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Applicability of joint regression and biplot models for stability analysis in multi-environment barley (*Hordeum vulgare*) trials

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ABSTRACT

GGE and AMMI biplot methods with Eberhart and Russell regression model were applied on the set of 18 barley (*Hordeum vulgare* L.) genotypes grown in 6 environments for quick and relevant method *vis-a-vis* to delineate genotype by environment interaction, stable genotypes and environmental discrimination. The average grain yield over the locations was depicted as 41.97 q/ha, which ranged from 31.82 (Karnal) to 55.52 q/ha (Bhatinda). The genotype DWRB 91 (47.51 q/ha) exhibited the highest grain yield followed by DWRB 121 (46.35 q/ha), DWRB 123 (46.04 q/ha) and DWRB 128 (44.70 q/ha) over the locations. In Eberhart and Russell model, the genotypes DWRB 124 and PL 880 were found suitable for favourable environments and DWRB 128 for poor environments. In AMMI analysis, IPCA 1 and IPCA 2 altogether captured 74.73% of the interaction mean squares, while in GGE biplot, PC 1 and PC 2 captured 36.51% and 26.44% interaction variation,respectively. The genotypes BH 992, DWRB 121, DWRB 123, RD 2897 and checks BH 902 and DWRB 91 were high yielding and as well as found stable in GGE and AMMI 1 biplot. The test environments Durgapura and Modipuram exhibited different niches, whereas, Hisar, Ludhiana, Bhatinda and Karnal were representative with better discriminating ability. Between biplot models applied, the GGE biplots were clear in visualization for polygon view, genotypic stability and environmental discrimination. The GGE method considered both G+GE for biplot generation and found most suitable for stability analysis.

Key words: AMMI and GGE biplots, GEI, Joint regression method, Stability

Barley (*Hordeum vulgare* L.) is a primitive sacred cereal grain, which contributes nearly 11-12% of the global coarse cereals production (Kumar *et al*. 2013, FAOSTAT 2016). During 2014, globally amongst cereals barley occupied fourth rank with 144.33 mt production, after maize (1021.61 mt), rice (740.95 mt) and wheat (728.96 mt) (FAOSTAT 2016). As per continents during 2014, the Europe ranked first with 64.8% of the total global barley production, while the highest production and productivity were showed by Russian Federation (20.44 mt) and Belgium (92.09 q/ha), respectively. The continent Asia produced 13.6% of the total world barley production and of which 9-9.5% was contributed from India. In India, barley is an important *rabi*, coarse cereal crop and always liked by marginal and small farmers, due to its better adaptability to problematic soils and low input requirements (Kumar *et al*. 2014).With urbanization, high living standards and open economy, barley demand is on rise for malting and brewing industry with an increase of consumption of health drinks, beer and similarly for other malt based products in India.

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Barley being self-pollinated crop the several advanced high yielding breeding lines after stringent selections being tested on multi-locations to culminate into superior varieties for further cultivation on farms. However, the changed relative ranking of these high yielding promising genotypes over the environments is always prime concern in genetic improvement. The unequal ranks over the environments are due to the occurrence of genotype × environment interaction (GEI), which is inevitable and restricts selection and further recommendation of varieties for the targeted environments (Asfaw *et al*. 2009, Kuchanur *et al*. 2015). To find out stable genotypes, several stability models based upon parametric, non-parametric and multivariate approaches stability were proposed and have been further reported by Flores *et al*. (1998) and Alwala *et al*. (2010). Some of these methods are Finlay and Wilkinson (1963), Eberhart and Russell (1966), Shukla (1972), Lin and Binns (1988), Gauch (1988), Yan *et al*. (2000) etc. Out of these models earlier the joint regression model of Eberhart and Russell was widely used in farm trials for stability analysis. However, biplot based models are present day popular methods for genotype by environment analysis because of quick view, mega environment delineation and environmental discrimination. The additive main effects and multiplicative interaction (AMMI) and genotype + genotype

by environment interaction (GGE) are visual biplots based on singular value decomposition (SVD) and biplot concepts (Gabriel 1971). AMMI is doubly-centered principal components (PC) model, refers SVD to the data minus the genotypic and environmental means, while GGE is environment-centered PC model, applies SVD to the data deducting the environment means (Gauch 2006). The GGE biplot model is further modification of AMMI, and considers the effects of the genotypes simultaneously with the G × E interaction, whereas, AMMI estimates these effects as additive effects (Sousa *et al*. 2015). Therefore, the present study was undertaken with 18 barley genotypes grown at 6 diverse production conditions to assess the genotype by environment interactions, identify stable genotypes, discriminating and representative environments *vis-a-vis* for the suitability of joint regression, AMMI and GGE methods for stability analysis.

MATERIALS AND METHODS

During *rabi*, 2013-14, the multi-environment trials (MET) were conducted at 6 diverse locations namely Durgapura (E1), Hisar (E2), Ludhiana (E3), Bhatinda (E4), Karnal (E5) and Modipuram (E6). The experimental material comprised 18 barley genotypes (Table 1), viz. BH990 (G1), RD2895 (G2), RD2896 (G3), RD2898 (G4), DWRB123 (G5), DWRB124 (G6), DWRB126 (G7), RD2897 (G8), PL880 (G9), DWRB125 (G10), PL881 (G11), DWRB128 (G12), DWRB91 (G13), BH902 (G14), DWRUB64 (G15), BH992 (G16), DWRB121 (G17) and BH991 (G18).

Out of 18 genotypes, 15 were advanced experimental strains and three were the commercial cultivars, i.e. G13, G14 and G15. The experiments were conducted in randomized complete block design (RCBD) in four replications having 6-row plots with row to row spacing of 18cm and row length of 5 m. All the standard package and practices were adopted to raise the good crop.The GGE and AMMI biplots were generated using Gen Stat 17.1 and Eberhart and Russell regression analysis was performed using SPAR. The brief models for regression analysis, AMMI and GGE biplots are as given below-

Linear regressions for each of the 18 genotypes were computed and the grain yield of each genotype at each location was regressed over the means of all genotypes at each of the 6 locations. The regression model was as followed -

$$Y_{ij} = \mu_i + b_i I_j + \delta_{ij} \quad (1)$$

In formulae (1), Y_{ij} is the yield of i^{th} genotype in j^{th} environment, μ is the yield of i^{th} genotype in overall environment, b_i represents the regression coefficient of i^{th} variety in varying environments, I_j denotes environmental index and $ä_{ij}$ is deviation from the regression of i^{th} variety at the j^{th} environment.

The deviations were squared and summed to draw estimates of deviation mean square (S^2d_i)-

$$\hat{S}^2d_i = [\sum_j \delta_{ij}^2/(n-2)] - S^2_e/r \quad (2)$$

where, S^2_e/r is the pooled error, n and rdenotes number of environments and replications, respectively.

Data were subjected to ANOVA and SVD in both AMMI (3) and GGE models (4). The AMMI model is doubly centered PCA and written as (Gauch 2006,Gauch*et al*. 2008)-

$$Y_{ijr} - \alpha_i - \beta_j + \mu = \sum_n \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij} + \varepsilon_{ijr} \quad (3)$$

The GGE biplot is based on Sites Regression (SREG) linear-bilinear multiplicative model and is environment centered (Yan *et al*. 2000). The GGE model is written as-

$$Y_{ijr} - \beta_j = \sum_n \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij} + \varepsilon_{ijr} \quad (4)$$

Table 1 Origin and parentage of 18 barley genotypes

Genotype	Code	Origin	Parentage
BH 990	G1	CCSHAU, Hisar	NDB1281/BH674
RD 2895	G2	RARI, Durgapura	DWR39/RD2651//RD2668
RD 2896	G3	RARI, Durgapura	CONGONA/BLLU//RD2668
RD 2898	G4	RARI, Durgapura	DWR46/RD2651//PL508
DWRB 123	G5	ICAR-IIWBR, Karnal	DWRUB54/DWR51
DWRB 124	G6	ICAR-IIWBR, Karnal	DWRUB54/DWRUB64
DWRB 126	G7	ICAR-IIWBR, Karnal	DWRUB62/BCU5754
RD 2897	G8	RARI, Durgapura	RD2035/IBON-6//DWR39
PL 880	G9	PAU, Ludhiana	PL426/BC473
DWRB 125	G10	ICAR-IIWBR, Karnal	DWRUB54/RD2668
PL 881	G11	PAU, Ludhiana	PL426/K537
DWRB 128	G12	ICAR-IIWBR, Karnal	DWRUB54/DWRUB75
DWRB 91	G13	ICAR-IIWBR, Karnal	DWR46/RD2552
BH 902	G14	CCSHAU, Hisar	BH495/RD2552
DWRUB 64	G15	ICAR-IIWBR, Karnal	DL472/PL705
BH 992	G16	CCSHAU, Hisar	RD2660/DWRUB52
DWRB 121	G17	ICAR-IIWBR, Karnal	DWRUB52/DWR28
BH 991	G18	CCSHAU, Hisar	28^{th}IBYT-3/RD2668

where, Y_{ijr} is the yield of genotype (i) in environment (j) for replicate r, μ is the grand mean, α_i represents genotype deviation, β_j denotes environment deviation, λ_n is singular value for component n, λ_{in} is the eigenvector value for i, $\delta_{jn}$is the eigen vector value for j, the residual is ρ_{ij} and ε_{ijr} is the error for genotype i, environment j and replicate r.

The AMMI stability value (ASV) values were also computed (Rad *et al*. 2013)-

$$ASV= \sqrt{[(SSIPCA1/SSIPCA2)(IPCA1score)]^2 + (IPCA score2)^2} \quad (5)$$

In equation 5, SSIPCA1/SSIPCA2 is the value by dividing the IPCA1 SS by the IPCA2 SS and IPCA1 and IPCA2 scores are the genotypic scores in the AMMI model.

RESULTS AND DISCUSSION

Analysis of variance for each location depicted significant genotypic mean squares and the pooled analysis of variance also revealed highly significant differences among genotypes and locations (P<0.001), indicating the presence of significant genetic and environmental variation. The G × E interaction mean squares were also significant and revealed the differential performances of the genotypes across the locations. The average grain yield over the locations was depicted as 41.97 q/ha, which ranged from 31.82 (Karnal) to 55.52 (Bhatinda) q/ha. Location-wise the highest mean grain yield was exhibited at Bhatinda (55.52 q/ha) followed by Durgapura (48.01 q/ha), Hisar (46.93 q/ha), Ludhiana (35.91 q/ha) locations etc. The genotype DWRB91 (47.51 q/ha) exhibited the highest grain yield followed by DWRB 121 (46.35 q/ha), DWRB 123 (46.04 q/ha), DWRB 128 (44.70 q/ha) etc. over the locations (Table 2).

Table 2 Stability parameters of Eberhart and Russell joint regression model

Genotype	Code	μ(Q/ha)	bi	S^2d_i
BH 990	G1	37.22	0.50	23.98
RD 2895	G2	36.35	0.46	67.35
RD 2896	G3	41.27	0.64	49.05
RD 2898	G4	41.74	1.29	16.00
DWRB 123	G5	46.04	1.09	-3.58
DWRB 124	G6	44.48	0.87	18.31
DWRB 126	G7	41.96	0.97	76.38
RD 2897	G8	43.16	1.33	26.11
PL 880	G9	43.18	1.16	9.23
DWRB 125	G10	41.63	1.03	12.48
PL 881	G11	37.97	1.00	105.69
DWRB 128	G12	44.70	0.64	41.58
DWRB 91	G13	47.51	1.38	16.87
BH 902	G14	43.02	1.05	10.71
DWRUB 64	G15	40.69	1.28	5.24
BH 992	G16	43.72	1.16	53.29
DWRB 121	G17	46.35	1.24	46.78
BH 991	G18	34.56	0.90	37.03
GM±SE	41.97±2.76	1±0.29		

Eberhart and Russell joint regression analysis

G × E interaction mean squares were further partitioned into linear and non-linear (pooled deviation) components. The linear interactions exhibited significant variation among the genotypes over the locations. The genotypes DWRB123 (μ=46.04 q/ha, b=1.09 and S^2d_i=3.58), DWRB124 (μ=44.48 q/ha, b=0.87 and S^2d_i=18.31) and BH902 (μ=43.02 q/ha, b=1.05 and S^2d_i=10.71) showed high mean grain yield accompanied with regression coefficient near to unity and exhibited low deviation from the regression (Table 2). Whereas, the genotypes BH992, DWRB91, DWRB121, PL 880 and RD 2897 depicted high grain yield with suitability for favourable environments, while the genotype DWRB128 was found better for poor environments.

AMMI analysis

Significant mean squares were exhibited for genotype (g), location (l) and genotype × location interaction (gl) in AMMI ANOVA (Table 3). The overall treatments mean squares (g+l+gl) explained significant variation (90.36%) of the total mean squares. The location effect showed 63.68% of the variation followed by genotype × location interaction (26.28%) and genotypic variation (10.04%), respectively (Table 3). The significant interaction again confirmed of changed relative rankings of genotypes over the locations. First two interaction components, i.e. IPCA 1 and IPCA 2 were found significant (P<.001) and explained for 56.28 and 18.45 % of the interaction mean squares, respectively. First two interaction principal components best explains the interaction sum of squares (Yan and Tinker 2006).

The genotypes, viz. G5 (DWRB 123), G6 (DWRB 124), G8 (RD 2897), G12 (DWRB 128), G13 (DWRB 91), G16 (BH 992) and G17 (DWRB 121) revealed low IPCA 2 scores and the environments E1 (Durgapura), E4 (Bhatinda) and E6 (Modipuram) depicted high IPCA 1 scores. AMMI stability values (ASV) were also calculated to determine stability of the genotypes and the genotypes with low ASV scores were considered as the consistent performers (Table 4). The genotypes DWRB 123 (0.58), DWRUB 64 (0.89), BH 902 (1.20), DWRB 125 (1.55), PL 880 (1.59), RD 2898 (2.99), BH 990 (3.21), DWRB 124 (3.40), RD 2896 (3.52) etc. showed low ASV. Based on IPCA 1 and IPCA 2 scores of ordinates with main effects on absicca and plotting of IPCA 1 with

Table 3 ANOVA for AMMI model

Source	df	SS	MS	F Pr	% SS
Total	431	56739.00	131.60		
Treatments	107	51271.00	479.20	<0.001	90.36
Genotypes	17	5149.00	302.90	<0.001	10.04
Environments	5	32649.00	6529.80	<0.001	63.68
Block	18	321.00	17.80	0.393\	
Interactions	85	13473.00	158.50	<0.001	26.28
IPCA 1	21	7583.00	361.10	<0.001	56.28
IPCA 2	19	2486.00	130.80	<0.001	18.45
Residuals	45	3403.00	75.60	<0.001	
Error	306	5147.00	16.80		

Table 4 Genotypic and environmental grain yield *per se* with AMMI IPCA scores and ASV

Genotype	Code	Mean (q/ha)	IPCA 1	IPCA 2	ASV	Environment	Code	Mean (Q/ha)	IPCA1	IPCA2
BH 990	G1	37.22	-0.84	-1.92	3.21	Durgapura	E1	48.01	-5.57	-0.51
RD 2895	G2	36.35	2.49	0.26	7.61	Hisar	E2	46.93	0.03	-1.15
RD 2896	G3	41.27	0.48	-3.20	3.52	Ludhiana	E3	35.91	0.14	1.90
RD 2898	G4	41.74	-0.98	-0.19	2.99	Bhatinda	E4	55.52	1.75	3.35
DWRB 123	G5	46.04	-0.15	0.36	0.58	Karnal	E5	31.82	0.65	-0.78
DWRB 124	G6	44.48	1.11	-0.13	3.40	Modipuram	E6	33.66	3.00	-2.81
DWRB 126	G7	41.96	2.47	1.41	7.67					
RD 2897	G8	43.16	-1.47	0.15	4.50					
PL 880	G9	43.18	0.24	1.42	1.59					
DWRB 125	G10	41.63	-0.37	-1.07	1.55					
PL 881	G11	37.97	2.56	-0.85	7.86					
DWRB 128	G12	44.70	1.99	0.29	6.09					
DWRB 91	G13	47.51	-1.59	1.11	4.97					
BH 902	G14	43.02	-0.03	1.20	1.20					
DWRUB 64	G15	40.69	0.18	0.69	0.89					
BH 992	G16	43.72	-2.26	0.56	6.91					
DWRB 121	G17	46.35	-2.14	0.77	6.56					
BH 991	G18	34.56	-1.72	-0.86	5.30					

IPCA 2 scores, AMMI1 and AMMI2 biplots were also obtained as per statistical analysis, respectively. After perusal of AMMI1 and AMMI2 biplots the genotypes, viz. DWRB 91, DWRB 121, DWRB 123, DWRB 124, DWRB 128, and RD 2897 were observed with high additive main effects and low interaction effects. While, the environments E1 and E4 were found with high interaction and main effects.

GGE analysis

Two principal components PC 1 and PC 2 accounted for total of 62.95% variation in GGE biplot analysis. In which won where pattern, the vertex genotypes were viewed as BH991, BH992, DWRB91, DWRB128, PL881 and RD2895. Equality lines of polygon indicated that BH992 was better performer at E1 (Durgapura), whereas DWRB91, DWRB124 and DWRB128 won at E5 (Karnal), E4 (Bhatinda) and E6 (Modipuram), respectively (Fig 1). The 6 environments were classified into the four different mega environments. The environments E2 (Hisar) and E3 (Ludhiana) were grouped together, while E4 (Bhatinda) and E5 (Karnal) represented the same group. Whereas, environments E1 (Durgapura) and E6 (Modipuram) created separate mega environments.

In AEC (Average Environment Coordination) view, the genotypes DWRB91 > DWRB121 > BH992 > RD2897 > DWRB123 > PL880 > BH902 were preferred as depicted high values on absicca and low interaction with less ordinate values. The genotypes BH990, BH991, PL881 and RD2895 were considered as poor performers as having low AEC absicca indicated the low grain yield *per se* across the locations.The desired genotypes had the high *per se* and stable performance in different environments (Yan and Tinker 2006). The environments E1 and E6 were found discriminating with long vectors, while the environments E2, E3, E4 and E5 revealed acute angles. Yan *et al*. (2000) and Yan and Tinker (2006) also emphasized that the environments with long vectors and less cosines are more discriminating and representative for consideration in future studies. Whereas, taking in account the discriminating ability and representativeness the environments Hisar,

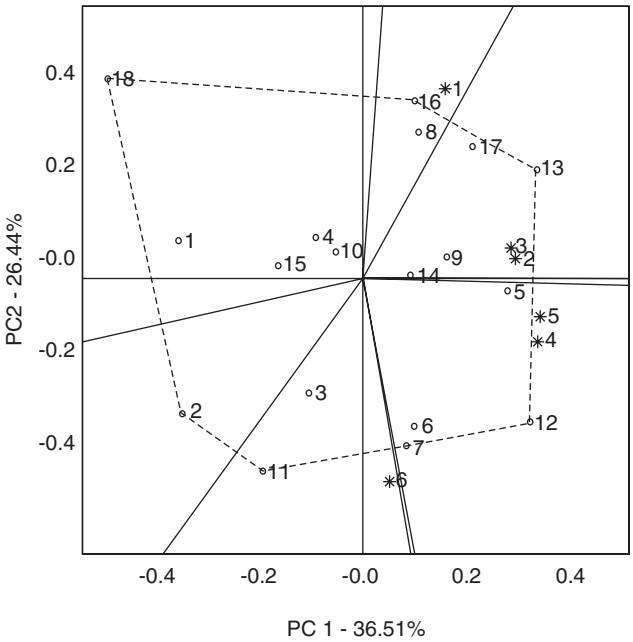

Fig 1 Which won where pattern in polygon view in GGE model *represents environments [Durgapura (E1), Hisar (E2), Ludhiana (E3), Bhatinda (E4), Karnal (E5) and Modipuram (E6)] and dot for genotypes [BH990 (G1), RD2895 (G2), RD2896 (G3), RD2898 (G4), DWRB123 (G5), DWRB124 (G6), DWRB126 (G7), RD2897 (G8), PL880 (G9), DWRB125 (G10), PL881 (G11), DWRB128 (G12), DWRB91 (G13), BH902 (G14), DWRUB64 (G15), BH992 (G16), DWRB121 (G17) and BH991 (G18)] in Fig 1&2

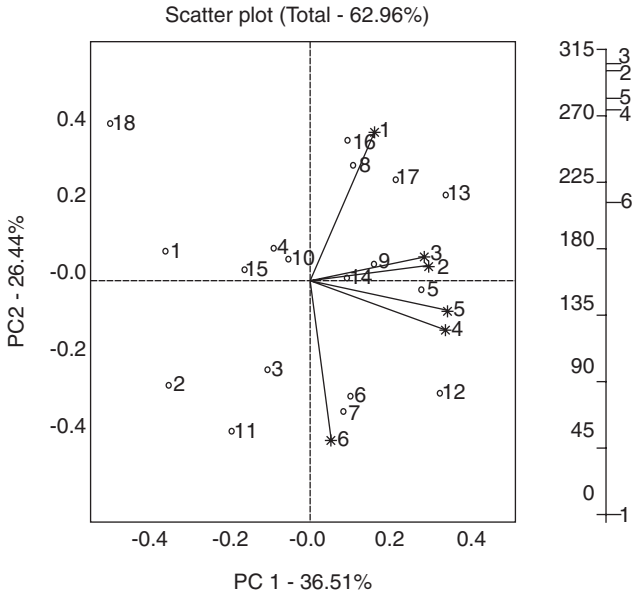

Fig 2 Test environments evaluation for discrimination and representativeness in GGE model.

Ludhiana, Bhatinda and Karnal were regarded as potential environments (Fig 2). The environments Durgapura and Modipuram were negatively correlated and exhibited separate niches from rest of the locations.

Delivering a high yielding and stable genotype over the environments is one of the prime objectives for plant breeders (Kuchanur *et al*. 2015). In AMMI analysis the genotypes BH902, BH992, DWRB91, DWRB121, DWRB123, DWRB124, DWRB128 and RD2897 were considered with low interaction effects. While also considering the AMMI stability values the genotypes BH902, DWRB91, DWRB123, DWRB124 and RD2897 were regarded with high main effects, low IPCA 2 scores and ASV. In two dimensional views, the ASV is the distance of the coordinate point from the origin for IPCA 1 scores against IPCA 2 scores in the AMMI model (Rad *et al*. 2013). In regression model, the genotypes namely BH902, DWRB123 and DWRB124 exhibited stable performance, while no information for environmental specific genotypes and environmental interactions could be generated. Eberhart and Russell model is widely adapted method but with inclusion of more number of genotypes and simultaneously the assumption of linear response of genotypes to environments restricts its application (Flores *et al*. 1998).

GGE biplot method is environment centered SVD model and graphically addresses which won where, genotypic stability and environmental discrimination etc. (Yan *et al*. 2000). The polygon view of GGE-biplot is very quick way to visualize the interaction patterns between genotypes and environments (Dehghani *et al*. 2006, Yan *et al*. 2007). In the present study the genotypes BH992, DWRB91, DWRB121, DWRB123, RD2897 etc. depicted high yield and low interaction with less ordinate values.Based on environmental vector lengths and cosine between environments the discriminating and representative environments were also studied. Discriminating and representative environments are useful to plant breeders to drop the non-informative environments and to curtail the financial cost. The environments Hisar, Ludhiana, Bhatinda and Karnal were discriminating and representative.

For visualization, GGE model was effective for polygon view and especially for environmental discrimination. It has been also emphasized by Yan *et al*. (2007) that GGE biplots are better for visualization, accommodating more number of genotypes and environments, test environment representativeness and discrimination, depiction of same units at absicca and ordinates etc. Silva *et al.* (2016) and Villegas *et al*. (2016) also used GGE biplots and reported that the method is very useful for biplots visualization and generates ample information for test sites and genotypic evaluation.

In conclusion, the present study indicated the significant effects for G, E and GEI and GEI also changed genotypic ranks over the locations. The genotypic selection in consensus was difficult for stability, however the genotypes BH992, DWRB121, DWRB123, RD2897 and checks BH902 and DWRB91 were found high yielding and consistent. The environments Durgapura, and Modipuram were different from rest of the environments and Hisar, Ludhiana, Bhatinda and Karnal were representative with better discriminating ability.The GGE model found suitable for stability analysis and biplotsgenerated werealso easy to view polygon, genotypic interactions and environmental ranks.

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