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Estimation of Genetic Variability of Malt Barley (*Hordeum vulgare* l.) Varieties for Yield, Yield Related Trait, North Eastern Ethiopia

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- Genotypic coefficient of variance; Phenotypic coefficient of variance; Genetics advance; Heritability

Abstract

The objectives of this study were to assess the genetic variability of yield, yield related traits and to estimate direct, indirect effects of trait associations. Seventeen varieties were evaluated and subjected to the analysis of variance using RCB design, in Eastern Amhara Ethiopia. The varieties differed significantly for most of the characters and had wide range of mean values, which indicated the existence of variations among the tested varieties. Estimates of phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) were generally low. The highest GCV and PCV values were recorded on grain yield (51) and plant height (60). The PCV values were slightly greater than the GCV values. Grain yield, plant height, protein content and grain size had relatively high heritability. Grain yield gives high heritability value accompanied by high genetic advance which is good indicator for selection. Grain yield had positively and significantly correlated with date of maturity. Grain yield negatively correlated with protein and positively associates with starch.

INTRODUCTION

Biological worlds were full of variability in which the real variability of each trait in plant breeding gave good opportunity to widen the scope of the breeding. Variability is the making of differences among individuals due to having differences in their genetic composition, the environment in which they are raised and gene and environment interaction [1,2]. When two individual express their characters separately when the influence of an environment were identical for both, differences in expression would result from genetic variation. Information on the nature and magnitude of genetic variability present in a crop species is important for developing effective crop improvement program [2-5].

When genetic variability is due to the genetic differences among individuals within a population, is the core of plant breeding which helps to magnified and widen the genetics base of a given population in trait level and support the proper management of diversity which produce permanent gain in the performance of plant and can buffer against seasonal fluctuations [4,6]. In addition, estimation the magnitude of variation within germplasm collection and traits found in cross ability parents for important plant attributes will enable breeders to exploit genetic diversity more efficiently [7].

The existing variability present in breeding populations can be assessed in the following way by using simple measures of variability, such as variance, standard deviation, coefficient of variability by estimating both phenotypic and genotypic various components of variance, heritability and genetic advance. Utilization of genetic resources requires proper and systematic evaluation of such resources. Therefore, the main objective of this experiment

- Assess genetic variability of malt barley for yield, yield related trait.
- Estimate direct and indirect effect of association between yield and yield related traits

MATERIALS AND METHODS

Description of the study area

The experiment was conducted in Amhara region at, Mekedella (south Wollo) in 2016 main growing season. Mekdella is located 500km North of Addis Ababa, at $11^{0}.57'$ N longitude and 39.02′ E latitudes, with the altitude of 2600 masl. The site received an average annual rainfall of 923mm. The soil types for both locations are litosols (GPS reading, and Kombolcha Metrological Station, 2016).

Experimental design and field lay out

The trial was laid out in Randomized Complete Block Design (RCBD) with three replications. The plot size was 1.60m wide

and 2.5 m long with a total area of 4 m^2 consisting of 8 rows. The spacing between rows, plot and replication was 20cm, 0.5m and 1m, respectively. Data were collected from the central six rows. The seed rate was 100 kg/ha, and seeds were drilled in each row. Fertilizer was applied in the form of Urea and Diamonium Phosphates (DAP) at the rates of 41/46 of (N/P_2O_5) per hectare. Half of the recommended rate was applied at planting and the remaining after 35 days of emergency for each location. All other agronomic management was applied as per recommendation.

Data collected

Data were collected and recorded both in the field and in the laboratory. Data which were collected like Days to heading, Days to maturity, Plant height , Harvest index, 1000 kernel weight, Gain yield (kg/ha),Spike length, Seeds per spike, Grain protein (GP): The grain protein content was analyzed by Infratic 1241grain analyzer; Near Infrared Reflect Spectroscope (NIRS). Around five hundred gram of malt barley grain sample was used to measure the protein content. The grains were inserted in the upper hole of NIRS then press the down arrow the NIRS start measuring the protein content. Kernel size (Sieve analysis): Kernel size distribution for malting barley was determined using European normal sorting sieve machine which has oblong (slotted) hole of 2.8, 2.5, 2.2 and less than 2.2mm in width. Hundred gram of malt barley seed sample were placed on the machine and shaking it for five minutes. Proportion of the seed trapped (passed) by each sieves was determined by measuring in gram and finally converted to percentage. Germination Energy (%): Counted 100 seed from each plot and allowed to germinate in Petri dish then after 120 hours the number of germinated seed divided by total seed in Petri dish and multiply by 100. Germination Capacity (%): For the determination of germination capacity 5ml of H_2O_2 diluted by 2000 ml of tape water and steeped 200 grain from each plot for forty eight hours in the petri dish and after forty eight hours the strain the grain replace by the same amount of water and hydrogen peroxide for the next forty eight hours. Finally strain the water and count ungerminated grain and converted to percentages, where kernel dormancy is suspected. Finally Calculate

$$GC = \frac{200}{2} - n(1)$$

where n, is ungerminated grain.

Hectoliter weight (HLW) (g/hl): The hectoliter weight was measured by grain analyzer instrument using 300 gram grain. Friability: Samples were analyzed using a pfeuffer Friabilimeter, which uses a pressure roller to grind the sample against a rotating screen. Low, medium and high friability malts were tested according to EBC Method 4.15 (EBC, 1998). Malt sample, 50g was allowed to run the friability meter for 8 min, and the non-friable fraction or retain one was weighed.

$$Friability(\%) = 100 - R * 2(2)$$

Where: R is the mass of non friable retained over the Friabilimeter sieve.

Fine grind hot water extract (HWE)

To determined fine grind hot water extract about 55 g malted barley of sample was weighted (at room temperature) in to tarred mash beaker and milled through mill set for standardized fineness of grind**.** The ground malt was collected in same mash beaker, carefully brushing malt particles remaining in mill in to mash beaker. Mix without delay the mash beaker was placed with content on balance accurate to within ± 0.05 fewer than 750g load and adjusted weight of malt to 50 ± 0.05g by removing excess in to tared dish for moisture determination. The mashing procedure was done by adding 200mL of distilled water at 45°C to 50 g of ground malt, and then the vessel was placed in a mashing apparatus. The sample was held at 45°C for 30 min, then the temperature was raised to 70°C by 1°C for every 1 min increase for 25 min, and then 100 mL 70°C distilled water was added to each sample and held at 70°C for 1 hour.

The extract obtained was converted and expressed in percentage on wet basis (% wb) and dry matter basis (% db) using the following equation.

$$\text{Extract dry basis} = \frac{(Ex100)}{(100 - M)}(3)$$

Where, P is an extraction in 100g wort, plato (P), M is moisture in the malt and E is extract as wet basis E= plato reading

Data analysis

Estimation of genetic parameter: In order to calculate the environmental effect on various characters that studied different genetic characters ,genetic variance (σ2g), Phenotypic variance (σ2p), phenotypic coefficients of variation (PCV), and genotypic coefficients of variation (GCV) were estimated based on the method of Burton et al., and Johnson et al. [8,9].

$$\sigma 2g = \frac{Msg - Me}{r}(4)$$

Where, $\sigma 2_g$= genetic variance, Ms_g =mean square due to genotype, M_e =environmental variance (error mean square) r =replication

$$\sigma 2P = \sigma 2g + \sigma 2e(5)$$

Where, σ_{2p} =Phenotypic variance, σ_{2g} =genotypic variance, σ_{2e} = Error variance

$$PCV = \sqrt{\frac{\text{phenotypic variance}}{\text{population mean for the character}}} * 100(6)$$

$$GCV = \sqrt{\frac{Genotypic\ \text{var}\ iance}{\text{population mean for the character}}} * 100(7)$$

Phenotypic and genotypic correlation coefficient (r)

A: Correlation coefficient (r): is measure of association of two or more variable or characters to determine the component of complex characters on grain yields by using, phenotypic correlation, genotypic correlation, interaction between variety and environment to know the inherent association between two variable were estimated as describe as by Pramoda HP et al., [10].

$$COV_{gxy} = \frac{MSPg - MSPe}{r}(8)$$

Where, COV_{GXY} Genotypic covariance between trait x and y, $MSPg$ = Genetic mean sum product of trait x and y

$MSPe$ = Environmental mean sum product of trait x and y, r =

replication

B: Heritability (H): Heritability in broad sense for all characters was computed using the formula given by Chand NS et al., [11].

$$\text{Heritability (H)} = \frac{\sigma_{g2}}{\sigma_{p2}} \times 100 (9)$$

Where: H = heritability in broad sense σ_{2p} = Phenotypic variance, σ_{2g} = Genotypic variance

Genetic advance under selection (GA): Expected genetic advance for each character at 5% selection intensity was computed using the methodology described by Sunil K Yadav et al., [12].

$GA = K. \sigma_p. H$ (10)

Where GA = expected genetic advance

K = constant (selection differential where K=2.056 at 5% selection intensity)

σ_p = phenotypic standard deviation on mean basis

H = heritability in broad sense

Genetic advance as percent of mean was calculated to compare the extent of predicted advance of different traits under ctin.

RESULTS

Phenotypic and genotypic coefficient of variation

The values of all the genotypic coefficient of variation (GCV) were low except for grain yield and plant height which were (16%), and (11%) respectively. The phenotypic coefficient variation (PVC), values were low to high (Table 1). The values of grain yield (23%), and spike length (25%). High heritability values obtained from plant height (60%) and protein (67%) and medium days to maturity (47%), grain yield (51%), and harvest index (56%). The other characters showed low heritability value. Grain yields (24%) and different seed sizes had higher genetic advances. Harvest index (19%) and plant height (18%) under medium genetic advance. The other characters showed that low genetic advance.

Phenotypic and genotypic correlation of grain yield with other related characters

Estimation of genotypic (r_g) and phenotypic (r_p) correlations between the yield and other character are presented in Table 2. The result of phenotypic correlation coefficient indicated that grain yield were positively and highly correlated with days to maturity (0.78), grain filling period (0.75) and significantly with harvest index (0.42), thousands seeds weight (0.31), plant height (0.49). The phenotypic association of other characters showed that days to maturity positively and significantly correlate with harvest index (0.36), thousand seed weight (0.38), and plant height (0.64). Thousands seed weight to plant height (0.40). Harvest index with thousands seed weight (0.30), and grain filling to harvest index (0.27).

Phenotypic and genotypic path coefficient analysis on grain yield

The phenotypic and genotypic direct and indirect effects of different characters and component in all possible combinations are presented in Table 3. Based on phenotypic path coefficient analysis, the highest positive and favorable direct effect exerted on grain yield was days to maturity (0.6826), grain filling (0.6289), followed by biomass (0.0182). The negative direct effect exerted on grain yield also by days to heading (-0.0372), plant height (-0.0250) and harvest index (-0.0281). The negative association and negative direct effect of days to heading on grain yields were expressed by the masking effects of positive indirect effect of days to heading through biomass and harvest index.

DISCUSSIONS

According to Whan et al. [13], phenotypic and genotypic values greater than 20% is considered as high, between; 10-20% is medium and below 10% as low and according to Pramoda et al. [10], heritability is categorized <40% low, between 40% - 59% medium, and 60% -79% high and above 80 very high. High heritability showed variation among the tested varieties as a result of the presence of difference due to the existing genetic, environmental influence and the interaction of genetic makeup and environment. High heritability values of yield, plant height, and protein and grain size were supported by [11,12]. Our finding on grain size showed relatively high heritability which supported by [14,15]. The value of most characters for heritability values ranged from low to medium. These were supported by previous workers [13]. According to Singh BD. [16], if heritability of a character is very high, selection for such a character should be fairly easy, because there would be a close correspondence between genotype and phenotype due to a relatively smaller contribution of environment to phenotype. Jalal-Al-Tabbal et al., and Blanco A. [17,18], reported that high heritability in days to heading in barley which in line with our finding. Character with low heritability should considerably difficult to practice phenotypic selection due to the masking effects of the environment.

The genetic advance as percent of mean was categorized into low (< 10%), moderate (10-20%) and high (> 20%) by (9). Higher heritability coupled with higher genetic advance was recorded for grain yield, and plant height at both locations which could helps for improving the grain yield in the tested environment. The higher heritability of the trait is an advantage in phenotypic selection and easy in crop improvement for the environment. This idea was supported by Khan AA [19]. Grain protein content showed higher heritability with low genetic advance. Different authors reported that characters possessing low genetic advance with high heritability indicate that the presence of none additive gene action, thus tell us simple selection procedure in early segregation generation may not be effective for generating desirable trait for future plant breeding. Likewise, high heritability with high genetic advance that the presence of additive gene action [9,20]. Singh BD. [20], Reported that genetic advance under selection refers to the improvement of characters which the value of the variety for the new population compared with the base population under one cycle of selection at a given selection intensity. Therefore, the current finding suggested that selecting the top 5% of the genotypes could result in an advance of 0.28% to 24.45 population mean for the listed characters. Genetic advance under selection value were low 0.28%, which indicates

Table 1: Range; mean; phenotypic; genotypic and environmental variance and genotypic and phenotypic coefficients of variance; broad sense heritability; genetic advance and Genetics advance of mean for different characters at Mekedella 2016.

Characters	Mean	SE(±)	Range	σ^2p	σ^2g	GCV (%)	PCV (%)	H^2 (%)	GA	GAM (%)
Dm (days)	111.0	1.183	105-120	8.03	3.83	1.77	2.56	47.72	2.79	2.52
GF (days)	39.0	4.037	28-60	59.18	10.29	8.2	19.67	17.38	2.76	7.06
HI (%)	0.39	0.025	0.29-0.44	0.005	0.003	12.73	16.95	56.42	0.08	19.73
GY (kg/ha)	1635	152.058	1178-2156	143037	73672	16.51	23.01	51.51	401.86	24.45
TKW (g)	40.4	1.549	33.3-47	8.13	0.93	2.39	7.06	11.43	0.67	1.66
PH (cm)	63.0	3.324	42.8-80.4	84.81	51.67	11.42	14.63	60.92	11.57	18.39
GC (%)	97.9	0.592	95-99	0.99	0.27	0.53	1.18	27.53	0.57	0.58
GE (%)	98.1	0.582	96-100	0.8	0.12	0.35	1.09	14.93	0.28	0.28
Pr.(%)	9.8	0.27	8.4-12	0.67	0.45	6.8	8.3	67.15	1.13	11.5
St(%)	65.4	0.531	61.9-68.5	1.97	1.13	1.62	2.15	57.1	1.65	2.53
Ex(%)	78.5	0.868	75-82	3.09	0.83	1.16	2.24	26.92	0.98	1.24
2.8mm.s.	15.8	4.127	0.7-62	209.52	158.43	79.66	91.61	75.62	22.58	142.91
2.5mm.s	54.9	2.66	29.4-78.2	144.98	123.75	20.26	21.92	85.36	21.2	38.61
2.8+2.5mm	70.8	4.539	48.4-92.1	205.88	144.06	16.95	20.27	69.97	20.71	29.26
2.2mm.s	21.1	2.928	5.3-42.2	90.88	65.16	38.33	45.27	71.7	14.1	66.95

Abbreviations: SE: Standard Error; σ^2p: Phenotypic Variance; σ^2g: Genotypic Variance; GCV: Genotypic Coefficient of Variance; PCV: Phenotypic Coefficient of Variance; H^2: Broad Sense Heritability; GA: Genetic Advance; GAM: Genetic Advance of Mean Express As Percentage; GF: Grain Filling; DM: Days to Maturity; GY: Grain Yield; PH: Plant Height; HI: Harvest Index; TKW: Thousands Seed Weight; GC: Germination Capacity; GE: Germination Energy; Pr: Protein; st: starch; Ex: Extract

Table 2: Genotypic (below diagonal) and phenotypic (above diagonal) correlation coefficient of 14 quantitative characters of malt barley varieties at Mekedella 2016/2017.

Characters	DH	DM	GF	BM	HI	GY	SKW	PH	SPS	HLW	GE	Protein	Starch	Extract
DH	1	-0.35*	-0.30*	0.32*	-0.93**	-0.43**	-0.28**	-0.16	0.02ns	-0.17ns	-0.01ns	0.12ns	0.11ns	-0.04ns
DM	-0.42*	1	0.18ns	-0.02ns	0.36**	0.78**	0.38**	0.64**	0.37ns	-0.19ns	-0.12ns	-0.17ns	0.19ns	0.12ns
GF	-0.48*	0.39ns	1	-0.13ns	0.27*	0.75**	0.09ns	0.12ns	0.1ns	0.11ns	-0.02ns	-0.2ns	0.03ns	-0.1ns
BM	0.47*	-0.22ns	-0.52*	1	0.04ns	-0.09ns	0.02ns	0.02ns	0.05ns	-0.11ns	-0.28ns	0.15ns	-0.07ns	0.06ns
HI	-0.97*	0.4ns	0.38ns	-0.23ns	1	0.42*	0.30*	0.17ns	0.23ns	0.13ns	-0.1ns	-0.06ns	-0.14ns	0.07ns
GY	-0.55*	0.78**	0.88**	-0.47*	0.48ns	1	0.31*	0.49*	0.31ns	-0.08ns	-0.11ns	-0.24ns	0.12ns	0.02ns
SKW	-0.3ns	0.25ns	0.18ns	-0.32ns	0.18ns	0.20ns	1	0.40*	-0.08ns	-0.16	-0.09ns	0.08ns	-0.18ns	0.1ns
PH	-0.2ns	0.65*	0.18ns	-0.12ns	0.2ns	0.43ns	0.46ns	1	0.21ns	-0.3	0.04ns	0.22ns	-0.12ns	0.01ns
SPS	0.25ns	0.34ns	0.34ns	-0.21ns	-0.06ns	0.39ns	-0.2ns	0.05ns	1	-0.1	-0.08ns	-0.25ns	0.12ns	0.03ns
HLW	0.02ns	-0.22ns	0.02ns	-0.17ns	-0.02ns	-0.17ns	-0.28ns	-0.41ns	-0.05ns	1	-0.28ns	-0.14ns	0.03	0.12ns
GE	-0.3ns	0.12ns	0.27ns	-0.36ns	0.25ns	0.24ns	0.28ns	0.36ns	0.28	-0.46	1	-0.02ns	0.02ns	0.04ns
Pro	0.21ns	-0.1ns	-0.24ns	0.26ns	-0.16ns	-0.21ns	-0.01ns	0.35ns	-0.4	-0.23	-0.3	1	-0.67ns	0.02ns
Sta	0.24ns	0.02ns	-0.13ns	-0.16ns	-0.31ns	-0.08ns	-0.22ns	-0.25ns	0.15ns	0.12ns	0.2ns	-0.67ns	1	-0.08ns
Extra	0.08ns	-0.15ns	-0.2ns	0.3ns	0.2ns	-0.21ns	0.03ns	-0.1ns	-0.11ns	0.28ns	-0.17ns	0.14ns	-0.26ns	1

Abbreviations: DH: Days to Heading; DM: Days to Maturity; GF: Grain Filling; BM: Biomass; HI: Harvest Index; GY: Grain Yield; SKW: Thousand kernel Weight; PH: Plant Height; SPS: Seed Per Spike; HLW: Hictoliter Weight; GE: Germination Energy; Pro: Protein; Sta: Starch; Extra: Extract

that improvements of characters of the variety genetic condition for new generation compare with base population under the first cycle selection is 0.28% at 5% selection intensity as the same time at high genetic advance the new population compare with the base population under first cycle selection 24.45% at 5% section intensity.

Phenotypic and genotypic correlation of grain yield with other related characters

Estimation of genotypic (r_g) and phenotypic (r_p) correlations between the yield and quality character is presented in Table 2.The result of phenotypic correlation coefficient indicated that

Table 3: Estimation of phenotypic path coefficient direct (diagonal) and indirect effects of 10 characters of malt barley on grain yield conducted at Mekedela 2016.

Variable	DH	DM	GF	BM	HI	TKW	PH	Protein	Starch	Extract	GY(rp)
DH	-0.0372	-0.2389	-0.1887	0.0058	0.0262	0.0001	0.0040	0.0000	-0.0013	0.0000	-0.43**
DM	0.0130	0.6826	0.1132	-0.0004	-0.0101	-0.0001	-0.0160	0.0001	-0.0022	0.0000	0.78**
GF	0.0112	0.1229	0.6289	-0.0024	-0.0076	0.0000	-0.0030	0.0001	0.0000	0.0000	0.75
BM	-0.0119	-0.0137	-0.0818	0.0182	-0.0011	0.0000	-0.0005	-0.0001	0.0008	0.0000	-0.09
HI	0.0346	0.2457	0.1698	0.0007	-0.0281	-0.0001	-0.0043	0.0000	0.0016	0.0000	0.42
TKW	0.0104	0.2594	0.0566	0.0004	-0.0084	-0.0003	-0.0100	0.0000	0.0021	0.0000	0.31*
PH	0.0060	0.4369	0.0755	0.0004	-0.0048	-0.0001	-0.0250	-0.0001	0.0014	0.0000	0.49*
Pro	-0.0045	-0.1160	-0.1258	0.0027	0.0017	0.0000	-0.0055	-0.0004	0.0078	0.0000	-0.24
Sta	-0.0041	0.1297	0.0000	-0.0013	0.0039	0.0001	0.0030	0.0002	-0.0116	0.0000	0.12
Extra	0.0015	0.0819	-0.0629	0.0011	-0.0020	0.0000	-0.0003	0.0000	0.0009	-0.0003	0.02

(0.0840)

Abbreviations: **; and * highly significant at 0.01% and 0.05%; level respectively; rp: Phenotypic Correlation. DH: Days to Heading; DM: Days to Maturity; GF: Grain Filling. BM: Biomass; HI: Harvest Index; SKW: Thousand Kernel Weight. PH: Plant Height. Pro: Protein; Sta: Starch; Extra: Extract.

grain yield were positively and highly correlated with certain characters. Wasif et al. [21], Reported that the significant correlation of plant height with grain yield which supported our findings. However, the author's finding also contradicted with the results of thousand seed weight and harvest index which had insignificantly correlation with grain yield. Days to heading (-0.43) negatively and highly correlated with grain yield. Balcha and Ahmadi et al. [22,23], observed that grain yield were negatively correlated with days to heading. These correlations indicated that varieties had an ability to escape moisture deficit. Grain yield insignificantly and negatively correlated with hectoliter weight, germination energy, protein and biomass and also insignificantly and positively correlated with the rest of the characters, which means improving of those characters would not help for grain yield improvement. According to Quan. [24], biomass was positively correlated with grain yield, which is contradicted to our findings. The phenotypic correlation coefficients (PCC) were less in magnitudes than genotypic correlation coefficient (GCC) which revealed the presence of high genetic relationship among the difference. Improve the maturity dates showed substantial yield increments since yield and days to maturity positively and significantly correlated. Days to heading with days to maturity (-0.35), and grain filling (-0.30) correlated significantly. These indicated that early heading date along with long time of maturity give reasonable yield at moisture deficits area. Here the crop tried to escape the stress [25].

At genotypic correlation coefficient days to maturity (0.78) and grain filling (0.88) positively and highly correlated with grain yield. The results of these findings were supported by Briggs. [13], grain yield were positively correlated with days to maturity, grain filling and plant height. Grain yield negatively and significantly correlates with days to heading (-0.55) and biomass (-0.47). These finding is similar with [22], these indicates that delayed days to heading and high biomass decrease grain yield, which means characters were highly compete the starch synthesis and biomass building. These might imply the varieties were stressed at the time of heading then plants forced to escape for grain filling for early reproduction.

Phenotypic and genotypic path coefficient analysis on grain yield

Phenotypic and Genotypic path coefficient analysis is presented in Table 3. The direct effect of characters on grain yield showed that the relationships between the characters were good contributors to the ultimate grain yield and these characters were the main component in the improvement of the grain. The positive association direct effect of biomass with grain yield supported by Alemu Dabi. [25], but contradict idea with Mitsiwa [26]. In the phenotypic path coefficient analysis of these finding revealed that improving date of maturity and grain filling were the main contributor to improve grain yield of malt barley variety. Days to heading, thousands seed weight, protein, starch, and extract were negative direct effect that influence on grain yield. The negative direct effects of the above characters on grain yield indicate that improving these characters should not help. The association of plant height was positive but the direct effect were negative these indicate that the negative direct effect influenced by the counterbalance indirect effect of plant height through days to maturity (0.4369). The phenotypic path coefficient residual value is low (0.0840), which indicates the characters in phenotypic path analysis explain 91.6% the variation on grain yield. It is suggest that maximum emphasis should be given the above character in selection of malt barley variety [27,28].

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