

## Grain protein content and genetic diversity of rice in north eastern India

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### ABSTRACT

Seed Protein content in rice is one of the important nutritional parameter. In the present investigation, 15 cultivars from north-eastern region of India along with two check (high protein containing 'ARC-10075' and low protein containing 'Basmati 370') were grown during wet season 2009 at experimental farm of CRRI at Cuttack. Highest crude protein (CP) was detected in Mykachak (11.09 per cent) and Full Badam (11.06 per cent), while lowest found in Basmati 370 (6.87 per cent). CP content was found negatively associated with seed yield as well as most of the important yield attributing traits like, number of seeds panicle<sup>-1</sup>. Therefore, more selection pressure for achieving more seed yield may negatively contribute to total seed protein. Genotypes were grouped under four clusters through D<sup>2</sup> analysis. Based on inter-cluster distances and D<sup>2</sup> values, Khasha, RCPL-1-87-4 and Pyzum white, having highest cluster mean for number of panicles per plant, number of seeds per panicle, seed yield per plant and protein yield per plant, but lowest crude protein content, located distantly from ARC-10075 having highest cluster mean for crude protein content and 100 seed weight.

**Key words:** rice, north eastern India, genetic diversity, crude protein content

Identification of high protein rice sources and development of modern rice varieties has been getting priority with the increasing attention to high-protein food products of rice in developed countries. Screening germplasm collections of cultivated rice for protein content showed that protein content in cultivated rice ranges from about 5 to 18% with an average of 9.5%, indicating the presence of genetic variability of high protein content and suggesting the feasibility of breeding high-protein rice cultivars. In spite of continuing efforts over the past five decades through conventional breeding and induced mutations (Khush and Juliano, 1984), lack of modern high-protein rice cultivars depicted that those efforts have been largely unsuccessful. The lack of success may have been caused by the universal complexity of the inheritance of endosperm traits, low heritability due to the significant environmental effects and negative correlation with yield and some eating/cooking quality criteria (Vasal, 2002). A very little understanding was acquired for genetical basis of inheritance of this quantitative trait (Shi *et al.*, 2006). North-eastern region of India, being the secondary centre of origin of rice and inaccessible geographic situation, still retain some valuable and unique

indigenous genotypes. These germplasm are having intermediate to poor vigor, shy tillering habit, open to semi-compact culm angle, fairly well panicle exertion, poor threshability and low yielding ability (Sardana, 1997). But some of their unique features, related to stress tolerance or nutritional quality can be incorporated in the rice breeding program for achieving food and nutritional security. In the present study, agromorphological parameters and protein content were measured and used in genetical analysis as well as selection of suitable cross combination for breeding high protein rice genotypes employing rice germplasm from north-eastern India.

Fifteen cultivars from north-eastern region of India along with two check varieties (high protein containing ARC-10075 and low protein containing Basmati 370) were planted for evaluation in wet season 2009 at CRRI farm, Cuttack (Table 1). They were planted in two replications in a randomized block design (RBD) with 20cm row to row and 15cm plant to plant distances. N:P:K ration was 80:40:40. Urea and MOP were applied in two split doses. Data were recorded on 10 plants from each replication. Crude protein

**Table 1. Varieties with their yield, yield contributing traits and protein content**

no	Variety	Days to maturity	Plant height (cm)	Panicle length (cm)	Panicle number plant <sup>-1</sup>	seed panicle <sup>-1</sup>	100 seed wt (g)	Crude protein (%)	seed wt plant <sup>-1</sup> (g)	protein yield plant <sup>-1</sup> (g)
1	Aduma	124.00	139.20	26.73	7.00	134.00	1.72	8.88	17.02	151.18
2	Garomalati	125.50	136.20	26.48	7.10	133.63	1.87	8.83	18.76	165.52
3	Makumi mokul	137.50	147.00	27.75	5.50	118.25	2.45	8.56	12.08	103.09
4	Mamy yathlok	123.50	127.70	23.35	10.00	128.25	1.84	10.80	18.14	196.31
5	Beti	128.50	144.17	22.38	10.67	104.13	1.82	9.44	18.70	176.34
6	Full Badam	122.50	112.50	19.90	9.80	94.50	1.91	11.06	15.45	170.96
7	Mykachak	115.50	118.70	23.85	8.70	124.75	1.91	11.09	14.30	158.76
8	White gelong	124.00	113.30	21.95	10.60	138.25	1.86	8.89	16.17	143.97
9	Ngoba	137.50	121.50	26.43	9.57	128.58	2.25	9.95	24.52	243.81
10	Kataktara	124.50	122.20	23.73	7.50	140.50	1.90	8.54	13.61	116.10
11	Khasha	152.00	151.50	27.08	16.17	216.75	1.41	7.70	34.62	266.65
12	Kali khasha	146.50	162.17	25.00	12.00	158.50	1.47	8.47	23.86	201.96
13	Binni	144.00	167.58	26.79	10.25	130.75	2.09	8.53	25.28	214.91
14	Pyzum white	153.00	112.25	26.83	12.25	235.20	2.00	8.13	37.96	308.72
15	RCPL-1-87-4-1	144.50	124.67	26.00	10.67	172.17	1.61	7.67	27.64	212.47
16	Basmati370	129.50	133.17	27.50	10.17	122.38	2.18	6.87	17.67	121.54
17	ARC-10075	144.00	166.20	27.48	7.70	122.75	2.77	10.43	21.20	220.24
	Mean	133.91	135.29	25.25	9.74	141.37	1.94	9.05	21.0	186.62
	SEm ±	1.27	3.31	0.78	1.44	15.14	0.05	0.18	1.53	14.34
	MS	271.7**	695.1**	10.74**	12.31	2675**	0.23**	3.08**	104.4**	6043**
	CV	1.39	3.56	4.51	21.57	15.61	3.88	2.91	10.59	11.2
	CD at 5%	3.93	10.22	2.41	4.46	46.77	0.16	0.56	4.71	44.31

content from rice seeds (after dehusking) was measured by standard Micro-Kjeldahl method. Analysis of genetic divergence was carried out by using Mahalanobis D<sup>2</sup> statistics. The genotypes were grouped in to clusters as per Tochar's method (Rao, 1952).

All the yield attributing traits were found significantly different except number of panicles per plant. Days to maturity, panicle length, panicle number per plant, seeds per panicle were significantly and

positively associated with seed yield per plant. But CP content was found negatively associated with seed yield ( $r = -0.41$ ) as well as most of the important yield attributing traits such as number of seeds/panicle ( $r = -0.61$ ) (Table 2).

Diversity of genotypes was found significant using D<sup>2</sup> statistics. CP contributed highest (51 per cent) followed by seed weight (14.7 per cent) and maturity (14 per cent) to the D<sup>2</sup> values. Genotypes were grouped

**Table 2. Correlation coefficients among different parameters**

Parameters	Maturity	Plant Height	Panicle length plant <sup>-1</sup>	Panicle number	Seeds panicle <sup>-1</sup>	100 seed wt	Crude protein
Maturity	1.00						
Plant Height	0.46**	1.00					
Panicle length	0.64**	0.51**	1.00				
Panicle number plant <sup>-1</sup>	0.66**	0.00	-0.12	1.00			
Seeds/panicle	0.76**	-0.11	0.43*	0.72**	1.00		
100 seed wt	0.01	0.16	0.33	-0.73**	-0.44**	1.00	
Crude protein	-0.51**	-0.2	-0.57**	-0.44**	-0.61**	0.27	1.00
Seed yield/plant	0.86**	0.12	0.43*	0.82**	0.93**	-0.3	-0.41*

\* significant at 5% level, \*\* significant at 1% level

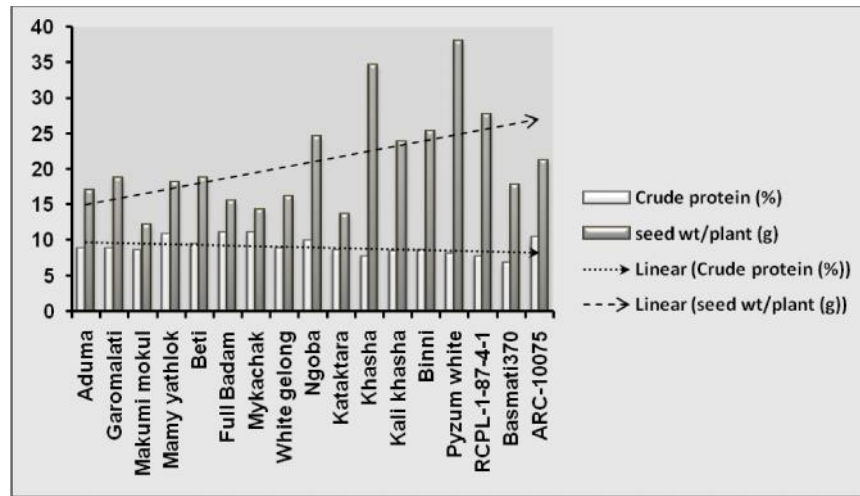


Fig 1. Graphical presentation of seed yield per plant and crude protein content of 17 varieties

under 4 clusters. Cluster-II contained three genotypes, viz. Khasha, RCPL-1-87-4 and Pyzum white. Cluster-III and Cluster-IV contained one genotype each. Ngoba and ARC-10075 belonged to Cluster-III and Cluster-IV, respectively. Rest of the varieties belonged to Cluster-I. Inter-cluster distance was highest (52.7) between cluster-II and Cluster-IV. Khasha, RCPL-1-87-4 and Pyzum white (in Cluster-II), having highest cluster mean for number of panicle per plant (13.03), seed per panicle (208.04), seed yield per plant (33.41g) and protein yield per plant (262.61g) could produce valuable diverse segregants while hybridizing with ARC-10075 (only genotype in cluster-IV) with highest mean CP content (10.43 per cent).

Seed protein content was found to be negatively correlated with grain yield in most of the varieties under this study (Fig. 1). Therefore, more selection pressure for achieving more grain yield may negatively contribute to total seed protein. Therefore, enhancement of grain protein content through hybridization and selection could have a positive impact on millions of poor and malnourished people in developing countries (Mahmoud *et al*, 2008). In the present study we found some genotypes with high crude protein content, like, Mykachak (11.09 per cent) and Full Badam (11.06 per cent). We also found some potential cross combination for developing high yielding and high protein rice

genotypes by using germplasm from north-eastern region of India.

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