many characters measured at the phenotype level; however, the isolated interpretation of the trend of a particular component of the yield may result in the low efficiency or intrinsic misconceptions of which progenies should be selected and directed to the next generations of breeding, which will result in a new superior genotype. In this context, it is possible to use the multicarter approach that allows to consider the tendency of the number of seeds per plant with the mass of these seeds, thus evidencing a single direction in the selection of the best progenies. However, selection strategies should be stratified for the segregating generation emphasized at the time of selection, because genetic and environmental events act distinctly in each situation, thus, the multicarter tendency specific for populations (F_2) and segregating families (F_3 and F_4) of common black bean was determined.

The variance components were decomposed from the total variance assigned to each segregating generation, with these estimates it was possible to determine that the phenotypic expression of the NS x SM phenotype index was based on 20%, 62% and 14% due to the additive and non additive genetic effects of the F_2, F_3 and F_4 generations, respectively.Broad sense heritability (H^2) provides to visualize the genetic variability (Annicchiarico, 2002) present in a given situation, superiority was evidenced for the generation of F_3 segregating families, these effects can be explained by the large number of families tested in this generation and originated of diverse populations, this culminates in the elevation of genetic variation and consequently potentiates this parameter, in contrast, its interpretation makes it possible to define the multicarter phenotype of generations F_2 and F_4, which are affected by more than 85% of environmental effects. The selection accuracies (Ac) are high in the generation of the F_3 segregating families, and indicate the possibility of selecting genotypes reliably for the multicarter increment (Resende and Duarte, 2007).

Predictions and ranking of the best linear unbiased prediction (BLUP)

For the multicarter approach to increase the number and mass of common black bean (PI NS x SM) seeds for the F_2 segregating generation, 33 populations were tested together with commercial controls BRSEsplendor (BE), BRSSupremo (BS) and IPRTiziu (IT), these were responsible for quantifying the effects of the environment and ranking the best genotypes against their predicted genetic value (Table 2). In this scenario, 30.6% of the evaluated populations were superior to commercial controls and expressed selection potential, being these 26, 9, 10, 23, 30, 7, 18, 21, 4, 19 and 20. When relating the multicarter genetic gain in relation to the commercial controls and the best F_2 population, it was verified the possibility of genetically increasing both components of seed yield of common black bean in 9.8%. Thus, as a criterion to specifically target selection and improve genetic gains, a minimum of +1.0 was used in predicted genetic units (G), which enabled the selection of populations 26, 9, 10, 23 and 30, in the general context 13.9% of the segregating genotypes have potential for high seed yield.

The F_3 generation was based on the measurement of 69 segregating families, of which 18.1% were higher than the commercial controls (Table 3) simultaneously for the number and seed mass produced per plant. In this situation, genetic gains of 2.0% were obtained through the families 64, 49, 51, 47, 36, 8, 50, 26, 62, 63, 9, 37 and 2, as these stand out as genetically superior to the agronomic attributes established by the controls. By using the criterion of at least +1.0 in predicted genetic units (G) it was possible to define that 11.1% of the F_3 families tested have the potential to increase both the number and the seed mass simultaneously, this will be possible by the specific selection of the genotypes 64, 49, 51, 47, 36, 8, 50 and 26.

For the F_4 generation, it was found that 38.6% of the segregating families were superior to commercial controls (Table 4), which revealed the possibility of genotypes with high genetic potential for seed production. In these conditions, the multicarter can be genetically increased by6.6% due to the selection of the 17 transgressive families, however, when applying the criterion of specific selection of at least +1.0 in predicted genetic units (G),genetic increments of 15.9% were observed in relation to the controls,being able to attribute as the best families 19, 1, 6, 33, 21, 3, 13 that have the potential to generate superior genotypes for the number and mass of seeds.

Genetic relations between the segregating generations F_2 x F_3 x F_4

Multivariate genetic trends for seed number and mass (PI NS × SM) are intrinsic to the generations, comprising 36 F_2 segregating populations, 72 F_3 segregating families and 44 F_3 segregating families. For the number of genotypes superior than the commercial controls, a reduction of 12.5% between the F_2 and F_3 generations was observed, as well as increases of 20.4% between F_3 and F_4, in this way, the selections acting between the F_2 population generation result in increases of 8.0% the magnitude of higher genotypes identified in generation F_4.Regarding the genetic gain weighted by the commercial controls, a reduction of 7.8% between the F_2 and F_3 generations was evidenced, but increases of 4.6% were obtained between the F_3 and F_4 generations, in the general scope there was a reduction in the genetic gain between F_2 generation population and the generation of F_4 segregating families.

Considering the criterion of specific selection of at least +1.0 in predicted genetic units (G), general increases of 2.0% in the number of genotypes selected between the F_2 and F_4

Table 1. Estimates of variance components and genetic parameters (REML) referring to the NSxSM index obtained for the F_2, F_3 and F_4 segregating generations of common black bean.

Variance components and genetic parameters*	F_2	F_3	F_4
V_G	2.34	10.85	2.09
V_E	8.73	6.63	12.48
VP	11.27	17.50	14.96
H^2	0.20	0.62	0.14
Ac	0.45	0.78	0.37
Overall mean	0.49	4.18	5.80

* V_G: genetic variance; V_E: residual variance; V_P: phenotypic variance; H^2: broad sense heritability; Ac: selection accuracy; Overall mean: overall mean of the experiment.

Table 2. Predictions for the best linear unbiased prediction (BLUP) for the NSxSM index obtained for the 33 F_2 segregating populations of common black bean.

R*	P	G	U + G	G(%)	NM
1	*26*	4.46	9.38	13.20	9.38
2	*9*	1.67	6.59	9.08	7.98
3	*10*	1.26	6.18	7.30	7.38
4	*23*	1.19	6.11	6.36	7.06
5	*30*	1.11	6.03	5.74	6.86
6	*7*	0.94	5.86	5.25	6.69
7	*18*	0.89	5.81	4.88	6.56
8	*21*	0.42	5.34	4.42	6.41
9	*4*	0.23	5.15	4.01	6.27
10	*19*	0.19	5.11	3.66	6.16
11	*20*	0.13	5.05	3.37	6.05
12	**IT**	0.00	4.92	3.09	5.96
13	**BE**	0.00	4.92	2.85	5.88
14	**BS**	0.00	4.92	2.65	5.81
15	*5*	-0.00	4.91	2.47	5.75
16	*3*	-0.01	4.90	2.31	5.70
17	*33*	-0.13	4.78	2.15	5.64
18	*29*	-0.15	4.76	2.01	5.59
19	*27*	-0.25	4.66	1.86	5.55
20	*22*	-0.39	4.52	1.71	5.49
21	*24*	-0.42	4.49	1.57	5.45
22	*14*	-0.49	4.42	1.43	5.40
23	*28*	-0.58	4.33	1.29	5.35
24	*2*	-0.58	4.33	1.16	5.31
25	*12*	-0.63	4.28	1.04	5.27
26	*31*	-0.66	4.25	0.93	5.23
27	*16*	-0.66	4.25	0.82	5.19
28	*17*	-0.67	4.24	0.72	5.16
29	*25*	-0.70	4.22	0.62	5.13
30	*13*	-0.71	4.20	0.53	5.10
31	*15*	-0.71	4.20	0.45	5.07
32	*31*	-0.73	4.18	0.36	5.04
33	*8*	-0.82	4.09	0.28	5.01
34	*11*	-0.92	3.99	0.19	4.98
35	*6*	-1.09	3.83	0.09	4.95
36	*1*	-1.12	3.79	0.00	4.92

* R: ranking; P: F_2 segregating population; G: genetic value; U + G: predicted genetic value; G (%) percentage of predicted genetic gain; NM: new mean predicted; BE: BRS Splendor control; BS: BRS Supreme control; IT: IPRTiziu control.

Table 3. Predictions for the best linear unbiased prediction (BLUP) for the NSxSM index obtained for the 69 F_3 segregating families of common black bean.

R	F	G	U + G	G (%)	NM	R	F	G	U + G	G (%)	NM
1	*64*	16.94	21.12	5.01	21.12	37	*4*	-0.93	3.25	0.81	5.30
2	*49*	15.46	19.64	4.48	20.38	38	*31*	-0.95	3.23	0.77	5.25
3	*51*	4.14	8.32	1.58	16.36	39	*24*	-0.95	3.23	0.73	5.20
4	*47*	4.03	8.21	0.10	14.33	40	*29*	-0.96	3.22	0.70	5.15
5	*36*	3.91	8.09	6.43	13.08	41	*11*	-0.97	3.21	0.66	5.10
6	*8*	3.59	7.77	5.79	12.19	42	*6*	-0.99	3.19	0.63	5.06
7	*50*	2.85	7.03	5.25	11.46	43	*28*	-1.01	3.18	0.60	5.01
8	*26*	1.12	5.30	4.70	10.69	44	*38*	-1.01	3.17	0.57	4.97
9	*62*	0.68	4.86	4.23	10.04	45	*67*	-1.06	3.12	0.54	4.93
10	*63*	0.57	4.75	3.85	9.51	46	*57*	-1.07	3.11	0.51	4.89
11	*9*	0.24	4.42	3.52	9.05	47	*68*	-1.08	3.10	0.48	4.85
12	*37*	0.23	4.41	3.24	8.66	48	*61*	-1.09	3.09	0.46	4.81

13	*2*	0.16	4.34	3.00	8.33	49	*23*	-1.10	3.08	0.43	4.78
14	**BS**	0.00	4.18	2.78	8.03	50	*39*	-1.11	3.07	0.41	4.74
15	**BE**	0.00	4.18	2.60	7.78	51	*14*	-1.14	3.04	0.38	4.71
16	**IT**	0.00	4.18	2.43	7.55	52	*44*	-1.14	3.04	0.36	4.68
17	*21*	0.00	4.18	2.29	7.35	53	*60*	-1.15	3.03	0.34	4.65
18	*48*	-0.08	4.10	2.16	7.17	54	*33*	-1.17	3.01	0.32	4.62
19	*52*	-0.21	3.97	2.04	7.00	55	*13*	-1.17	3.01	0.29	4.59
20	*10*	-0.25	3.93	1.93	6.85	56	*53*	-1.20	2.98	0.27	4.56
21	*25*	-0.26	3.93	1.83	6.71	57	*22*	-1.22	2.96	0.25	4.53
22	*1*	-0.45	3.73	1.73	6.58	58	*69*	-1.23	2.95	0.23	4.50
23	*40*	-0.45	3.73	1.64	6.45	59	*46*	-1.24	2.94	0.21	4.48
24	*30*	-0.46	3.72	1.56	6.34	60	*58*	-1.26	2.92	0.20	4.45
25	*43*	-0.55	3.63	1.48	6.23	61	*19*	-1.28	2.90	0.18	4.43
26	*35*	-0.57	3.61	1.41	6.13	62	*41*	-1.29	2.89	0.16	4.40
27	*42*	-0.69	3.49	1.34	6.03	63	*54*	-1.31	2.87	0.14	4.38
28	*45*	-0.71	3.47	1.27	5.94	64	*15*	-1.33	2.85	0.12	4.35
29	*66*	-0.77	3.41	1.21	5.85	65	*16*	-1.34	2.84	0.11	4.33
30	*3*	-0.83	3.35	1.15	5.77	66	*12*	-1.35	2.83	0.09	4.31
31	*27*	-0.83	3.35	1.09	5.69	67	*17*	-1.36	2.82	0.08	4.29
32	*32*	-0.85	3.33	1.04	5.62	68	*7*	-1.37	2.81	0.06	4.26
33	*55*	-0.86	3.32	0.99	5.55	69	*18*	-1.39	2.79	0.04	4.24
34	*65*	-0.88	3.30	0.94	5.48	70	*56*	-1.40	2.78	0.03	4.22
35	*59*	-0.88	3.30	0.90	5.42	71	*34*	-1.41	2.77	0.01	4.20
36	*5*	-0.89	3.29	0.85	5.36	72	*20*	-1.44	2.74	0.00	4.18

* R: ranking; F: F$_3$ segregating family; G: genetic value; U + G: predicted genetic value; G (%) percentage of predicted genetic gain; NM: new mean predicted; BE: BRS Splendor control; BS: BRS Supreme control; IT: IPRTiziu control.

Table 4. Predictions for the best linear unbiased prediction (BLUP) for the NSxSM index obtained for the 44 F$_4$ segregating families of common black bean.

R	F	G	U + G	G (%)	NM	R	F	G	U + G	G (%)	NM
1	*19*	3.33	9.13	8.82	9.13	23	*28*	0.10	5.70	1.70	6.44
2	*1*	1.88	7.69	6.90	8.41	24	*29*	0.13	5.67	1.62	6.41
3	*6*	1.41	7.21	5.85	8.01	25	*16*	0.18	5.63	1.53	6.38
4	*33*	1.24	7.04	5.20	7.77	26	*41*	0.26	5.54	1.45	6.35
5	*21*	1.20	7.00	4.80	7.61	27	*18*	0.39	5.41	1.36	6.31
6	*3*	1.18	6.98	4.52	7.51	28	*5*	0.40	5.40	1.27	6.28
7	*13*	1.11	6.91	4.29	7.42	29	*27*	0.41	5.39	1.19	6.25
8	*31*	0.79	6.59	4.02	7.32	30	*29*	0.46	5.34	1.11	6.22
9	*22*	0.76	6.56	3.79	7.23	31	*20*	0.58	5.22	1.02	6.19
10	*34*	0.64	6.44	3.58	7.15	32	*25*	0.59	5.21	0.94	6.16
11	*9*	0.45	6.26	3.37	7.07	33	*36*	0.60	5.20	0.87	6.13
12	*4*	0.41	6.21	3.18	7.00	34	*32*	0.66	5.14	0.79	6.10
13	*26*	0.22	6.02	2.98	6.93	35	*28*	0.67	5.13	0.72	6.07
14	*17*	0.21	6.01	2.81	6.86	36	*30*	0.72	5.08	0.64	6.04
15	*40*	0.10	5.90	2.64	6.80	37	*23*	0.78	5.02	0.57	6.02
16	*2*	0.05	5.85	2.48	6.74	38	*24*	0.95	4.85	0.49	5.99
17	*15*	0.04	5.84	2.34	6.68	39	*37*	1.03	4.77	0.41	5.95
18	**BS**	0.00	5.80	2.21	6.64	40	*7*	1.07	4.73	0.32	5.92
19	**BE**	0.00	5.80	2.09	6.59	41	*14*	1.08	4.72	0.25	5.89
20	**IT**	0.00	5.80	1.99	6.55	42	*10*	1.19	4.61	0.16	5.86
21	*35*	0.07	5.74	1.89	6.51	43	*11*	1.25	4.55	0.09	5.83
22	*8*	0.07	5.73	1.79	6.48	44	*12*	1.37	4.43	0.00	5.80

* R: ranking; F: F$_4$ segregating family; G: genetic value; U + G: predicted genetic value; G (%) percentage of predicted genetic gain; NM: new mean predicted; BE: BRS Splendor control; BS: BRS Supreme control; IT: IPRTiziu control.

Table 5. Correlation coefficients between the phenotypic and genetic approach predicted for the NSxSM index obtained for the F$_2$, F$_3$ and F$_4$ generations.

	PG_F$_2$	P_F$_3$	PG_F$_3$	P_F$_4$	PG_F$_4$
P_F$_2$	0.75*	0.12	0.25	-0.09	-0.07
PG_F$_2$	-	0.18	0.32	-0.07	-0.06
P_F$_3$		-	0.89*	-0.04	-0.07
PG_F$_3$			-	-0.02	-0.05
P_F$_4$				-	0.75*

* P_F$_2$: phenotypic index NSxSM obtained in the F$_2$ segregating generation; PG_F$_2$: predicted genetic index NSxSM obtained in the F$_2$ segregating generation; P_F$_3$: phenotypic index NSxSM obtained in the F$_3$ segregating generation; PG_F$_3$: predicted genetic index NSxSM obtained in the F$_3$ segregating generation; P_F$_4$: phenotypic index NSxSM obtained in the F$_4$ segregating generation; PG_F$_4$: predicted genetic index NSxSM obtained in F$_4$ segregating generation.

generations were observed, but decreases of 2.8% were obtained from F_2 to F_3 and increases of 4.8% between F_3 and F_4, justifying that the management of the superior families preserving the genealogy can result in positive genetic gain and increase in the probability of identifying superior genotypes. In relation to the genetic value added by the phenotypic average (U + G) it was verified that the multicarter (PI NS × SM) shows accentuated increases between the F_2 population generation and the F_3 segregating families, however, this variation is diluted between generations F_2 and F_4.

In order to verify the multicarter phenotypic trends for the number and mass of seeds with the genetic predictions, the linear correlation was estimated (Table 5). In this context, coefficients of positive linear association between phenotypic measurements and genetic predictions of the multicarter index for all segregating generations (F_2, F_3 and F_4) were evidenced, indicating that the genotypic trends expressed in this study are supported by the measured phenotypic magnitudes, and these inferences can be used for future selection strategies that recommend obtaining common black bean genotypes with high seed yield.

Materials and methods

Conduction of study and experimental design

This experiment was carried out in 2017 in the municipality of TenentePortela - RS, located at the coordinates: latitude 27°22 '16''S and longitude 53°45'30''W, with an altitude of 420 meters. Soil is classified as a Ferric Red Latosol (Streck, 2008), and the climate is characterized by Köppen as subtropical humid Cfa.

The experimental design was augmented blocks, where the BRS Esplendor (BE), BRS Supremo (BS) and IPR Tiziu (IT) genotypes were used as controls arranged in four replicates, the other treatments were organized in a unique way in the experiment , the F_2 segregating generation being represented by 36 common black bean populations, F_3 segregating generation composed of 72 families and the F_4 segregating generation formed by 44 families, all genotypes are genetically linked, F_4 families being selected according to the best F_3 families , as well as, the F_3 families were formed by the identification of the superior individuals present in the F_2 populations.

The experimental units consisted of two lines with two meters in length, spaced by 0.5 meters. For sowing, 12 seeds per linear meter were used in the population density of 24 plants per m^2. For the basic fertilization 250 kg ha-1 of N, P2O5, K2O (10-20-20) was used. For top dressing, 70 kg ha-1 of nitrogen was applied at the phenological stage V_4. Crop treatments, weed and pest insects controls were carried out according to the need of the crop.

Characters measured

The agronomic characters were measured in ten plants per experimental unit, these being: *Number of seeds per plant (NS)*, obtained after the pod track, where the total number of seeds produced per plant was measured, results in units. *Seed mass per plant (SM)*, the cleaned seeds were submitted to the measurement of the mass in a precision scale, results in grams.

Due to the attributes of the seed production show a similar economic importance, they were combined in a multicarter index in order to express a unique tendency (NUNES et al., 2017). This multicarter was called the NS x SM phenotypic index, and was obtained by the following equation:

$$\text{PINSxSM}=\left(\left(\frac{NS}{S_{NS}}\right)\times\left(\frac{SM}{S_{SM}}\right)\right)$$

Where: PI NS x SM: refers to the phenotypic index NS x SM, NS: corresponds to the observed value of the character number of seeds per plant, SM: corresponds to the observed value of the seed mass per plant, S_{NS}: refers to the standard deviation of the NS character, S_{SM}: refers to the standard deviation of the SM character.

Statistical analysis

The data obtained were submitted to a 5% probability analysis with the purpose of testing the model additivity, residue normality and homogeneity of variances (Ramalhoet al., 2012). Subsequently, the Deviance (LRT) analysis was performed at 5% probability by the chi-square test (X^2), in order to verify the significance of the variance components and genetic parameters (REML), based on the model $y = Xr + Zg + e$, where y: is the data vector, r: are the effects of the repetitions assumed to be fixed, g: are the genetic effects assumed to be random, e: correspond to the effects of the residuals assumed to be random.

Genetic variance (V_G), residual variance (V_L), phenotypic variance (V_P), broad sense heritability (H^2), accuracy of selection (Ac) and the overall mean of the experiment were estimated. The *best linear unbiased prediction* (BLUP) was used to obtain the components of the means for ranking (R), obtaining the genetic value (G), predicted genetic value (U + G), percentage of genetic gain (G%) and the new predicted mean (NM) of the F_2 segregating populations and the F_3 and F_4 segregating families of common black bean. Subsequently, the linear correlation was performed in order to prove the association between the multicharacter phenotypic value and the genetic predictions, where the significance of the coefficients were obtained through the *t*-test at 5% of probability.

Conclusion

The multicarter phenotypic index provides the simultaneous selection for the number and mass of seeds per plant, independent of the segregating generation of common black bean. Multicarter genetic variation is superior for the F_3 segregating generation, with pronounced environmental effects on the F_4 generation.The F_4 segregating families express superiority to the genetic gain and magnitude of superior genotypes in relation to the commercial controls, where high genetic increase is exposed between the selections F_3 to F_4.The use of the phenotypic index expresses applicability to the selection of common black bean genotypes to increase seed yield.

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