Appraisal of Genetic Variability and Seasonal Interaction for Yield and Quality Traits in Maize (*Zea mays* L.)

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Abstract Knowledge of the genetic components of variances and inter-relationships between yield and its quality traits will improve the efficiency of breeding programmes through the use of appropriate selection indices, taking into consideration for ten inbreds of maize obtained from All India Co-ordinated Maize Improvement Project. Ten inbreds were evaluated in a Randomized Block Design with three replications. Highest PCV and GCV were observed for oil content preceded by days to 50% tasseling and days to 50% silking. High heritability were observed for days to 50% tasseling, days to 50% silking, protein content, starch content and number of kernels row^{-1}. High heritability with high genetic advance were observed for days to 50% tasseling and days to 50% silking which indicated that most likely the heritability was due to the influence of additive genes and selection may be effective for such traits. Highest significant and positive correlation were found between days to 50% tasseling and days to 50% silking followed by association of ear height and plant height; number of kernels row^{-1} and ear length; ear diameter and ear length. Significant and negative association were found between ear height and days to 50% tasseling; ear height and days to 50% silking; starch content and oil content. Oil content was recorded maximum positive direct effect on yield. Direct effect of ear length, ear diameter, 100 kernel weight, oil content and starch content on yield was positive and high.

Keywords Correlation; Path coefficients; Oil; Variances

Introduction

Maize (*Zea mays* L.) is one of the most important food crops in the world with highest production and productivity. It is grown in more than 166 countries in diverse seasons for diverse uses in different agro-ecological conditions due to its high yield potential. The major maize growing countries are USA, China, Mexico, Brazil, Argentina and India (FAO, 2007).

The success of any crop improvement programme is dependent not only on the amount of genetic variability present in the population, but also on the extent to which it is heritable, therefore, is a key component of breeding programmes for broadening the gene pool of crops (Ahmad et al., 2011). Yield is a complex quantitative character controlled by many genes interacting with the environment and is the product of many factors called yield components. Selection of parents based on yield alone is often misleading. The appropriate knowledge of such interrelationships between yield and its contributing components can significantly improve the efficiency

of breeding programmes through the use of appropriate selection indices (Mohammadia et al., 2003).

Path coefficient analysis furnishes information of influence of each contributing trait to yield directly as well as indirectly (Farshadfar, 2004) and also enables breeders to rank the genetic attributes according to their contribution and thus, useful in indirect selection and of elite genotypes from diverse genetic populations. Therefore, availability of good knowledge of these genetic parameters existing in different yield contributing characters and the relative proportion of genetic information in various quantitative traits is a pre-requisite for effective crop improvement.

Results

Analysis of variance (ANOVA) indicated that the seasons were significant for DTT, DTS, PH, ED, KR, PY, OC, PC, SC and SuC. Interactions were non-significant for all the traits. Treatments were significant for almost all the characters which indicated that lot of genetic variability were present among the different genotypes. The ANOVA is given in Table 1.

Table 1 Analysis of variance of Randomized Block Design for 10 characters in maize inbreds

Traits	Replications	Seasons	Interactions	Treatments	Error
DF	2	1	2	9	45
DTT	8.3167	10.4167**	1.1167	6676.4240**	5.9085
DTS	8.7167	6.6667*	1.2167	6677.4520**	7.2030
PH	148.0940	62.4240**	4.3620	915.2533**	70.9114
EH	97.6940	20.1260	41.0221	903.0864**	94.2227
EL	4.1024	3.9015	1.2881	19.6470**	2.2976
ED	0.0800	0.2483*	0.0788	0.9595**	0.1169
KR	8.0773	73.6377**	1.7391	106.9913**	5.6895
KRE	0.0627	0.1017	0.0304	8.8596**	1.8975
KW	15.3672	0.3227	4.1102	33.0023**	8.3909
PY	329.5623	3621.9080**	34.2694	1807.3710**	432.7575
PtY	0.0007	0.0118	0.0512	0.2500**	0.0452
OC	0.0020	2.2714**	0.0084	2.3771**	0.1780
PC	0.0020	0.0053**	0.0002	0.1931**	0.0056
SC	0.0052	13.9291**	0.0725	24.5729**	1.1932
SuC	0.0194	0.2851**	0.0067	0.3136**	0.0304

Note: *,** significant at 5% and 1% probability levels, respectively

Phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV) for all the characters studied, which indicated that environment also played a considerable role in expression of these characters. There was a close resemblance between PCV and GCV for all the characters indicating that selection for these characters would be effective.   The PCV ranged from 43.16 for OC to 4.03 for SC. Highest PCV was recorded for OC followed by DTT and DTS. Lowest PCV was recorded for SC followed by PC and PH. Highest GCV was observed for DTT followed by DTS and OC. Lowest GCV was observed for SC succeeded by PC and KR. The highest environmental coefficient of variation (ECV) was accorded for PY followed by OC and PtY and lowest for SC succeeded by PC and DTT.

High heritability was recorded for DTT, DTS followed by PC, SC and KR. Moderate heritability were observed for OC, PH followed by SuC, EH, EL and ED. Rest of the characers exhibited low heritability.

High genetic advance were recorded for traits *viz.,* DTT followed by DTS and PH. Rest of the attributes recorded low genetic advance. The genetic advance as percentage of mean were accorded for characters *viz.,* DTT, DTS, OC, KR, EH and PtY. High heritability with high genetic advance was recorded for DTT and DTS (Table 2).

Highest significant and positive correlation was observed between DTT and DTS followed by EL and KR, PH and EH, ED and KR, EL and ED, KR and KRE, correlation of DTT and DTS with KRE, ED and KRE, KRE and OC, PC and SuC, PC and SC, EH and KW, EL and KRE. A high significant and positive correlation was found for DTT and DTS with ED and EL, between KR and OC, EH and SuC, EH and OC, KW and SuC, PH and KW and SC and SuC (Table 3).

Significant and negative association was found between KR and PC, ED and PC, KRE and SuC, EL and SuC, PH and KRE, EH and ED, DTT and DTS with SuC, DTS and KW, EH and KRE, PH and ED, KRE and PC, KW and PC, OC and SC, KW and SC, correlation of DTT and DTS with PH, OC and PC and correlation of DTT and DTS with EH.

Direct or indirect effects are categorized as follows, negligible when values are between 0.00~0.09, low when the values range from 0.10~0.19, moderate for values between 0.20~0.29, high for values 0.30~0.99 and values more than 1.00 are categorized as very high (Lenka and Mishra, 1973). The path analysis first suggested by Wright (1921) and later illustrated by Dewey and Lu (1959) provides an effective measure of direct and indirect causes of association and depicts the relative importance of each factor involved in contributing to the final product.

Direct and positive effect on grain yield was exhibited by DTT, PH, EH, EL, ED, KW, OC, PC and SC where

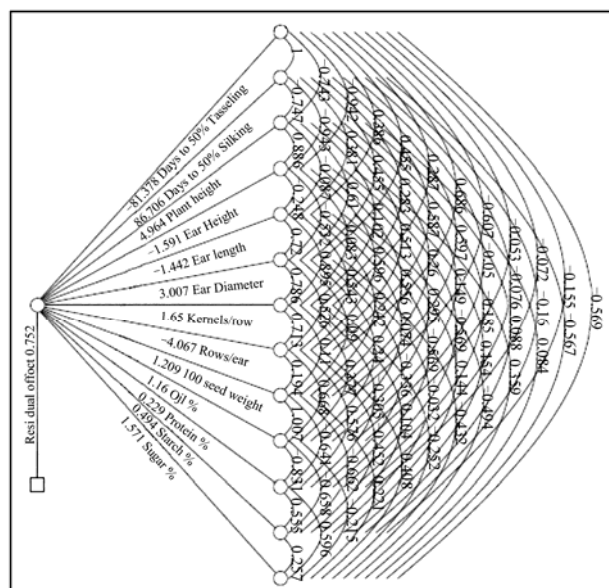as direct and negative effects were exhibited by DTS, KR, KRE and SuC (Table 4).

Among these, PH recorded negligible positive directs, whereas the direct effect of EH and PC was positive and low. The direct contribution of DTT on yield was positive and very high whereas, the direct contribution

of DTS was negative and very high. Direct effect of EL, ED, KW, OC and SC on grain yield was positive and high. Negative and high direct effects were observed for KR. KRE and SuC showed negative and low direct effects. OC recorded maximum positive direct effect on yield (Figure 1).
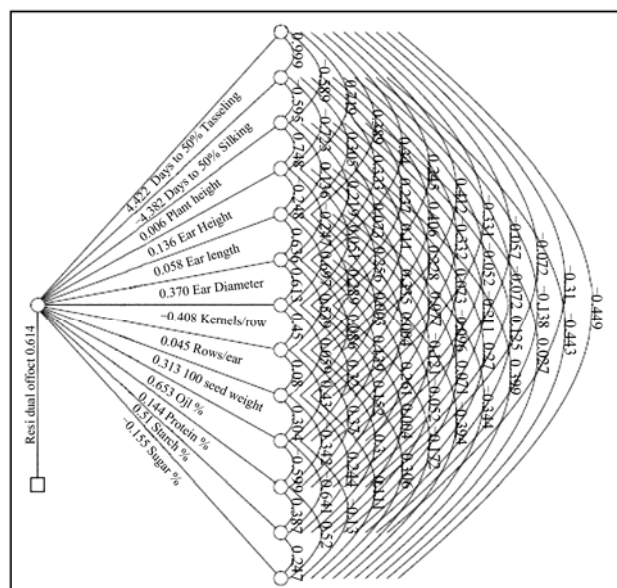
Figure 1 Phenotypical and genotypical path diagrams showing the direct and indirect effects on yield

Discussion

The knowledge of genetic variation is important for selection in crop improvement programmes. The success of any crop improvement programme is dependent not only on the amount of genetic variability present in the population, but also on the extent to which it is heritable, which sets the limit of progress that can be achieved through selection (Sumathi et al., 2005; Najeeb et al., 2009; Hussain et al., 2011; Khan et al., 2011 and Wang et al., 2011).

The phenotypic expression of a character is the manifestation of genotype, environment and interaction between the genotype by environment. The genotypic coefficient of variation measures the extent of genetic variability present in a crop species and also enables to quantify the extent of variability present in different characters. Therefore, the total variance needs to be partitioned into heritable and non-heritable components to assess the true breeding nature of that particular trait.

Phenotypic coefficient of variation (PCV) was slightly

higher than the genotypic coefficient of variation (GCV) for all the characters studied, which indicated that environment also played a considerable role in expression of these characters being in consonance with Kumar et al (2011). There was a close resemblance between PCV and GCV for all the characters indicating that selection for these characters would be effective. This is in conformity with the findings of Alake et al (2008).

Heritability is a measure of phenotypic variance attributable to genetic causes providing information on the extent to which a particular morphogenetic character can be transmitted to successive generations. Knowledge of heritability influences the choice of breeding procedures, to predict gain from selection and to determine the relative importance of genetic effects (Kashiani et al., 2010; Laghari et al., 2010).

The most important function of heritability in genetic studies of quantitative characters is its predictive role to indicate the reliability of phenotypic value as a guide to breeding value (Falconer and Mackay, 1996).

Characters with high heritability can easily be fixed with simple selection resulting in quick progress. However, it has been accentuated that heritability alone has no practical importance without genetic advance (Najeeb et al., 2009). Genetic advance shows the degree of gain obtained in a character under a particular selection pressure.

DTT, DTS, KR, PC and SC recorded high heritability in broad sense, which indicates that though the character is least influenced by the environmental effects, selection may not be useful as broad sense heritability is based on total genetic variance which includes both fixable and non-fixable variances. It would be useful only when the fixable proportion is known. KRE and KW recorded low heritability which indicated that the character is highly influenced by environmental effects and genetic improvement through selection will be difficult due to masking effects of environment on the genotypic effects.

DTT and DTS recorded high genetic advance which indicates that the character is governed by additive genes and selection will be rewarding for improvement of such trait (Reddy and Agarwal, 1992; Singhal et al., 2006; Najeeb et al., 2009; Muhammad Rafiq et al., 2010). Low genetic advance were observed for EL, ED, KR, KRE, KW, OC, PC, SC and SuC elucidating that the character is governed by non-additive genes and heterosis breeding may be useful in such a situation. High heritability with high genetic advance was recorded for DTT and DTS which indicated that most likely the heritability is due to the influence of additive genes and selection may be effective for such traits.

If correlation between two traits is significant and positive, it indicates that increase in one character will lead to a simultaneous increase in the paired character and if the correlation is significant and negative, increase or decrease in one character, will lead to increase or decrease in the other paired character or vice-versa. Yield is complex trait and is dependent on several contributing traits. Hence, trait association was studied to assess the relationship among yield, its components enhancing the usefulness of selection. Genotypic correlations reveal the existence of real associations, whereas the phenotypic correlations may occur by chance. Significant phenotypic correlations

without genotypic association are of no value. If the genotypic correlation is significant and phenotypic is not, it means the existing real association is masked by environment effect. This indicates the importance of genotypic correlation compared to phenotypic correlation.

Zozulya (1971) found significant positive correlation between oil content and plant yield of maize. Chmeleva et al (1988) studied significant positive correlation between protein and oil contents. Proksza and Harmati (1988) revealed that oil yield were usually high in hybrids with moderate oil content coupled with high yielding capacity. Lambert et al (1997) reported high oil hybrids with increased oil content were found to be inferior in grain yield than normal hybrids. Mittal et al (1998) reported that DTS and DTT were important parameters for estimating maturity under Indian conditions.

Yield attributing traits such as EL, ED, KR, KRE, TW showed significant association with yield and negative association with DTT, DTS, PH and EH. These similar findings were supported by Sofi and Rather (2007), Muhammad Rafiq et al (2010), Pavan et al (2011), Raghu et al (2011) and Ravi et al (2012).

Path coefficient provides more information among variables than do correlation coefficients since this analysis provides the direct effects of specific yield components on yield, and indirect effects via other yield components (Garcia Del Moral et al., 2003). Path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921).

Direct and positive effect on grain yield was exhibited by DTT, PH, EH, EL, ED, KW, OC, PC and SC indicating the effectiveness of direct selection whereas direct and negative effects were exhibited by DTS, KR, KRE and SuC indicating the effectiveness of indirect selection. These findings were in corroboration with Muhammad Rafiq et al (2010), Pavan et al (2011), Raghu et al (2011) and Ram Reddy et al (2012).

High positive direct effect of test weight was also reported by Singhal et al (2006), Saidaiah et al (2008), Zarei et al (2012). The high direct effect of this trait appears to be the main factor for their strong association with grain yield. Hence, direct selection

for these traits would be effective.

Conclusion

From the above experiment, it can be concluded that all the genotypes interacted with seasons differently for different traits *viz.,* DTT, DTS, PH, ED, KR, PY, OC, PC, SC and SuC. Some of the traits showed stability which elucidated that no effect of season's were observed on them *viz.,* EH, PH, KRE, KW, PtY. High heritability with high genetic advance were observed for days to 50% tasseling and days to 50% silking. The inter relationship between component traits is also valuable in selection criteria because they directly or indirectly influence economic quality traits

such as OC, PC, SC and SuC which can help to produce specialty corns.

Materials and Methods

The present investigation entitled "Utility of Quality and Morphological traits as a selection criterion of yield improvement in specialty corns (*Zea mays* L.)" was carried out during *Rabi* 2011-2012 and *Kharif* 2012 season at the Research Farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi. The experimental material consisted of ten inbreds of maize obtained from the All India Co-ordinated Maize Improvement Project, Varanasi. Details of ten inbred is presented in Table 5.

Table 5 Inbreds used in experiment and their morphology

S. No.	Genotypes	Center	Duration	Plant height	Kernel type	Kernel colour
1	HUZM-53	Varanasi	Late	Medium	Flint	Yellow
2	HUZM-265	Varanasi	Late	Dwarf	Dent	Yellow
3	HUZM-478	Varanasi	Late	Medium	Flint	Yellow
4	HUZQPM-01	Varanasi	Late	Medium	Semi flint	White
5	HUZQPM-03	Varanasi	Late	Dwarf	Flint	White
6	HUZQPM-05	Varanasi	Late	Medium	Flint	White
7	HUZQPM-06	Varanasi	Late	Medium	Flint	White
8	HIGH OIL	DMR, Delhi	Medium	Medium	Flint	White
9	DMHOC-15	DMR, Delhi	Medium	Medium	Semi flint	Yellow
10	DMHOC-09	DMR, Delhi	Medium	Medium	Dent	White

Ten inbreds were sown in a Randomized Block Design with three replications. Each entry was sown as single row of 4 meter length with row-to-row and plant-to-plant distance of 60 cm and 20 cm respectively. Initially two seeds per hill were sown and later on one plant was thinned to maintain single plant per hill. Two border rows were also planted to avoid the border effect. The crop was raised as per the recommended package of practices. Observations *viz.,* days to 50% tasseling (DTT), days to 50% silking (DTS), plant height (PH) (cm), ear height (EH) (cm), ear length (EL) (cm), ear diameter (ED) (cm), number of kernels row^{-1} (KR), number of kernel rows ear^{-1} (KRE), 100 kernels weight (KW) (g), plant grain yield (PY) (g), plot yield (PtY) (kg), oil content (OC) (%), protein content (PC) (%) , starch content (SC) (%) and sugar content (SuC) (%) were recorded on ten plants selected randomly from each inbred in each replication. Later on it was adjusted at 15% moisture and 80% shelling. Moisture percentage was measured

by taking kernel samples from the bulk and recorded by electronic moisture meter. The kernels taken for quality analyses were used from self pollinated plant as to avoid xenia effect.

Quality analysis was done by FOSS Infratec™ 1241 NIRS. Near Infrared measurements of grain have performance when measuring in transmittance (570~1050 nm) and reflectance (1100~2500 nm) mode. The model for analyses of variance included seasons, replications, genotypes and genotype by season interaction. An analysis using means over replications allowed the generation of entry least square means. For each trait, inbred means were the average values calculated from all the replications in both seasons. Calculation of correlation coefficients involved trait values paired by inbred. The statistical analysis was done by using Indostat Version 8.1.

The mean data will be subjected to following statistical analyses: Variances, mean, range and

coefficient of variability will be assessed following Panse and Sukhatme, 1967; Computation of correlation coefficients will be done as per Searle, 1961; Path coefficient analysis (Dewey and Lu, 1959).

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Table 2 Components of variability of yield and yield contributing traits in maize inbreds

S. No.	Traits	Mean	Range		ECV (%)	GCV (%)	PCV (%)	h²b (%)	GA		GA as % of mean	
			Min.	Max.					(5%)	(1%)	(5%)	(1%)
1	DTT	87.68	49.83	122.00	2.77	38.03	38.13	99.50	68.51	87.79	78.13	100.12
2	DTS	90.93	53.00	125.00	2.95	36.67	36.79	99.40	68.46	87.74	75.29	96.49
3	PH	139.55	127.63	164.36	6.03	8.50	10.43	66.50	19.93	25.54	14.28	18.30
4	EH	65.35	49.06	83.61	14.85	17.77	23.16	58.90	18.35	23.52	28.08	35.98
5	EL	12.16	9.47	14.37	12.47	13.99	18.74	55.70	2.62	3.35	21.51	27.57
6	ED	3.88	3.02	4.46	8.82	9.67	13.09	54.60	0.57	0.73	14.71	18.85
7	KR	20.79	13.47	28.94	11.47	19.76	22.85	74.80	7.32	9.38	35.21	45.11
8	KRE	12.74	11.05	14.67	10.81	8.45	13.72	37.90	1.37	1.75	10.73	13.75
9	KW	21.04	18.05	25.42	13.77	9.63	16.80	32.80	2.39	3.06	11.36	14.56
10	PY	77.57	66.25	116.67	26.82	19.51	33.17	34.60	18.35	23.51	23.65	30.31
11	PtY	0.89	0.53	1.11	23.92	20.78	31.69	43.00	0.25	0.32	28.07	35.97
12	OC	1.71	0.99	2.71	24.67	35.41	43.16	67.30	1.02	1.31	59.84	76.69
13	PC	3.39	3.11	3.77	2.21	5.21	5.67	84.70	0.34	0.43	9.86	12.67
14	SC	56.00	51.27	58.39	1.95	3.52	4.03	76.60	3.56	4.56	6.35	8.14
15	SuC	2.11	1.69	2.46	8.25	10.29	13.19	60.80	0.35	0.45	16.53	21.19

Table 3 Estimates of genotypic (rg) and phenotypic (rp) correlation coefficients among 10 characters in maize germplasm

Traits		DTT	DTS	PH	EH	EL	ED	KR	KRE	KW	OC	PC	SC	SuC	PY
DTT	g	1	1.00 **	−0.74 **	−0.94 **	0.38 **	0.45 **	0.29	0.68 **	−0.60	−0.05	−0.07	−0.15	−0.57**	−0.15
	p	1	1.00 **	−0.59 **	−0.72 **	0.31 *	0.34 **	0.24	0.41 **	−0.33 **	−0.05	−0.07	−0.12	−0.44 **	−0.06
DTS	g		1	−0.75 **	−0.94 **	0.38 **	0.45 **	0.28	0.68 **	−0.59 **	−0.05	−0.07	−0.15	−0.56 **	−0.15
	p		1	−0.59 **	−0.72 **	0.30 *	0.33 **	0.24	0.40 **	−0.33 **	−0.05	−0.07	−0.13	−0.44 **	−0.07
PH	g			1	0.88 **	−0.09	−0.61 **	−0.10	−0.51 **	0.26 *	0.14	−0.18	0.08	0.08	0.14
	p			1	0.75 **	0.13	−0.22	−0.07	−0.10	0.22	0.07	−0.21	0.12	0.02	0.29
EH	g				1	−0.25	−0.53 **	−0.08	−0.58 **	0.55 **	0.29*	−0.05	0.15	0.35 **	0.32
	p				1	−0.08	−0.25	−0.06	−0.25 *	0.33 **	0.07	−0.09	0.26 *	0.39 **	0.27
EL	g					1	0.72 **	0.89 **	0.54 **	−0.24	0.07	−0.17	0.14	−0.49 **	0.60
	p					1	0.63 **	0.70 **	0.28 *	−0.01	−0.01	−0.12	0.07	−0.34 **	0.49
ED	g						1	0.78 **	0.62 **	0.08	0.24	−0.33 **	−0.06	−0.43	0.62
	p						1	0.61 **	0.53 **	0.08	0.13	−0.26 *	−0.05	−0.39 **	0.48
KR	g							1	0.713	0.10	0.37 **	−0.30 *	0.10	−0.26	0.72
	p							1	0.46 **	0.05	0.32 *	−0.18	0.01	−0.17	0.38
KRE	g								1	0.19	0.6084	−0.62 **	−0.46	−0.40 **	0.28
	p								1	0.08	0.43 **	−0.36 **	−0.29 *	−0.30 *	0.24
KW	g									1	0.01	−0.64 **	−0.66 **	0.27 *	0.35
	p									1	0.30 *	−0.34 **	−0.24	0.11	0.35
OC	g										1	−0.83 **	−0.65 **	−0.21	0.54
	p										1	−0.59 **	−0.64 **	−0.12	0.23
PC	g											1	0.56 **	0.59 **	−0.51
	p											1	0.38 **	0.51 **	−0.31
SC	g												1	0.25 *	0.05
	p												1	0.24	0.13
SuC	g													1	−0.50
	p													1	−0.21
PY	g														1
	p														1

Note: *,** significant at 5% and 1% probability levels, respectively

Table 4 Direct and indirect effect of different characters on plant yield per plant at genotypic and phenotypic level in maize inbreds

Traits		DTT	DTS	PH	EH	EL	ED	KR	KRE	KW	OC	PC	SC	SuC
DTT	G	−81.38	−81.38	60.49	76.66	−31.40	−36.99	−23.37	−55.82	49.40	4.32	5.90	12.59	46.28
	P	4.42	4.42	−2.61	−3.18	1.37	1.50	1.08	1.82	−1.47	−0.25	−0.32	−0.57	−1.99
DTS	G	86.71	86.71	−64.74	−81.78	33.00	39.47	24.50	59.58	−51.79	−4.33	−6.58	−13.85	−49.18
	P	−4.38	−4.38	2.61	3.17	−1.34	−1.46	−1.04	−1.78	1.45	0.23	0.31	0.61	1.94
PH	G	−3.69	−3.71	4.96	4.40	−0.43	−3.03	−0.51	−2.55	1.29	0.74	−0.92	0.44	0.42
	P	0.00	0.00	0.01	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
EH	G	1.50	1.50	−1.41	−1.59	0.39	0.85	0.13	0.93	−0.88	−0.47	0.08	−0.25	−0.57
	P	−0.10	−0.10	0.10	0.14	−0.01	−0.03	−0.01	−0.03	0.05	0.01	−0.01	0.04	0.05
EL	G	−0.56	−0.55	0.12	0.36	−1.44	−1.04	−1.29	−0.78	0.35	−0.11	0.26	−0.21	0.71
	P	0.16	0.15	0.07	−0.04	0.51	0.32	0.35	0.15	0.00	0.00	−0.06	0.04	−0.17
ED	G	1.37	1.37	−1.83	−1.60	2.17	3.01	2.36	1.88	0.27	0.72	−1.01	−0.19	−1.30
	P	0.10	0.10	−0.07	−0.08	0.19	0.31	0.19	0.17	0.03	0.04	−0.08	−0.02	−0.12
KR	G	0.47	0.47	−0.17	−0.14	1.48	1.30	1.65	1.18	0.18	0.62	−0.50	0.17	−0.43
	P	−0.10	−0.10	0.03	0.02	−0.28	−0.25	−0.41	−0.19	−0.02	−0.13	0.07	0.00	0.07
KRE	G	−2.79	−2.79	2.09	2.38	−2.21	−2.55	−2.90	−4.07	−0.79	−2.47	2.55	1.88	1.66
	P	−0.02	−0.02	0.00	0.01	−0.01	−0.02	−0.02	−0.04	0.00	−0.02	0.02	0.01	0.01
KW	G	−0.73	−0.72	0.31	0.67	−0.29	0.11	0.13	0.23	1.21	1.22	−0.77	−0.80	0.33
	P	−0.10	−0.10	0.07	0.10	0.00	0.03	0.02	0.03	0.31	0.10	−0.11	−0.08	0.03
OC	G	−0.06	−0.06	0.17	0.34	0.09	0.28	0.44	0.71	1.17	1.16	−0.96	−0.76	−0.25
	P	−0.04	−0.03	0.05	0.05	0.00	0.09	0.21	0.28	0.20	0.65	−0.39	−0.42	−0.08
PC	G	−0.02	−0.02	−0.04	−0.01	−0.04	−0.08	−0.07	−0.14	−0.15	−0.19	0.23	0.13	0.14
	P	−0.01	−0.01	−0.03	−0.01	−0.02	−0.04	−0.03	−0.05	−0.05	−0.09	0.14	0.06	0.08
SC	G	−0.08	−0.08	0.04	0.08	0.07	−0.03	0.05	−0.23	−0.33	−0.32	0.28	0.49	0.13
	P	−0.07	−0.07	0.06	0.14	0.04	−0.03	0.00	−0.15	−0.12	−0.33	0.20	0.51	0.13
SuC	G	−0.89	−0.89	0.13	0.56	−0.78	−0.68	−0.41	−0.64	0.43	−0.34	0.94	0.40	1.57
	P	0.07	0.07	0.00	−0.06	0.05	0.06	0.03	0.05	−0.02	0.02	−0.08	−0.04	−0.16
PY	G	−0.15	−0.15	0.14	0.33	0.60	0.62	0.72	0.28	0.35	0.54	−0.51	0.06	−0.50
	P	−0.06	−0.07	0.29	0.27	0.49	0.48	0.38	0.24	0.35	0.23	−0.31	0.13	−0.21

Note: Underlined numbers denote the direct effects; Phenotypic residual effect (p)=0.7525; Genotypic residual effect (g)=0.6144