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Investigation on association analysis of quantity and quality traits of rice (*Oryza sativa* L.) landraces

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Abstract

Investigated were the relationships between different yield features and the pattern of influences on rice grain yield. In order to establish selection criteria for a greater grain yield, it is crucial to evaluate the direct and indirect impacts of different features on yield. A randomized complete block design was used to examine 23 rice landrace genotypes. According to the results of the character association analysis, there is a substantial strong correlation between the number of productive tillers per plant, the harvest index, the number of fertile spikelets per panicle, and the biological yield. Path coefficient analysis expressed that number of fertile spikelets per panicle, panicle length, days to 50% flowering, number of tillers per plant, thousand grain weight and biological yield were showing high positive effect on the grain yield per plant. For accurate selection, it is necessary to validate important yield- and quality-related factors by molecular characterization of the rice genotypes.

Keywords: Rice, correlation, path coefficient analysis, grain yield and direct effect

Introduction

For around half of the world population, rice is considered to be primary source on energy intake. Over a hundred of nation's farm rice on around 158 million hectares, which yielding 470 million tons of white rice per year (Anonymous, 2021) [23]. Rice landraces have been farmed and nourished since the dawn of civilization, and they play a critical role in livelihood and food security. Rice landraces have a wide range of agro-morphological characteristics, and some of them show promise in terms of yield. Some rice landraces provide surprising health benefits such as protection against several chronic diseases such as cardiovascular disease, type-2 diabetes, obesity, cancer and have the potential to heal certain disorders like hemorrhage, diarrhoea, fertility, fever and many more (Sanghamitra *et al.*, 2017 [24], Pokhrel *et al.*, 2020) [12]. Due to the increasing awareness of health benefits in rice landraces, there is a rising need for the rice variety with good cooking and nutritive qualities (Asghar *et al.*, 2012) [15]. There always been a need for increase in the food production to curtail the hunger of raising human population. Though the rice landraces have a low yielding potential, they are believed to have more local adaptability and better-quality traits (Tiwari *et al.*, 2014) [20]. The breeder can determine the size and direction of selection for the enhancement of the character with the use of correlation studies, which offer information on the kind and degree of link between yield and its component qualities. Plant breeders can rank the hereditary traits according to the contribution they make according to path coefficient analysis, which further divides the correlation coefficients into direct and indirect impacts (Nanda *et al.*, 2019) [1]. The purpose of the current study is to determine the nature of the relationship between grain yield and quality traits, the direct and indirect contributions of these components to grain yield, and the best combinations of these yield components to use as selection criteria for creating high yielding rice genotypes using rice landraces.

Materials and Methods

The present investigation was conducted during the *kharif*-2021 at Bagusala farm, Centurion University of Technology and Management, Parlakhemundi, Odisha. In terms of topography and fertility, the experimental area was rather uniform. Coordination is the location. 84.139883°E, 18.806853°N. The experimental material consists of 23 germplasm lines of rice genotypes obtained from Seed Farms from Telangana (Table 1). These lines were laid out in a randomized block design and planted in the spacing 20 X 20 cm with three replications.

The recommended package of practices was followed to raise a normal crop, including irrigation with alternate wetting and drying and necessary plant protection measures. Fertilizers

were applied to the main field at the rate of 150:50:50 NPK kg/ha at different crop stages including transplanting, early tillering and booting stage.

Table 1: List of Rice Landraces

S. No	Genotypes	Sources
1	Thalam Gour	JVKS Agrotech Pvt. Ltd, Telangana
2	Phodisi	JVKS Agrotech Pvt. Ltd, Telangana
3	Halla batta	JVKS Agrotech Pvt. Ltd, Telangana
4	Jhadjadhan	JVKS Agrotech Pvt. Ltd, Telangana
5	Phuda Malu	JVKS Agrotech Pvt. Ltd, Telangana
6	Daddigha	JVKS Agrotech Pvt. Ltd, Telangana
7	Kaala Jeera	JVKS Agrotech Pvt. Ltd, Telangana
8	Krishtampeta gold	JVKS Agrotech Pvt. Ltd, Telangana
9	Dhomdha	Arsan Agro Business Pvt. Ltd, Telangana
10	Kukuda Munde	Arsan Agro Business Pvt. Ltd, Telangana
11	Mudimuringi	Arsan Agro Business Pvt. Ltd, Telangana
12	Nagara	Arsan Agro Business Pvt. Ltd, Telangana
13	Pohaki	Arsan Agro Business Pvt. Ltd, Telangana
14	Eesakawada	Arsan Agro Business Pvt. Ltd, Telangana
15	Ghalima	Arsan Agro Business Pvt. Ltd, Telangana
16	Gadakadhiya Mahi	Arsan Agro Business Pvt. Ltd, Telangana
17	Kumar Gorla	Arsan Agro Business Pvt. Ltd, Telangana
18	Aashudhee	JMD Trading Groups, Telengana
19	Agma Kundha	JMD Trading Groups, Telengana
20	Bhairajlu	JMD Trading Groups, Telengana
21	Vedhuru Sanna	JMD Trading Groups, Telengana
22	Tharang	JMD Trading Groups, Telengana
23	Akshaya ponni	JMD Trading Groups, Telengana

Data recordings

The rice landraces were examined based on the 21 quantitative and quality traits. The data was collected on 1) days to 50% flowering, 2) days to maturity, 3) number of tillers per plant, 4) number of effective tillers per plant, 5) plant height, 6) panicle length, 7) number of fertile spikelets per panicle, 8) spikelet fertility, 9) panicle density, 10) thousand grain weight, 11) biological yield, 12) harvest index, 13) grain yield per plant, 14) grain length, 15) grain breadth, 16) kernel length breadth ratio, 17) elongation ratio, 18) water uptake ratio, 19) alkali spread value, 20) amylose content and 21) protein content. In these traits, protein content was estimated with Lowry's method, rest of traits were measured or recorded as per the guidelines of DUS (Distinctiveness, Uniformity and Stability) from Directorate of Rice Research (Shobha *et al.*, 2006) [9]. These data on 21 traits were recorded from 5 randomly selected representative plants in all the genotypes, except for the trait days to 50% flowering and days to maturity, where observation was made on plot-by-plot basis.

Data analysis

The data from the 21 quantitative and quality traits were analyzed in 'Studio (4.1.2)' using various packages. Correlation and Path Coefficient Analysis were done using the 'Variability' package.

Result and Discussion

Correlation analysis

Genotypic correlation showed, Days to maturity has significantly strong positive association ($r_g = 0.99$) to days to 50% flowering. Likewise, Panicle density ($r_g = 0.50$) and Water Uptake Ratio ($r_g = 0.51$) has significantly moderate positive association to days to 50% flowering and alkali

spread value ($r_g = 0.43$) has significantly moderate weak association to days to 50% flowering. Genotypically, number of tillers per plant ($r_g = 0.98$), number of fertile spikelets per panicle ($r_g = 0.65$), grain yield per plant ($r_g = 0.88$), biological yield ($r_g = 0.64$) and harvest index ($r_g = 0.68$) showed significantly strong and positive correlation with number of effective tillers per plant. Panicle density expressed weak but significant direct association with days to 50% flowering ($r_p = 0.27$) and days to maturity ($r_p = 0.24$) and moderately strong but inverse association with panicle length ($r_p = -0.54$), at Genotypic level. Unlike genotypic level, thousand grain weight has positive but moderately weak association with grain yield per plant ($r_p = 0.47$), biological yield ($r_p = 0.36$), harvest index ($r_p = 0.35$), spikelet fertility ($r_p = 0.35$) and grain breadth ($r_p = 0.31$); weak positive association with number of tillers per plant ($r_p = 0.29$), plant height ($r_p = 0.25$) and panicle length ($r_p = 0.23$), at phenotypic level.

Similarly, number of effective tillers per plant ($r_p = 0.58$), grain yield per plant ($r_p = 0.63$), plant height ($r_p = 0.79$), and number of tillers per plant ($r_p = 0.56$) were happen to have strong positive correlation with biological yield at phenotypic level also. Thousand grain weight ($r_p = 0.36$), number of fertile spikelets per panicle ($r_p = 0.38$) and grain breadth ($r_p = 0.29$) showed weak positive association but grain length showed weak negative association. Negative association has been seen on grain breadth ($r_p = -0.68$), panicle length ($r_p = 0.42$), elongation ratio ($r_p = 0.33$), grain yield per plant ($r_p = -0.28$), plant height ($r_p = -0.25$) and number of tillers per plant ($r_p = -0.24$), on which grain breadth was strong ($r_p = -0.68$); panicle length and elongation ratio were moderately weak, rest were weak. At genotypic level, only alkali spread value ($r_g = -0.48$) was significant correlation to amylose content, which was also moderately weak negative correlation. At genotypic level, protein content didn't show any significant correlation,

even though non-significant weak correlation seen on water uptake ratio ($r_g = 0.35$) and days to maturity ($r_g = 0.37$).

The analysis of character association concluded that the grain yield per plant has strong positive significant correlation with number of tillers per plant, number of effective tillers per plant, harvest index, number of fertile spikelets per panicle and biological yield; moderate strong and positive association was absorbed for grain breadth and thousand grain weight (Table 2). Thus, selection based on these traits will be help to improve grain yield per plant. A positive and substantial correlation was found between plant height and grain yield per plant. Sindhumole *et al.*, 2015 [18], Anyaoha *et al.*, 2018 [2] and Zafar *et al.*, 2020 [22] all confirmed this finding. Similarly, Fentie *et al.*, 2014 [5], Bhati *et al.*, 2015 [3], and Nikhil *et al.*, 2019 [10] found a positive and substantial relationship between biological yield and grain yield per plant. Grain yield per plant had a substantial and positive relationship with grain breadth. It agreed with the findings of Madhubabu *et al.*, 2020 [8]. Krishnamurthy *et al.*, 2016 [7], Edukondalu *et al.*, 2017 [4], Gour *et al.*, 2017 [6] and Thippani *et al.*, 2017 [19] found a positive and substantial relationship between number of tillers per plant and grain yield per plant.

Path Coefficient Analysis

At genotypic level revealed, the direct effect of various traits on the grain yield per plant revealed out of 20 traits, 14 traits gave positive direct effect and 6 traits gave negative direct effect. Among the positive traits, number of fertile spikelets per panicle, panicle length, days to 50% flowering, number of tillers per plant, thousand grain weight and biological yield were showing high effect on the grain yield per plant; alkali spread value and protein content were showing moderate effect; low effect was exhibited by the traits such as elongation ratio, grain length and panicle density, remaining positive traits like number of effective tillers per plant, kernel length breadth ratio and amylose content showed very low effect. Similarly, negative effects were shown by 6 traits. On

that, water uptake ratio, spikelet fertility and plant height were showing high negative effect and harvest index, days to maturity and grain breadth were showing moderately negative effect on grain yield per plant.

At phenotypic level, path coefficient analysis, out of 20 traits, 9 traits were showing positive effect and 11 traits were showing negative effect on grain yield per plant. In the traits with positive effect, only two have high effect i.e., number of effective tillers per plant and harvest index; number of fertile spikelets per panicle has moderate effect and low effect was shown by thousand grain weight, biological yield and plant height. Irrespective of the direction of effect, the rest of the traits were showing very effect only, which were days to 50% flowering, kernel length breadth ratio and protein content for positive effect and alkali spread value, grain breadth, amylose content, elongation ratio, panicle density, water uptake ratio, spikelet fertility, days to maturity, panicle length, number of tillers per plant and grain length.

Path coefficient analysis expressed that grain yield per plant has 14 traits gave positive direct effect and 6 traits gave negative direct effect, at genotypic level (Table 3). Among the positive traits, number of fertile spikelets per panicle, panicle length, days to 50% flowering, number of tillers per plant, thousand grain weight and biological yield were showing high effect on the grain yield per plant; alkali spread value and protein content were showing moderate effect; Similarly, negative effects were shown by 6 traits. On that, water uptake ratio, spikelet fertility and plant height were showing high negative effect and harvest index, days to maturity and grain breadth were showing moderately negative effect on grain yield per plant. Among the positive traits, number of fertile spikelets per panicle, panicle length, days to 50% flowering, number of tillers per plant, thousand grain weight and biological yield were showing high effect on the grain yield per plant. Similar results were reported by Yadav *et al.*, 2010 [21], Sindhumole *et al.* 2015 [18], Bhati *et al.* 2015 [3], Rashid *et al.* 2017 [14], Ranjith *et al.* 2018 [13] and Samudin *et al.* 2019 [16].

Table 2: Phenotypic and genotypic correlation coefficient estimate for 21 yield and quality traits

Characters		DFP	DM	NT	NET	PH	PL	NFSPP	SF	PD	TGW	BY	HI
		P	P	P	P	P	P	P	P	P	P	P	P
DFP		1**											
DM	G	0.999**	1**										
NT	G	-0.251	-0.315	1**									
NET	G	-0.278	-0.334	0.984**	1**								
PH	G	-0.127	-0.154	0.283	0.285	1**							
PL	G	-0.428*	-0.437*	0.242	0.238	0.731**	1**						
NFSPP	G	0.194	0.105	0.573**	0.645**	0.157	0.155	1**					
SF	G	0.081	0.023	0.002	-0.06	0.107	0.226	-0.006	1**				
PD	G	0.59**	0.58**	-0.01	-0.137	-0.299	-0.746**	0.318	-0.044	1**			
TGW	G	0.003	-0.073	0.364	0.285	0.262	0.304	0.153	0.443*	-0.203	1**		
BY	G	-0.144	-0.205	0.62**	0.641**	0.862**	0.588**	0.414*	0.231	-0.199	0.39	1**	
HI	G	0.063	-0.021	0.675**	0.678**	-0.233	-0.064	0.808**	-0.021	0.152	0.399	0.138	1**
GL	G	-0.089	-0.178	-0.151	-0.109	0.23	-0.15	-0.262	0.332	-0.043	0.078	0.215	-0.369
GB	G	-0.114	-0.138	0.398	0.409	0.403	0.472*	0.516*	-0.141	0.144	0.343	0.348	0.436*
KLBR	G	0.249	0.2	-0.342	-0.335	-0.254	-0.551	-0.173	0.331	0.224	-0.177	-0.155	-0.246
ER	G	-0.165	-0.155	-0.036	-0.193	0.347	0.698*	0.326	0.479*	-0.346	0.226	0.273	0.054
WU	G	0.512*	0.505*	-0.265	-0.366	-0.172	-0.397	0.034	0.066	0.27	-0.15	-0.065	-0.133
ASV	G	0.425*	0.323	-0.114	-0.224	-0.032	-0.429*	-0.108	0.178	0.461*	0.163	0.142	-0.163
AC	G	0.004	0.141	-0.073	0.014	-0.24	-0.208	-0.256	-0.177	-0.151	0.02	-0.274	0.008
PC	G	0.198	0.303	-0.174	-0.138	-0.016	0.089	-0.069	0.155	-0.23	-0.021	-0.082	-0.083
GYP	G	-0.03	-0.113	0.859**	0.881**	0.319	0.291	0.829**	0.06	-0.04	0.511*	0.639**	0.832**

*, ** significant at 5% and 1% level, respectively. Correlation at the phenotypic level (P) is indicated by a value above the unity diagonal, and correlation at the genotypic level (G) is indicated by a value below the unity diagonal

Table 2: Cont....

Characters		GL	GB	KLBR	ER	WU	ASV	AC	PC	GYP
		P	P	P	P	P	P	P	P	P
DFE	G	-0.075	-0.134	0.196	-0.123	0.349**	0.267*	0.006	0.196	-0.037
DM	G	-0.15	-0.145	0.145	-0.107	0.319**	0.194	0.109	0.246*	-0.116
NT	G	-0.152	0.323**	-0.245	-0.037	-0.203	-0.038	-0.037	-0.13	0.791**
NET	G	-0.096	0.277*	-0.219	-0.029	-0.141	-0.093	0.019	-0.079	0.821**
PH	G	0.216	0.327**	-0.251	0.195	-0.119	-0.017	-0.227	-0.016	0.293*
PL	G	-0.094	0.298*	-0.42**	0.437**	-0.203	-0.259*	-0.15	0.109	0.218
NFSPP	G	-0.244*	0.403**	-0.182	0.136	-0.014	-0.098	-0.24*	-0.063	0.759**
SF	G	0.23	-0.161	0.216	0.199	0.004	0.126	-0.152	0.093	0.095
PD	G	-0.08	0.017	0.13	-0.1	0.234	0.206	-0.096	-0.16	0.067
TGW	G	0.087	0.315**	-0.18	0.132	-0.133	0.152	0.012	-0.022	0.469**
BY	G	0.185	0.29*	-0.131	0.173	-0.033	0.135	-0.259*	-0.067	0.633**
HI	G	-0.326**	0.336**	-0.224	0.059	-0.073	-0.104	0.005	-0.06	0.835**
GL	G	1**	-0.294*	0.557**	-0.205	0.039	0.171	-0.095	0.077	-0.187
GB	G	-0.323	1**	-0.686**	0.183	-0.47**	-0.249*	-0.215	-0.206	0.46**
KLBR	G	0.632**	-0.814	1**	-0.33**	0.552**	0.44**	-0.075	0.274*	-0.288*
ER	G	-0.52*	0.538**	-0.514*	1**	-0.033	-0.082	-0.128	-0.056	0.084
WU	G	0.029	-0.58*	0.679**	-0.378	1**	0.421**	-0.228	0.377**	-0.116
ASV	G	0.178	-0.293	0.488*	-0.216	0.638**	1**	-0.444	-0.23	-0.043
AC	G	-0.086	-0.25	-0.096	-0.167	-0.287	-0.49*	1**	0.125	-0.115
PC	G	0.076	-0.204	0.292	-0.153	0.35	-0.262	0.13	1**	-0.081
GYP	G	-0.192	0.56**	-0.321	0.123	-0.184	-0.077	-0.126	-0.101	1**

*, ** significant at 5% and 1% level, respectively.

Correlation at the phenotypic level is indicated by a value above the unity diagonal, and correlation at the genotypic level is indicated by a value below the unity diagonal

Table 3: Path coefficient analysis showing the direct and indirect effect of 20 traits on the Grain Yield per Plant at genotypic level

	DFE	DM	NT	NET	PH	PL	NFSPP	SF	PD	TGW	BY	HI
DFE	0.408	0.408	-0.103	-0.113	-0.052	-0.175	0.079	0.033	0.241	0.001	-0.059	0.026
DM	-0.257	-0.257	0.081	0.086	0.040	0.112	-0.027	-0.006	-0.149	0.019	0.053	0.005
NT	-0.102	-0.128	0.407	0.400	0.115	0.099	0.233	0.001	-0.004	0.148	0.252	0.275
NET	-0.020	-0.024	0.072	0.073	0.021	0.017	0.047	-0.004	-0.010	0.021	0.047	0.049
PH	0.077	0.094	-0.172	-0.173	-0.608	-0.444	-0.095	-0.065	0.182	-0.159	-0.524	0.142
PL	-0.183	-0.187	0.104	0.102	0.313	0.428	0.066	0.097	-0.319	0.130	0.252	-0.027
NFSPP	0.125	0.068	0.370	0.417	0.101	0.100	0.645	-0.004	0.205	0.098	0.267	0.522
SF	-0.038	-0.011	-0.001	0.028	-0.050	-0.106	0.003	-0.470	0.021	-0.208	-0.108	0.010
PD	0.072	0.071	-0.001	-0.017	-0.037	-0.091	0.039	-0.005	0.122	-0.025	-0.024	0.019
TGW	0.001	-0.028	0.141	0.111	0.102	0.118	0.059	0.172	-0.079	0.388	0.152	0.155
BY	-0.051	-0.072	0.217	0.225	0.303	0.206	0.145	0.081	-0.070	0.137	0.351	0.048
HI	-0.013	0.004	-0.141	-0.142	0.049	0.013	-0.169	0.004	-0.032	-0.084	-0.029	-0.209
GL	-0.013	-0.026	-0.022	-0.016	0.034	-0.022	-0.038	0.049	-0.006	0.011	0.032	-0.054
GB	0.032	0.039	-0.111	-0.114	-0.113	-0.132	-0.144	0.040	-0.040	-0.096	-0.097	-0.122
KLBR	0.006	0.005	-0.008	-0.008	-0.006	-0.013	-0.004	0.008	0.005	-0.004	-0.004	-0.006
ER	-0.027	-0.025	-0.006	-0.031	0.056	0.112	0.052	0.077	-0.056	0.036	0.044	0.009
WU	-0.202	-0.199	0.105	0.144	0.068	0.156	-0.014	-0.026	-0.107	0.059	0.026	0.052
ASV	0.106	0.081	-0.029	-0.056	-0.008	-0.107	-0.027	0.045	0.115	0.041	0.035	-0.041
AC	0.000	0.003	-0.001	0.000	-0.005	-0.004	-0.005	-0.003	-0.003	0.000	-0.005	0.000
PC	0.048	0.074	-0.042	-0.034	-0.004	0.022	-0.017	0.038	-0.056	-0.005	-0.020	-0.020
r _g with GYP	-0.030	-0.113	0.859	0.881	0.319	0.291	0.829	0.060	-0.040	0.511	0.639	0.832

Bold values indicate direct effects;

Table 3: Cont....

	GL	GB	KLBR	ER	WU	ASV	AC	PC
DFE	-0.036	-0.047	0.102	-0.067	0.209	0.174	0.002	0.081
DM	0.046	0.036	-0.052	0.040	-0.130	-0.083	-0.036	-0.078
NT	-0.062	0.162	-0.139	-0.015	-0.108	-0.047	-0.030	-0.071
NET	-0.008	0.030	-0.024	-0.014	-0.027	-0.016	0.001	-0.010
PH	-0.140	-0.245	0.154	-0.211	0.105	0.019	0.146	0.010
PL	-0.064	0.202	-0.236	0.299	-0.170	-0.184	-0.089	0.038
NFSPP	-0.169	0.333	-0.111	0.210	0.022	-0.069	-0.165	-0.045
SF	-0.156	0.066	-0.155	-0.225	-0.031	-0.084	0.083	-0.073
PD	-0.005	0.018	0.027	-0.042	0.033	0.056	-0.018	-0.028
TGW	0.030	0.133	-0.069	0.088	-0.058	0.063	0.008	-0.008

BY	0.076	0.122	-0.054	0.096	-0.023	0.050	-0.096	-0.029
HI	0.077	-0.091	0.052	-0.011	0.028	0.034	-0.002	0.017
GL	0.147	-0.047	0.093	-0.076	0.004	0.026	-0.013	0.011
GB	0.090	-0.280	0.228	-0.151	0.162	0.082	0.070	0.057
KLBR	0.015	-0.019	0.023	-0.012	0.016	0.011	-0.002	0.007
ER	-0.084	0.087	-0.083	0.161	-0.061	-0.035	-0.027	-0.025
WU	-0.011	0.229	-0.268	0.149	-0.394	-0.252	0.113	-0.138
ASV	0.044	-0.073	0.122	-0.054	0.159	0.250	-0.122	-0.065
AC	-0.002	-0.005	-0.002	-0.003	-0.006	-0.010	0.020	0.003
PC	0.019	-0.050	0.071	-0.037	0.085	-0.064	0.032	0.244
r_g with GYP	-0.192	0.560	-0.321	0.123	-0.184	-0.077	-0.126	-0.101

Bold values indicate direct effects; Residual values (G) = 0.0346

Conclusion

The analysis of correlation concluded that the grain yield per plant has strong positive significant correlation with number of tillers per plant, number of effective tillers per plant, harvest index, number of fertile spikelets per panicle and biological yield; moderate strong and positive association was absorbed for grain breadth and thousand grain weight. Thus, selection based on these traits will be help to improve grain yield per plant.

Path coefficient analysis expressed that grain yield per plant has 14 traits gave positive direct effect and 6 traits gave negative direct effect Among the positive traits, number of fertile spikelets per panicle, panicle length, days to 50% flowering, number of tillers per plant, thousand grain weight and biological yield were showing high effect on the grain yield per plant; Similarly, negative effects were shown by 6 traits. On that, water uptake ratio, spikelet fertility and plant height were showing high negative effect and harvest index, days to maturity and grain breadth were showing moderately negative effect on grain yield per plant.

Future Scope

According to the results of correlation and path analysis, the following traits should be used to create high-yielding rice genotypes: number of tillers per plant, number of productive tillers per plant, harvest index, number of fertile spikelets per panicle, grain breadth, thousand grain weight, and biological yield. It is recommended that additional work be done on the molecular characterization of the rice genotypes previously found in order to offer more exact measurements of genetic diversity and validate key yield and quality-related variables with associated molecular markers for precision selection.

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