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Analysis of Seed protein of Rice genotype percentage due to the effect of micronutrients and their interaction

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Abstract
Seed biology is a major area under discussion in plant research, although most studies have been focused on seed dormancy and germination mechanisms. The present study deals with the seed protein percentage of Rice due to the effect of micronutrients and their interaction. The result indicates that PAC-708 applied with the combined levels of Multiplex +Znso4 +FYM giving significantly highest seed protein (9.21%) than other genotype (IR-36, JR-345). Mean percentage of seed protein of PAC-708 is 8.04 which also higher than IR- 36 (7.56%) JR-345 (7.82%).

Keywords: *Oryza sativa*, seed protein, micronutrients, genotype.

1. Introduction
Rice (Oryza sativa L.) is an important food grain of the country. India is largest rice growing country and rice is our major food crop .Madhya Pradesh contributes nearly 6.5 percent to the national rice production. Seeds are important plant storage organs that play a central role in the life cycle of plants because they are essential for plant reproduction and the initial stages of offspring formation (Yang *et al.*, 2009) [10]. Rice (*Oryza sativa*) seed storage proteins (SSPs) are synthesized and deposited in storage organelles in the endosperm during seed maturation as a nitrogen source for germinating seedlings. Kawakatsu et al. 2010, generated glutelin, globulin, and prolamin knockdown lines and have examined their effects on seed quality of rice (*Oryza sativa*) seed storage proteins (SSPs) are synthesized and deposited in storage organelles in the endosperm during seed maturation as a nitrogen source for germinating seedlings. Rice provides insufficient vitamin A, iron, and lysine, an essential amino acid, resulting in serious malnutrition in these countries (Sautter *et al*. 2006) [7].

2. Material and Method
The present experiment was conducted at the regional Agricultural research station, Kuthulia Rewa (M.P.). The field experiments carry out during rainy season. Firstly soil sample were collected randomly through a soil auger up to 15cm depth from 10 different spots of the experimental plot and mixed them to form composite sample. The field experiment laid out in split–plot design during both the seasons. The treatments comprised of three genotype of rice and eight micronutrient levels thus forming twenty four treatment combinations. These treatments were randomly arranged in each replication, keeping in all three replications. The genotype were taken in the main-plots, and the micronutrient levels in the layout plan as depicted

Treatments	Symbol
Main-plots treatments (Genotypes 3)	
IR-36	G1
JR -345	G2
PAC-708	G3

Sub-plot treatment (Micronutrient levels 8)

No Micronutrient (Control)	M0

25 Kg Zn So4/ha (Soil application) M1
FYM@10 tones/ha M2
FYM+25kg ZnSo4/ ha M3
Multiplex (Foliar spray thrice) M4
Multiplex+ ZnSo4 M5
Multiplex+FYM M6
Multiplex+ ZnSo4+ FYM M7

Treatments' combinations: 24

1. G1M0	9. G2M0	17. G3M0
2. G1M1	10. G2M1	18. G3M1
3. G1M2	11. G2M2	19. G3M2
4. G1M3	12. G2M3	20. G3M3
5. G1M4	13. G2M4	21. G3M4
6. G1M5	14. G2M5	22. G3M5
7. G1M6	15. G2M6	23. G3M6
8. G1M7	16. G2M7	24. G3M7

Details of layout in the field
Experiment design: Split plot
Replications: three
No. of plot in one replications: 24
Gross plot size: 3.4m ×4.5m= 15.3 m^2
Net plot size: 4.0m × 3.0m= 12m2
Row and plant spacing: 20cm and 10cm
No. of rows per plot: 10
Replication border: 1.0m
Main plot and subplot border: 0.5m
Total no. of plot: 72

Table 1: Seed protein (%) as influenced by rice genotypes and micronutrients and their interactions

Micronutrient level (M)	Genotype (G)			Mean
	IR-36	JR-345	PAC-708	
Control	7.20	7.28	7.45	**7.31**
ZnSo4 (25kg/ha)	7.45	7.65	7.63	**7.57**
FYM(10 t/ha)	7.51	7.79	8.00	**7.76**
ZnSo4+ FYM	7.61	7.93	7.98	**7.84**
Multiplex spray (thrice)	7.26	7.77	7.78	**7.6o**
Multiplex+ ZnSo4	7.75	7.82	7.87	**7.81**
Multiplex+ FYM	7.75	7.97	8.43	**8.05**
Multiplex+ ZnSo4 +FYM	8.00	8.42	9.21	**8.54**
Mean	**7.56**	**7.82**	**8.04**	

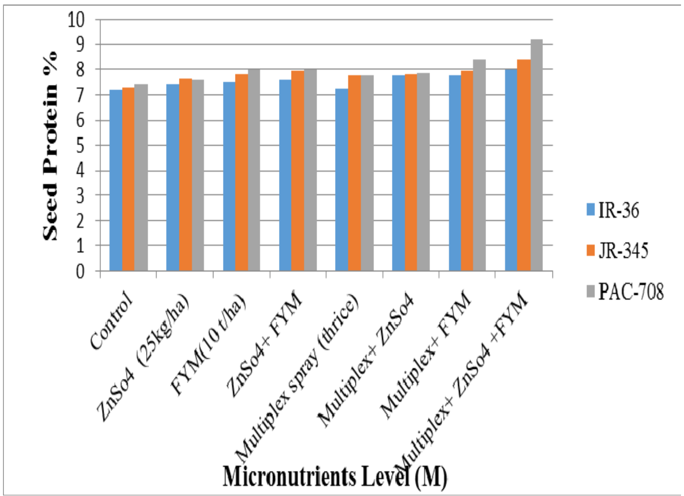

Fig 1: Seed protein percentage of rice genotype due to the effect of micronutrients and their interaction.

3. Result and Discussion

The seed protein in rice was deviated significantly due to change in the genotypes and micronutrient levels as well as their interactions, PAC-708 recorded maximum seed protein (8.04%) being significantly superior to IR-36 and JR-3-45. JR-3-45 was found significantly superior to IR-36, thus the lowest seed protein (7.56%) was recorded in case of IR-36 (Table 1).

The present study relevant with the findings Taheri Asghari M. & Mir Alizade Fard R. (2015) that treatment of 40 t/ha of FYM showed the highest effect on Crude protein content (8.393%) (P<0.01. The treatment of 300 kg/ha of nitrogen fertilizer on crude protein content (8.330%) were significant (P<0.01). The interaction effect of 40 t/ha of FYM and 300 kg/ha nitrogen fertilizer showed the highest effect on crude protein content (8.94%) (P<0.01). The significantly highest seed protein (8.54%) was obtained in case of Multiplex +$ZnSO_4$ +FYM as compared to those of all the rest of the treatments (Fig 1). The overall picture indicated that this parameter was encouraged with the increase in the micronutrient levels. Thus, the minimum seed protein (7.31%) was recorded in case of control treatment. Muni et al 2015 also suggest that fly ash, nitrogen, phosphorous and potassium (NPK) fertilizer and farm yard manure treatments changed the protein contents of the rice varieties and also changed the banding patterns

The Genotype and Micronutrients interaction, the best interaction was PAC-708 applied with the combined levels of Multiplex +Znso4 +FYM giving significantly highest seed protein (9.21%) over all the remaining interactions. On the hand, the lowest seed protein (7.20%) was noted in case of IR-36 without application of any micronutrients. The protein content background values for green gram and maize plant are 24 g/100 g and 4.3 g/100 g, respectively. The average protein content of maize was found to be approximately 3.2 g/100 g in control, FYM, NPK, and FYM + NPK treatments. NPK + FYM showed best result for protein (2.9 g/100 g) content among the groups that received Cr and fertilizers Dheeba Et al., 2015

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