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Research Article

Genetic variability and association studies in F_2 population of rice under sodicity

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Abstract

Rice is the major staple food crop in Asia and it feeds more than 70 per cent population of India. A study was carried out in rice using F₂ segregating population of three cross combinations *viz.*, ASD 16 × CSR 23, ASD 16 × Anna (R) 4 and MDU 6 × Ezhome1 in a non-randomized experimental design under sodic soil condition. Observations were recorded on 12 morphometric traits *viz.*, days to flowering, plant height, flag leaf length, flag leaf width, number of productive tillers, panicle length, number of grains per panicle, spikelet fertility percentage, chlorophyll content, thousand grain weight, grain length breadth ratio and single plant yield. Genetic variability parameters and correlation varied from cross to cross and the traits number of productive tillers and number of grains per panicle showed high PCV and GCV. These characters also showed high positive correlation towards single plant yield with high direct effects in path analysis. Hence, these traits could be relied upon as selection indices under sodic soil conditions in rice.

Keywords

Rice, F₂ population, variability, correlation and path analysis.

Introduction

Rice is considered to be one of the most staple food crops with an annual production of 759. 6 million tonnes (FAOSTAT, 2018). China, India and Indonesia account for about 30.85 percent, 20.12 percent and 8.21 percent of total global rice production respectively. It feeds more than 70 percent population in India and contributes immensely towards the global food bowl.

According to a study conducted by the Economics of Salt-Induced Land Degradation and Restoration Forum (2014), an average of 2000 ha irrigated lands across 75 countries is being degraded by salt every year. About 6.73 million hectares of salt affected soils exist in India. Out of which, 2.96 million hectares is saline and remaining 3.77 million hectares area is classified as sodic soils (Sharma and Chaudhari, 2012). Sodium chloride is one of the most abundant salts released from the soil. Rice is considered to be one of the most salt sensitive cereal crop. Generally, it cannot grow in soils with Electrical Conductivity (EC) level of above 5dSm⁻¹. It is reported to control the transport of salts initially by selective uptake by root cells and ions entering into the root along with water through symplastic and apoplastic pathways (Das et al., 2015).

Selection of the genotypes based on the quantitative characters is the most important criteria in the crop improvement programme.

Statistical measures *viz.*, genetic variability, correlation and path coefficient analysis will be useful for the identification of appropriate genotypes for any environmental condition. Genetic variability indicates the presence of variations within the genotypes and the correlation studies aides in identifying the traits that influence yield. With this background, a study was formulated to assess the genetic variability and character association in segregating population of rice for the traits contributing to yield under sodicity.

Materials and Methods

An experiment was conducted at Anbil Dharmalingam Agricultural College and Research Institute, Tamil Nadu Agricultural University, Trichy during Samba season of 2018 to study the genetic variability and trait association among rice genotypes under sodic soil condition. Three F₂ populations viz., ASD 16 \times CSR 23, ASD 16 \times Anna (R) 4 and MDU $6 \times$ Ezhome1 (Table 1) along with their respective parents. The trial was laid out in natural sodic soil condition with a pH of 8.9 and EC of 2.5 dSm^{-1} . The three cross combinations ASD $16 \times CSR$ 23, ASD $16 \times Anna$ (R) 4 and MDU $6 \times$ Ezhome1 are represented as cross I, cross II and cross III respectively.

The F_2 seeds of three cross combinations were sown in a nursery along with the parents. Twenty



seven days old seedlings were transplanted as single seedling per hill in the main field with a spacing of 20 cm \times 20 cm in a Non-Randomized Block design. All agronomic practices and crop protection measures were followed at appropriate times as per the recommendations during the entire crop growth period. Observations were recorded on 12 yield contributing traits viz., days to flowering, plant height, flag leaf length, flag leaf width, number of productive tillers, panicle length, number of grains per panicle, spikelet fertility percentage, chlorophyll content (by Soil Plant Analysis Development (SPAD) chlorophyll meter), thousand grain weight, grain length breadth ratio and single plant yield in 300 randomly selected plants in each cross combinations.

Analysis of variance was estimated as per the procedure proposed by Panse and Sukhatme (1967). Heritability was calculated based on the formula given by Lush (1940) and genetic advance by Johnson *et al.* (1955). Correlation coefficients were estimated by the procedure suggested by Pearson (1897) and path coefficients by Dewey and Lu (1959) for all the traits.

Results and Discussion

The knowledge on variability present in any breeding population for traits of interest and their gene action is of paramount importance to undertake any successful selection for realization of tangible improvement. This information can be obtained from parameters like mean, range, Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), heritability, genetic advance and genetic advance as percent of mean. An attempt was made to study the above parameters in three F_2 populations of rice *viz.*, ASD 16 × CSR 23 (cross I), ASD 16 × Anna (R) 4 (cross II) and MDU 6 × Ezhome1 (cross III) and their corresponding parents.

Based on the mean performance, the highest single plant yield was obtained in segregants of cross III (18.60 g) followed by cross II (15.96 g) and cross I (11.38 g). A simple variability measure, range showed quite high variation for all the characters studied (Table 2). In cross I, plant height ranged from 79 cm to 128 cm, flag leaf width varied from 0.7 cm to 1.8 cm and panicle length varied from 13.4 cm to 28.3 cm. In F₂ population of cross II, days to flowering ranged from 72 days to 98 days, number of productive tillers varied from 3 to 25, spikelet fertility percentage ranged from 66.8 to 100, chlorophyll content ranged from 35 to 38 and single plant yield 7.43 g to 48.65 g. Range of flag leaf length varied from 15.1 cm to 28.9 cm, number of grains per panicle varied from 55 to 245, test weight ranged from 21.2 g to 29.9 g and grain

length breadth ratio varied from 1.25 to 3.75 were observed in segregants of cross III. The present findings were in accordance with the results of Ali *et al.* (2018) in rice for days to flowering, number of productive tillers, panicle length, number of grains per panicle, spikelet fertility percentage and single plant yield; Bharath *et al.* (2018) in rice for plant height, flag leaf length, flag leaf width, number of productive tillers, panicle length, number of grains per panicle, test weight and grain length breadth ratio. These results indicated the existence of good amount of variability presenting scope for selection to identify good segregants under sodic soil condition.

In the present study, PCV values were observed to be higher as compared to GCV for all the traits but their difference was minimum, except for single plant yield (Table 2). This suggested that, apart from single plant yield and numbers of productive tillers, all the other characters were predominantly influenced by genetic factors. In all the crosses, number of productive tillers, number of grains per panicle and single plant yield had higher values for both PCV and GCV. Similar findings were reported by Shet et al. (2012), Bharath et al. (2018) and Badri et al. (2016) for number of productive tillers, Acharya et al. (2018) for number of grains per panicle, Yadav et al. (2010) and Acharya et al. (2018) for single plant yield in rice. Among the three cross combinations, single plant yield in all cross combinations and number of productive tillers in cross II showed wide difference between PCV and GCV which might be due to modifying or masking effect of environment. Abarshahr et al. (2011), Abhilash et al. (2018), Adhikari et al. (2018) also reported environmental influence on inheritance of traits viz., number of productive tillers and single plant yield. Hence, the character number of grains per panicle may be used as a selection criterion for crop improvement in sodic soil.

Moderate values of PCV and GCV were obtained for the characters *viz.*, plant height, panicle length and grain length breadth ratio in cross I. In cross II, the characters panicle length, grain length breadth ratio and thousand grain weight showed moderate PCV and GCV. The characters plant height, flag leaf length, flag leaf width, panicle length and chlorophyll content in cross III, recorded moderate PCV and GCV. These results are in conformity with the findings of Yadav *et al.* (2010) and Abhilash *et al.* (2018) for thousand grain weight and panicle length, Karim *et al.* (2016) for grain length breadth ratio, Shet *et al.* (2016) for chlorophyll content.



The characters days to flowering and spikelet fertility percentage recorded lower estimates of PCV and GCV in all cross combinations. Similar results were registered in rice crop by Karim et al. (2016) for days to flowering and Singh et al. (2014) for spikelet fertility percentage. In cross I and cross II low PCV and GCV values were obtained for the characters flag leaf length and chlorophyll content. The trait thousand grain weight in cross I and cross III had low PCV and GCV values. Similar findings are in accordance with the results of Lingaiah (2018) for test weight and Kumar et al. (2015) for chlorophyll content. This indicated the lack of variability among the segregants for the above mentioned traits. Hence, selection of sodicity tolerant genotypes based on these characters may be less effective.

Except for the characters of chlorophyll content, for all other traits, high heritability was observed in cross I. In case of cross II, all characters were observed to have high heritability, whereas in the case of cross III, low heritability was recorded in chlorophyll content, spikelet fertility and grain length breadth ratio. Though heritability reflects the amount of genetic variability inherited from parent to their progenies (Lush, 1940), selection of traits could be more precisely done by taking into consideration the genetic advance along with heritability (Johnson *et al.*, 1955).

In cross I, the characters flag leaf width and grain length breadth ratio possessed high heritability accompanied with high genetic advance which indicated the preponderance of additive gene action. Similar results were reported by Yadav et al. (2010) for flag leaf width and Bharath et al. (2018) for grain length breadth ratio. Single plant yield and number of productive tillers were observed to have high heritability with moderate genetic advance. This indicated that these characters were governed by additive and nonadditive gene action. Similar results were obtained in cross II for the character number of productive tillers, which had high heritability along with low genetic advance. In cross III, the number of productive tillers had high heritable value coupled with moderate genetic advance and the chlorophyll content had moderate heritability coupled with moderate genetic advance. Similar result was obtained for chlorophyll content by Kumar et al. (2015). Flag leaf and width showed high heritability along with high genetic advance. The characters days to flowering, plant height, flag leaf length, panicle length, number of grains per panicle, single plant yield, and thousand grain weight studied in this experiment showed high heritability with low genetic gain which may be due to non-additive gene action and it can be

improved by intermating of superior genotypes in this segregating population for selection in further generations. These results were in agreement with the findings of Abhilash *et al.* (2018) for days to flowering, plant height, thousand grain weight, panicle length, spikelet fertility percentage and single plant yield.

To develop a suitable plant type, information on association of desirable traits is an essential criterion. Correlation studies help a breeder to select the elite genotypes based on the information on the association of characters with the yield. The result of correlation analysis is furnished in Tables 3a, 3b and 3c. In cross I, number of productive tillers, panicle length, number of grains per panicle and thousand grain weight had highly significant positive correlation with single plant yield (Table 3a). Spikelet fertility percentage showed positive association with the single plant yield and the same results were obtained in cross III also (Table 3c). The highest positive correlation were recorded for the characters days to flowering, plant height, number of productive tillers, panicle length, number of grains per panicle, chlorophyll content with single plant yield at one percent level of significance and flag leaf width was positively correlated with single plant yield at five percent level of significance in cross II (Table 3b). In cross III, plant height, number of productive tillers, panicle length and number of grains per panicle showed highly significant positive correlation with single plant yield.

The characters number of productive tillers, panicle length and number of grains per panicle showed high positive correlation with yield across all the crosses. These results are in accordance with the findings of Abhilash *et al.* (2018) for panicle length and number of productive tillers; Fiyaz *et al.* (2011) for number of grains per panicle with grain yield. These results revealed that selection for number of productive tillers, panicle length and number of grains per panicle will result in simultaneous increase in single plant yield. Hence, these characters would be better selection parameters while selecting for high yielding segregants under sodic soil conditions.

Path analysis is a statistical measure which was developed by Wright (1921). It separates the direct correlation as direct and indirect effects towards the dependent variable. The results of path coefficient analysis are presented in Tables 4a, 4b and 4c. The traits number of productive tillers and number of grains per panicle showed high positive direct effects on yield in cross II (Table 4b) and cross III (Table 4c) but it had positive negligible direct effect in cross I (Table 4a). Thousand grain weight



showed high positive direct effect on single plant yield in cross I. Panicle length in cross II showed negative direct effects on yield but it had high positive indirect effect through number of grains per panicle. In cross III, days to flowering and plant height are considered as the second most important characters which have low positive direct effects on yield. The characters number of productive tillers and number of grains per panicle had high positive direct effects in all the three cross combinations. Similar results were reported by Abhilash et al. (2018) and Sameera et al. (2016) for the character number of productive tillers and Nandeshwar et al. (2010) for number of grains per panicle. These results revealed that number of productive tillers and number of grains per panicle would be the suitable parameter for the selection of best segregants under sodic condition.

The results of the present study revealed that number of grains per panicle is the most dependable traits for direct selection, as this trait possessed high PCV and GCV values with narrow difference between them. Results of correlation study clearly indicated that yield in rice can be improved indirectly by selecting F_2 segregants with more number of productive tillers and number of grains per panicle as these characters had high positive correlation with yield. Path coefficient analysis also reveals that number of productive tillers and number of grains per panicle had high direct effects under sodic condition.

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S. No	Parents	Parentage	Characteristics
1.	ASD 16	ADT 31 / CO 39	Short duration, short bold grain type and sensitive to salt affected soil. Its average yield is about 5.6 tonnes ha ⁻¹ .
2.	MDU 6	MDU5 / ACM 96136	Short duration, long slender grain type and sensitive to salt affected soil. Its average yield is about 7 tonnes ha ⁻¹ .
3.	CSR 23	IR64//IR4630-22-2-5-1- 3 / IR9764- 45-2-2	Medium duration, medium slender grain type and tolerant salt affected soil. Its average yield is about 3.2 tonnes ha ⁻¹ .
4.	Anna (R) 4	Pant Dhan 10 / IET 9911	Short duration, long slender grain type. Its average yield is about 3.7 tonnes ha ⁻¹ .
5.	Ezhome 1	Jaya / Kuthiru	A red rice, short duration, short bold grain type and tolerant to salt affected soil. Its average yield is about 3.5 tonnes ha ⁻¹ .

Table 1. Characteristic features of parents involved in the cross combinations



Cross	Characters	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
~	Mean	87	98.98	24.27	1.26	10	18.68	85	93.33	35.22	21.13	2.59	11.38
CSR 23	Range	73 - 97	79 - 128	21.5 - 27	0.7 -1.8	3 - 23	13.4 - 28.3	35 - 223	72.82 - 99.31	33.8 - 36.8	18.9 - 28.8	2.3 -3.13	8.0 - 42.70
	PCV %	5.71	11.03	6.51	16.53	31.75	15.79	33.92	3.87	2.48	8.6	14.29	50.46
	GCV%	4.45	11.02	6.43	15.54	30.64	15.74	31.95	3.84	1.86	8.55	13.28	27.44
ASD 16×	h^2	95.91	99.85	97.48	88.38	93.09	99.38	88.71	98.54	56.34	98.72	86.3	98.02
SD	GA	1.98	1.33	1.01	0.48	1.75	0.99	5.69	1.34	0.88	0.92	0.66	1.82
¥	GAM	2.28	1.34	4.15	38.59	17.5	5.29	6.69	1.44	25.42	4.36	2.5	15.96
-	Mean	82	91.2	22.2	1.4	11	18.1	88	92.7	2.6	20	36.4	14.3
na 4	Range	72 - 98	80 - 102	21.0 - 23.5	1.2 - 1.6	3 - 25	12 - 27	58 - 195	66.80 - 100	35 - 38	14.26 - 25.4	1.5 - 3.5	7.43 - 48.65
Anna	PCV %	5.66	6.86	3.37	9.42	34.61	13.57	27.15	5.59	18.94	12.32	2.45	42.74
	GCV%	5.22	6.85	3.25	7.31	29.96	13.45	26.19	4.09	17.67	12.3	2.41	19.22
ASD 16×	h^2	99.06	99.64	93.37	60.22	74.95	98.16	93.01	53.5	87.09	99.75	97.11	99.67
VSI	GA	1.37	1.26	0.84	0.36	2.14	1.17	4.8	2.07	0.75	0.72	0.78	1.21
V	GAM	1.67	1.38	3.8	25.48	19.29	6.45	5.49	2.24	29.03	3.61	2.14	8.49
-	Mean	79	90.7	23.3	1.5	10	18.6	110	94.5	33.6	27.4	2.9	18.6
me	Range	75 - 88	74 - 109	15.1 - 28.9	1.2 - 1.8	4 - 23	13.2 - 23.6	55 - 245	58.90 - 99.44	30 - 37.21	21.2 - 29.9	1.25 - 3.75	8.73 - 45.21
pho	PCV %	4.37	10.99	12.41	13	39.15	10.91	32.38	4.04	6.12	6.47	15.65	41.81
E	GCV%	4.65	10.99	12.37	11.74	38.26	10.68	31.68	1.85	2.16	6.43	8.95	30.36
MDU 6× Ezhome	h ²	97.49	99.95	99.37	81.58	95.49	95.79	95.7	20.99	32.67	98.97	12.46	99.63
D	GA	1.88	1.1	4.22	32.42	17.88	6.85	4.87	0.84	1.06	3.16	14.24	7.6
Σ	GAM	1.49	1	0.98	0.49	1.8	1.27	5.36	0.8	0.36	0.87	0.41	1.41



Traits	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
DTF	1	0.031	0.039	0.032	-0.014	-0.109	-0.136*	0.052	0.049	-0.084	0.056	-0.056
PH		1	-0.020	0.099	0.051	-0.011	-0.068	-0.029	0.108	-0.001	-0.028	-0.037
FLL			1	-0.040	-0.003	-0.003	0.029	0.002	-0.094	0.056	0.057	0.049
FLW				1	-0.014	0.039	-0.002	-0.005	0.025	-0.077	0.090	-0.050
NPT					1	-0.037	-0.065	0.09	0.022	0.330**	0.014	0.327**
PL						1	0.840^{**}	0.167^{**}	0.053	0.428^{**}	-0.04	0.443**
NGP							1	0.193**	0.024	0.481^{**}	-0.011	0.504^{**}
SF%								1	0.117^{*}	0.129^{*}	0.109	0.125^{*}
CC									1	0.102	-0.027	0.059
TGW										1	-0.066	0.950^{**}
GLB											1	-0.079
SPY												1

*Significant at 5 per cent level

** Significant at 1 per cent level



Traits	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
DTF	1	0.054	-0.018	0.180^{**}	0.134^{*}	0.205**	0.176**	-0.003	0.134*	0.069	0.045	0.313**
PH		1	0.043	0.007	-0.005	0.084	0.067	0.143*	0.036	-0.049	0.052	0.174^{**}
FLL			1	0.002	-0.079	0.107	0.085	-0.019	0.037	-0.045	0.018	0.083
FLW				1	0.077	0.122^{*}	0.101	-0.061	-0.015	0.027	0.002	0.144^{*}
NPT					1	-0.042	-0.060	-0.106	0.094	0.034	0.033	0.433**
PL						1	0.731**	0.025	0.073	0.028	0.017	0.445^{**}
NGP							1	0.120^{*}	0.119^{*}	0.066	0.009	0.585^{**}
SF%								1	-0.012	0.073	0.006	0.042
CC									1	0.060	0.022	0.150^{**}
TGW										1	-0.288**	0.089
GLB											1	0.093
SPY												1

Table 3b. Correlation matrix for biometrical traits in F ₂ population of cross II	[(ASD 16 × Anna (R) 4)

*Significant at 5 per cent level

** Significant at 1 per cent level



Traits	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
DTF	1	0.078	0.102	0.019	-0.035	-0.042	-0.006	0.052	-0.047	0.013	0.030	0.071
РН		1	0.004	-0.051	0.140^{*}	0.097	0.115^{*}	0.010	0.124^{*}	-0.056	0.093	0.276^{**}
FLL			1	-0.011	-0.003	0.267^{**}	0.100	0.110	-0.121*	-0.018	0.098	0.086
FLW				1	0.011	-0.105	-0.090	0.027	0.001	-0.009	-0.003	-0.019
NPT					1	0.048	0.123*	-0.085	-0.006	0.016	-0.033	0.458^{**}
PL						1	0.605^{**}	0.263**	-0.039	-0.105	0.019	0.390^{**}
NGP							1	0.252^{**}	0.037	-0.053	-0.018	0.596**
SF%								1	-0.022	0.033	0.043	0.127^{*}
CC									1	-0.033	-0.006	0.012
TGW										1	-0.023	-0.051
GLB											1	0.015
SPY												1

Table 3c. Correlation matrix for biometrical traits in F ₂ population of cross III (MDU 6 × Ezhome 1)
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*Significant at 5 per cent level

** Significant at 1 per cent level



Table 4a. Direct and indirect effects of different traits as partitioned by path an	nalysis for the cross I (ASD 16 × CSR 23)

Traits	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
DTF	0.0352	-0.0011	-0.0003	0.0008	-0.0005	0.0006	-0.0104	-0.0003	-0.0018	-0.0765	-0.0013	-0.0560
PH	0.0011	-0.0335	0.0001	0.0025	0.0018	0.0001	-0.0052	0.0002	-0.0039	-0.0005	0.0007	-0.0370
FLL	0.0014	0.0007	-0.0069	-0.0010	-0.0001	0.0000	0.0022	0.0000	0.0034	0.0508	-0.0014	0.0490
FLW	0.0011	-0.0033	0.0003	0.0256	-0.0005	-0.0002	-0.0001	0.0000	-0.0009	-0.0700	-0.0022	-0.0500
NPT	-0.0005	-0.0017	0.0000	-0.0004	0.0352	0.0002	-0.0050	-0.0006	-0.0008	0.3006	-0.0003	0.3270^{**}
PL	-0.0038	0.0004	0.0000	0.0010	-0.0013	-0.0053	0.0644	-0.0011	-0.0019	0.3899	0.0010	0.4430**
NGP	-0.0048	0.0023	-0.0002	-0.0001	-0.0023	-0.0045	0.0767	-0.0012	-0.0009	0.4382	0.0003	0.5040^{**}
SF%	0.0018	0.0010	0.0000	-0.0001	0.0032	-0.0009	0.0148	-0.0063	-0.0042	0.1179	-0.0026	0.1250^{*}
CC	0.0020	0.0009	-0.0004	0.0023	0.0005	0.0002	-0.0008	-0.0007	0.0010	-0.0601	-0.0240	-0.0790
TGW	-0.0030	0.0000	-0.0004	-0.0020	0.0116	-0.0023	0.0368	-0.0008	-0.0037	0.9118	0.0016	0.9500^{**}
GLB	0.0017	-0.0036	0.0007	0.0007	0.0008	-0.0003	0.0018	-0.0007	-0.0360	0.0932	0.0006	0.0590

Residual effect = 0.089;

Diagonal and bold indicates the direct effects

*Significant at 5 per cent level

** Significant at 1 per cent level



Traits	DTF	PH	FLL	FLW	NPT	PL	NGP	SF%	CC	TGW	GLB	SPY
DTF	0.1349	0.0068	-0.0012	0.0048	0.0599	-0.0006	0.1001	0.0000	0.0014	0.0039	0.0034	0.3130**
PH	0.0072	0.1263	0.0029	0.0002	-0.0022	-0.0003	0.0378	0.0002	0.0004	-0.0028	0.0039	0.1740^{**}
FLL	-0.0024	0.0054	0.0679	0.0001	-0.0351	-0.0003	0.0483	0.0000	0.0004	-0.0025	0.0014	0.0830
FLW	0.0243	0.0008	0.0002	0.0263	0.0345	-0.0004	0.0573	-0.0001	-0.0002	0.0015	0.0002	0.1440^{*}
NPT	0.0181	-0.0006	-0.0053	0.0020	0.4471	0.0001	-0.0340	-0.0002	0.0010	0.0019	0.0025	0.4330**
PL	0.0276	0.0106	0.0073	0.0032	-0.0187	-0.0031	0.4149	0.0000	0.0008	0.0016	0.0013	0.4450^{**}
NGP	0.0238	0.0084	0.0058	0.0027	-0.0268	-0.0022	0.5676	0.0002	0.0013	0.0037	0.0006	0.5850^{**}
SF%	-0.0005	0.0181	-0.0013	-0.0016	-0.0472	-0.0001	0.0682	0.0017	-0.0001	0.0041	0.0005	0.0420
CC	0.0181	0.0046	0.0025	-0.0004	0.0421	-0.0002	0.0674	0.0000	0.0106	0.0034	0.0017	0.1500**
TGW	0.0093	-0.0062	-0.0030	0.0007	0.0153	-0.0001	0.0374	0.0001	0.0006	0.0565	-0.0217	0.0890
GLB	0.0061	0.0066	0.0012	0.0001	0.0147	-0.0001	0.0048	0.0000	0.0002	-0.0163	0.0753	0.0930

Table 4b. Direct and indirect effects of different traits as partitioned by path analysis for the cross II (ASD 16 × Anna (R) 4)

Residual effect = 0.388

Diagonal and bold indicates the direct effects

*Significant at 5 per cent level

** Significant at 1 per cent level



Traits	DTF	PH	FLL	FLW	NPT	FPL	NGP	SF%	CC	TGW	GLB	SPY
DTF	0.0747	0.0122	0.0007	0.0006	-0.0132	-0.0023	-0.0030	0.0006	0.0008	-0.0002	0.0005	0.0710
PH	0.0059	0.1560	0.0001	-0.0017	0.0525	0.0053	0.0574	0.0001	-0.0021	0.0009	0.0016	0.2760^{**}
FLL	0.0085	0.0025	0.0064	-0.0002	0.0014	0.0151	0.0516	0.0013	0.0021	0.0002	0.0017	0.0860
FLW	0.0014	-0.0080	0.0000	0.0337	0.0043	-0.0058	-0.0451	0.0003	0.0000	0.0002	-0.0001	-0.0190
NPT	-0.0026	0.0218	0.0000	0.0004	0.3757	0.0026	0.0616	-0.0010	0.0001	-0.0003	-0.0006	0.4580^{**}
PL	-0.0031	0.0151	0.0018	-0.0036	0.0179	0.0546	0.3018	0.0031	0.0007	0.0018	0.0003	0.3900^{**}
NGP	-0.0005	0.0180	0.0007	-0.0030	0.0464	0.0331	0.4986	0.0030	-0.0006	0.0009	-0.0003	0.5960^{**}
SF%	0.0039	0.0016	0.0007	0.0009	-0.0320	0.0143	0.1257	0.0118	0.0004	-0.0006	0.0007	0.1270^{*}
CC	-0.0035	0.0193	-0.0008	0.0000	-0.0022	-0.0021	0.0183	-0.0003	-0.0173	0.0006	-0.0001	0.0120
TGW	0.0010	-0.0087	-0.0001	-0.0003	0.0060	-0.0058	-0.0266	0.0004	0.0006	-0.0167	-0.0004	-0.0510
GLB	0.0022	0.0145	0.0006	-0.0001	-0.0123	0.0010	-0.0091	0.0005	0.0001	0.0004	0.0174	0.0150

Table 4c. Direct and indirect effects of different traits as partitioned by path analysis for the cross III (MDU 6 × Ezhome 1)

Residual effect = 0.458

Diagonal and bold indicates the direct effects

*Significant at 5 per cent level

** Significant at 1 per cent level



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