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CORRELATION AND PATH ANALYSIS FOR GRAIN NUMBER AND GRAIN WEIGHT USING SOME BIOCHEMICAL PARAMETERS IN RICE

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ABSTRACT

Genotypic correlation and path coefficient analyses of grain number and grain weight with total chlorophyll content, soluble proteins, peroxidase, mitochondrial ATPase and succinic dehydrogenase were carried out on eight rice genotypes at boot stage, flowering, 10- and 20 days after flowering. Correlation coefficients and direct and indirect effects varied with developmental stages. Soluble proteins showed significantly positive correlation with grain number per panicle at boot stage and with grain weight at flowering while mitochondrial ATPase activity indicated close association with grain number at flowering, with grain weight at 20 days after flowering.

KEY WORDS: Path Analysis, Biochemical Parameters, Rice

Correlation studies help in designing appropriate selection strategies while path analysis reveals the cause of association and pin-points the actual parameters to be manipulated. Several workers have reported the relevance of correlation and path analysis for grain yield improvement in rice using morphological parameters (Sharma, 1993; Katoch *et al.* 1993). However, physiological efficiency is also greatly influenced by various biochemical parameters particularly during reproductive stages (Srivastava, 1983; Sharma and Mani, 1990) but they have been least investigated. The present investigation was undertaken with a view to assess the utility of chlorophyll content, soluble proteins, peroxidase, mitochondrial ATPase and succinic dehydrogenase as the selection parameters for high yield in rice.

MATERIALS AND METHODS

The experimental material comprised of eight

Narendra 1, IR46830A x Narendra 1, Basmati 370, IR46830A x Basmati 370, Mahsuri and IR46830A x Mahsuri. These were planted in randomised block design with three replications. Each replication consisted of 4 rows each of 3.0 m length. The spacing adopted was 20x15 cms. Nitrogen was applied at 120 kg/ha in three split doses with no P and K application because *tarai* soil of Uttar Pradesh contained P and K in abundant amount.

A sample size of 0.5 g of chopped leaf material taken from flag leaf at boot stage, flowering, 10 days and 20 days after flowering from each genotype in each replication was used for analyses.

Total Chlorophyll content was estimated according to Mackinney (1941) by measuring absorbance at 652 nm using 80% acetone as blank. Soluble proteins were determined by dye binding method of Bradford (1976) and BSA was used as

standard. Peroxidase activity was assayed as per t

method of Mahadevan and Sridhar (1983). One unit of enzyme activity was change in absorbance in one minute under standard condition of assay. Mitochondrial ATPase was estimated as suggested by Wayne (1955) and the amount of inorganic phosphorus liberated was determined by procedure of Fiske and Subba Row (1925). Unit activity of ATPase was the amount of enzyme producing one mole of phosphorus in one minute. Succinic dehydrogenase was quantified at 600 nm by method of Jayaraman (1981). Unit change in absorbance in one mint represented one unit of the enzyme activity. Number of grains per panicle and 1000 grain weight were recorded at maturity from five randomly selected plants. Genotypic correlation and path co-efficient analyses were computed by statistical procedures of Singh and Choudhary (1985).

RESULTS AND DISCUSSION

Correlation and path analyses at genotypic level between number of grains per panicle and chlorophyll content, soluble proteins, peroxidase, mitochondrial ATPase and succinic dehydrogenase are given in table 1 and that of 1000 grain weight in table 2. Total chlorophyll content showed positive correlation with number of grains per panicle but negative with grain weight. Though the correlation was positive for grain number, the direct effects were negative except at 20 days after flowering. The genotypic correlation was also positively significant. Direct selection for chlorophyll content at this stage would improve grain number per panicle. But the negative effect on grain weight indicated the difficulty to increase grain yield through selection for higher chlorophyll content.

Table 1. Direct and indirect effects of the characters on number of grains per panicle at boot stage (a), flowering (b), 10 days after flowering (c) and 20 days after flowering (d), in rice

Characters	Direct effect	Indirect effect through					1000 grain weight	Genotypic correlation coefficient
		Chlorophyll content	Soluble proteins	Peroxidase	Mitochondrial AT Pase	Succinic dehydrogenase		
Chlorophyll content	a	-1.539	0.685	0.711	0.101	0.030	0.130	0.091
	b	-1.215	-0.638	1.095	0.635	0.034	0.315	0.288
	c	-0.152	0.075	-0.447	0.455	0.201	0.008	0.140
	d	1.311	-0.415	0.100	0.485	-0.020	-0.023	0.475*
Soluble proteins	a	1.132	-0.894	0.065	0.117	-0.030	0.105	0.494*
	b	1.386	0.559	-0.942	-0.417	-0.038	0.720	-0.173
	c	0.332	-0.034	0.914	-0.729	-0.605	-0.133	-0.256
	d	-0.386	0.996	0.500	-0.686	-0.304	-0.016	-0.001
Peroxidase	a	0.944	1.159	0.078	0.044	0.061	0.105	0.025
	b	1.291	-1.031	-1.012	0.629	0.044	0.363	0.283
	c	-1.334	-0.051	-0.227	1.040	0.632	0.075	-0.135
	d	1.031	-0.174	1.233	-0.692	0.534	0.001	0.146
Mitochondrial AT Pase	a	0.203	-0.764	0.650	0.203	-0.011	-0.009	0.272
	b	0.836	-0.926	-0.692	0.971	1.031	0.231	0.457*
	c	1.107	-0.062	-0.218	-0.254	0.674	0.136	-0.110
	d	-0.927	0.650	1.314	-0.538	-0.422	-0.038	-0.338
Succinic dehydrogenase	a	-0.068	0.683	0.504	-0.850	0.032	-0.148	0.153
	b	0.049	-0.838	-1.089	1.150	0.629	0.246	0.146
	c	-0.742	-0.041	-0.270	-1.137	1.005	0.093	0.207
	d	0.617	0.043	0.917	0.654	-0.663	0.003	0.258
1000 grain weight	a	-0.650	0.308	-0.182	-0.083	0.003	-0.015	-0.619*
	b	-1.206	0.318	0.828	0.299	-0.160	-0.100	-0.619*
	c	-0.684	0.001	0.04	0.095	0.152	-0.070	-0.621*
	d	0.057	-0.523	0.521	-0.084	-0.637	-0.034	-0.620*

Table 2. Direct and indirect effects of the characters on 1000 grain weight at boot stage (a), flowering (b), 10 days after flowering (c) and 20 days after flowering (d), in rice

Characters	Direct effect	Indirect effect through					No. of grains per panicle	Genotypic correlation coefficient
		Chlorophyll content	Soluble proteins	Peroxidase	Mitochondrial ATPase	Succinic dehydrogenase		
Chlorophyll content	a	-2.154	0.971	0.732	0.169	0.200	0.199	-0.200
	b	-0.991	-0.531	0.886	0.510	0.048	-0.184	-0.261
	c	-0.521	0.198	-0.449	0.591	0.241	-0.068	-0.208
	d	0.460	0.156	0.048	-1.337	-0.055	0.329	-0.399
Soluble proteins	a	1.671	-1.154	0.067	0.195	-0.201	-0.641	-0.161
	b	1.153	0.456	0.762	-0.334	-0.055	0.139	0.597
	c	0.882	-0.117	0.918	-0.946	-0.726	0.124	-0.135
	d	0.206	0.350	0.240	-1.903	0.825	-0.001	-0.281
Peroxidase	a	0.972	-1.622	0.116	0.073	0.407	-0.033	-0.087
	b	1.044	-0.841	-0.842	0.504	0.062	-0.228	-0.301
	c	-1.340	-0.175	-0.604	1.350	0.759	-0.065	-0.075
	d	-0.363	-0.061	-0.136	1.922	-1.449	0.101	0.014
Mitochondrial ATPase	a	0.340	-1.069	0.959	0.209	-0.072	0.353	0.014
	b	0.669	-0.756	-0.576	0.786	0.053	-0.368	-0.192
	c	1.437	-0.215	-0.581	-1.259	0.809	-0.053	0.138
	d	2.698	-0.228	-0.145	-0.259	-1.143	-0.268	0.655*
Succinic dehydrogenase	a	-0.452	0.956	0.744	-0.875	0.054	-0.191	0.228
	b	0.070	-0.689	-0.906	0.930	0.506	-0.118	-0.204
	c	0.891	-0.141	-0.719	-1.142	1.304	-0.100	0.094
	d	-1.675	0.015	-0.114	-0.311	1.841	0.178	-0.058
No. of grains per panicle	a	-1.297	-0.197	0.827	0.025	-0.093	-0.069	-0.619*
	b	-0.387	-0.226	-0.199	0.296	0.306	0.010	-0.619*
	c	-0.484	-0.073	-0.050	-0.181	0.159	0.184	-0.612*
	d	0.691	0.219	0.000	-0.053	-1.046	-0.432	-0.620*

* Significant at 5% level

Direct effects of soluble proteins were positive for both number of grains/panicle and 1000-grain weight but genotypic correlations were negative except with grain number at boot stage (0.494) and grain weight at flowering (0.597). Associations of soluble proteins with photosynthesis and nutrient cycling were observed in rice plants during senescence period (Uchida *et al.*, 1982). Selection based on this character will be useful at boot and flowering stages.

Genotypic correlations of peroxidase activity were either poor or negative with either of the panicle traits even though direct effects varied from positive to negative. The results revealed that under normal condition of growth and development peroxidase does not exhibit any characteristic association.

Path analysis for mitochondrial ATPase revealed that direct effects were mostly positive but genotypic correlation was significant with grain number only at flowering while it was significant at 20 days after flowering with grain weight. The genotypic correlations were positive with grain number in the initial two stages while in the later two, correlations become positive for grain weight. Therefore, as the development proceeded correlations indicated shift from grain number to grain weight. It points to the close involvement of ATPase with physiological processes regulating metabolite movements determining both grain number and grain weight. Association of ATPase activity with various yield components has been reported in heterotic hybrids of maize (Jin, 1986) and rice (Sharma and Mani, 1990). Succinic dehydrogenase showed positive correlation with grain number at all stages but were non-significant.

Slow succinate dehydrogenase decline in leaves was related to higher panicle dry weight in different rice varieties (Debata and Murthy, 1982).

The results indicated that genotypic correlation of total soluble proteins at boot and of mitochondrial ATPase activity at flowering are better biochemical indicators for predicting number of filled grains per panicle, while genotypic correlation of total soluble proteins at flowering and mitochondrial ATPase activity at 20 days after flowering for enhanced grain weight.

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WEED MANAGEMENT IN PIGEONPEA - GROUNDNUT INTERCROPPING SYSTEM

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ABSTRACT

Field experiments were conducted for three years, to study the effect of different weed management practices in pigeonpea + groundnut intercropping system. The study revealed that the first 30 days after sowing is the critical period of weed management for pigeonpea + groundnut system. Weed free environment upto 30 days after sowing produced significantly higher yield which was on par with weed free upto 45, 60 days and weed free till maturity. Similar trend was observed for both the main and intercrops.)

KEY WORDS : Pigeonpea, Groundnut, Weed Management, Intercropping

Pigeonpea is a major pulse crop grown under rainfed condition during *kharif* season. The special requirement and nature of growth of this crop offer good scope for intercropping short duration compatible crops under such conditions. Efficient use of applied inputs and scarce soil moisture is of

timely and effective control of weeds, robing the soils, of nutrients and moisture (Masood Ali *et al.*, 1982). The extent of loss caused by weeds in pigeonpea systems varies with the intensity and nature of weeds, soil fertility and stage of crop (Mittal and Singh, 1983). If timely weeding is not