

Estimates on Characters Association and Path Coefficient Analysis in Maize (*Zea mays* L.) Varieties in District Satna of Madhya Pradesh

Deepak Kumar, Rajbeer Singh Gaur, Ayodhya Prasad Pandey, Brindaban Singh and Neeraj Verma

Department of Genetics and Plant Breeding
Faculty of Agriculture Science and Technology
AKS University, Satna- 485001 (M.P.)

Abstract:

Twenty six different maize cultivars were planted in a Completely Randomized Block Design (CRBD) at AKS University, Satna, in November 2021 during the Rabi season. Twelve quantitative traits were examined, and data was gathered and analyzed for variance, correlation coefficient, and path coefficient. The experimental design showed significant variations in all traits as a result of the treatments. The analysis of variance for the twenty six maize genotypes revealed a considerable amount of variability among the genotypes for all traits under study. The direction of genotypic and phenotypic correlation was similar for almost all the characters. In general, genotypic correlation was higher than phenotypic ones in magnitude for all the characters except correlation between day to 50% pollen shedding and number of kernel per row, length of flag leaf and cob diameter, length of flag leaf and number of kernel per row, days to maturity and number of kernel per row, days to maturity and grain yield/plant, number of kernel per row and seed index. Path coefficient analysis revealed that seed index followed by days to maturity, plant height, days to 50% pollen shedding, number of kernel per row and cob height had exerted maximum direct effect on seed yield at genotypic level. Kernel per cob and cob diameter had exhibited negative direct effect on seed yield at genotypic level. At phenotypic level, path coefficient analysis revealed that kernel per cob followed by cob length, seed index, cob diameter and plant height had exerted maximum direct effect on seed yield. Number of kernel per row, day to maturity and days to 50% silking had exhibited negative direct effect on seed yield at genotypic level. The R Square and Residual effect was (0.9206 and 0.2818), respectively. Residual effect value was moderate and indicating that some of characters affecting seed yield has to be include in

the future study.

Keyword: Maize, correlation coefficient, and path coefficient.

Introduction

Maize (*Zea mays* L.; $2n = 20$) is a monoecious and third maximum vital cereal crop of the sector after wheat and rice. It is also known as queen of cereals because of its highest genetic yield potential among the cereals. Maize is a significant source of daily calories in the diets of people in various developing countries in Africa and Latin America, where animal protein is limited and costly (Prasanna et al. 2001). It is cultivated for consumption by low-income families in Ethiopia and incorporated into various dishes. Despite its widespread dependence, the conventional variety of maize lacks two crucial amino acids, lysine and tryptophan, which are essential for protein synthesis (Vasal 2002). The kernels of opaque-2 maize were characterized by a dull and chalky appearance, weighed 15 to 20% less, and were more susceptible to diseases and insects [Ignjatovic et al. 2008]. Consequently, scientists lost interest in further research on this variety.

Maize is one of the few food vegetation that is diploid species with a simple set of ten chromosome with the number of chromosomes are $2n = 20$. It's miles used as grain as well as fodder at various level of plant increase, specifically from tasselling onward. Maize is miles grown from fifty eight°N to forty°S, from underneath sea degree to altitudes more than 3000 m, and in areas with 250 mm to higher than 5000 mm of rainfall according to yr (Shaw, 1988) and (Dowswell et al. 1996).

It is cultivated in nearly 201 m ha with a production of 1162 m tonnes and productivity of 5754.7 kg/ha all over the world, having wider diversity of soil, climate, biodiversity and management practices (FAOSTAT 2020). *Teosinte* and *Tripsacum*, are monoecious, i.e. they've separate staminate and pistillate flora at the selfsame plant, and this changed into the reason maize and its relatives were as soon as grouped right into a separate taxonomic tribe the Maydeae (syn. Tripsaceae). (Stebbins and Crampton 1961) revised this category and put down *Zea* and *Tripsacum* in the Andropogoneae. Other contributors of the Andropogoneae endemic to the brand new world are mainly Coix, Trilobachne,

Polytoxa, Schleracne, Chionacne, as well as the important grasses sugarcane and sorghum (Kellogg, 1998). the vagaries of weather change/ variability desires to be addressed with suitable breeding methods to add new germplasm for the benefit of goal environments (Cairns et al. 2012) and to increase extra weather resilient maize structures (Cairns et al. 2013).

Correlation coefficients typically indicate connections between independent traits and the strength of the linear relationship between them. The route analysis first counseled via (Wright, 1921) and later illustrated by using (Dewey and Lu, 1959). Correlation coefficients typically indicate the connections between independent attributes and the extent of their linear relationship. However, when a causal connection between these attributes is required, this relationship alone is not enough (Toker and Cagirgan 2004). Therefore, understanding the interdependencies between grain yield and its contributing factors enhances the effectiveness of breeding programs by employing suitable selection indices (Belay 2018, Mohammadi et al. 2003). The performance of breeding programme depends especially on the path and magnitude of association between yield and its additive traits and also the relative significance of every aspect concerned in contributing to grain yield (Jakhar et al. 2017). So, the aim of this study is to workout inter relationships among twelve traits in maize and their direct and indirect effects on grain yield.

Materials and Methods

The present investigation entitled “**Estimates on characters association and path coefficient analysis in maize (*Zea mays* L.) Varieties in district Satna of Madhya Pradesh**” was carried out along with the techniques applied and materials used. The current study's field experiment took place in Kharif, 2022 at the Research Farm of Genetics and Plant Breeding at AKS University in Sherganj, Satna, Madhya Pradesh. Geographically, Sherganj is located at 24058' N latitude, 80083' E longitude, and approximately 3 km away from the district headquarters of Satna. It is situated at an elevation of 322 meters above the mean sea level.

The collections of 26 varieties/strains of maize (*Zea mays* L.) germplasm comprising indigenous genotypes, constituted the experimental materials for this study. These genotypes exhibiting wide spectrum of variability for various agronomic and morphological characters were obtained from the, Pusa BISA Bihar, KVK Hariharpur (Vaishali) Bihar, Farmers fields, and Department of Genetics and Plant Breeding, AKS University Sherganj, Satna M.P.

The study was carried out to assess 26 maize germplasm under irrigated conditions, utilizing a Completely Randomized Block Design. The entire experimental field was divided into 3 blocks of equal size, with each block containing 26 plots. Each plot consisted of 3 rows measuring 2 meters in length, with a row-to-row spacing of 60 cm and a plant-to-plant spacing of 20 cm. Recommended cultural practices were implemented to ensure a successful crop yield. The characters studied were days to 50% tasseling, days to 50% silking, length of flag leaf (cm), plant height (cm), ear height (cm), cob length (cm), cob diameter (cm), grain rows per cob, no. of karnels per row, grains per cob, 100 grain weight (g), grain yield/plant (g).

The basic relationships between various characters at genotypic and phenotypic levels were established by examining characters as proposed by Searle (1961). Path coefficient analysis was conducted using the formula recommended by Dewey & Lu (1959).

Result and Discussion

Analysis of variance (ANOVA) for the design of experiment.

The analysis of variance for the design of the experiment involving 26 maize strains/varieties were evaluated in Randomized Block Design with three replications for the twelve quantitative characters. The design of the experiment (mean sum of squares) indicated highly significant differences for all the characters suggesting the presence of appreciable genetic variability among the experimental material under study. Non-significant differences due to replications were observed for all the characters (**Table 1**). Thus, there is enough of area and scope for advancement of different polygenic and oligogenic traits through selection. Similar finding on presence of significant variability for various traits in the maize genotypes was also reported by many investigators in their

investigation (**Kumar et al. 2015; Kandel et al. 2018**). Also similar results were reported by **Vavilov (1951)** and **Asins (2002)**.

Correlation coefficient:

The crop's grain yield is determined by the interplay of various interconnected traits. Hence, the selection process should focus on these individual traits and their correlation with the grain yield. The association between different traits provides valuable insights into their mutual relationship, serving as a crucial parameter for making decisions on the appropriate selection approach to enhance the studied crop.

This indicated that though there was a strong inherent association between the different traits studied, phenotypic expression of the correlation was depressed under the influence of environment. Similar were the findings of **Saxena and Asthana (1962)**. In the present investigation correlation coefficient was worked out at genotypic and phenotypic levels for all the twelve traits of 26 genotypes and has been presented in **Table 2**.

The direction of genotypic and phenotypic correlation was similar for almost all the characters. In general, genotypic correlation was higher than phenotypic ones in magnitude for all the characters except correlation between day to 50% pollen shedding and number of kernel per row, length of flag leaf and cob diameter, length of flag leaf and number of kernel per row, days to maturity and number of kernel per row, days to maturity and grain yield/plant, number of kernel per row and seed index.

Day to 50% pollen shedding showed significant positive correlation at 5% probability level with plant height (0.441) and days to 50% silking (0.412) at only genotypic level.

Days to 50% silking showed highly positive significant correlation with plant height (0.813**), at 1% probability level (0.425*), at 5% probability level cob diameter (0.604**) 1% probability level (0.431*) at 5% probability level at both the genotypic and phenotypic levels, respectively and with seed index (0.427*) at 5% probability level at genotypic level only.

Length of flag leaf showed highly positive significant correlation with Plant Height (0.611** and 0.478*) at both the genotypic and phenotypic levels, respectively and with Cob Height 0.396* and Seed Index 0.459* at genotypic level only.

Day to maturity showed negative but significant correlation with Seed Index (-0.389*) at genotypic level only.

Plant height showed highly positive significant correlation with cob height (0.724** and 0.608**), cob diameter (0.651** and 0.477*), kernel per cob (0.562** and 0.418*) and grain yield/plant (0.526** and 0.457*) at both the genotypic and phenotypic levels, respectively.

Cob height showed highly positive significant correlation with grain yield/plant (0.755** and 0.636**) followed by kernel per cob (0.726** and 0.658**), number of kernel per row (0.660** and 0.572**) and cob diameter (0.620** and 0.522**) at both the genotypic and phenotypic levels, respectively. Cob height also showed positive significant correlation with cob length (0.462*) and seed index (0.418*) at genotypic level only.

Cob length exhibited highly positive significant correlation with grain yield/plant (0.974** and 0.838**) followed by seed index (0.787** and 0.598**), kernel per cob (0.741** and 0.649**) number of kernel per row (0.679** and 0.632**) cob diameter (0.544** and 0.476*) at both the genotypic and phenotypic levels, respectively.

Cob diameter exhibited positive significant correlation with grain yield/plant (0.772** and 0.618**) followed by seed index (0.628** and 0.456*), kernel per cob (0.489* and 0.423*) and number of kernel per row (0.475* and 0.410*) at both the genotypic and phenotypic levels, respectively.

Kernel per cob exhibited positive significant correlation with number of kernel per row (0.932** and 0.815**) at both the genotypic and phenotypic levels, respectively. Also kernel per cob exhibited positive significant correlation with grain yield/plant (0.788**) at phenotypic level only.

Number of kernel per row exhibited high positive significant correlation with grain yield/plant (0.745** and 0.687**) at both the genotypic and phenotypic levels, respectively. Seed Index also exhibited positive significant correlation with grain yield/plant (0.636** and 0.621**) at both the genotypic and phenotypic levels, respectively.

The above findings of correlation indicate that the plant height, cob height, cob length, cob diameter number of kernel per row, and seed index showed high significant correlation with grain yield/plant will also show better performance in terms of grain yield. This indicated that possibility of simultaneous improvement of these traits by a single selection programme. The association of grain yield was also reported by **Murthy & Roy (1957)**, & **Rupak et al. (1979)**. Also **Najeeb et al. (2009)**, **Parvez and Rather (2004)**, **Jayakumar et al. (2007)**, **Venugopal et al. (2003)**, **Venkatesh et al. (2003)**, **Manivannan (1998)**. **Umakanth et al. (2000)**, **Hossian et al. (2004)** reported that grain weight was positively and highly significantly correlated with plant height, number of leaves per plant, weight of cobs, grain weight and 100 grain weight and positive and significantly correlated with number of cobs per plant. Highly significant positive correlation was between ear girth and grain weight supports the present findings. Also similar results was reported by **Jawaharlal et al. (2011)**, for Grain yield and **Bello & Olaoye (2009)**, **Shalyagina (1990)**, & **Nemati et al. (2009)** for number of seeds per ear & 100 seed weight.

Path coefficient analysis:

The yield is determined by a combination of various component characters that have a direct or indirect impact on it. The correlation studies revealed a mutual association among the characters, while the path coefficient analysis helps in understanding the specific contributions of each character to the final yield, such as grain yield. By partitioning the correlation coefficient into direct and indirect effects, we can gain insights into how other characters affect the grain yield. The genotypic and phenotypic correlation coefficients of seed yield with the other characters were further analyzed through path coefficient analysis, with the results presented in Table 3, Table 4, Figure 1, and Figure 2.

Path coefficient analysis revealed that seed index (0.7036) followed by days to maturity (0.478), plant height (0.2462), days to 50% pollen shedding (0.2249), number of kernel per row (0.1972) and cob height (0.114) had exerted maximum direct effect on seed yield at genotypic level. Kernel per cob (-0.6234) and cob diameter (-0.365) had exhibited negative direct effect on seed yield at genotypic level.

Plant height (0.1085) via days to 50% pollen shedding, seed index (0.3003) and plant height (0.2001) via days to 50% silking, seed index (0.3228) and plant height (0.1502) via length of flag leaf, no of kernel per row (0.2831) and seed index (0.2239) via plant height, no of kernel per row (0.7897), seed index (0.2942) and plant height (0.1781) via cob height, no of kernel per row (0.8127) and seed index (0.5535) via cob length, no of kernel per row (0.5681), seed index (0.4415), plant height (0.1603) and day to maturity (0.106) via cob diameter, plant height (0.1385), seed index (0.1216) and no of kernel per row (0.1155) via kernel per cob, seed index (0.118) via no of kernel per row, no of kernel per row (0.2008) via seed index had exerted substantial positive indirect effect on seed yield per plant at genotypic level. The R Square and Residual effect was (0.9051 and 0.3081), respectively at genotypic level.

At phenotypic level, path coefficient analysis revealed that kernel per cob (0.4462) followed by cob length (0.3198), seed index (0.2805), cob diameter (0.1711) and plant height (0.0815) had exerted maximum direct effect on seed yield. Number of kernel per row (-0.0616), day to maturity (-0.0334) and days to 50% silking (-0.115) had exhibited negative direct effect on seed yield at genotypic level.

Kernel per cob (0.1229) via days to 50% pollen shedding, seed index (0.1013) via length of flag leaf, kernel per cob (0.1868) via plant height, kernel per cob (0.2936) and cob length (0.1237) via cob height, kernel per cob (0.2899) and seed index (0.1678) via cob length, kernel per cob (0.1891), cob length (0.1522) and seed index (0.128) via cob diameter, cob length (0.2077) via kernel per cob, kernel per cob (0.3639) and cob length (0.2022) via number of kernel per row, cob length (0.1912) via seed index had exerted substantial positive indirect effect on seed yield per plant at phenotypic level. The R Square and Residual effect was (0.9206 and 0.2818), respectively. Residual effect value

was moderate and indicating that some of characters affecting seed yield has to be include in the future study.

On the basis of path coefficient analysis showed that seed index followed by days to maturity, plant height, days to 50% pollen shedding, number of kernel per row and cob height were important characters that could be taken into consideration for selection and improvement of seed yield in maize. The above findings of the path studies are in accordance with the findings of **Mohammadi *et al.* (2003)**, **Aycicek & Yildirim (2006)** & **Pavan *et al.* (2011)**. **Shi *et al.* (2008)** for ear height, seed index and kernel numbers per row; **Bello *et al.* (2010)** for ear weight and number of grains per ear; **Seyedzavar *et al.* (2015)** for number of rows per ear **Begum *et al.* (2016)** for plant height, ear length and kernel rows per ear. Ear length had the lowest positive direct effect on grain yield. In contrast, to this high positive direct effect was observed by **Reddy *et al.* (2012)** for Days to 50% anthesis and anthesis-silking interval, ear girth exhibited a direct and negative effect.

Table 1. Analysis of variance for twelve quantitative characters in Maize.

Source of Variation	Degree of Freedom	Mean sum of squares											
		Day to 50% pollen shedding	Day to 50% silking	Length of flag leaf	Day to maturity	Plant Height	Cob Height	Cob length	Cob Diameter	No of Kernel per Cob	No of kernel per row	Seed Index	Grain Yield/Plant
Replication	2	2.176	367.258	0.389	14.432	8202.346	743.108	4.435	0.402	6762.838	62.401	169.846	365.632
Treatments	25	81.211**	22.672**	206.274**	156.237**	1761.324**	841.277**	6.566**	2.396**	12081.098**	85.142**	27.985**	1060.315**
Error	50	1.636	6.398	3.868	8.609	557.989	109.369	1.063	0.453	1584.614	10.267	9.416	210.424

*Significant at 5% probability level.

**Significant at 1% probability level.

Table 2. Genotypic and Phenotypic correlation coefficient for 12 quantitative traits in maize.

Traits	Ch. 1	Ch. 2	Ch. 3	Ch. 4	Ch. 5	Ch. 6	Ch. 7	Ch. 8	Ch. 9	Ch. 10	Ch. 11	Ch. 12	
Ch. 1	Gen	1.000	0.412*	0.198	-0.040	0.441*	0.118	0.135	0.107	0.297	0.049	0.134	0.298
	Phe	1.000	0.357	0.189	-0.039	0.341	0.097	0.130	0.093	0.275	0.057	0.108	0.262
Ch. 2	Gen		1.000	0.122	-0.190	0.813**	0.154	0.212	0.604**	-0.121	-0.200	0.427*	0.207
	Phe		1.000	0.100	-0.150	0.425*	0.096	0.134	0.431*	-0.092	-0.199	0.237	0.105
Ch. 3	Gen			1.000	-0.231	0.611**	0.396*	0.184	0.071	0.172	-0.026	0.459*	0.358
	Phe			1.000	-0.218	0.478*	0.366	0.167	0.073	0.158	-0.035	0.361	0.319
Ch. 4	Gen				1.000	0.188	-0.057	0.080	0.222	0.198	0.012	-0.389*	0.029
	Phe				1.000	0.155	-0.054	0.066	0.210	0.184	0.024	-0.282	0.046
Ch. 5	Gen					1.000	0.724**	0.246	0.651**	0.562**	0.237	0.318	0.526**
	Phe					1.000	0.608**	0.177	0.477*	0.418*	0.222	0.252	0.457*
Ch. 6	Gen						1.000	0.462*	0.620**	0.726**	0.660**	0.418*	0.755**
	Phe						1.000	0.387	0.522**	0.658**	0.572**	0.299	0.636**
Ch. 7	Gen							1.000	0.544**	0.741**	0.679**	0.787**	0.974**
	Phe							1.000	0.476*	0.649**	0.632**	0.598**	0.838**
Ch. 8	Gen								1.000	0.489*	0.475*	0.628**	0.772**
	Phe								1.000	0.423*	0.410*	0.456*	0.618**
Ch. 9	Gen									1.000	0.932**	0.173	0.870
	Phe									1.000	0.815**	0.131	0.788**
Ch. 10	Gen										1.000	0.168	0.745**
	Phe										1.000	0.198	0.687**
Ch. 11	Gen											1.000	0.636**
	Phe											1.000	0.621**
Ch. 12	Gen												1.000
	Phe												1.000

*Significant at 5% probability level. **Significant at 1% probability level.

Ch-1= Day to 50% pollen shedding, Ch-2= Days to 50% silking, Ch-3= Length of flag leaf, Ch-4= Day to maturity, Ch-5= Plant Height, Ch-6= Cob Height, Ch-7= Cob length, Ch-8= Cob Diameter, Ch-9= Kernel per Cob, Ch-10= No of kernel per row, Ch-11= Seed Index, Ch-12= Grain Yield/Plant

Table 3. Direct and indirect effect for different characters on seed yield per plant at genotypic level in maize.

S.N.	Trait	Ch. 1	Ch. 2	Ch. 3	Ch. 4	Ch. 5	Ch. 6	Ch. 7	Ch. 8	Ch. 9	Ch. 10	Ch. 11	Ch. 12
1	Ch. 1	0.2249	0.0927	0.0445	-0.009	0.0991	0.0266	0.0304	0.0241	0.0667	0.0111	0.0302	0.2978
2	Ch. 2	0.021	0.0511	0.0062	-0.0097	0.0415	0.0078	0.0108	0.0308	-0.0062	-0.0102	0.0218	0.2066
3	Ch. 3	0.0103	0.0064	0.0523	-0.0121	0.0319	0.0207	0.0096	0.0037	0.009	-0.0014	0.024	0.3583
4	Ch. 4	-0.0191	-0.0906	-0.1105	0.478	0.0897	-0.0272	0.0384	0.106	0.0945	0.0059	-0.186	0.0293
5	Ch. 5	0.1085	0.2001	0.1502	0.0462	0.2462	0.1781	0.0605	0.1603	0.1385	0.0582	0.0783	0.526
6	Ch. 6	0.0135	0.0175	0.0451	-0.0065	0.0825	0.114	0.0527	0.0707	0.0828	0.0752	0.0477	0.7553
7	Ch. 7	0.0089	0.0139	0.0121	0.0053	0.0162	0.0304	0.0658	0.0358	0.0488	0.0447	0.0518	0.9742
8	Ch. 8	-0.039	-0.2203	-0.0257	-0.0809	-0.2376	-0.2264	-0.1984	-0.365	-0.1782	-0.1732	-0.229	0.7716
9	Ch. 9	-0.1848	0.0754	-0.1074	-0.1232	-0.3506	-0.4528	-0.4618	-0.3043	-0.6234	-0.5808	-0.1077	0.8697
10	Ch. 10	0.059	-0.2398	-0.0313	0.0149	0.2831	0.7897	0.8127	0.5681	0.1155	0.1972	0.2008	0.7448
11	Ch. 11	0.0945	0.3003	0.3228	-0.2737	0.2239	0.2942	0.5535	0.4415	0.1216	0.118	0.7036	0.6355

R Square = 0.9051

Residual effect = 0.3081

Ch-1= Day to 50% pollen shedding, Ch-2= Days to 50% silking, Ch-3= Length of flag leaf, Ch-4= Day to maturity, Ch-5= Plant Height, Ch-6= Cob Height, Ch-7= Cob length, Ch-8= Cob Diameter, Ch-9= Kernel per Cob, Ch-10= No of kernel per row, Ch-11= Seed Index, Ch-12= Grain Yield/Plant

Note: Diagonal & Bold font = Direct path

Table 4. Direct and indirect effect for different characters on seed yield per plant at phenotypic level in maize.

S.N.	Trait	Ch. 1	Ch. 2	Ch. 3	Ch. 4	Ch. 5	Ch. 6	Ch. 7	Ch. 8	Ch. 9	Ch. 10	Ch. 11	Ch. 12
1	Ch. 1	0.0597	0.0213	0.0113	-0.0023	0.0204	0.0058	0.0078	0.0055	0.0164	0.0034	0.0064	0.2618
2	Ch. 2	-0.0411	-0.115	-0.0115	0.0173	-0.0489	-0.011	-0.0154	-0.0496	0.0106	0.0229	-0.0273	0.1052
3	Ch. 3	0.0045	0.0024	0.0236	-0.0051	0.0113	0.0087	0.004	0.0017	0.0037	-0.0008	0.0085	0.3189
4	Ch. 4	0.0013	0.005	0.0073	-0.0334	-0.0052	0.0018	-0.0022	-0.007	-0.0061	-0.0008	0.0094	0.0461
5	Ch. 5	0.0278	0.0347	0.039	0.0126	0.0815	0.0496	0.0144	0.039	0.0341	0.0181	0.0205	0.4566
6	Ch. 6	0.0025	0.0025	0.0094	-0.0014	0.0156	0.0256	0.0099	0.0134	0.0169	0.0146	0.0076	0.6356
7	Ch. 7	0.0416	0.0428	0.0535	0.0212	0.0565	0.1237	0.3198	0.1522	0.2077	0.2022	0.1912	0.8383
8	Ch. 8	0.0159	0.0738	0.0125	0.0359	0.0818	0.0894	0.0815	0.1711	0.0725	0.0702	0.0781	0.6182
9	Ch. 9	0.1229	-0.0411	0.0703	0.0819	0.1868	0.2936	0.2899	0.1891	0.4462	0.3639	0.0582	0.7884
10	Ch. 10	-0.0035	0.0123	0.0021	-0.0015	-0.0137	-0.0352	-0.039	-0.0253	-0.0502	-0.0616	-0.0122	0.6875
11	Ch. 11	0.0302	0.0666	0.1013	-0.079	0.0706	0.0837	0.1678	0.128	0.0366	0.0555	0.2805	0.6212

R Square = 0.9206

Residual effect = 0.2818

Ch-1= Day to 50% pollen shedding, Ch-2= Days to 50% silking, Ch-3= Length of flag leaf, Ch-4= Day to maturity, Ch-5= Plant Height, Ch-6= Cob Height, Ch-7= Cob length, Ch-8= Cob Diameter, Ch-9= Kernel per Cob, Ch-10= No of kernel per row, Ch-11= Seed Index, Ch-12= Grain Yield/Plant

Note: Diagonal & Bold font = Direct path

Genotypical Path Diagram for Grain Yield/Plant

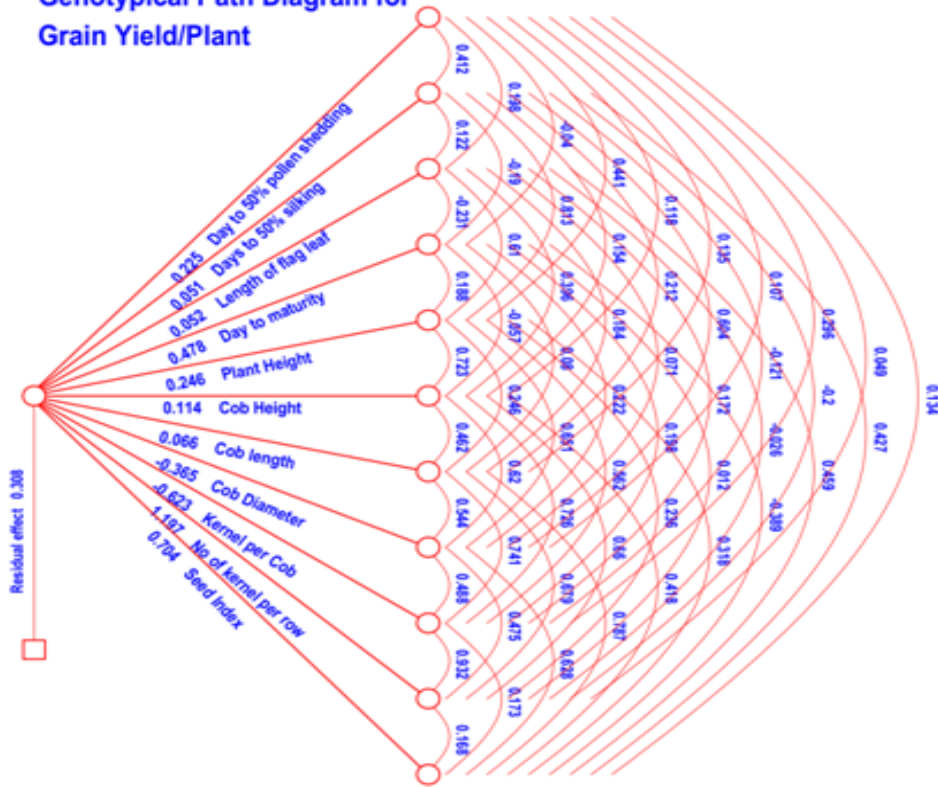


Figure 1. Genotypic path diagram

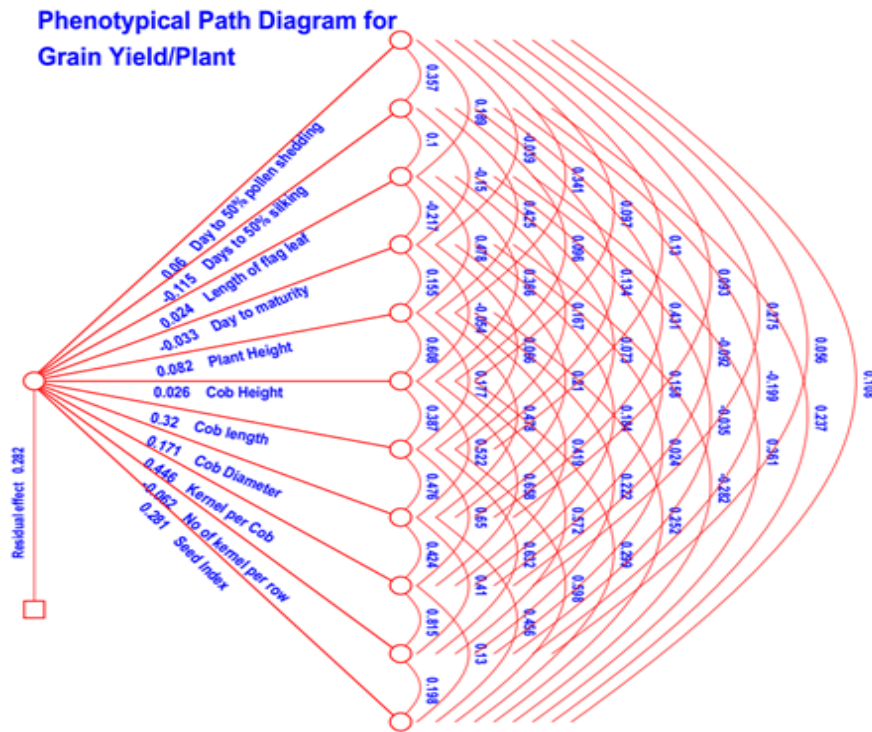


Figure 2. Phenotypic path diagram

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