

Original Research Article

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## Genetic Exploration on Crude Protein Estimation in Traditional Rice Landraces of Southern India

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### ABSTRACT

Rice (*Oryza sativa* L.) is the foremost important food crop in the world especially in Asiatic Continent. It is ranking second to the wheat among the most cultivated cereals in the world. Rice has widest germplasm collection than other cereal crops. It has to be made productive through several achievements in rice breeding programme, especially in sustainable food grain production with quality concern and it is undoubtedly the most important cereal of the world providing 21 per cent of global human per capita energy and 15 per cent of per capita protein. The mature rice grain, after removal of the hull (husk), again consists of the embryo and the starchy endosperm, surrounded by the seed coat, comprised of remnant tissues of testa and pericarp. The seed coat, embryo and the aleuronic layer from the bran is removed during the milling (often called polishing in rice) process. Most of the seed proteins are located in the rice bran. Thus is a need to collect, exploit and evaluate the untapped germplasms of Rice. Keeping this in view, an attempt was made to evaluate a set of thirty eight traditional land races with high yielding ruling varieties of protein content estimation this study will definitely impact for better parental selection in future crop breeding point of view.

#### Keywords

Indigenous rice,  
Protein,  
Variability,  
GCV, PCV

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### Introduction

Rice (*Oryza sativa* L.) is the most important crop of India and it occupies 23.3 per cent of gross cropped area of the country. Rice contributes 43 per cent of total food grain production and 46 per cent of total cereal

production. It continues to play vital role in the national food grain supply. It is the staple food of nearly half of the world's population. It ranks third after wheat and maize in terms of worldwide production. One third of Asia's rice production is consumed in China and one fifth in India (www.fao.org.in1992).

The germplasm provides immense scope for wide variability. Genetic divergence is an efficient tool for an effective choice of parents for hybridization programme. Such study also selects the genetically divergent parents to obtain desirable combinations in the segregating generations. Protein is one of the most significant factors facing in developing world.

Only twenty per cent of the world people are affluent enough to have access to nutritious diet. Protein energy malnutrition (basic hunger or under nutrition) affects 850 million people worldwide. Most of the people eat the rice and rice based products, so improve the protein content in rice is most important target. It is estimated that under nutrition is the cause of half of all the cases of child mortality. In India, over 50% of all children receive insufficient calories everyday to meet their potential growth and development requirements (Mahendra *et al.*, 2004).

Oko *et al.*, (2012) reported that about eighty per cent of all malnourished children in the developing countries that boasted food surpluses. With more than seventy per cent of the world's malnourished children, South Asia is expected to remain "Black Spots" of child malnutrition in 2020.

A substantial decrease in the availability of legumes over three decades, from an average of 64.4 g during the Pre-Green Revolution decade to about 33.6 g per capita per day during 1996 to 2002 in our country has been largely responsible for protein malnutrition. The quality of a rice protein is always determined by its amino acid profile. Studies conducted in the 1950s and 1960s on children recovering from protein energy malnutrition demonstrated that essential amino acids like lysine and tryptophan were important in improving nitrogen retention when cereals like wheat, rice or corn was the staple food

(Pellett and Ghosh, 2004). Riza *et al.*, (2004) studied the precision of the study that showed that protein content of tested rice varieties ranged from 5.8 to 8.8 per cent for parboiled rice and from 5.5 to 7.5 per cent for unparboiled rice and also found that protein variations from 6.30 to 9.10 per cent in 438 rice cultivars, while rice germplasm lines of core collections had 5.00 to 9.50 per cent variation for protein in milled grains.

Deepa *et al.*, (2008) reported that *Njavara*, a medicinal landrace of rice had higher protein when compared with Jyothi and IR64. They also stated that protein ranged from 4.30 to 18.20 per cent in different polished white rice samples. Banerjee *et al.*, (2011) studied the protein content in 258 rice lines ranged from 4.91 to 12.08 per cent and five lines *viz.*, Harad Guni, Koliha Cheriha, Hardeshi and Dudhiya Danwar were excelled more than 9.00 per cent protein. This implies not only the loss of a nutritionally valuable rice component in human diets but also a reduction of the quantity of rice available for human nutrition by around 10 to 15 per cent. In rice, polishing removes 15 per cent of the protein and also results in a significant loss of other nutrients

## **Materials and Methods**

This investigation was carried out the protein estimation of traditional rice germplasm at the Department of Rice (Paddy Breeding Station), Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU), Coimbatore. The station is located at 11° N latitude and 77° E longitude with an elevation of 426.72 m above the mean sea level.

## **Rice flour preparation for experiment**

The sample powder was grinded by using small volume (150 mg) powder mixer for

biochemical quality analysis. For analysis talc like powder sample was needed, when grinding the samples the sediment powder samples obtained were used for biochemical analysis.

### Crude protein content estimation

For detecting the protein content (Fig. 1). The following reagents and buffers were prepared for extraction and estimation of protein from the rice flour. 2% Sodium carbonate in 0.1 N Sodium hydroxide (Reagent A) 0.5% Copper sulphate ( $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ ) in 1% potassium sodium tartrate (Reagent B) Alkaline copper solution: 50ml of reagent A and 1ml of reagent B were mixed prior to use (Reagent CFolin-Ciocalteau reagent (reagent D): The commercial reagent was diluted 1:1 with water and used. Protein solution (Stock standard): 50 mg of bovine serum albumin was taken accurately and dissolved in distilled water and made upto 50 ml in a standard flask Working standard :10 ml of the stock solution was diluted to 50ml with distilled water in a standard flask Phosphate buffer 0.1 M (pH 7).

Rice flour samples (500 mg) were taken and extracted with 5 ml of buffer solution and centrifuged. The supernatant was collected separately. The residues were re extracted with 5 ml buffer solution centrifuged twice and the collected supernatants were pooled and made upto 100 ml. 0.5 ml of sample extracts were pipetted out and made upto 1 ml with distilled water. Different volumes of 0.2, 0.4, 0.6, 0.8, 1.0 ml of working standard solutions were pipetted into series of test tubes and made upto 1 ml each with distilled water. A test tube with 1.0 ml distilled water was used as blank. Then 5 ml of reagent C was added to all the tubes thoroughly mixed and allowed it to stand for 10 minutes. Then 0.5 ml of reagent D was added, mixed well and incubated at room temperature in the dark for 30 minutes. The absorbance of developed

blue color was measured at 660 nm using UV- visible spectrophotometer (Elico, Mini Spec SL171) and readings were noted.

### Variability studies

#### Phenotypic and genotypic variances

These were estimated according to the formulae given by Lush (1940).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M1 + M2}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \sigma^2_e$$

#### Phenotypic and genotypic coefficients of variability (PCV and GCV)

For each character, phenotypic and genotypic coefficients of variability (PCV and GCV) were computed based on the method given by Burton (1952)

$$\text{PCV } (\%) = \frac{\sqrt{\sigma^2_p}}{\text{Grand mean}} \times 100$$

$$\text{GCV } (\%) = \frac{\sqrt{\sigma^2_g}}{\text{Grand mean}} \times 100$$

#### Heritability

Heritability ( $h^2$ ) in a broad sense was calculated according to Lush (1940)

$$= \frac{\sigma^2_{gh^2}}{\sigma^2_p} \times 100$$

The range of heritability was categorized as suggested by Johnson *et al.*, (1955)

### Genetic advance

Genetic advance was derived according to the method given by Johnson *et al.*, (1955) for each character.

$$\text{Genetic advance} = \frac{\sigma^2_g}{\sigma_p} \times K$$

Where,

$\sigma^2_g$  = genotypic variance

$\sigma_p$  = phenotypic standard deviation

K = selection differential, the value of which is 2.06 at 5% selection intensity.

Genetic advance was expressed as percentage

of mean by using the formula suggested by Johnson *et al.*, (1955). The range of genetic advance as percent of mean was classified as described by Johnson *et al.*, (1955).

### Results and Discussion

This trait showed a range of variability from 7.63 per cent (Arupatham samba) to 12.88 per cent (Kullakar) with a grand mean of 9.56 percent Table 1. The phenotypic and genotypic variances were 1.43 and 1.11 respectively. The phenotypic and genotypic coefficients of variations were 12.61 and 11.11 respectively (Fig.1).

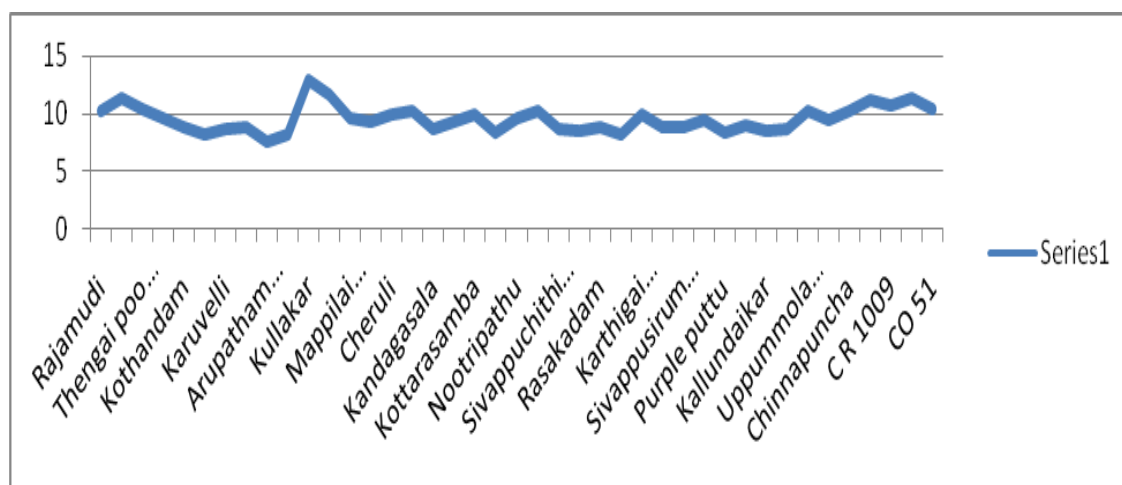
**Table.1**

S.NO	Genotype	Grain protein Content (%)
1	Rajamudi	10.33
2	Athurkitchali	11.31
3	Thengai poo samba	10.43
4	Valaan	9.59
5	Kothandam	8.79
6	Athira	8.23
7	Karuvelli	8.72
8	Karunkuruvai	8.82
9	Arupatham samba	<b>7.63</b>
10	Seeraga samba	8.19
11	Kullakar	<b>12.88</b>
12	Thondi	11.66
13	Mappilai samba	9.59
14	Marnellu	9.38
15	Cheruli	9.98
16	Kaliyan samba	10.26
17	Kandagasala	8.72
18	Kappakar	9.38
19	Kottarasamba	9.98
20	Karuppukavuni	8.4
21	Nootripathu	9.59
22	Vellaichithiraikar	10.22

23	Sivappuchithiraikar	8.75
24	Mohini samba	8.58
25	Rasakadam	8.93
26	Kakarathan	8.3
27	Karthigai samba	9.87
28	Ottadayan	8.82
29	Sivappusirumani	8.89
30	Kattikar	9.56
31	Purple puttu	8.4
32	Norungan	9.03
33	Kallundaikar	8.58
34	Velsamba	8.68
35	Uppummolagai	10.26
36	Kallundai	9.52
37	Chinnapuncha	10.22
38	Swarna	11.13
39	C R 1009	10.71
40	IR 20	11.31
41	CO 51	10.43
	<b>Mean</b>	<b>9.56</b>
	<b>Maximum</b>	<b>12.88</b>
	<b>Minimum</b>	<b>7.63</b>
	<b>SE (D)</b>	<b>0.56</b>
	<b>CD 5%</b>	<b>1.14</b>



**Fig.1** Rice flour digestion for protein estimation



**Fig.2** Mean performance of protein content of rice genotypes

High heritability of 78 percent and moderate genetic advance of 20.15 as a per cent of mean was recorded by this trait. The content protein showed high phenotypic and genotypic coefficient of variations. These results were in accordance with the findings of Luisa *et al.*, (2008), Seyoum *et al.*, (2012) and Shejul *et al.*, (2013). Moderate GCV and PCV were recorded in the protein content and carbohydrate content (Fig. 2).

These results were accorded with the findings of Rao *et al.*, (2010) and Paikhomba *et al.*, (2014). And also protein content showed high heritability likewise the similar results were reported by Purusoatham (2010), Ukaoma *et al.*, (2013) and Paikhomba *et al.*, (2014). Based on this study we explored the protein content in rice showed a range of variability.

It is high for Thondi, Kullakar, Thengai poo samba, athur kitchali, Kaliyan samba and low for Arupatham samba, Nootripathu, Kakarathan and Low for Kallundaikar kar, Kaaruppu kavuni, Arupatham samba, seeraga samba. Similar results were reported by in Riza *et al.*, (2004) who found that protein variations from 6.30 to 9.10 per cent in 438 rice cultivars, while rice germplasm lines of core collections had 5.00 to 9.50 per cent variation for protein in milled grains.

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ranged which from 4.91 per cent to 12.08 per cent and five lines viz., Harad Guni, Koliha Cheriha, Hardeshi and Dudhiya Danwar were excelled more than 9.00 per cent protein.

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