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ANALYSIS OF BIOCHEMICAL PARAMETERS AT BOOT STAGE IN RICE (*ORYZA SATIVA* L.)

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ABSTRACT

Correlation analysis was carried out in seven genotypes of rice for five biochemical parameters, namely, chlorophyll content, soluble protein content, mitochondrial ATPase, succinic dehydrogenase and peroxidase activity at boot stage and grain yield per plant at maturity. Soluble protein content and mitochondrial ATPase had highly significant genotypic correlations (0.74 and 0.51) and significant phenotypic correlations (0.65 and 0.50) with grain yield per plant. It is concluded that these two biochemical parameters can be used to predict the performance of rice genotypes at boot stage.

Key words: Correlation analysis, biochemical parameters, boot stage, grain yield, rice, *Oryza sativa* L.

A number of studies in rice on morphological characters have shown that grain yield per plant is a function of several yield contributing characters [1 – 3]. It is now known that not only morphology but many biochemical parameters also have a control on harvestable products in plants [4, 5]. However, correlation analysis between grain yield and biochemical parameters during growth and development of the phenotype has been least investigated in rice and hence this formed the objective of the present study.

MATERIALS AND METHODS

The material for the study consisted of lines IR 46830A, Saket 4, Narendra 1, Basmati 370, F_1 hybrids IR 46830A x Saket 4, IR 46830A x Narendra 1, and IR 46830A x Basmati 370. All the genotypes were transplanted in R.B.D. with three replications. A sample of 0.5 g leaf material was collected at boot stage from each replication and crushed in a 3.0 ml cold phosphate buffer (pH 6.0). The homogenate so obtained was centrifuged at 5000 g twice.

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The sediment which contained chloroplasts was dissolved in 80% acetone. The supernatent was centrifuged at 10,000 g for 20 min to sediment mitochondria and the supernatent devoid of chloroplasts and mitochondria was retained for estimation of peoxidase and soluble protein content.

Chlorophyll content was estimated as per Mackinney [6] by taking absorbance at 652 nm. Soluble proteins were determined by dye binding method Bradford [7] using BSA as standard protein. Mitochondrial ATPase was assayed according to Wayne [8] at 32°C using ATP (sodium salt) as substrate and the reactions was terminated by addition of 2.0 ml of cold 10% TCA. The amount of Pi liberated was determined by the method of Fiske and Subba Row [9]. One unit of enzyme activity was defined as the µmole of phosphorus produced in one min under standard conditions of assay. Succinic dehydrogenase was estimated as described by Jayaraman [10]. Unit activity of the enzyme was calculated on the basis of change produced in absorbance using molar extinction coefficient of dichlorophenol indophenol. The method of Mahadevan and Sridhar [11] was applied for estimation of peroxidase. One unit of peroxidase activity was the amount of enzyme causing a unit change of absorbance per min. Genotypic, phenotypic and environmental correlation coefficients were estimated by the standard statistical procedure.

RESULTS AND DISCUSSION

The genotypic, phenotypic and environmental correlation coefficients between different biochemical parameters at boot stage and grain yield per plant at maturity are presented in Table 1. Chlorophyll content had positive correlation with all the parameters except succinic dehydrogenase activity. High genotypic ($r = 0.56$ and 0.63) and significant phenotypic ($r = 0.51$ and 0.50) correlation coefficients were obtained for soluble proteins and peroxidase activity with chlorophyll content. Soluble proteins were positively associated with all the traits studied. However, high genotypic and phenotypic correlations of soluble proteins were recorded with mitochondrial ATPase ($r = 0.62, 0.54$) and grain yield per plant ($r = 0.74, 0.65$). Subsequently the correlations of mitochondrial ATPase and peroxidase activity were significant with grain yield per plant ($r = 0.50, 0.69$). Estimates of environmental correlations were either negative or weak.

Chlorophyll is the photosynthetic pigment. It synthesizes food from raw inorganic material in presence of light. Its weak correlations with mitochondrial ATPase and grain yield per plant indicate that chlorophyll content at boot stage is not a limiting factor for grain yield under normal conditions. Several studies have revealed that the amount of chlorophyll in an ordinary leaf of rice plant was considerably higher than necessary [12, 13]. Soluble proteins comprise both enzymatic and nonenzymatic proteins which play pivotal role in growth and development. High genotypic and significant phenotypic correlations of soluble

Table 1. Genotypic (rg), phenotypic (rp) and environmental (re) correlation coefficients for biochemical parameters at boot stage and grain yield per plant in rice

Parameter	Correlation type	Soluble protein	Mitochodrial ATPase	Peroxi-dase	Succinic de-hydrogenase	Yield per plant
Chlorophyll content	rg	0.56^{*}	0.26	0.63^{**}	$–0.53^{*}$	0.40
	rp	0.51^{*}	0.24	0.50^{*}	–0.40	0.39
	re	0.21	–0.07	–0.32	0.32	0.00
Soluble protein	rg		0.62^{**}	0.35	0.38	0.74^{**}
	rg		0.54^{*}	0.35	0.40	0.65^{**}
	re		0.09	0.34	0.46^{*}	–0.01
Mitochondrial ATPase	rg			0.44^{*}	0.30	0.51^{*}
	rp			0.38	0.23	0.50^{*}
	re			0.06	–0.13	–0.11
Peroxidase	rg				$–0.46^{*}$	0.77^{**}
	rp				$–0.42^{*}$	0.69^{**}
	re				–0.31	0.62^{**}
Succinic dehydrogenase	rg					0.24
	rp					0.19
	re					–0.39

*,**Significant at 5% and 1% levels, respectively.

proteins with mitochondrial ATPase and grain yield per plant point out that at this stage of development large proportion of soluble proteins might be represented by enzymatic proteins involved in vital physiological processes. Moreover, a parallel decline in photosynthesis and soluble proteins has been observed during senescence of rice leaves [14]. Subsequently their breakdown products are transported to sink regions (grains). Chen et al. [15] reported that heterotic hybrids had more soluble proteins than their parents during leaf senescence. Higher protein content in hybrid grains could be attributed to the rapid translocation of these soluble proteins in the hybrids. Mitochondrial ATPase is involved in generation of energy currency ATP and also provides energy to various biochemical reaction by hydrolysing ATP [16]. The significant correlation of mitochondrial ATPase activity at boot stage with grain yield per plant at maturity suggests that mitochondrial ATPase plays a contributory role in grain yield. Jin [17] observed in certain maize hybrids that higher ATPase activity was associated with number of grains per cob, 1000-grain weight, and grain yield per plant. A positive correlation between the ATPase activity of the grain and filling velocity has been reported [18]. It seems that ATPase provides necessary driving force to various biochemical reactions taking part during grain filling. Peroxidase activity did not prove to be a reliable contributor to grain yield as environmental correlation in this case was also significantly high (r = 0.62). Succinic dehydrogenase, which is responsible for providing electrons to the electron transport chain, may not have significant bearing on grain yield as it showed weak correlation with grain yield per plant.

The correlation analysis leads to the conclusion that soluble protein content and mitochondrial ATPase activity are the two biochemical parameters at boot stage that can be used to predict the yield performance of genotypes at maturity. This study also reveals that not only morphological traits but biochemical traits need to be investigated to formulate a more suitable ideotype in a crop plant.

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