

Path Analysis, Genetic Variability and Correlation Studies of Related Characters for Forage

Soybean (Glycine max (L.) Merill)

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Research Article

ABSTRACT

Article History: Received: 18.01.2023 Accepted: 06.04.2023 Published online: 05.07.2023

Keywords: Path analysis Genetic variation Soybean Heritability Correlation variability, reveal the genetic correlation among the traits and partition the genetic correlations into direct and indirect effects so as to estimate the direct and indirect effects of various traits on forage yield. 4 soybean varieties and lines were used at the experiment. The experiment design was a Randomized Block Design with six replications. The genotypic coefficient of variation (GCV) was lower than the phenotypic coefficient of variation (PCV). However, the difference in variability between these two estimates-was very close for some characters, very large for some others, and moderate in the rest. Regarding the genetic parameters, for forage yield, number of nodes, days to 50% flowering, and dry matter yield recorded high values for heritability (h^2) in the broad sense, genetic advance (GA), and also for genetic advance in percent (GAM%). The phenotypic correlation coefficients (r_p) were lower than genotypic correlation coefficients (r_g) for all traits all traits hence there was assigned a strong, natural connection between trait pairs. Forage yield results were positive and significant (P<0.05) for genotypic, phenotypic, and environmental correlation coefficients except for first pod height, days to 50% flowering, and crude protein ratio. Days to maturity had the greatest direct impact on forage yield, according to path coefficient analysis.

This study was conducted to evaluate the extent and pattern of genetic

Yemlik Soyada (Glycine max (L.) Merill) İlgili Karakterlerin Path Analizi, Genetik

Değişkenliği ve Korelasyon Çalışmaları

Araștirma Makalesi	OZ							
<i>Makale Tarihçesi:</i> Geliş tarihi: 18.01.2023 Kabul tarihi:06.04.2023	Bu çalışma, genetik değişkenliğin kapsamını ve modelini değerlendirmek, karakterler arasındaki genetik korelasyonu ortaya çıkarmak ve çeşitli karakterlerin yeşil ot verimi üzerindeki doğrudan ve							
Online Yayınlanma: 05.07.2023	dolaylı etkilerini tahmin etmek için yapılmıştır. Deneme, 4 soya çeşidi							
Anahtar Kelimeler: Yol analizi Genetik varyasyon Kalıtım derecesi Korelasyon	ve hattı ile Tesadüf Blokları Deseninde ve altı tekerrürlü olarak yapılmıştır. Genotipik varyasyon katsayısından (GCV) fenotipik varyasyon katsayısı (PCV) daha düşük bulunmuştur. Ancak tüm karakterler için bu iki tahmin arasındaki fark değişkenliği bazılarında cok yakın bazılarında cok büyük ye diğerlerinde orta düzeyde tespit							
Soya	edilmiştir. Genetik parametrelerle ilgili olarak, yeşil ot verimi, boğum sayısı, %50 çiçeklenme gün sayısı ve kuru ot verimi için geniş anlamda kalıtım derecesi (h ²), genetik ilerleme (GA) ve ayrıca genetik ilerleme							

yüzdesi (%GAM) için yüksek değerler kaydedilmiştir. Genotipik korelasyon katsayıları (r_g), tüm karakterlerde fenotipik korelasyon katsayılarından (r_p) daha büyük bulunmuştur. Bu nedenle karakter çiftleri arasında güçlü bir doğal ilişki belirlenmiştir. Yem verimi ile genotipik, fenotipik ve çevresel korelasyon katsayılarının sonuçları ilk bakla yüksekliği, %50 çiçeklenme gün sayısı ve ham protein oranı dışında pozitif ve anlamlı bulunmuştur (P<0.05). Yol katsayısı analizi, olgunlaşma gün sayısı yem verimine maksimum doğrudan katkısı olduğunu ortaya çıkardı. Yol katsayısı analizlerine göre, yem verimi üzerinde en büyük doğrudan etki olgunlaşma gün sayısı tespit edilmiştir.

1. Introduction

Soybean is one of the most widely used plants in industry and animal nutrition because it contains 40-42% protein, 18-22% fat, 30% carbohydrates, 5% mineral substances, and many vitamins (Nazlıcan, 2010; Sirtioglu, 2019). Soybean is a food raw material that cannot be substituted, especially since it meets the protein and energy needs in poultry nutrition (Kutlu, 2008). It is used as soybean grain, pulp, green and dry grass in the nutrition of ruminant animals, especially in cattle breeding (Kutlu, 2021). Moreover, many warm climate cereals are cultivated with legumes and wheat forage crops, sometimes alone or mixed in different proportions, and are widely used as silage in animal feed almost all over the world (Ergin and Kızıl Aydemir, 2018). It has been reported that the protein and energy contents of the feed content of silages obtained from a mixture of warm climate cereals and legume forage plants are superior to silages obtained from warm climate cereals alone (Altınok et al., 2005; Ayaşan, 2011; Kızıl Aydemir, 2018).

Although soybean cultivation has been carried out in Turkey for many years, the use of soybean as forage and the development of forage varieties is quite new. During the literature study, many important studies investigating the grain yield and grain yield characteristics of soybean were found, but no study was found on forage soybean varieties or lines (Basavaraja et al., 2005; Malik et al., 2006; Reni and Rao, 2013; Vaidya, 2019; Kuswantoro et al., 2021). Soybean forage varieties are taller than other soybean varieties, have higher green and dry grass content, and are more suitable for mixed cultivation with warm climate cereals such as corn for silage production (K1z1l Aydemir, 2018). In this study, data collected from the characteristics containing yield components of soybean and candidate forage soybean lines were used.

Studies conducted on soybean have shown that yield and traits that affect yield vary according to genetic and environmental conditions (Ghanbari et al., 2018). It is necessary to reveal the relationships between the characters in the breeding programs (Bhuva et al., 2020; Mehra et al., 2020; Karyawati and Puspitaningrum, 2021). The correlation coefficient is generally used to determine the level of relations between traits. However, the level of interaction between independent features is determined by the correlation coefficient. Therefore, the result examined in biological events is formed by the joint effects of interrelated features. The correlation coefficient is generally used to determine the level

To Cite: Hızlı H., Cubukcu P., Şahar AK. Path Analysis, Genetic Variability and Correlation Studies of Related Characters for Forage Soybean (*Glycine max* (L.) Merill). Osmaniye Korkut Ata Üniversitesi Fen Bilimleri Enstitüsü Dergisi 2023; 6(2): 1513-1528.

of relations between traits. However, the level of interaction between independent features is determined by the correlation coefficient. Therefore, the result examined in biological events is formed by the common effects of interrelated features. Therefore, while the correlation coefficient calculated between traits is insufficient alone for successful breeding programs, it is crucial to know the direct and indirect effects of traits on each other (Al-Jibouri et al., 1958; Dewey and Lu, 1959).

The success of an animal or plant breeding program is influenced by genetic diversity and the heritability of the traits. Breeders can choose a plan and employ precise selection criteria for the desired improvement with the use of genetic variability and heredity analysis. This study's objective was to estimate genetic variability, heritability and expose the genetic correlations among the traits of potential fodder soybean genotypes and lines in order to assess the direct and indirect effects of fourteen traits on green grass yield.

2. Materials and Methods

Materials

Forage soybean variety development studies were conducted at the EMARI from 2000. 1530, 517, Nazlıcan, and Turksoy varieties were used as a material in this experiment. The Experiment design was a Randomized Block Design with six replications. The number of genotypes is low but the number of replications is high because there were no forage soybean standard varieties during this study. After this trial results, Turkey's first forage soybean varieties were registered.

Statistical Analyses

Data were recorded for forage yield (FY), number of branches per plant (NB), plant height (PH), days to maturity (DM), number of nodes per plant (NN), first pod height (FPH), stem thickness (ST), weight of fresh pods per plant (WFP), days to 50% flowering (DF), dry matter ratio (DMR), dry matter yield (DMY), crude protein ratio (CP), Neutral Detergent Fiber (NDF), and Acid Detergent Fiber (ADF). Using the admitted formulas, the parameters phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) (Burton, 1952), heritability (broad sense) h^2 (Lush, 1940), genetic advance (GA), and genetic advance as a percentage of the mean (GAM%) (Johnson et al., 1955) were estimated. The direct and indirect effects of Path analysis were also calculated for different components of forage yield using the procedure given by Dewey and Lu (1959). The GCV and PCV categories were evaluated using the Sivasubramanian and Madhavamenon (1973) scale (low 10%; moderate 10-20%; high >20%), the h^2 category using the Robinson (1966) scale (low 30%; moderate 30-60%; high >60%), and the GA and GAM% categories using the Johnson et al. (1955) scale (low 10%, moderate 10-20%, and high >20%). TNAUSTAT statistical software was used to do the variance analysis of PV, GV, GCV, h^2 , GA, and GAM% parameters for the assessment of genetic variability, as well as the correlation and path coefficients study (Manivannan, 2014).

3. Results and Discussion

In the present study, the analysis of variance revealed highly significant differences except for first pod height, NDF, and ADF characters among the forage soybean lines and cultivar in the other all characters, which indicates the existence of considerable genetic variability for selection and breeding (Table 1). Chandrawat et al. (2017), Neelima et al. (2018), Erbil (2021), Reni and Rao (2013), Goonde and Ayana (2021), and Urdă et al. (2021) have also documented significant diversity in soybean.

	Mean Squares													
Source of variance	Df	FY	DM	РН	FPH	NN	ST	NB						
Genotype	3	2793514.86*	532.15**	795.95**	6.52	86.66**	3.19**	1.62*						
Replication	5	68198.43	3.38*	33.25	4.05	0.37	0.33	1.50*						
Error	15	113897.72	2.02	23.50	3.05	1.85	0.66	0.44						
Source of variance	Df	WFP	DF	DMY	DMR	CPR	NDF	ADF						
Genotype	3	2980.18*	478.06**	644997.94**	33.49**	13.13**	24.26	19.82						
Replication	5	124.42	5.37**	8777.53	1.02	0.55	12.28	4.79						
Error	15	716.16	1.26	13622.27	0.95	2.14	9.53	5.85						

Table 1. Analysis of variance for silage soybean lines and varieties

*: P<0.05; **: P<0.001; Df: Degrees of freedom; FY: Forage yield (kg/da), DM: Days to maturity (days), PH: Plant height (cm), FPH: First pod height (cm), NN: Number of nodes per plant(number), ST: Steam thickness (mm), NB: Number of branches per plant (number), WFP: Weight of fresh pods per plant (g), DF: Days to 50% flowering (days), DMY: Dry matter yield (kg/da), DMR: Dry matter ratio (%), CPR: Crude protein ratio (%), Neutral Detergent Fiber % (NDF); Acid Detergent Fiber % (ADF)

Range of variation, general mean (GMean), standard errors (S.E), coefficient of variation CV (%) as descriptive statistics estimates for the 14 characters studied in the silage soybean genotypes examined are shown in Table 2.

		Gen	otypes	Descriptive statistics							
Characters	517	517 1530 N		Turksoy	Range	GMean	S.E.	CV	CD 5%		
FY	4849.85	6310.95	5763.88	5001.87	4531.3 - 6771	5481.64	137.78	6.16	415.03		
DM	111.5	127.83	120.5	106.67	105 - 130	116.63	0.58	1.22	1.75		
PH	119.83	147.6	133.6	129.6	116 - 151.8	132.66	1.98	3.65	5.96		
FPH	6.03	4.33 4.63 6.47		6.47	2.4 - 9.4	5.37	0.71	32.52	2.15		
NN	20.8	28.4	24.57	20.2	18.2 - 30.6	23.49	0.56	5.8	1.67		
ST	10.16	11.22	10.38	9.45	8.08 - 12.3	10.3	0.33	7.85	1		
NB	3.8	4.3	4.57	3.4	2.4 - 5.8	4.02	0.27	16.51	0.82		
WFP	95.33	124.4	125.93	80.67	50.8 - 175.2	106.58	10.93	25.11	32.91		
DF	42.5	25.67	32	22.17	21 - 44	30.58	0.46	3.66	1.38		
DMY	1294.83	2046.32	1748.58	1477.25	1226 - 2234.4	1641.75	47.65	7.11	143.53		
DMR	26.71	32.42	30.33	29.54	25.5 - 33.25	29.75	0.4	3.27	1.2		
CPR	14.68	11.58	12.07	13.93	10.4 - 17.2	13.07	0.6	11.2	1.8		
NDF	42.08	46.28	42.3	42.43	34 - 51.9	43.28	1.26	7.13	3.8		
ADF	33.33	36.27	37.23	37.1	31.4 - 42	35.98	0.99	6.72	2.97		

Table 2. The estimates of range of variation, means, standart errors (S.E), coefficient of variation CV (%)

FY: Forage yield (kg/da), DM: Days to maturity (days), PH: Plant height (cm), FPH: First pod height (cm), NN: Number of nodes per plant(number), ST: Steam thickness (mm), NB: Number of branches per plant (number), WFP: Weight of fresh pods per plant (g), DF: Days to 50% flowering (days), DMY: Dry matter yield (kg/da), DMR: Dry matter ratio (%), CPR: Crude protein ratio (%), Neutral Detergent Fiber % (NDF); Acid Detergent Fiber % (ADF)

Forage yield (6310.95 kg/da), days to maturity (127.83 days), plant height (147.60 cm), number of nodes per plant (28.40), stem thickness (11.22 mm), dry matter yield (2046.32 kg/da), dry matter ratio (32.42%), NDF (46.28%) were found highest in the 1530 genotype. Forage yield ranged from 4531.3 -6771 kg/da. Forage yield was recorded in 1530 (6310.95 kg/da), Nazlıcan (5763.88 kg/da), and Turksoy (5001.87 kg/da), respectively. Days to maturity results were supported by Mesfin (2018), while reported lower by Malik et al. (2006), Chandrawat et al. (2017), Neelima et al. (2018), Kuswantoro et al. (2021), and higher by Vaidya (2019). In addition, Kuswantoro (2018) reported that the days to maturity were influenced by environmental factors. Some scientists have reported lower plant height (Aditya et al., 2011; Chandrawat et al., 2017; Mesfin, 2018; Neelima et al., 2018; Vaidya, 2019; Kuswantoro et al., 2021). The first pod height ranged from 2.4 cm to 9.4 cm, being maximum (6.47 cm) in Turksov, and above the general average of 5.37 cm, and the coefficient of variation between all genotypes was 32.52%. The first pod height range was reported higher by Joseph et al. (1983) and Malik et al. (2006). The number of nodes per plant results were supported by Kuswantoro et al. (2021). The number of branches (4.57), the weight of pods per plant (125.934 g), and ADF (37.23%) were found maximum in Nazlıcan. The number of branches results were supported by Aditya et al. (2011); Kuswantoro et al. (2021) while reported lower by Rasaily et al. (1986); Malik et al. (2006); Reni and Rao (2013); Malek et al. (2014), and higher by Chandrawat et al. (2017), and Jain

et al. (2018). The days to 50% flowering and crude protein ratio ranged from 21 to 44 days and from 10.4% to 17.2%, and were maximum in the 517 genotype i.e. 42.5 days and 14.68% respectively, while while these were minimum in the 1530 genotype i.e. 25.67 days and 11.58% respectively. The days to 50% flowering results were supported by Neelima et al. (2018), Kuswantoro et al. (2021) while reported lower by Chandrawat et al. (2017), and higher by Malik et al. (2006), Aditya et al. (2011), Vaidya (2019). Dry matter yield ranged from 1226 kg/da to 2234.4 kg/da, and contribution from the 1530 genotype, Nazlıcan and Turksoy was 2046.32 kg/da, 1748.58 kg/da, and Turksoy 1477.25 kg/da, respectively.

The analysis of phenotypic variance (PV), genotypic variance (GV), phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability (broad sense) h^2 , genetic advance (GA), and genetic advance as percent of the mean (GAM%) estimates for the investigational traits is shown in Table 3.

	Components											
Characters	PV	GV	PCV	GCV	h ²	GA	GAM%					
FY	560500.57	446602.8	13.66	12.19	79.68	1228.85	22.42					
DM	90.38	88.36	8.15	8.06	97.77	19.15	16.42					
РН	152.24	128.74	9.3	8.55	84.56	21.49	16.2					
FPH	3.62	0.58	35.47	14.18	15.98	0.63	11.68					
NN	15.99	14.13	17.02	16	88.41	7.28	31					
ST	1.08	0.42	10.07	6.31	39.2	0.84	8.13					
NB	0.64	0.2	19.87	11.04	30.89	0.51	12.64					
WFP	1093.5	377.34	31.03	18.23	34.51	23.51	22.05					
DF	80.72	79.47	29.38	29.15	98.44	18.22	59.58					
DMY	118851.55	105229.3	21	19.76	88.54	628.78	38.3					
DMR	6.37	5.42	8.48	7.83	85.16	4.43	14.88					
CPR	3.97	1.83	15.25	10.36	46.11	1.89	14.49					
NDF	11.98	2.46	8	3.62	20.5	1.46	3.38					
ADF	8.18	2.33	7.95	4.24	28.47	1.68	4.66					

Table 3. The estimates of genetic components for traits of forage soybean lines and varieties.

FY: Forage yield (kg/da), DM: Days to maturity (days), PH: Plant height (cm), FPH: First pod height (cm), NN: Number of nodes per plant(number), ST: Steam thickness (mm), NB: Number of branches per plant (number), WFP: Weight of fresh pods per plant (g), DF: Days to 50% flowering (days), DMY: Dry matter yield (kg/da), DMR: Dry matter ratio (%), CPR: Crude protein ratio (%), Neutral Detergent Fiber % (NDF); Acid Detergent Fiber % (ADF)

Firstly, the relative magnitude of PCV and GCV for different characters was comparatively examined. PCV was higher than the GCV in all examined characters. Similar results were reported by Aditya et al. (2011) and Vaidya (2019). The fact that PCV is greater than GCV suggests that environmental factors may influence the characters. However, while for some characters this difference was quite small, for others it was larger, showing how the characters are affected by inheritance factors as well as environmental factors. The phenotype of any quantitative character arises under the influence of genotypic and environmental factors and has different averages in different environments, so with phenotypic and genotypic variances, it is not possible alone to determine the extent of inheritance variation by the degree of PCV and the GCV (Chandrawat et al., 2017; Jain et al., 2018; Guleria et al., 2019). The difference between PCV and GCV in characters such as the first pod height, stem thickness, number of branches, weight of pods per plant, crude protein ratio, NDF and ADF, was quite large, which indicates that the role of the environment was also high. Heritability is a reliable measure of genetic improvement under selection for polygenic traits. The heritability of the characters the first pod height, stem thickness, number of branches, weight of pods per plant, crude protein ratio, NDF, and ADF was found to be 15.98, 39.2, 30.89, 34.51, 46.11, 20.5, and 28.47, respectively. The difference between PCV and GCV in the characters forage yield, days to maturity, plant height, number of nodes per plant, days to 50% flowering, dry matter yield, and dry matter ratio were quite less. According to the above-mentioned expression, we can see that the role of the environment is also minimum. The characters of days to maturity, plant height, dry matter ratio, NDF and ADF showed the lowest PCV and GCV, with similar results reported by Chavan et al. (2014), Chandrawat et al. (2017), Neelima et al. (2018), and Dutta et al. (2021) for days to maturity and by Guleria et al. (2019) for plant height. The heritability of the characters the forage yield, days to maturity, plant height, number of nodes per plant, days to 50% flowering days, dry matter yield, and the dry matter ratio were found to be 79.68, 97.77, 84.56, 88.41, 98.44, 88.54, and 85.16, respectively. Similar results of high heritability were reported by Chavan et al. (2014), Chandrawat et al. (2017), Guleria et al. (2019), Dutta et al. (2021) for the number of days to flowering; Chavan et al. (2014), Chandrawat et al. (2017), Neelima et al. (2018), Dutta et al. (2021) for the number of days to maturity; Chavan et al. (2014), Neelima et al. (2018), Guleria et al. (2019), Dutta et al. (2021), Kuswantoro et al. (2021) for plant height; Chandrawat et al. (2017) for crude protein ratio. The presence of high GCV is indicative of good scope for breeding by hybridization followed by selection (Chavan et al., 2014). High heritability coupled with high genetic advance as GAM was recorded for the forage yield, the number of nodes per plant, the weight of pods per plant, the days to 50% flowering, and dry matter yield revealing the influence of additive gene action for these traits. Hence the improvement of these traits can be made through direct phenotypic selection. High heritability with low GAM was recorded for days to maturity, plant height, and dry matter ratio indicating the effect of non-additive gene action in crop improvement like heterosis breeding may be beneficial.

		DM	PH	FPH	NN	ST	NB	WFP	DF	DMY	DMR	CPR	NDF	ADF
	rg	0.9731**	0.9611**	-0.6657*	0.9844**	0.9779**	0.8971**	0.9819**	-0.3987	0.9936**	0.9422**	-0.6886*	0.5558*	0.5448*
ΓV	r _p	0.8776**	0.868**	-0.5665*	0.8933**	0.5609*	0.5298*	0.6393*	-0.3657	0.9707**	0.7741*	-0.6546*	0.4725*	0.3151
ΓY	r _e	0.2792	0.4467*	-0.2781	0.321	0.0407	0.226	0.3412	-0.2227	0.8921**	-0.0116	0.0158	0.114	0.1459
	r	0.9547**	0.9428**	-0.9433**	0.9839**	0.8575**	0.7737**	0.8719**	-0.3923	0.989**	0.9093**	-0.9741**	0.8203**	0.464
	r_{g}		0.8368**	-0.9875**	0.9976**	0.7437**	0.6878*	0.7323**	0.9731**	0.9101**	0.753**	-0.9685**	0.9844**	0.2355
DM	r _p		0.7532*	-0.5779	0.9274**	0.6884*	0.5138*	0.6704*	0.8776**	0.8708**	0.7169**	-0.6984*	0.4971	0.1498
DM	r _e		-0.1319	-0.4162	-0.0008	0.2011	-0.3677	0.4402	0.2792	0.4757	0.5187	-0.4391	0.4231	0.2019
	r		0.8214**	-0.9777**	0.9849**	0.9612**	0.8554**	0.9377**	0.9547**	0.903**	0.7462*	-0.8953**	0.7821*	0.2041
	rg			-0.7064*	0.9129**	0.7802**	0.5941*	0.7335*	0.9611**	0.9937**	0.9056**	-0.7026**	0.8551**	0.7142**
РН	r _p			-0.4826*	0.8752**	0.5867*	0.3946	0.5088	0.868**	0.919**	0.8737**	-0.5563	0.4308	0.2869
	r _e			-0.282	0.6419*	0.4487	0.2785	0.3541	0.4467	0.4454	0.1348	0.3073	-0.179	-0.1914
	r			-0.7786**	0.9058**	0.7201*	0.5245*	0.6596*	0.9428**	0.9796**	0.9804**	-0.9096**	0.8908**	0.5729
	r_{g}				-0.9212**	-0.884**	-0.9769**	-0.7893**	-0.9354**	-0.8613**	-0.6779*	0.9636**	-0.9875**	-0.5457*
EDU	r _p				-0.6109	-0.5436*	-0.4081	-0.8652**	-0.5665*	-0.5279*	-0.4051	0.3385	-0.3552	-0.06
ггп	r _e				-0.4502	-0.3354	-0.1179	-0.812**	-0.2781	-0.257	-0.0941	-0.0695	-0.216	0.0727
	r				-0.9488**	-0.8941**	-0.9347**	-0.9844**	-0.9433**	-0.8862**	-0.7363*	0.9289**	-0.6543*	-0.3075
	r_{g}					0.9566**	0.8818**	0.9843**	0.9754**	0.97**	0.8556**	-0.7046*	0.7513	0.3355
NINI	r _p					0.7417**	0.5766*	0.6675*	0.8933**	0.8975**	0.7651*	-0.6017*	0.5443	0.2412
ININ	r _e					0.5329*	0.4089	0.4494	0.321	0.341	0.1734	0.236	0.2764	0.2529
	r					0.9344**	0.7756*	0.881**	0.9839**	0.9566**	0.8386**	-0.9226**	0.8592	0.2988
	r_{g}						0.9323**	0.8467**	0.9779**	0.8864**	0.654*	-0.9317**	0.461	-0.116
ST	r _p						0.4583	0.4993	0.5609*	0.5615*	0.4675	-0.3435	0.448	0.0412
	r _e						0.2065	0.1812	0.0407	0.1489	0.2982	0.092	0.2034	0.1212

Table 4. Genotypic, phenotypic, environmental and simple correlation coefficients among traits

	r	0.7581**	0.8535**	0.8575**	0.7916*	0.5974*	-0.743*	0.8091**	-0.057
	r _g		0.9454**	0.8971**	0.8027**	0.6293*	-0.6151*	0.5921*	0.3665
ND	r _p		0.5031*	0.5298*	0.4456	0.2372	-0.2571	0.0469	0.0292
IND	r _e		0.1287	0.226	0.0916	-0.2671	0.259	-0.1378	-0.113
	r		0.9818**	0.7737*	0.6848*	0.5061*	-0.8044**	0.3489	0.2306
	r _g			0.0394	0.8977**	0.7216**	-0.7564*	0.7775**	0.3941
WFD	r _p			0.0459	0.5788*	0.4024	-0.3164	0.1885	0.019
VV 1 1	r _e			0.227	0.3016	0.036	0.2439	-0.0254	-0.1528
	r			0.04	0.7956*	0.623*	-0.8738**	0.5203*	0.2477
	r _g				-0.5261*	-0.7483*	0.4834	-0.5293*	-0.9804**
DE	r _p				-0.5061*	-0.6999*	0.3649	-0.3091	-0.5646*
DF	r _e				-0.3525	-0.3073	0.4277	-0.6413*	-0.4318
	r				-0.5225*	-0.7394*	0.4505	-0.4325	-0.834**
	r _g					0.9732**	-0.7316**	0.734**	0.6438*
DMV	r _p					0.9021**	-0.7137**	0.5233*	0.3792
DMI	r _e					0.4378	-0.1425	0.2315	0.1954
	r					0.9598**	-0.9693**	0.8417**	0.5502*
	r _g						-0.9955**	0.9848**	0.8576**
DMD	r _p						-0.7125*	0.5192*	0.4688
DWK	r _e						-0.3136	0.3136	0.1426
	r						-0.9191**	0.7896**	0.7228**
	r _g							-0.7472**	-0.6614*
CDD	r _p							-0.6326*	-0.5513*
Urk	r _e							-0.6155*	-0.5019*
	r							-0.6885*	-0.6181*

	r _g	-0.1182
NDF	r _p	0.517*
	r _e	0.7235*
	r	0.1689

FY: Forage yield (kg/da), DM: Days to maturity (days), PH: Plant height (cm), FPH: First pod height (cm), NN: Number of nodes per plant(number), ST: Steam thickness (mm), NB: Number of branches per plant (number), WFP: Weight of fresh pods per plant (g), DF: Days to 50% flowering (days), DMY: Dry matter yield (kg/da), DMR: Dry matter ratio (%), CPR: Crude protein ratio (%), Neutral Detergent Fiber % (NDF); Acid Detergent Fiber % (ADF)

Table 4 shows that genotypic correlation coefficients (r_g) were found to be larger than phenotypic correlation coefficients (r_p) . In such cases, it shows that there is a strong natural relationship between these character pairs. The results of the genotypic, phenotypic, and environmental correlation coefficients (r_e) given in Table 4 show that the forage yield has positive and significant (P<0.05) correlation with days to maturity, plant height, number of nodes per plant, stem thickness, number of branches, weight of fresh pods per plant, dry matter yield, dry matter ratio, NDF and ADF. At genotypic level, forage yield showed highly significant positive correlation with days to maturity ($r_g =$ 0.9731), plant height ($r_g = 0.9611$), number of nodes per plant ($r_g = 0.9844$), stem thickness ($r_g = 0.9731$) 0.9779), number of branches ($r_g = 0.8971$), weight of fresh pods per plant ($r_g = 0.9819$), dry matter yield ($r_g = 0.9936$), dry matter ratio ($r_g = 0.9422$), NDF ($r_g = 0.5558$) and ADF ($r_g = 0.5448$). On the other hand, forage yield showed highly significant negative correlation with the first pod height ($r_g = -$ 0.6657) and the crude protein ratio ($r_g = -0.6886$). The environmental correlation coefficient of forage yield was positive and significant with dry matter yield ($r_e = 0.8921$), positive and nonsignificant with dry matter ratio ($r_e = 0.2792$), plant height ($r_e = 0.4467$), number of nodes per plant ($r_e = 0.321$), stem thickness ($r_e = 0.0407$), number of branches ($r_e = 0.226$), weight of fresh pods per plant ($r_e = 0.3412$), crude protein % ($r_e = 0.0158$), NDF ($r_e = 0.114$), ADF ($r_e = 0.1459$).

Estimates of direct effect and indirect effect are presented in Table 5. In the current investigation, forage yield was considered as the resultant (dependent) variable, and days to maturity, plant height, first pod height, number of nodes per plant, stem thickness, number of branches, weight of fresh pods per plant, days to 50% flowering, dry matter yield, dry matter ratio, NDF and ADF were causal (independent) variables. Days to maturity had the highest positive direct effect (0.1409) on forage yield. Small and negligible negative indirect effect of this trait on forage yield was registered through plant height, first pod height, number of nodes per plant, and weight of fresh pods per plant. Relatively high and positive correlation between days to maturity (0.9731) was largely due to the highest positive direct effect and a positive indirect effect through NDF, number of branches per plant, dry matter yield, days to 50% flowering, ADF, crude protein ratio, and stem thickness (Table 5).

	DM	РН	FPH	NN	ST	NB	WFP	DF	DMY	DMR.	CPR	NDF	ADF	r _g
DM	0.1409	-0.0261	-0.0211	-0.0059	0.027	0.0028	-0.0019	0.0041	0.0033	-0.2001	0.0087	0.0016	0.0054	0.9731**
PH	0.1371	-0.0268	-0.0183	-0.0062	0.0268	0.0031	-0.0022	0.0044	0.0009	-0.1833	0.0078	0.0015	0.0024	0.9611**
FPH	0.1354	-0.0224	-0.0219	-0.0049	0.0245	0.0022	-0.0013	0.0031	0.0055	-0.2001	0.0083	0.0018	0.0071	-0.6657*
NN	-0.1783	0.0353	0.0227	0.0047	-0.0336	-0.0035	0.0031	-0.0047	-0.0011	0.24	-0.0114	-0.0015	-0.0055	0.9844**
ST	0.1417	-0.0267	-0.02	-0.0059	0.0268	0.0029	-0.0019	0.0041	0.0022	-0.1954	0.0083	0.0016	0.0034	0.9779**
NB	0.1378	-0.0288	-0.0171	-0.0057	0.0273	0.0029	-0.002	0.0044	-0.0006	-0.1785	0.0075	0.0016	-0.0012	0.8971**
WFP	0.1264	-0.0273	-0.013	-0.0067	0.0236	0.0027	-0.0021	0.0053	-0.0014	-0.1617	0.0088	0.0009	0.0037	0.9819**
DF	0.1383	-0.0285	-0.0161	-0.0052	0.0264	0.003	-0.0027	0.0042	-0.0003	-0.1808	0.0093	0.0012	0.0039	-0.3987
DMY	-0.0562	0.0028	0.0144	0.0006	-0.0072	0.0002	-0.0004	0.0002	-0.0083	0.106	-0.0039	-0.0008	-0.0098	0.9936**
DMR	0.14	-0.0244	-0.0218	-0.0056	0.026	0.0025	-0.0017	0.0038	0.0044	-0.2014	0.0085	0.0016	0.0064	0.9422**
CPR	0.1327	-0.0202	-0.022	-0.0047	0.0229	0.0019	-0.0013	0.003	0.0062	-0.196	0.008	0.0015	0.0086	-0.6886*
NDF	-0.1533	0.026	0.0226	0.0066	-0.0278	-0.0027	0.0024	-0.0048	-0.004	0.2138	-0.008	-0.0011	-0.0066	0.5558*
ADF	0.1487	-0.0264	-0.026	-0.0046	0.029	0.0031	-0.0013	0.0033	0.0044	-0.2144	0.006	0.0015	-0.0012	0.5448*

Table 5. Genotypic path analysis with direct (bold phase) and indirect components to forage yield silage soybean

FY: Forage yield (kg/da), DM: Days to maturity (days), PH: Plant height (cm), FPH: First pod height (cm), NN: Number of nodes per plant(number), ST: Steam thickness (mm), NB: Number of branches per plant (number), WFP: Weight of fresh pods per plant (g), DF: Days to 50% flowering (days), DMY: Dry matter yield (kg/da), DMR: Dry matter ratio (%), CPR: Crude protein ratio (%), Neutral Detergent Fiber % (NDF); Acid Detergent Fiber % (ADF)

The dry matter ratio showed the highest negative direct effect (-0.2014) on forage yield. The indirect effects of weight of fresh pods per plant, number of nodes per plant, first pod height, and plant height were negative but low in magnitude. The total correlation for dry matter ratio was significant and positive (0.9422) which was mainly due to the indirect positive contribution of days to maturity (0.14). According to the results of this study, indirect selection *via* days to maturity will be most effective for increasing forage yield (Table 5). Number of nodes per plant, stem thickness, number of branches per plant, days to 50% flowering and dry matter ratio had positive and direct effect on forage yield (0.0047), (0.0268), (0.0029), (0.0042), (0.008) respectively. Plant height, first pod height, weight of fresh pods per plant, dry matter yield, NDF and ADF had negative and direct effect on forage yield (-0.0268), (-0.0219), (-0.0083), (-0.0011) and (-0.0012) respectively.

4. Conclusion

The analysis of variance revealed highly significant changes between the genotypes of all traits tested, indicating that the data from the aforementioned diverse material was highly variable. PCV values were higher than GCV, although the range between these two estimations for each character varied widely in some cases, moderately in others, and very significantly in a few. Regarding the genetic parameters, for forage yield, the number of nodes per plant, days to 50% flowering, and dry matter yield was recorded as high values for h² in the broad sense, for GA and also for GAM. It was suggested that soybean forage yield can be improved by the direct selection of genotypes with high values of forage yield, the number of nodes per plant, days to 50% flowering, and dry matter yield. The phenotypic correlation coefficients were lower than the genotypic correlation coefficients in all characters. Therefore, there determines a robust spontaneous relationship between character pairs. The results of the genotypic, phenotypic, and environmental correlation coefficients with the forage yield are positive and significant except for first pod height, days to 50% flowering, and crude protein ratio. An increase in these traits will eventually boost forage yield. The path coefficient study showed that days to maturity had the greatest direct contribution to forage yield.

Statement of Conflict of Interest

Authors have declared no conflict of interest.

Author's Contributions

The contribution of the authors is equal.

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