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Diallel Analysis of Nutritional Composition Among Parents and F1 Hybrids in Rice (*Oryza sativa* L.)

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Abstract
A field to lab experiment was conducted to evaluate the nutritional composition among parents and F1 hybrids in rice. On the field, seven parents namely: FARO 26, FARO 64, FARO 57, FARO 33, FARO 66, FARO 44 and FARO 31 were crossed in all possible combinations to obtain 21 F1 hybrids. The parents and F1 hybrids were evaluated in the field for both quantitative and qualitative traits. Sample of the seeds obtained after evaluating the parents and F1 hybrids were subjected to laboratory analysis to determine their nutritional composition. Parameters assessed include: percentage crude protein, crude fiber, crude fat and moisture content. Results obtained showed that there was significant difference among the entries used.

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I. Introduction

Human health is desirous of food with higher nutritional value. Rice being the most popular grain globally and the primary staple for more than 3.5 billion people around the world is considered as single most important source of dietary energy in West Africa and the third most important in sub-Saharan Africa. It also provides at least 20% of dietary protein, 3% of dietary fat and other essential nutrients. Improvement of the nutritional quality of rice is therefore crucial to improving the overall health of African populations.

Selection through breeding is one of the several factors that influence the nutritional content of rice (Das *et al.,* 2020). A successful and efficient hybridization program relies on the knowledge of parental lines or germplasm, hence, understanding the nature and magnitude of gene action helps in the selection of suitable parents for hybridization and also in choosing the appropriate breeding programme and procedures for the crop improvement. Among different methods to assess the nature of gene action in the parents, the diallel cross technique is a systematic method that has been widely utilized in estimating the nature and magnitude of genetic variability and interactions involved in the inheritance of desired traits in crops (Verma, 2003; Chinyere and Ignatius, 2015). When crosses are made in all possible combinations using the technique, it is possible to produce new genetic combinations that might have improved performances over the parents. Combining ability of the parents gives useful genetic information regarding the selection of parents in terms of the performance of their hybrids.

Therefore, in the present study, diallel mating design without reciprocal has been made to estimate the genetic components of variance and gene action in F1 including parents with respect to yield.

In recent times, contemporary agriculture is focusing on human nutritional improvement by generating improved varieties of staple crops such as rice grain. Human nutrition is completely dependent on plant systems directly or indirectly. Efforts have been taken for long to improve the nutritional quality by generating improved varieties of staple crops as these are the main sources of food (Ricachenevsky *et al*., 2019).

II. Materials And Methods

Rice grain samples from seven parents and 21 hybrids were evaluated/assessed for crude protein content, crude fat, crude fibre and moisture content using both the Kjeldal method and magnetic resonance imaging machine at the Grand Cereal industry in Jos Plateau State, Nigeria.

KJELDAHL METHOD FOR PROTEIN ANALYSIS

2.0 gram of each rice sample were weighed as W1, 7.0 g of K_2SO_4 was added and also 0.80 g $CuSO_4$ was added. The whole content were transferred into a digesting tube and 12 ml of concentrated H_2SO_4 was added and the sample were digested in a digester for 2 hours at 420^{o}C, the sample were removed and cooked.

70 ml of water added and the tube was fixed in the distiller and 60 ml of concentrated NaOH were dispensed. 25 ml of 4% boric acid were collected in conical flask and distilled the sample which were titrated with 0.1N HCl. A blank was conducted (that is same procedure above without sample).

$$\% \text{ Protein titre} = \frac{\text{blank} \times 14.01 \times \text{Conc. of HCl} \times 6.25 \times 100}{W_1 \text{ (weight of sample)}}$$

Crude Fibre Analysis

2.0g of dried defated sample (W1) was put into 250 ml flat bottom flask, 100ml of crude fibre reagent was added to the sample and refluxed for 45 minutes, it was cooled and filtered digested using filter paper and were rinsed using methylated spirit and water. the residue were transferred from filter paper into a crucible and dried in the oven at 120 – 130^{o}C for 45 minutes and were cooled and weighed as W2. The content were ashed using a furnace at 600^{o}C for 6 hours then cooled and weighed as W3.

$$\% \text{ Crude Fibre} = \frac{W2-W3}{W1} \times 100$$

Moisture Content Procedure (Oven Method)

A washed dried cooled dish was weighed as W2. Using the weighing balance, 5.00g of sample was weighed as W1 and were oven dried for 3 hours at 105^{o}C, cooled in a dessicator and weighed as W3

$$\% \text{ Moisture Content, MC} = \frac{(W1 + W2) - W3}{W1} \times 100$$

Fat Analysis

3 grams of a sample were weighed as W1 and empty dried flask as W2, the thimble were inserted into an extractor. Hexain was measured 2/3 of a flask filled and were refluxed for 3 hours, the thimble were removed and excess solvent drained. The solvent were recovered into the flask. the flask containing the oil was dried for 3 hours. It was cooled and weighed as W2.

$$\% \text{ Fat} = \frac{W3 - W2}{W1} \times 100$$

Statistical Analysis: Data obtained were analysed using Excel Plant Breeding tools (PB tools 1.3, 2013), statistical tools for Agricultural Research (STAR 2.0.1 2013).

III. Results

Mean values of the parents and F1 hybrids were shown in table 1 shows mean values of crude protein, crude fat, moisture content and crude fibre recorded from the experiment. The values of crude protein recorded ranges from minimum of 5.49 and maximum of 9.64. This range is higher than the range recorded by Edeogu *et al.* (2007) with a range between 1.58 to 6.22%. The percentage fat obtained ranges between 1.55 – 2.52% which is also in agreement with earlier results obtained by Julianor (1985). Crude fibre obtained ranged between 2.98 – 5.18 exceeds the range recorded by Oko and Ugwu (2010) range 1.50 – 2.0 while moisture content obtained ranges between 6.47 – 8.97 which was lower than that recorded by Oko and Ugwu (2011) 3.6 – 18.0.

Table 2 shows mean square and genetic variances for nutritional composition of rice grain samples. Analysis of variance on general combining ability and specific combining ability shows significant differences. However, differences recorded among parents and hybrid might be due to dominance gene effect as genetic parameters shown from the table shows higher degree of dominance than additive gene effect. The result is in conformity with the findings of Gaballah *et al.* (2022) who observed that the dominance variance due to specific combining ability was much higher than the additive variance due to the general combining ability in novel hybrid rice parental lines studied. This indicates the superiority of dominance gene action in the inheritance of characters (Zaazaa and Anis, 2014).

Table 3 shows GCA and SCA effects on nutritional composition of rice grain samples shows that the GCA effects were recorded on parents (P1) and P2 for crude protein were significant while P2 and P7 were significant for crude fat. P2 recorded highest GCA effect compared to SCA means, indicating a preponderance of additive gene effect for protein. This indicates that the parent P2 will make progress in selection of crosses involving the parent. This is because the performance of a single cross progeny can be adequately predicted on the basis of GCA when SCA mean squares are not significant (Ojo *et al.*, 2001).

Table 1: Mean values for nutritional compositions

ENTRIES	CRUDE PROTEIN	CRUDE FAT	MOISTURE CONTENT	CRUDE FIBRE
P1	8.540	1.410	6.640	3.210
P1xP2	5.860	1.230	6.190	3.080
P1xP3	6.140	2.520	6.210	2.630
P1xP4	9.340	2.010	5.950	2.630
P1xP5	7.080	1.960	7.200	3.450
P1xP6	6.910	2.220	6.900	2.410
P1xP7	6.960	1.960	6.700	3.960
P2	9.640	1.070	6.030	3.240
P2xP3	6.060	2.320	8.400	2.860
P2xP4	6.080	2.110	8.970	4.050
P2xP5	7.690	1.890	5.770	2.750
P2xP6	8.100	1.780	6.720	2.540
P2xP7	9.280	1.960	6.950	3.050
P3	9.140	1.170	6.030	2.440
P3xP4	9.110	1.540	7.020	2.810
P3xP5	9.400	1.210	6.470	1.980
P3xP6	6.510	1.200	7.820	3.010
P3xP7	8.220	1.340	5.900	2.770
P4	6.940	1.090	5.470	2.630
P4xP5	5.520	1.220	6.690	2.930
P4xP6	8.090	1.150	5.970	2.690
P4xP7	5.960	1.200	6.160	2.750
P5	6.400	1.650	5.940	3.200
P5xP6	8.410	1.070	6.270	3.110
P5xP7	6.360	1.340	5.260	2.870
P6	7.330	1.740	6.140	2.930
P6xP7	5.490	1.090	5.090	2.310
P7	5.790	1.010	6.290	5.180
Mean	7.370	1.552	6.470	2.981
Min	5.49	1.01	5.09	1.98
Max	9.64	2.52	8.97	5.18

Table 2: Mean Square and Genetic Variances for nutritional composition

	Mean Square			Variance Components		Genetic Parameters				
Parameters	ANOVA	GCA	SCA	GCA	SCA	VA	VD	h2	H2	Dominance Ratio
Crude protein	5.47**	1.2019	2.0021**	0.0000	2.0021	0.0000	2.0021	0.0000	1.0000	
Crude fat	0.60**	0.1849	0.2037**	0.0000	0.2037	0.0000	0.2037	0.0000	1.0000	
Moisture content	2.23**	0.5741	0.7901**	0.0000	0.7901	0.0000	0.7901	0.0000	1.0000	
Crude fibre	1.14**	0.5941	0.3202**	0.0304	0.3202	0.0609	0.3202	0.1597	1.0000	3.2438

Key: * = significant at 0.05 probability, ** = significant at 0.01 probability, ns = not significant, GCA = general combining ability, SCA = specific combining ability, VA = additive variance, VD = dominance variance, h2 = narrow sense heritability, H2 = broad sense heritability

Table 3: GCA and SCA Effects on the Nutrients

	Entries	CRUDE PROTEIN		CRUDE FAT		MOISTURE CONTENT		CRUDE FIBRE	
	P1	-0.350	*	-0.130	ns	0.050	ns	0.260	ns
	P2	0.470	**	0.230	*	0.380	ns	0.110	ns
	P3	0.290	ns	-0.200	ns	0.530	ns	0.010	ns
GCA	P4	0.020	ns	-0.080	ns	-0.110	ns	-0.110	ns
	P5	-0.090	ns	0.030	ns	-0.190	ns	-0.050	ns
	P6	-0.100	ns	-0.120	ns	-0.090	ns	-0.050	ns
	P7	-0.230	ns	0.270	*	-0.570	ns	-0.170	ns
	S. Error	0.173		0.107					
	P1xP2	-0.170	ns	0.110	ns	-1.930	ns	-0.690	ns
	P1xP3	-0.130	ns	0.190	ns	-1.800	ns	0.710	ns
	P1xP4	-0.020	ns	-0.080	ns	2.030	ns	0.310	ns
	P1xP5	0.830	**	0.360	*	-0.150	ns	0.200	ns
	P1xP6	1.060	**	0.090	ns	-0.420	ns	0.460	ns
	P1xP7	0.950	**	0.380	**	0.110	ns	0.320	ns
	P2xP3	0.460	*	0.050	ns	-2.220	ns	0.650	ns
SCA	P2xP4	1.900	**	0.590	**	-1.560	ns	0.560	ns
	P2xP5	0.070	ns	0.010	ns	0.130	ns	0.270	ns
	P2xP6	-0.360	ns	-0.420	**	0.440	ns	0.160	ns
	P2xP7	0.240	ns	-0.540	**	2.100	ns	0.460	ns
	P3xP4	-0.010	ns	0.050	ns	1.320	ns	0.090	ns
	P3xP5	0.060	ns	-0.490	**	1.690	ns	-0.300	ns
	P3xP6	0.790	**	0.070	ns	-1.300	ns	-0.310	ns
	P3xP7	0.090	ns	-0.140	ns	0.890	ns	-0.050	ns
	P4xP5	-0.040	ns	-0.040	ns	-1.550	ns	-0.170	ns
	P4xP6	-0.110	ns	0.050	ns	0.920	ns	-0.240	ns
	P4xP7	-0.090	ns	-0.380	**	-0.730	ns	-0.070	ns
	P5xP6	-0.050	ns	0.310	*	1.320	ns	-0.390	ns
	P5xP7	-0.480	*	-0.270	ns	-0.250	ns	0.000	ns
	P6xP7	-0.630	**	-0.560	**	-1.220	ns	-0.250	ns
	S. Error	0.504		0.311					

Key: * = significant at 0.05 probability, ** = significant at 0.01 probability, ns = not significant, GCA = general combining ability, SCA = specific combining ability

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