

Critical Analysis of Correlation and Direct and Indirect Effects of Some Economic Characters in Silkworm (*Bombyx mori* L.)

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ABSTRACT

*Ten economic traits were taken to detect the relationship as well as find out direct and indirect effects among the characters of ten silkworm (*Bombyx mori* L.) lines. Correlation analysis revealed that Y/100 DFSL showed a positive correlation with all the characters except SR% at both the phenotypic and genotypic levels. But Y/100 DFSL significantly correlated with all the characters except renditta at both the phenotypic and genotypic levels indicating the effectiveness for directional selection for genetic improvement of yield and suggested that with the increases of those characters Y/100 DFSL will be increased. In case of path coefficient analysis, characters ERRwt, SSwt and denier at phenotypic level and all the characters except Wt10ML and SSwt at genotypic level exhibited a direct positive effect on Y/100 DFSL which revealed their contribution to the yield and selection can be made by using these characters. It was noted that in path coefficient analysis ERRwt showed the highest direct effect on Y/100 DFSL both at phenotypic and genotypic levels. From the results of correlation and path coefficient analysis, it can be concluded that ERRwt was the most important yield contributing character as it exhibited significant positive correlation and highest direct effect on Y/100 DFSL both at phenotypic and genotypic levels followed by denier since denier showed positive direct effect both at genotypic and phenotypic levels.*

Keywords: *Correlation, Direct and Indirect Effects, Silkworm.*

INTRODUCTION

Silkworm (*Bombyx mori* L.) which is a domesticated insect reared by the farmers to produce silk is one of the most economically important insects because of its importance in the silk industry. Sericulture provides gainful employment, economic development and improvement in the quality of life of the

people in rural areas and therefore plays an important role in anti-poverty programme in several developing countries and also plays an important role in the national economy of Bangladesh (FAO, 2003). The cultivation of mulberry plant, rearing of silkworm, reeling and weaving of silk provide employment to millions of people.

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As sericulture holds the merit of employment generation through its different steps of activities the government has taken sericulture as one of the potential sectors for employment generation, poverty reduction and women empowerment. Sericulture, therefore, has all the amenities and facilities to become a major caretaker of the rural economy of Bangladesh. The soil and the climatic condition, availability of land especially in hilly region, labour, unemployment and existence of wide agricultural tradition are the major advantages for exploiting sericulture in the country and because of these advantages, 505 hectare of land is under mulberry plantation with 418.00 MT annual cocoon production as well as 41.60 MT raw silk productions (Rahman, 2015). Looking to the importance of this crop, greater attention is needed for its improvement. In this regard, efforts should be made to develop high yielding varieties through breeding research. The aim of silkworm breeding is the genetic improvement of economic traits of silkworm to increase profitability and to provide benefits to the sericulture industry. The success of a breeding programme depends on the consequence of the genetic variability in the breeds and their proper utilization. The estimation of genetic parameters such as correlation and path co-efficient analysis is essential to achieve the success of a breeding programme and to predict the contingencies up to which level a particular character could be improved. In case of character selection, the knowledge of genotypic and phenotypic association within and between yield and yield contributing characters plays an important role as yield is the ultimate objective to the breeders.

Correlations between traits are a measurement of the degree of common factors causing the variation in each of two traits while genetic correlation in particular is of great importance in a breeding programme and provides an understanding of the genetic background of each trait with more accurate predictions of breeding values (Talebi et al., 2010). Again path co-efficient analysis has been useful in identifying indirect selection criteria for complex quantitative traits in crops as well

as animal breeding programmes because correlations do not always mean causal relationships and complex traits can be better studied as cumulative influences direct and indirect of component trait. For the improvement of yield and yield contributing traits, it will be helpful in effective selection. Therefore, the present investigation was taken to estimate the relationship of various traits of ten silkworm lines and to find out direct and indirect effects of the yield components towards yield and it is hoped that results obtained herein would be of value for silkworm breeders.

MATERIALS AND METHODS

Ten multivoltine lines, viz. BSR-03/5(P), BSR-04/4, BSR-05/2, BSR-05/4(M), BSR-06/4(SL), BSR-07/2(P), BSR-07/2(P)GY, BSR-08/2(W), BSR-08/5 and BSR-(W) were drawn from the germplasm bank of Bangladesh Sericulture Research and Training Institute (BSRTI), Rajshahi and were reared in four rearing seasons considered as environment viz. Jaistha-E₁ (May-June'18), Bhaduri-E₂ (August-September'18), Agrahayoni-E₃ (October-November'18) and Chaita-E₄ (February-March'19) in the laboratory of BSRTI, Rajshahi.

In each season, 5 DFLS (disease free layings) of each race was brushed separately and reared up to 2nd moult in mass bed. After that all the races were reared in two replications each with 300 larvae retained after 2nd moult. Rearing was done in control weather suggested by Krishnaswami (1978) and Rahman (1983). The data on 10 quantitative traits such as weight of 10 mature larvae (Wt10ML), effective rate of rearing by number (ERRno), effective rate of rearing by weight (ERRwt), yield per 100 disease free laying (Y/100 DFLS), single cocoon weight (SCwt), single shell weight (SSwt), shell ratio% (SR%), length of filament (LF), denier and renditta were recorded and evaluated. The collected data were analyzed following the biometrical technique of analysis as developed by Mather (1949) based on the mathematical model of Fisher et al. (1932). Again, for the

study of correlation and path coefficient, the analysis of both variance and co-variances are required Miller et al. (1958). Therefore, co-variances were calculated between all possible pairs of characters. The path-coefficient analysis was carried out using the formula of Wright (1921 & 1923) as illustrated by Dewey and Lu (1959). Analysis of correlation coefficient and path-coefficient are as follows:

I. Character association

Correlation coefficient at phenotypic (r_p) and genotypic (r_g) levels were estimated following Singh and Chaudhary (1976) as follows:

$$r_p = \sigma^2 P_{12} / (\sigma^2 P_{11} \times \sigma^2 P_{22})^{1/2},$$

$$r_g = \sigma^2 G_{12} / (\sigma^2 G_{11} \times \sigma^2 G_{22})^{1/2}$$

Where, $\sigma^2 P_{12}$ and $\sigma^2 G_{12}$ represent phenotypic and genotypic covariance of character 1 and 2, $\sigma^2 P_{11}$ and $\sigma^2 G_{11}$ represent phenotypic and genotypic variances of character 1 and $\sigma^2 P_{22}$ and $\sigma^2 G_{22}$ represent phenotypic and genotypic variances of character 2.

II. Path-coefficient

The path-coefficient analysis was done both at phenotypic and genotypic levels by solving the simultaneous equation using matrix algebra as follows:

$$r_{xy} = p_{xy} + r_{x2} p_{2y} + r_{x3} p_{3y} + \dots + r_{xn} p_{ny}$$

Where, r_{xy} = correlation between one component's character and yield, p_{xy} = path-coefficient between the same character and yield and $r_{x2}, r_{x3}, \dots, r_{xn}$ = represent correlation coefficient between that character and each of the other yield component in turn.

RESULTS AND DISCUSSION

In the present investigation, correlation studies showed that genotypic correlation was higher than the respective phenotypic correlation in most of the cases (Table 1). This situation was also marked in the path-coefficient analysis. The high genotypic correlation indicated the strong inherent associations between pairs of characters which do not always reflect the nature and magnitude of phenotypic variation. A higher magnitude of genotypic correlation than phenotypic one was also found by several workers viz. Kumaresan et al. (2000), Ahsan and Rahman (2008), Ahsan et al. (2010),

Talebi and Subramanya (2010) and Ahsan (2010 & 2011) in silkworm.

In the present work, trait Y/100 DFSLs showed positive significant correlation with all the characters except SR% and renditta while SR% showed a negative but significant correlation and renditta expressed positive but non-significant correlation with Y/100DFSLs both at the phenotypic and genotypic levels. But Y/100 DFSLs significantly correlated with all the characters except renditta both at the phenotypic and genotypic levels. The above information indicates that these characters are genetically related with Y/100 DFSLs more than those of the other yield components. The significant correlation of Y/100 DFSLs with these characters indicated the effectiveness of directional selection for genetic improvement of yield and suggested that Y/100 DFSLs will be increased with the increase of those characters. The character Wt10ML was positively correlated with ERRno, ERRwt, SCwt, SSwt, LF and denier both at phenotypic and genotypic levels. The highest correlation value was observed when Wt10ML was correlated with SCwt at phenotypic level and SSwt at genotypic levels. And Wt10ML significantly correlated with all the characters except SR% and renditta at phenotypic level. ERRno expressed positive and significant correlation with all the characters both at phenotypic and genotypic levels except LF at phenotypic level and SR% and renditta both at phenotypic and genotypic levels. SR% and renditta showed a negative correlation with this character while SR% was significantly correlated with ERRno but renditta showed a non-significant correlation. ERRno exhibited the highest correlation value with ERRwt both at phenotypic and genotypic levels. ERRwt showed a negative correlation with SR% both at phenotypic and genotypic levels and the rest of the characters were positively correlated with ERRwt at both the phenotypic and genotypic levels. The correlation value was higher when ERRwt correlated with SR%. In this case only renditta was non-significantly correlated with this character.

The character SCwt was significantly correlated with all the characters both at phenotypic and genotypic levels except renditta at the phenotypic level. Again SCwt expressed a negative correlation with SR% at both the levels and with renditta at the phenotypic level. Further correlation value was higher between SCwt and SSwt in case of this character. SSwt significantly correlated with LF and denier both at phenotypic and genotypic levels while this character showed significant result with SR% at phenotypic level. All the values were positive except its correlation with SR% at the genotypic level and renditta at both levels. In case of SR%, the character was significantly correlated with all the characters and positive correlation was exhibited with only LF at both the levels. LF expressed significant but negative correlation with denier and renditta both at phenotypic and genotypic level while denier showed significant positive correlation with renditta at both the levels. A significant and positive correlation was found by different workers such as Kumaresan et al. (2000), Ahsan and Rahman (2008), Ahsan et al. (2010), Talebi and Subramanya (2010), Seidavi (2010) and Ahsan (2010 & 2011) in silkworm.

The correlation coefficient was partitioned into direct and indirect effects by path analysis (Table 2 and Table 3 as well as Figure 1 and Figure 2). Characters ERRwt, SSwt and denier at phenotypic level and all the characters except Wt10ML and SSwt at genotypic level exhibited a direct positive effect on Y/100 DFSL that means they contribute to the yield and hence selection can be made by using these traits. On the other hand, traits viz. Wt10ML, ERRno, SCwt, SR%, LF and renditta at phenotypic level and Wt10ML and SSwt at genotypic level showed a negative direct effect on Y/100 DFSL. These characters also failed to contribute to yield due to its negative direct effect and thus, an increase of yield through direct selection for these traits should be avoided whereas indirect selection should be more appropriate to apply. Trait ERRwt

followed by denier showed the highest direct effect on Y/100 DFSL both at phenotypic and genotypic levels.

From the Table 2 and 3 it was found that Wt10ML had the negative direct effect of -0.1310 on Y/100 DFSL at phenotypic level while at genotypic level the direct effect was -0.0797. The character had negative indirect effect via ERRno, SCwt and LF at the phenotypic level and via SSwt, SR% and renditta at the genotypic level. ERRno had a negative direct effect on Y/100 DFSL at the phenotypic level and a positive direct effect at the genotypic level. In this case positive indirect effect was observed via ERRwt, SSwt, SR%, denier and renditta at phenotypic level and via ERRwt, SCwt, LF and denier at phenotypic level. The positive direct effect of ERRwt on Y/100 DFSL was 1.5483 and 1.1063 at phenotypic and genotypic levels, respectively which were the highest positive direct effect among all the characters. The character expressed positive indirect effect via SSwt, SR% and denier at phenotypic level and via ERRno, SCwt, LF, denier and renditta at genotypic level. SCwt expressed a negative direct effect on Y/100 DFSL at phenotypic level while at genotypic level the character exhibited a positive direct effect. At the phenotypic level, the character exhibited a positive indirect effect via ERRwt, SSwt, SR%, denier and renditta while via all the characters except Wt10ML, SSwt and SR% at the genotypic level. Regarding SSwt the direct effect was positive at the phenotypic level but at a genotypic level, the character showed a negative direct effect. This character showed a positive indirect effect via ERRwt, denier and renditta at phenotypic level and via ERRno, ERRwt, SCwt, LF and denier at genotypic level. In the result of SR% the direct effect was found to be as negative at the phenotypic level and positive at the genotypic level. SR% expressed positive indirect effect via Wt10ML, ERRno, SCwt, SSwt and renditta at phenotypic level and via Wt10ML, SSwt and LF. The character LF exhibited a negative direct effect at the phenotypic level and in

case of genotypic level, the value was positive. In respect of indirect effect positive value was expressed via ERRwt, SSwt and renditta at the phenotypic level and via ERRno, ERRwt, SCwt and SR% at the genotypic level. Denier showed a positive direct effect both at the phenotypic and genotypic levels. This character showed positive indirect effect via ERRwt, SSwt, SR% and LF at phenotypic level and via ERRno, ERRwt, SCwt and renditta. The character renditta expressed a negative direct effect on Y/100 DFLS at the phenotypic level but a positive direct effect at the genotypic level. Renditta had an indirect positive effect through all the characters except SSwt at phenotypic level and ERRno, SR% and LF at genotypic level.

Path analysis revealed that characters ERRwt, SSwt and denier exhibited a positive direct effect on Y/100 DFLS at phenotypic level and all the characters except Wt10ML and SSwt at the genotypic level indicating their contribution to the yield and with the help of these characters effective selection can be done. On the other hand characters with negative direct effects should be avoided because of their poor contribution to yield whereas in this situation indirect selection should be suitable to apply. These results are in agreement with the findings of Mukherjee et al. (2000), Jayaswal et al. (2001), Bashir et al. (2015) and Chandrakanth et al. (2016).

Table 1: Phenotypic (r_p) and genotypic (r_g) correlation coefficients between yield and yield contributing characters in silkworm

Characters	ERRno	ERRwt	SCwt	SSwt	SR%	LF	Denier	Renditta	Y/100 DFLS	
Wt10 ML	0.5852**	0.8089**	0.8686**	0.7315**	-0.1737 ^{NS}	0.3627*	0.5803**	-0.0794 ^{NS}	0.8017**	P
	0.8581**	0.9253**	0.9740**	0.9896**	-0.2407*	0.4434*	0.7245**	-0.2050*	0.9231**	G
ERR no.		0.9008**	0.5642**	0.2952**	-0.3957**	0.1626 ^{NS}	0.3898**	-0.0442 ^{NS}	0.9016**	P
		0.9967**	0.9575**	0.8045**	-0.6190**	0.3136**	0.7849**	-0.0004 ^{NS}	0.9977**	G
ERRwt.			0.8155**	0.5468**	-0.4024**	0.1874*	0.5700**	0.0496 ^{NS}	0.9996**	P
			0.9949**	0.8916**	-0.5031**	0.3251**	0.7775**	0.1539 ^{NS}	0.9999**	G
SCwt				0.8029**	-0.2827**	0.2921**	0.6641**	-0.0204 ^{NS}	0.8124**	P
				0.8979**	-0.4851**	0.3283**	0.7598**	0.3665**	0.9953**	G
SSwt					0.2745**	0.5021**	0.3763**	-0.0053 ^{NS}	0.5414**	P
					-0.0508 ^{NS}	0.6285**	0.4456**	-0.1586 ^{NS}	0.8913**	G
SR%						0.4241**	-0.4964**	-0.4058**	-0.4048**	P
						0.4179**	-0.7719**	-0.9975**	-0.5072**	G
LF							-0.3514**	-0.6874**	0.2662**	P
							-0.3685**	-0.9032**	0.3239**	G
Denier								0.2583**	0.5694**	P
								0.9729**	0.7763**	G
Renditta									0.0579 ^{NS}	P
									0.1680 ^{NS}	G

Where, NS, * and ** indicate non-significant, significant at 5% and 1% levels, respectively.

Table 2: Path coefficient analysis of yield and yield contributing characters in silkworm at phenotypic level

Characters	Wt10 ML	ERRno	ERRwt	SCwt	SSwt	SR%	LF	Denier	Renditta	Total effect
Wt10 ML	-0.1310	-0.2017	1.2524	-0.9618	0.6987	0.1079	-0.0148	0.0243	0.0280	0.8019
ERR no.	-0.0767	-0.3447	1.3946	-0.6248	0.2819	0.2458	-0.0066	0.0163	0.0156	0.9015
ERRwt.	-0.1060	-0.3105	1.5483	-0.9030	0.5222	0.2500	-0.0076	0.0238	-0.0180	0.9997
SCwt	-0.1138	-0.1945	1.2627	-1.1073	0.7669	0.1756	-0.0119	0.0278	0.0072	0.8126
SSwt	-0.0958	-0.1017	0.8466	-0.8891	0.9551	-0.1700	-0.0205	0.0157	0.0019	0.5416
SR%	0.0228	0.1364	-0.6230	0.3130	0.2621	-0.6210	-0.0173	-0.0210	0.1432	-0.4050
LF	-0.0475	-0.0560	0.2902	-0.3234	0.4795	-0.2630	-0.0408	-0.0150	0.2426	0.2665
Denier	-0.0760	-0.1344	0.8825	-0.7354	0.3594	0.3083	0.01430	0.0418	-0.0910	0.5694
Renditta	0.0104	0.0152	0.0769	0.0225	-0.0050	0.2521	0.0280	0.0108	-0.3530	0.0579

Residual effect: 0.0816

Table 3: Path coefficient analysis of yield and yield contributing characters in silkworm at genotypic level

Characters	Wt10 ML	ERRno	ERRwt	SCwt	SSwt	SR%	LF	Denier	Renditta	Total effect
Wt10 ML	-0.0797	0.0033	1.0237	0.3185	-0.4250	-0.0540	0.0559	0.0840	-0.0040	0.9230
ERR no.	-0.0684	0.0038	1.1027	0.3131	-0.3460	-0.1380	0.0395	0.0910	-0.000007	0.9977
ERRwt.	-0.0738	0.0038	1.1063	0.3253	-0.3830	-0.1120	0.0410	0.0901	0.0027	0.9999
SCwt	-0.0777	0.0037	1.1007	0.3269	-0.3860	-0.1080	0.0414	0.0881	0.0064	0.9953
SSwt	-0.0789	0.0031	0.9864	0.2936	-0.4300	-0.0110	0.0793	0.0517	-0.0030	0.8912
SR%	0.0192	-0.0024	-0.5570	-0.1586	0.0218	0.2234	0.0527	-0.0890	-0.0170	-0.5070
LF	-0.0354	0.0012	0.3597	0.1073	-0.2700	0.0934	0.1261	-0.0430	-0.0160	0.3239
Denier	-0.0578	0.0030	0.8602	0.2484	-0.1920	-0.1720	-0.0465	0.1159	0.0169	0.7762
Renditta	0.0163	-0.000001	0.1704	0.1198	0.0682	-0.2230	-0.1139	0.1128	0.0174	0.1681

Residual effect: 0.0249

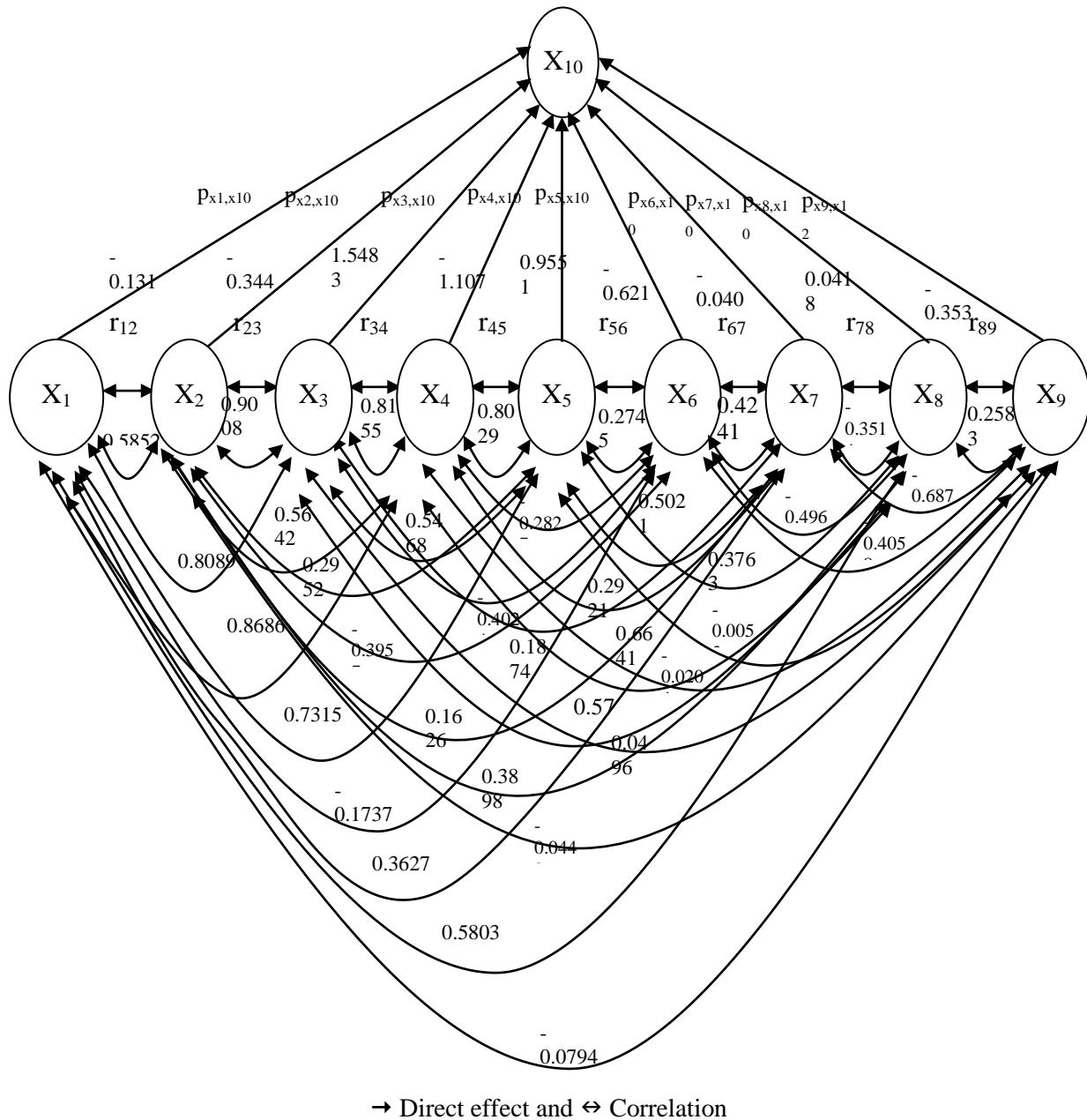


Fig. 1: Path diagram of different yield contributing characters on yield at phenotypic level

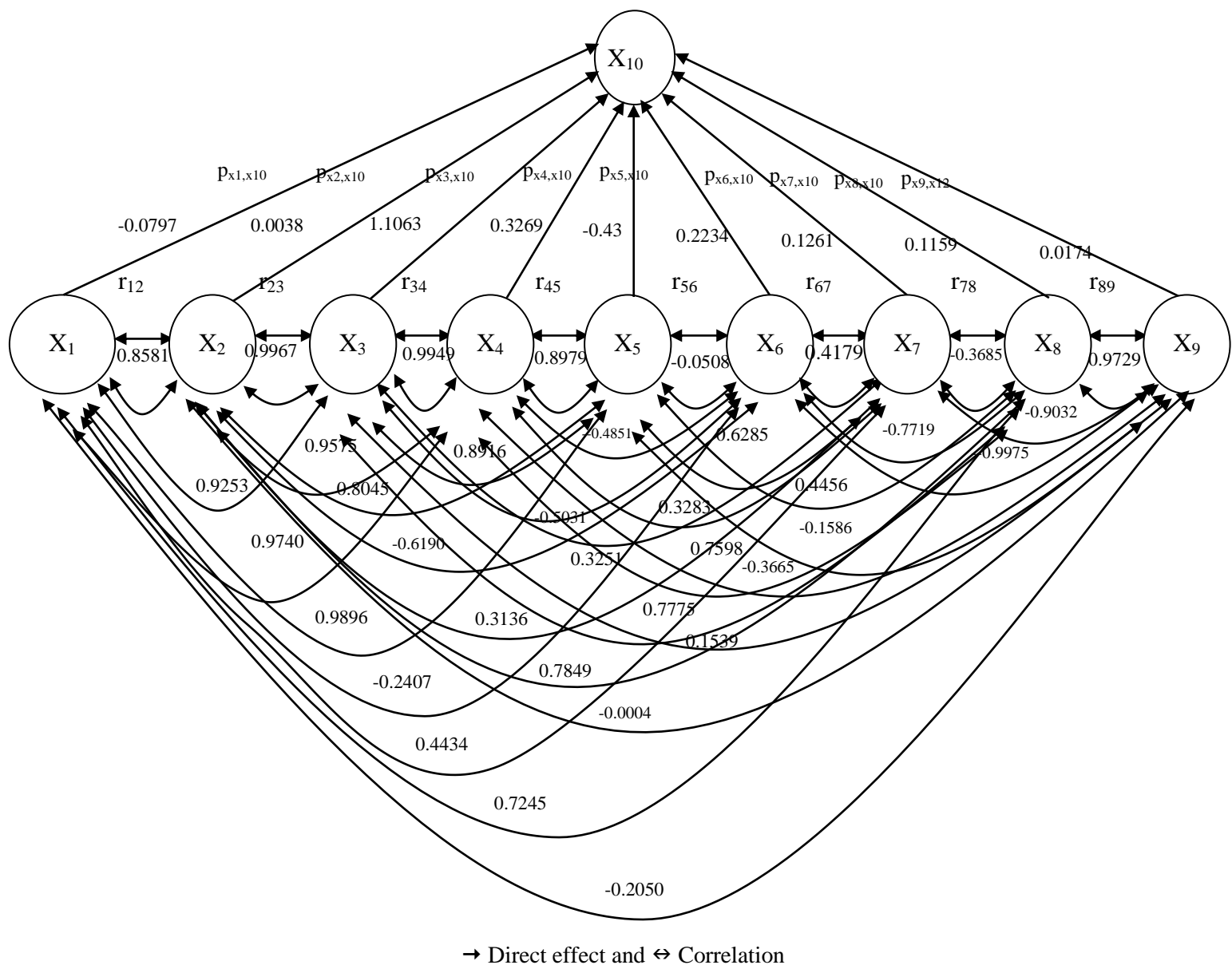


Fig. 2: Path diagram of different yield contributing characters on yield at genotypic level

CONCLUSION

In this study, Y/100 DFSLs showed a positive correlation with all the characters except SR% at both the phenotypic and genotypic levels. Again, Y/100 DFSLs significantly correlated with all the characters except renditta at both the phenotypic and genotypic levels. From the path analysis, ERRwt followed by denier showed the highest direct effect on Y/100 DFSLs both at phenotypic and genotypic levels. From the results of correlation and path coefficient analysis, it can be concluded that ERRwt was the most important yield contributing character as it exhibited significant positive correlation and highest

direct effect on Y/100 DFSLs both at phenotypic and genotypic levels followed by denier showed positive direct effect both at phenotypic and genotypic levels.

Disclosure Statement

No potential conflict of interest was reported by the authors.

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