STUDIES ON GENETIC CORRELATION AND CAUSATION AMONG SEED YIELD AND ITS COMPONENT TRAITS IN MEDIUM DURATION RICE (*ORYZA SATIVA* L.) GENOTYPES GROWN OVER SIX SEASONS UNDER COASTAL ECO-SYSTEM

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Abstract

Seed yield evinced positive and significant genetic association with a number of grains per panicle and harvest index, consistently over the seasons. Seed yield had negative and significant genotypic association with days to 50% flowering and plant height in S_3 only. In the remaining analysis, it witnessed neutral associations at the genotypic level. Genetic causation studies revealed the importance of number of grains per panicle and harvest index in the determination of seed yield, consistently over the seasons. Hence, selection and manipulation of number of grains per panicle and harvest index are likely to improve seed yield under the coastal eco-system. The primary importance has given to harvest index. Genetic correlation and causation do depend on season and genotype × season interaction determines the direction and magnitude of genetic correlation as well as causation. It necessitated the over season analyses of seed yield and their component traits.

*Keywords***:** Rice, Six seasons, Correlation, Path analysis.

Introduction

Rice is the stable food for most of the Asians and also Africans. In Tamilnadu rice is grown in 2.04 Million hectares, with production of 7.98Million tonnes. The average productivity in Tamilnadu is 3918 kg/hectare (2015-2016, Agricultural Statistics at a glance 2016). Despite the increase production, the rural peoples are not taking three course meals for three times per day. This may be due to the poor purchasing capacity. To increase the purchasing capacity the breeder has to increase the production and productivity still higher. It necessitated to increase the production and productivity. One among all the possible ways to increase the production is to extend the area of cultivation. East coast area accounts for 15% of area in India. It suffers from salinity. Hence, the breeder has ought to find a genetic solution to identify suitable trait for selection and manipulation to increase the seed yield under the coastal eco-system. The present study was conducted over six seasons to identify the trait which would be useful to augment the productivity in the coastal eco-system.

Materials and Methods

The present inquiry was conducted at the plant breeding farm, Department of Genetics and Plant breeding, Annamalai University, Annamalai Nagar (Altitude – 5m MSL). The EC of the soil is 4.2 dS m^{-1} and EC of irrigation water 1.7 dS m^1. Twenty six medium duration rice genotypes were obtained from the Tamilnadu Rice Research Institute (TNAU), Aduthurai. Seeds were sown in raised beds. The seedlings were transplanted 28 days after sowing in 4.5 m length plot of two rows, with a spacing of 20×15cm. The crop was raised in three replications in RBD. The experiment was conducted during navarai and samba from 2013 to 2018. Recommended agronomic practices and need based plant protection measures were judiciously followed. Observations were recorded on ten randomly selected plants, leaving border rows and plants, for ten agronomic traits. The traits *viz.,* X1) Days to 50% flowering, X2) Plant height, X3) Number of tillers per plant, X4) Number of productive tillers per plant, X5) Panicle length, X6) Number of grains per panicle, X7) 100 Seed Weight, X8) Total dry matter production, X9) Harvest Index and X10) Seed yield per plant. The data were subjected to statistical analyses as per the method given by Dewey and Lu (1959). The statistical analyses were done with the use of Genres.

Results and Discussion

Correlation studies revealed that seed yield had positive and significant genotypic association with X3, X6, X8 and X9 in S_1. In S_2, it had positive and significant genotypic association with the

aforementioned traits. Seed yield had positive and significant genotypic association with X4, X5, X6 and X9 in S_3. In S_4 also, the same associations were observed. In S_5, seed yield had positive and significant genotypic association with X8 only. In S_6, seed yield had positive and significant genotypic association with X2, X3, X4, X6 and X9. In the pooled analysis, seed yield had positive and significant genotypic association with X2, X3, X6, X8 and X9. The overall association pattern indicated that X6 and X9 had positive and significant genotypic association with seed yield, consistently.

The *inter se* correlation among the component traits indicated that X2 had a positive and significant association with the X5 and X8 are being positively associated. X5 and X8 are being positively associated. X3 had a positive and significant association with X4 and X8. Number of productive tillers (X4) evinced neutral association with X8 positive and significant association with X9, in S_1 (Table 1). In S_2, X2 had a positive and significant association with X8. Total number of tillers (X3) registered positive and significant association with X4, X8 and X9. Number of grains per panicle (X6) witnessed positive and significant association with X9 (Table 3). In S_3, X1 had a positive and significant association with X2, X3, X4 and X7 and negative significant association with the X5, X8 and X9. Plant height (X2) had a positive and significant association with X8. It also had negative and significant association with X3, X4, X5, X9 and X10. Total number of tillers (X3) had a positive and significant association with X4 and X7. It had a negative and significant association with the X6. X4 had a positive and significant association with X7 and X9. X5 had positive and significant genotypic association with X6 and X9. Similarly, X8 had a positive and significant association with X3, X4 and X5. Plant height (X2) had a positive and significant association with X9 (Table 5). In S_4, X1 had a positive and significant association with X3, X4 and X5. Plant height (X2) had positive and significant association with X8 and X9and negative and significant association with X3. Total number of tillers per plant negatively association with panicle length. Panicle length evinced positive and significant association with X6 and X9. X6 had a positive and significant association with X9. X8 had a negative and significant association with X9 (Table 7). In S_5, X1 evidenced positive and significant genotypic association with X2, X4, X5, X6 and X8. X3 showed positive and significant association with X4. X4 had a negative and significant association with X6. X6 had a positive and significant association with X8. X8 witnessed negative and significant association with X9 (Table 9). In S_6, X2 had a positive and significant association with X7. X3 had a

positive and significant association with X4. X6 exhibited positive and significant association with X9 (Table 11). In the pooled analysis, X2 had a positive and significant association with X5 and X8. X3 showed positive and significant association with X4 and X7. X4 had a negative and significant association with the X6. X5 had a positive and significant association with the X6. X6 had a positive and significant association with X9. X6 was negative and significant association with X7 (Table 13).

Seed yield is a complex entity and is associated with a number of other characters. Correlation is a simple measure of association of characters and does not indicate the relative contribution of causal factors to seed yield. The component characters are themselves interrelated such inter- dependence of the contributory factor often affects their direct relationship with seed yield, thereby making the correlation coefficients unreliable as selection indices.

Path coefficient analysis permits the separation of the direct effects from indirect effects through other related characters by partitioning the correlation coefficients. Accordingly, to Dewey and Lu (1959), correlation simply measures the mutual association without regard to causation while the path coefficient analysis specifies the causes and measures their relative importance. Path analysis is usually done by adopting the method suggested by Dewey and Lu (1959). It is used to partition the genotypic correlation coefficients into direct and indirect effects.

Out of two traits *viz.*, number of grains per panicle and harvest index, which portrayed positive and significant genotypic association in almost all the analyses, X6 exerted negative direct effect in S_1. And negligible positive direct effect S_2. In S_3 and S_4 exerted moderate positive direct effect towards seed yield. In S_5 and S_6, it exerted a low positive direct effect. In the pooled analysis, X6 exerts high positive direct effect. Harvest index exerted a positive direct effect towards seed yield per plant, which were close to genetic correlation coefficients in almost all the analyses and gains momentum.

In S_1, X3 and X5 had a high positive direct effect (Table 2). In S_2, X8 exerted a moderate positive direct effect (Table 4). In S_3, X4, X5 and X6 exerted considerable positive direct effects towards seed yield. In X7 and X9 exerted negative direct effects towards seed yield per plant (Table 6). In S_4, X2, X3 and X8 exerted moderate to high positive direct effect (Table 8). In S_5, X3 exerted low positive direct effect (Table 10). In S_6, X3, X7 and X8 showed low to high positive direct effect (Table 12). In the pooled analysis, X3, X4, X6,

X8 and X9 exerted positive direct effect towards seed yield per plant (Table 14).

Correlation and causation studies have revealed the importance of the number of grains per panicle and harvest index in the seed yield improvement under the coastal eco-system. Hence, selection and manipulation of the number of seeds per panicle and harvest index would be useful and could be declared as choice of traits under coastal ecosystem. It was also found out that the direction and magnitude of correlations under the effects of component traits towards seed yield per plant was depend on season. Hence, correlation and causation studies should be conducted over the seasons.

References

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Table 1: Genotypic correlation coefficients among various traits for 26 rice genotypes in S_1

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	0.361	0.211	0.359	0.330	0.000	-0.116	0.143	0.125	0.030
X2		1.000	0.572**	0.303	0.806**	0.336	-0.035	0.414*	0.343	0.350
X3			1.000	0.703**	0.363	0.161	0.077	0.461*	0.317	0.468*
X4				1.000	0.257	-0.057	-0.253	0.127	0.420*	0.221
X5					1.000	0.146	0.147	0.480*	0.220	0.075
X6						1.000	-0.386	0.247	0.383	0.493*
X7							1.000	0.030	-0.086	-0.289
X8								1.000	0.289	0.493*
X9									1.000	0.688**
X10										1.000

Table 2: Path co-efficient analysis among various traits in 26 rice genotypes for S_1

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation coefficients
X1	0.2852	-0.5756	0.5869	-0.9481	0.4104	-0.0003	0.1760	-0.0906	0.1864	0.030
X2	0.1028	-1.5963	1.5909	-0.8017	1.0038	-0.2513	0.0530	-0.2613	0.5104	0.350
X3	0.0602	-0.9134	2.7805	-1.8564	0.4518	-0.1202	-0.1163	-0.2910	0.4731	0.468*
X4	0.1023	-0.4843	1.9534	-2.3969	0.3203	0.0423	0.1383	-0.0799	0.6255	0.221
X5	0.0939	-1.2865	1.0086	-0.6794	1.2455	-0.1092	-0.2227	-0.3029	0.3279	0.075
X6	0.0001	-0.5357	0.4463	0.1493	0.1816	-0.7489	0.5862	-0.1560	0.5705	0.493*
X7	-0.0330	0.0557	0.2131	0.6677	0.1828	0.2893	-1.5175	-0.0190	-0.1284	-0.289
X8	0.0409	-0.6606	1.2813	-0.3346	0.5974	-0.1850	-0.0458	-0.6315	0.431	0.493*
X9	0.0356	-0.54676	0.8827	-1.1091	0.2741	-0.2866	0.1307	-0.1826	1.4904	0.688**

Residual Effect = 0.1240

Table 3: Genotypic correlation coefficients among various traits for 26 rice genotypes in S_2

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	0.353	0.046	0.259	0.336	0.031	-0.246	0.242	0.072	0.025
X2		1.000	0.328	0.171	0.568**	0.222	-0.023	0.476*	0.285	0.308
X3			1.000	0.556**	0.053	0.283	-0.026	0.480*	0.536**	0.594**
X4				1.000	-0.009	0.325	-0.367	0.106	0.346	0.252
X5					1.000	0.238	0.134	0.045	0.203	-0.012
X6						1.000	-0.247	0.294	0.534**	0.516**
X7							1.000	-0.018	-0.195	-0.170
X8								1.000	0.349	0.612**
X9									1.000	0.779**
X10										1.000

Table 4 : Path co-efficient analysis among various traits in 26 rice genotypes for S$_2$

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation coefficients
X1	-0.0200	0.0275	0.0085	-0.0392	-0.0738	0.0047	0.0098	0.0659	0.0411	0.025
X2	-0.0070	0.0781	0.0601	-0.0259	-0.12492	0.0340	0.0009	0.1298	0.1632	0.308
X3	-0.0009	0.0256	0.1832	-0.0843	-0.01162	0.0433	0.0010	0.1308	0.3068	0.594**
X4	-0.0051	0.0133	0.1018	-0.1517	0.0020	0.0497	0.0146	0.0289	0.1983	0.252
X5	-0.0067	0.0444	0.0096	0.0014	-0.2199	0.0365	-0.0053	0.0123	0.1160	-0.012
X6	-0.0006	0.0173	0.0518	-0.0492	0.0245	0.1263	0.0098	0.0801	0.3055	0.516**
X7	0.0049	-0.0017	-0.0047	0.0557	-0.0295	-0.0378	-0.0400	-0.0049	-0.1114	-0.170
X8	-0.0048	0.0372	0.0878	-0.0160	-0.0099	0.0450	0.0007	0.2728	0.1986	0.612**
X9	-0.0014	0.0222	0.0981	-0.0525	-0.0445	0.0818	0.0077	0.0951	0.5726	0.779**

Residual Effect = 0.1517

Table 5: Genotypic correlation coefficients among various traits for 26 rice genotypes in S$_3$

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	-1.000	0.8633**	0.552**	1.7103**	-11.7152**	0.3573	2.2832**	-2.087**	-1.2220**	-2.9982**
X2		1.000	-0.8503**	-0.5860**	-0.4180*	-0.154	-0.0165	0.4652*	-0.6133**	-0.3895*
X3			1.000	0.6564**	-0.2399	-0.5047**	0.6085**	-0.0647	0.0284	0.1772
X4				1.000	0.3877	-0.2346	0.5379**	0.0050	0.5316**	0.5708**
X5					1.000	0.6724**	-0.2604	0.2823	0.6194**	0.7283**
X6						1.000	-0.2463	-0.2814	0.6393**	0.4494
X7							1.000	0.1053	-0.2480	-0.0361
X8								1.000	-0.4936*	0.3094
X9									1.000	0.6945**
X10										1.000

Table 6: Path co-efficient analysis among various traits in 26 rice genotypes for S$_3$

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation Coefficients
X1	-0.1077	-1.5110	-0.9047	4.6264	-6.7828	0.4500	-2.4531	0.0116	3.7360	-2.9982**
X2	0.0929	-1.7501	1.3856	-1.5852	-0.2420	-0.1951	0.0178	0.0114	1.8750	-0.3895*
X3	0.0598	1.4881	-1.6296	1.7757	-0.1389	-0.6356	-0.6537	-0.0015	-0.0868	0.1772
X4	0.1842	1.0256	1.0894	2.7049	0.244	-0.2955	-0.5779	0.0001	-1.6252	0.5708**
X5	-1.2618	0.7318	0.3909	1.0488	0.5789	0.8469	0.2797	0.0069	-1.8938	0.7283**
X6	0.0384	0.2714	0.8225	-0.6348	0.3893	1.2593	0.2646	-0.0069	-1.9544	0.4494
X7	0.2459	0.0290	-0.9916	1.4552	-0.1507	-0.3102	-1.0744	0.0025	0.7582	-0.0361
X8	-0.2249	-0.8142	0.1056	0.0137	0.1634	-0.3545	-0.1131	0.0245	1.5090	0.3094
X9	-0.1316	1.0734	-0.0463	1.4380	0.3586	0.8051	0.26649	-0.0121	-3.0571	0.6945**

Residual Effect = 0.1298

Table 7: Genotypic correlation coefficients among various traits for 26 rice genotypes in S$_4$

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	0.305	0.883**	0.626**	0.390*	-0.107	-0.219	0.125	0.169	0.262
X2		1.000	-1.511**	-1.322**	0.171	0.115	0.336	0.843**	-0.614**	-0.122
X3			1.000	0.255	-0.719**	-0.352	0.072	-0.099	-0.097	-0.105
X4				1.000	-0.290	-0.221	-0.052	0.307	0.344	0.534**
X5					1.000	0.893**	0.192	0.280	0.540**	0.611**
X6						1.000	0.080	-0.074	0.553**	0.511**
X7							1.000	-0.102	-0.126	-0.267
X8								1.000	-0.425*	0.373
X9									1.000	0.650**
X10										1.000

Table 8 : Path co-efficient analysis among various traits in 26 rice genotypes for S_4

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation Coefficients
X1	0.0146	0.1323	0.2301	0.0012	-0.4312	-0.0791	-0.0073	0.1335	0.2679	0.262
X2	0.0044	0.4339	-0.3938	-0.0026	-0.1895	0.0850	0.0112	0.9035	-0.9740	-0.122
X3	0.0129	-0.6558	0.2605	0.0005	0.7946	-0.2603	0.0024	-0.1066	-0.1532	-0.105
X4	0.0092	-0.5737	0.0665	0.0020	0.3206	-0.1637	-0.0017	0.3297	0.5453	0.534**
X5	0.0057	0.0744	-0.1873	-0.0005	-1.1053	0.6611	0.0063	0.3001	0.8565	0.611**
X6	-0.0015	0.0498	-0.0916	-0.0004	-0.9870	0.7403	0.0026	-0.0790	0.8774	0.511**
X7	-0.0032	0.1459	0.01877	-0.0001	-0.2119	0.0590	0.0333	-0.1088	-0.2001	-0.267
X8	0.0018	0.3656	-0.0259	0.0006	-0.3094	-0.0545	-0.0033	1.0723	-0.6741	0.373
X9	0.0024	-0.2664	-0.0251	0.0007	-0.5968	0.4095	-0.0042	-0.4557	1.5862	0.650**

Residual Effect = 0.1342

Table 9 : Genotypic correlation coefficients among various traits for 26 rice genotypes in S_5

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	0.023	0.298	0.405*	-0.227	-0.238	-0.090	-0.027	-0.157	-0.179
X2		1.000	-0.071	-0.259	0.658**	0.404**	0.014	0.467*	-0.384	0.154
X3			1.000	0.853**	-0.087	-0.313	0.192	0.320	-0.071	0.334
X4				1.000	-0.340	-0.542**	0.253	0.113	-0.042	0.112
X5					1.000	0.078	0.286	0.310	-0.119	0.205
X6						1.000	-0.327	0.518**	-0.277	0.361
X7							1.000	0.035	0.001	0.062**
X8								1.000	-0.514**	0.683
X9									1.000	0.257
X10										1.000

Table 10 : Path co-efficient analysis among various traits in 26 rice genotypes for S_5

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation coefficients
X1	-0.0172	-0.0011	0.0371	-0.0296	0.0074	-0.0163	-0.0044	-0.0284	-0.1260	-0.179
X2	-0.0004	-0.0499	-0.0087	0.0188	-0.0215	0.0277	0.0007	0.4945	-0.3076	0.154
X3	-0.0051	0.0035	0.1244	-0.0623	0.0028	-0.0214	0.0095	0.3393	-0.0566	0.334
X4	-0.0069	0.0129	0.1061	-0.0730	0.0111	-0.0371	0.0125	0.1196	-0.0334	0.112
X5	0.0039	-0.0328	-0.0108	0.0248	-0.0327	0.0053	0.0141	0.3287	-0.0955	0.205
X6	0.0040	-0.0202	-0.0389	0.0395	-0.0025	0.0686	-0.0162	0.5481	-0.2219	0.361
X7	0.0015	-0.0007	0.0238	-0.0184	-0.0093	-0.0224	0.0496	0.0370	0.0007	0.062**
X8	0.0004	-0.0233	0.0398	-0.0082	0.192	0.0355	0.0017	1.0589	-0.4118	0.683
X9	0.0027	0.0192	-0.0088	0.0030	0.0039	-0.0190	0.0000	-0.5448	0.8004	0.257

Residual Effect = 0.1460

Table 11: Genotypic correlation coefficients among various traits for 26 rice genotypes in S_6

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	-0.236	-0.068	-0.126	0.139	0.024	0.030	0.048	0.088	0.106
X2		1.000	0.078	0.074	0.310	0.281	0.392*	0.020	0.332	0.403*
X3			1.000	1.016**	-0.223	-0.027	0.050	0.328	0.191	0.591**
X4				1.000	-0.323	-0.044	-0.012	0.347	0.156	0.565**
X5					1.000	0.348	0.186	-0.265	0.383	0.210
X6						1.000	-0.242	-0.232	0.687**	0.583**
X7							1.000	0.214	0.158	0.341
X8								1.000	-0.555	0.072
X9									1.000	0.768**
X10										1.000

Table 12 : Path co-efficient analysis among various traits in 26 rice genotypes for S_6

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation Coefficients
X1	0.0272	-0.0025	-0.0222	0.0049	-0.0025	0.0039	0.0451	0.0208	0.0179	0.106
X2	-0.0064	0.0105	0.0253	-0.0029	-0.0055	0.0461	0.0547	0.0087	0.2719	0.403*
X3	-0.0018	0.0008	0.3256	0.0399	0.0040	-0.0044	0.0070	0.1428	0.1567	0.591**
X4	-0.0034	0.0007	0.3308	-0.0393	0.0058	-0.0072	-0.0016	0.1514	0.1278	0.565**
X5	0.0037	0.0032	-0.0726	0.0126	-0.0180	0.0571	0.0259	-0.1156	0.3138	0.210
X6	0.0006	0.0029	-0.0087	0.0017	-0.0062	0.1643	-0.0336	-0.1012	0.5631	0.583**
X7	0.0018	0.0041	0.0164	0.0004	-0.0033	-0.0397	0.1393	0.0931	0.1292	0.341
X8	0.0013	0.0002	0.1067	-0.0136	0.0047	-0.0381	0.0297	0.4359	-0.4551	0.072
X9	0.0024	0.0035	0.0622	-0.0061	-0.0069	0.1128	0.0219	-0.2420	0.8198	0.768**

Residual Effect = 0.1496

Table 13: Genotypic correlation coefficients among various traits for 26 rice genotypes in Pooled analysis

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10
X1	1.000	0.130	0.043	0.289	0.207	0.058	-0.198	-0.041	0.115	-0.079
X2		1.000	0.067	0.082	0.527**	0.359	0.015	0.636**	0.040	0.451*
X3			1.000	0.931**	-0.018	-0.348	0.501**	0.126	0.349	0.452*
X4				1.000	0.139	-0.420*	0.147	0.122	0.221	0.275
X5					1.000	0.396*	-0.052	0.258	0.181	0.211
X6						1.000	-0.428*	0.021	0.421*	0.431*
X7							1.000	-0.009	-0.184	-0.167
X8								1.000	-0.317	0.451*
X9									1.000	0.564**
X10										1.000

Table 14: Path co-efficient analysis among various traits in 26 rice genotypes for Pooled Analysis

Traits	X1	X2	X3	X4	X5	X6	X7	X8	X9	Genetic correlation coefficients
X1	-0.1771	-0.0038	0.0013	0.0857	-0.0452	0.0246	-0.0043	-0.0270	0.0666	-0.079
X2	-0.0231	-0.0297	0.0021	0.0242	-0.1153	0.1529	0.0003	04159	0.0232	0.451*
X3	-0.0075	-0.0019	0.0325	0.2766	0.0040	-0.1479	0.0109	0.0824	0.2026	0.452*
X4	-0.0511	-0.0024	0.0303	0.2970	-0.0304	-0.1788	0.0032	0.0795	0.1281	0.275
X5	-0.0365	-0.0157	-0.0006	0.0413	-0.2188	0.1686	-0.0011	0.1685	0.1048	0.211
X6	-0.0102	-0.0106	-0.0113	-0.1247	-0.0867	0.4257	-0.0093	0.0136	0.2444	0.431*
X7	0.350	-0.0004	0.0163	0.1043	0.0113	-0.1822	0.0218	-0.0173	-0.1065	-0.167
X8	0.0070	-0.0189	0.0041	0.0361	-0.0564	0.0089	-0.0020	0.6536	-0.1838	0.451*
X9	-0.0203	-0.0012	0.0113	0.0656	-0.0395	0.1794	-0.0040	-0.2072	0.5800	0.564**

Residual Effect = 0.1389