



## Research Article

# Genetic Variability and Heritability of Nodulation, and Root Morphology and Their Association with Yield Contributing Characters in Soybean

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ARTICLE INFO	ABSTRACT
<p><b>Article history</b>            Received: 21 Oct 2022            Accepted: 06 Dec 2022            Published: 31 Dec 2022</p> <p><b>Keywords</b>            Soybean (<i>Glycine max</i>),            Roots,            Nodules,            Yield per plant,            Pods per plant</p> <p><b>Correspondence</b>            Arif Hasan Khan Robin            ✉: <a href="mailto:gpb21bau@bau.edu.bd">gpb21bau@bau.edu.bd</a></p> <p> OPEN ACCESS</p>	<p>Soybean is widely grown for its edible beans that have a high nutritive value and numerous uses. An experiment was conducted to find out the genetic variability and heritability of root morphology and nodulation traits of ten soybean genotypes and to observe the relationship between nodulation and root morphology with yield contributing characters of soybean. The experiment was carried out in field conditions where morphological data were collected from standing crops at age of four months. Then, few plants were uprooted from 40cm soil depth to collect root and nodulation traits. Analysis of variance revealed significant differences among soybean genotypes for plant height, ground area, leaves/plant, leaflets/plant, leaf area index, shoot fresh and dry weight, nodules/plant, nodule fresh and dry weight, root fresh and dry weight, primary root length, lateral roots/plant, pods/plant, 100-seeds weight, and yield/plant. A high heritability estimate was found in case of plant height, ground area, leaves/plant, leaflets/plant, leaf area index, nodules/plant, hundred seed weight and yield/plant while other traits showed low to medium heritability. Correlation study showed a significant relationship among the root-shoot traits in terms of yield traits. The principal component analysis explored the most vital traits contributing to the variations among the genotypes. The soybean genotype PM-78-6-3-13 (S13) showed the maximum plant height, nodule fresh and dry weight, highest root fresh weight and the maximum number of lateral roots per plant, pods/plant, and 100-seeds weight. This finding suggested the inclusion of nodulation and root traits for yield improvement of soybean would be useful.</p>
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## Introduction

Soybean (*Glycine max* L.) is considered as an important economic food legume cultivated worldwide for seed protein and oil content, and also for its atmospheric nitrogen-fixing capacity with soil-borne microorganisms through symbiosis process (Schmutz et al., 2010). Despite having suitable climatic and edaphic conditions, the yield of soybean is very low ( $1.2 \text{ t ha}^{-1}$ ) in Bangladesh compared to the average yield of soybean in the world ( $3.0 \text{ t ha}^{-1}$ ) (SAIC, 2007). Because of low production, most of the soybean in Bangladesh is imported (Miah and Mondol, 2017). To improve production of soybean we need to understand its root morphology as improving yield is intimately related to the root system. Previous investigations revealed relations between root traits and yield in rice (Samejima et al., 2005; Wang et al., 2006; Yang et al., 2008).

The morphology of plants root system includes length and diameter of main root axis, density, diameter and

length of lateral branches and root hairs. In tap root systems, exemplified by crop plants such as legumes, *Brassica* and *Arabidopsis*, there is a single main root axis, the primary roots which remains the largest root with smaller lateral roots originating from primary roots (Figure 1, Dickison, 2000; Doussan et al., 2006). The root system of soybean is allorhizic comprising primary (tap root) and lateral roots (Ao et al., 2010; Fenta et al., 2014) (Figure 1). As a legume plant, soybean has the ability to form a symbiotic relationship with nitrogen-fixing bacteria like rhizobia, which cause the small swellings on the root system called nodules. The legumes become the model agricultural crop for nitrogen-fixing ability in root nodules as requiring limited nitrogen fertilizers. As the effect of nodulation properties and root traits in the yield of soybean is not clearly elucidated yet, exploring the influence of root traits and nodulation in the yield of soybean has become one of the major concerns for soybean breeders.

## Cite This Article

Rima, M.N., Hannan, A., Rahman, S. and Robin, A.H.K. 2022. Genetic Variability and Heritability of Nodulation, and Root Morphology and Their Association with Yield Contributing Characters in Soybean. *Journal of Bangladesh Agricultural University*, 20(4): 373-382. <https://doi.org/10.5455/JBAU.123297>

However, the challenge behind such study is difficult in phenotyping. As there is no easy method of root phenotyping and the ordinary techniques are too laborious. Therefore, this study was conducted to find out the genetic variability and heritability of different root morphological traits including nodulation related traits and also to observe the relationship among root morphology, nodulation and yields of soybean in different genotypes. Because a thorough understanding on root and nodulation traits and their linkage with each other and also with the yield contributing characteristics of soybean would be helpful to make new steps in the roots and nodulation breeding endeavors.

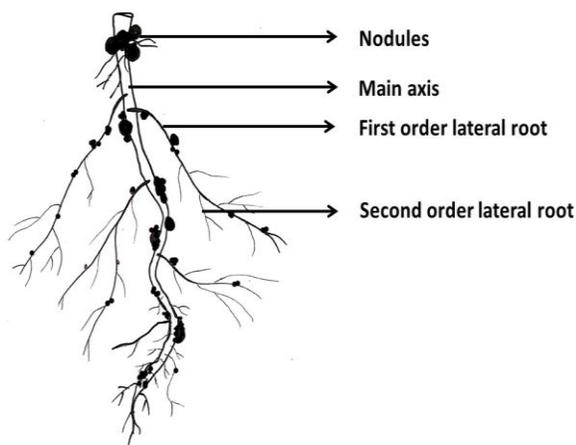


Figure 1. Allorhizic root system of soybean plant with nodules

## Materials and Methods

### Plant culture and management

An upland soil in the Field Laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh was used for conducting the experiment. The experimental duration

was from November 2018 to April 2019. The place was geographically located at about 24°75' North latitude and 90°50' East longitude and 18 meters above sea level (FAO, 1988; Khan, 1997). As the experimental site was in a sub-tropical climate zone, in the month of May to September there occurred heavy rainfall whereas very light rainfall in the remaining year. Ten soybean genotypes (Table 1) were used for integrating nodulation and root morphology with yield contributing characters of soybean. The experiment was done by following Randomized Complete Block Design (RCBD) with three replications. The individual plot size was 3 m × 2 m. Seeds were sown in lines with a spacing of 30 cm × 5 cm. The experimental plot was brought to a fine tilth by ploughing and harrowing. Manures and fertilizers such as cowdung (5000 kg/ha), Urea (60 kg/ha), TSP (150 kg/ha) and MP (70 kg/ha) were applied during cultivation following recommended doses (Alam et al., 1988). Weeding and proper intercultural operations were performed. In the case of intercultural operation, thinning was done 15 days after sowing. Weeding of the field was done two times. The first one was done within 15-20 days of sowing seeds and the second time was within 35-40 days of sowing. Irrigation was given once to raise the experimental crops. As soybean is a leguminous plant and has the unique ability of nitrogen fixation into the soil through rhizobial symbiosis at root zones, the bacterial inoculum (*Rhizobium* inoculants) @ 25g/kg seed was mixed with seed before sowing. The plants were destructively harvested at full maturity when leaves became yellow with completion of leaf shedding and the pod colour mostly became dark brown. Different varieties were harvested at different dates as days to maturity differed among varieties.

Table 1. List of experimental materials with source

Name of the genotypes	Source
Lokon (S3), Acc-1222 (S4), Shohag (S5), Santarosa (S10), PM-78-6-3-13 (S13), Davis (S20), Bragg (S23), BS-13 (S25), H1H5-W1H5 (S26), Tainans (S38)	Experimental farm of Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh, Bangladesh.

### Measurements and data collection

Morphological data were collected from the four-month aged standing crops. After morphological characterization 3 plants from all of the genotypes of 3 replications were uprooted from the soil to study root (Figure 2). The depth of the uprooted portion was 40 cm (Figure 2A and Figure 2B). After cleaning the roots, data on main root axis length (cm) (Figure 2C), lateral root number, maximum lateral root length (cm), nodules per plant (Figure 2D), root weight (fresh and dry) and nodule weight (fresh and dry) were measured in the laboratory. Yield data such as pods per plant,

hundred seeds weight per plant and yield per plant were also collected.

### Statistical analyses of data

Data were analyzed using Minitab 17 statistical software package (Minitab Inc., State College, PA, USA). One way Analysis of variance (ANOVA) was performed to reveal deviations among genotypes. A post hoc analysis was executed following Tukey's pairwise comparisons for separating means. Genotypic variance (GV), phenotypic variance (PV) and heritability in broad sense (Hb) (%) were estimated according to the formula given by Johnson et al. (1955). Genotypic co-efficient of

variations (GCV) and phenotypic co-efficient of variations (PCV) values were estimated according to the formula given by Burton (1952) and Singh and Chaudhury (1985). Genetic advance in percent of mean (GA %) was calculated by the formula of Comstock and Robinson (1952).



**Figure 2.** (A) Process of uprooting plant uprooting soybean plant from the field for recording root data (B) Uprooted soybean plant (C) Measuring root length with normal centimetre ruler (D) Soybean root system with nodules

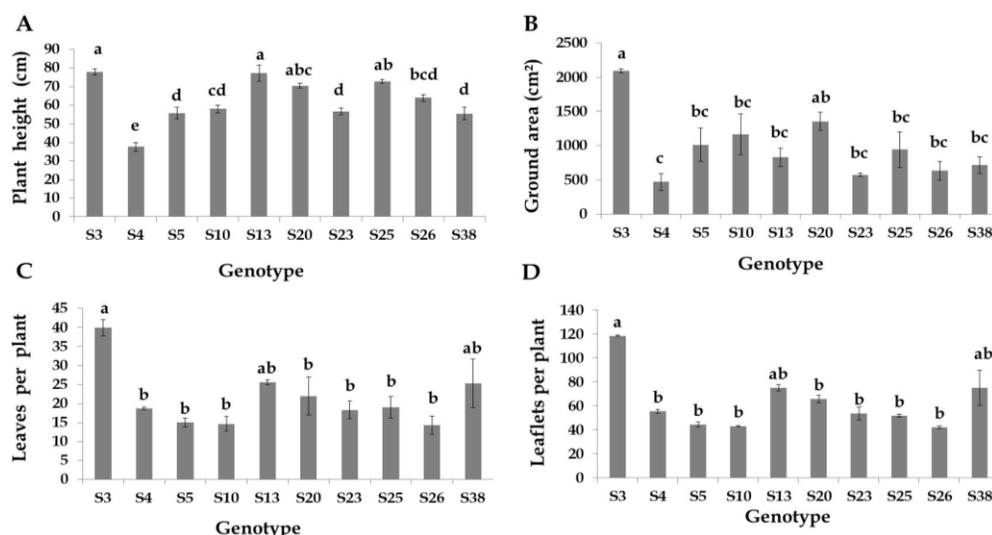
A principal component analysis (PCA) was conducted to investigate association among the yield contributing traits and root traits. ANOVA of the PC scores was performed for genotypes following a similar one-way

ANOVA model. A Pearson correlation analysis was carried out to explore relationships among the selected traits.

## Results and Discussion

### Varietal differences

Analysis of variance for the different shoot and root traits of ten soybean genotypes was presented in the Table 2. The results of the analysis of variance indicated a possible amount of variability among the genotypes for plant height, ground area, leaves per plant, leaflets per plant, leaf area index, shoot fresh and dry weight, nodules per plant, nodule fresh and dry weight, root fresh and dry weight, lateral roots per plant, primary root length, pods per plant, 100-seeds weight and yield per plant (Table 2). This would give the breeder an opportunity to improve these traits through selection and hybridization. The current study revealed that plant height was highly significant ( $P$ -value < 0.001) for the soybean genotypes (Table 2) where genotype Lokon (S3) and PM-78-6-3-13 (S13) showed the maximum plant height and Acc-1222 (S4) showed the minimum height (Figure 3A). This variation in plant height showed conformity with a previous results that indicated significant differences among the soybean genotypes studied (Haque, 2005). The genotype Lokon (S3) also showed the highest ground area (Figure 3B), the maximum number of leaves (Figure 3C), leaflets per plant (Figure 3D), shoot fresh weight (Figure 4B) whereas genotype Acc-1222 (S4) showed the lowest ground area (Figure 3B), the lowest number of nodules per plant (Figure 5A), lowest nodule fresh (Figure 5B) and dry weight (Figure 5C), also lowest root fresh (Figure 6A) and dry weight (Figure 6B). In *Brassica campestris*, it was also found that defoliation during the late anthesis stage reduced seed yield (Freyman et al., 1973).

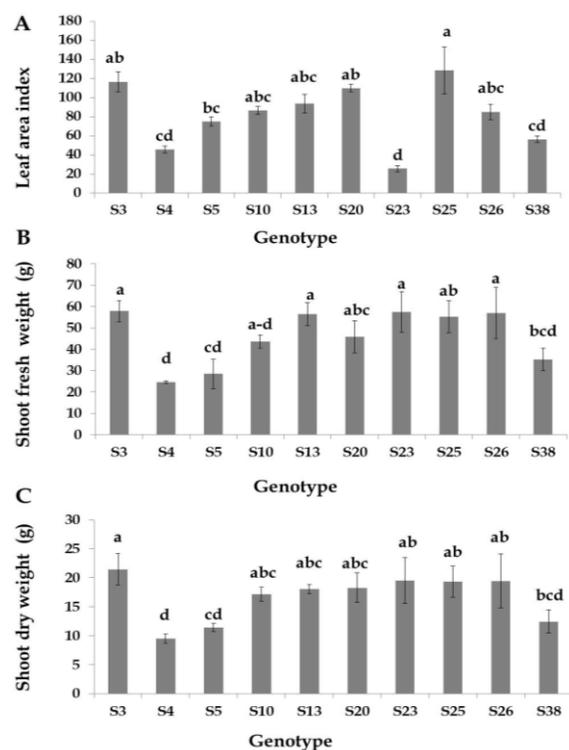


**Figure 3.** Genotypic differences for (A) Plant height in centimeter; (B) Ground area in centimeter square; (C) Number of leaves per plant; (D) Number of leaflets per plant of ten genotypes of soybean in field condition. Vertical bars indicate standard error of mean against each variable. Different letter indicates significant difference among data. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa, S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans

**Table 2.** Analysis of variance table for the studied shoot and root traits of ten soybean genotypes

Traits		PH	GA	L/P	LL/P	N/P	NFW	NDW	RFW	RDW
Genotype	MS	462.95	685678	179.59	1605.69	9092	3.876	0.2788	40872	0.4037
	F value	24.63	7.54	6.37	5.83	5.56	3.66	3.80	2.80	2.42
	P value	< 0.001	< 0.001	0.001	0.001	0.001	0.008	0.006	0.027	0.048
Traits		SFW	SDW	MLRL	PRL	LR/P	P/P	100-SW	Y/P	
Genotype	MS	490.3	49.04	25.32	28.547	89.87	479.5	35.208	59.430	
	F value	3.36	2.49	1.68	2.97	5.13	4.46	18.37	7.81	
	P value	0.011	0.043	0.160	0.020	0.001	0.003	< 0.001	< 0.001	

Here, MS= Mean squares, P= Probability of statistical significance, PH= Plant height, GA= Ground area, L/P= Leaves per plant, LL/P= Leaflets per plant, LAI= Leaf area index, N/P= Nodules per plant, NFW= Nodules fresh weight, NDW= Nodules dry weight, RFW= Root fresh weight, RDW= Root dry weight, SFW= Shoot fresh weight, SDW= Shoot dry weight, MLRL= Maximum lateral root length, PRL= Primary root length, LR/P= Lateral roots per plant, P/P= Pods per plant, 100-SW= Hundred seeds weight, Y/P= Yield per plant.



**Figure 4.** Genotypic differences for (A) Leaf area index; (B) Shoot fresh weight in gram; (C) Shoot dry weight in gram of ten genotypes of soybean in field condition. Vertical bars indicate standard error of mean against each variable. Different letter indicates significant difference among data. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa, S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans

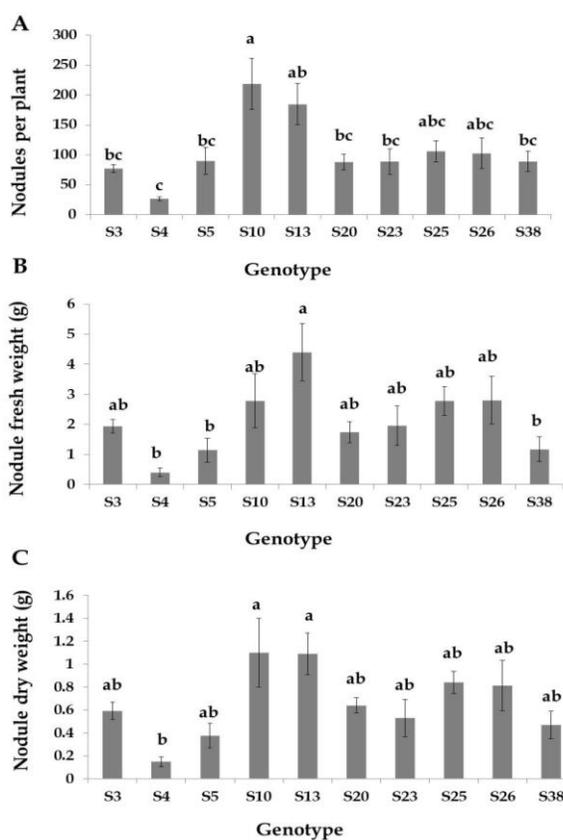
The highest number of nodules per plant (Figure 5A) was observed in the genotype Santarosa (S10) while PM-78-6-3-13 (S13) showed the maximum nodule fresh weight (Figure 5A), and both Santarosa (S10) and PM-78-6-3-13 (S13) had the maximum nodule dry weight (Figure 5C). Primarily, the legume crops form nodules in their root. In rapidly developing soybean plants, a short time after the plant emergence root nodules are started to form. Annually around 16.4 million metric tons of combined nitrogen was contributed through symbiotic nitrogen fixation by soybean plants accounting for 77% of the total N assimilated by legume crops (Herridge et al., 2008). This nodulation can encounter 50-60% demand of nitrogen for soybean plants throughout their whole life ensuring proper growth and development (Salvagiotti et al., 2008). Similarly, in this study both the genotypes with high nodulation

capacity, Santarosa (S10) and PM-78-6-3-13 (S13), performed well in terms of leaf area index (Figure 4A), shoot fresh weight (Figure 4B), shoot dry weight (Figure 4C), pods per plant (Figure 7A) and hundred seed weight (Figure 7B). Moreover, PM-78-6-3-13 (S13) also demonstrated maximum plant height (Figure 3A), higher number of leaves per plant (Figure 3C) and leaflets per plant (Figure 3D); indicating clear effect of nodulation on plant growth and development. Literature supporting our study found that rhizobia inoculation has clear effects on plant growth which subsequently affects the yield contributing traits and total yield of the legumes (Mabrouk et al., 2018).

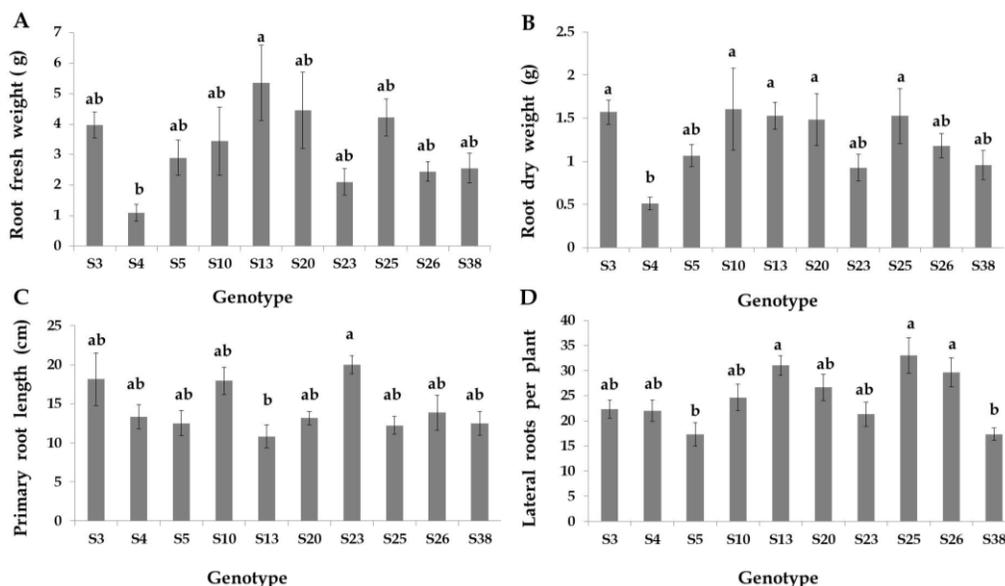
Besides, two genotypes Santarosa (S10) and PM-78-6-3-13 (S13) showed good performance for root related traits such as the highest root dry weight (Figure 6B) was observed in Santarosa (S10), and the maximum root fresh weight was observed in PM-78-6-3-13 (S13) (Figure 6A). Additionally, both PM-78-6-3-13 (S13) and BS-13 (S25) showed the highest number of lateral roots per plant (Figure 6D). All three genotypes, S10, S13 and S25 demonstrated higher number of pods per plant (Figure 7A) which indicates root trait such as number of lateral roots per plant had an association with yield of soybean. In contrast, both Shohag (S5) and Tainans (S38) showed the lowest number of lateral roots per plant (Figure 6D) which ultimately results in lower hundred seed weight (Figure 7B) and lower yield per plant (Figure 7C). Similar to our study, it was reported in eggplant (*Solanum melongena* L.) that, genotypes with more lateral roots produce more percentage of fruits compared to the genotypes with less lateral roots (Rouhani et al., 1987).

So, overall it had been found from the study that soybean genotype PM-78-6-3-13 (S13) showed the maximum plant height, higher number of nodules per plant, maximum nodule fresh and dry weight, and highest root fresh and dry weight, contained the maximum number of the lateral roots per plant. It also produced the maximum pods per plant and 100-seeds weight though the yield per plant was comparatively low (Figure 7C). Probably, the number of seeds per pod was lower in this genotype which results in reduced yield instead of having maximum value for pods per plant and 100-seeds weight. However, further

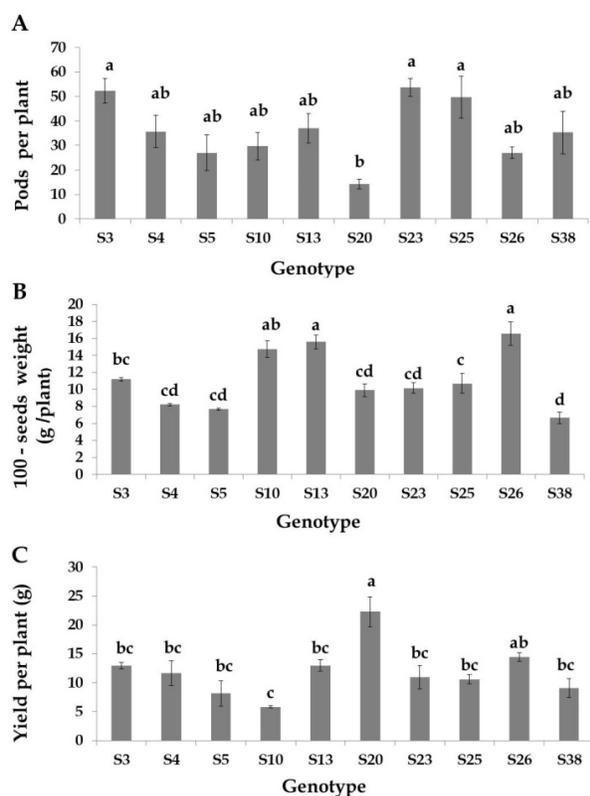
investigation is needed to confirm that. Another genotype, H1H5-W1H5 (S26) was also promising as it showed the highest shoot fresh weight, higher number of nodules per plant, higher nodules fresh and dry weight, the maximum number of lateral roots per plant, higher root fresh and dry weight and higher primary root length. The best thing about H1H5-W1H5 (S26) is the highest value for hundred seed weight and also higher performance in pods per plant and yield per plant.



**Figure 5.** Genotypic differences for (A) The numbers of nodules per plant; (B) Nodule fresh weight in gram; (C) Nodule dry weight in gram of ten genotypes of soybean in field condition. Vertical bars indicate standard error of mean against each variable. Different letter indicates significant difference among data. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa, S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans



**Figure 6.** Genotypic differences for (A) Root fresh weight in gram; (B) Root dry weight in gram; (C) Primary root length in centimeter; (D) Number of lateral roots per plant of ten genotypes of soybean in field condition. Vertical bars indicate standard error of mean against each variable. Different letters indicate significant difference among data. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa, S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans



S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans

#### Analysis of genetic parameters

Genetic parameters for all the studied shoot and root traits of ten soybean genotypes were presented in Table 3. Estimation of heritable and non-heritable portion of total genetic variability in any population is necessary for selection and breeding (Shashikala, 2006; Shukla et al., 2006; Desheva and Kyosey, 2015). For majority of the traits in this study, PCV was slightly higher than the corresponding GCV value. The highest value for GCV was observed for nodules per plant, N/P (46.49%) whereas the highest PCV was observed for nodules fresh weight, NFW (66.98%). On contrast, maximum lateral root length (MLRL) showed the lowest value for GCV (7.78%) and PCV (18.10%). Here, the close difference between GCV and PCV for most of the traits indicates that these traits are less influenced by environment (Mohammadi and Amri, 2013). Similar results were found from previous studies on soybean (Aditya et al., 2011; Baraskar et al., 2014; Kuswantoro, 2017), while contrasting result was also available in literature (Jain et al., 2017).

**Figure 7.** Genotypic differences for (A) Pods per plant; (B) Hundred seeds weight in gram; (C) Yield per plant in gram of ten genotypes of soybean in field condition. Vertical bars indicate standard error of mean against each variable. Different letters indicate significant difference among data. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa,

**Table 3.** Genetic parameters of shoot and root traits of ten soybean genotypes

Traits	GV	PV	GCV	PCV	Hb	GA	GA%
PH	148.05	166.84	19.44	20.64	88.74	22.88	36.56
GA	198262.67	289152.67	45.42	54.86	68.57	741.35	75.63
L/P	50.46	78.66	33.35	41.64	64.15	11.46	53.80
LL/P	443.40	718.90	33.57	42.74	61.68	33.33	53.14
LAI	963.23	1250.83	37.65	42.90	77.01	54.59	66.23
N/P	2485.33	4121.33	46.49	59.87	60.30	78.07	72.81
NFW	0.94	1.99	45.91	66.98	46.98	1.34	63.76
NDW	0.07	0.14	39.64	57.06	48.25	0.37	55.76
RFW	1.04	2.78	31.37	51.24	37.48	1.27	39.05
RDW	0.08	0.25	22.75	40.13	32.15	0.32	26.28
SFW	114.80	260.70	23.21	34.97	44.04	14.42	31.24
SDW	9.77	29.49	18.75	32.58	33.14	3.66	21.98
PRL	6.31	15.93	17.38	27.61	39.61	3.21	22.22
MLRL	3.42	18.49	7.78	18.10	18.48	1.63	6.85
LR/P	24.11	41.64	20.02	26.30	57.90	7.54	30.74
P/P	124.03	231.43	30.79	42.06	53.59	16.48	45.58
100-SW	11.10	13.01	29.90	32.38	85.27	6.15	55.18
Y/P	17.27	24.88	34.90	41.88	69.41	6.96	58.44

Here, GV= Genotypic variance, PV= Phenotypic variance, GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, Hb= Heritability in broad sense, GA= Genetic advance, GA%= Genetic advance in percent of mean, PH= Plant height, GA= Ground area, L/P= Leaves per plant, LL/P= Leaflets per plant, LAI= Leaf area index, N/P= Nodules per plant, NFW= Nodules fresh weight, NDW= Nodules dry weight, RFW= Root fresh weight, RDW= Root dry weight, SFW= Shoot fresh weight, SDW= Shoot dry weight, PRL= Primary root length, MLRL= Maximum lateral root length, LR/P= Lateral roots per plant, P/P= Pods per plant, 100-SW= Hundred seeds weight, Y/P= Yield per plant

Estimation of heritability is also important as it indicates the scope of improving traits through selection (Robinson et al., 1949). Here, heritability in broad sense (Hb) ranged from 18.48% to 88.74% where higher heritability (>60%) was found mostly for soybean growth and yield related trait such as plant height, ground area, leaf and leaflets per plant, leaf area index, hundred seed weight and yield per plant (Table 3). Previous studies also found high heritability in case of plant height (Adity et al., 2011; Baraskar et al., 2014), hundred seed weight (Kuswanto, 2017) and yield per plant (Adity et al., 2011). Surprisingly, root related traits including nodulation demonstrated low to medium heritability except for nodules per plant (60.3%), as nodulation traits are associated with the availability and activity of nodule forming bacteria. However, heritability along with genetic advance gives a better prediction of genetic gain comparing heritability calculation alone (Bhargava et al., 2003; Anshuman et al., 2013). Here, a high heritability coupled with high genetic advance was observed only for ground area, leaf area index, nodules per plant, hundred seed weight and yield per plant (Table 3) which indicated maximum improvement in soybean is possible for these traits through selection in advanced generation.

#### Association study among the traits

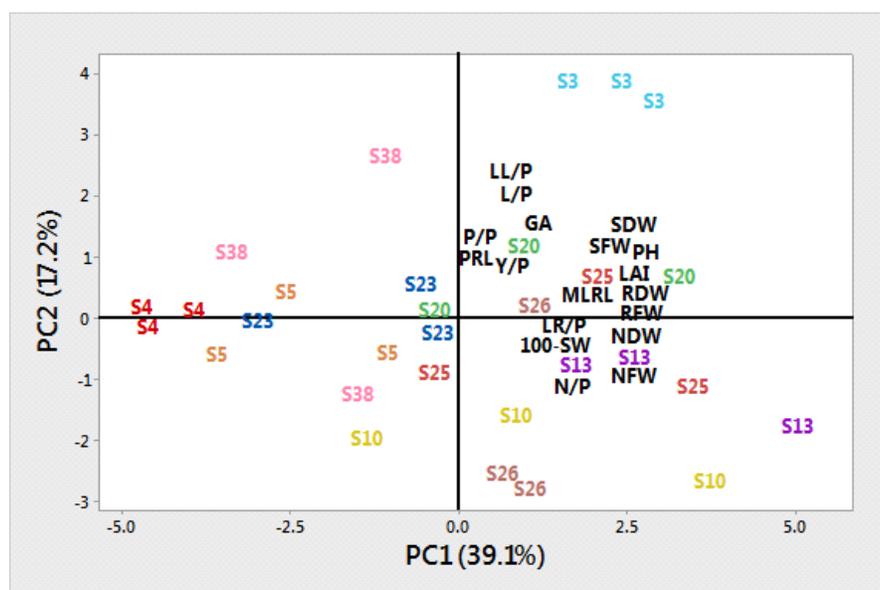
Root is one of the most vital and fundamental parts of a plant. Previous literature revealed a close association between root morphology and physiology with the growth and development of the above-ground portion of the plants (Waines and Ehdai, 2007; Yang et al., 2008). Thus, the presence of a relationship among the root-shoot traits in terms of yield traits is inevitable. A study on wheat roots revealed that root area is closely associated with the surface growth of the plant (Ward et al., 1978). In addition, lateral root traits are heritable

(Lynch, 2007). Both PCA and Pearson correlation analysis revealed the relationship among the nodulation and root morphology with yield contributing characters in this study (Figure 8, Tables 4, 5). Principal component analysis (PCA) revealed that the first five principal components (PC) explained 81.4% of the total data variation for the studied root and shoot traits of ten soybean genotypes. PC1 and PC2 explained 39.1% and 17.2% data variation, respectively, which was above 50% of the total variation. Variation in PC1 was mostly contributed by the positive coefficients of root dry weight (0.334), plant height (0.324), root fresh weight (0.323) and nodule fresh weight (0.311) (Table 4). Whereas negative coefficient of nodules per plant (-0.295), nodule dry weight (-0.271), 100-seeds weight (-0.258) and positive coefficients of leaves per plant (0.479), leaflets per plant (0.478) and ground area (0.316) contributed to the variation of PC2 (Table 4). PC scores evidently separated ten genotypes of soybean (Table 4) by their contrasting setting in PCA-biplot (Figure 8) and by their differing mean PC scores (Table 4). From the biplot, it was seen that PC1 scores of the genotype PM-78-6-3-13 (S13) were completely separated from those of Acc-1222 (S4) whereas PC2 scores of the genotype Lokon (S3) was completely separated from the other genotypes (Figure 8, Table 4). From PCA, it was clear that variation in the genotype PM-78-6-3-13 (S13) occurred due to the major contribution of the traits like root dry weight, plant height, root fresh weight and nodule fresh weight (Figure 8, Table 4).

**Table 4.** Coefficients of PCs from PCA and mean PC scores with standard deviation of each soybean genotype

Variable	PC1	PC2
Plant height (cm)	0.324	0.115
Ground area (cm <sup>2</sup> )	0.171	0.316
Leaves per plant	0.121	0.479
Leaflets per plant	0.110	0.478
LAI (Leaf area index)	0.242	0.068
Nodules per plant	0.240	-0.295
Nodule fresh weight (g)	0.311	-0.241
Nodule dry weight (g)	0.307	-0.271
Root fresh weight (g)	0.323	0.016
Root dry weight (g)	0.334	0.002
Shoot fresh weight (g)	0.286	0.073
Shoot dry weight (g)	0.276	0.107
Primary root length (cm)	0.039	0.120
Max. lateral root length (cm)	0.224	0.084
Lateral roots per plant	0.221	-0.189
Pods per plant	0.051	0.222
100-seeds weight (g)	0.205	-0.258
Yield per plant (g)	0.115	0.128
% Variation explained	39.1	17.2
P value	<0.001	<0.001

Mean PC scores with standard deviation		
Genotype	PC1	PC2
Lokon (S3)	2.31±0.57 a	3.81±0.16 a
Acc-1222 (S4)	-4.49±0.40 c	0.05±0.05 bc
Shohag (S5)	-2.37±1.40 bc	-0.33±0.41 bc
Santarosa (S10)	1.00±2.58 ab	-2.06±0.56 c
PM-78-6-3-13 (S13)	3.12±1.88 a	-1.00±0.62 bc
Davis (S20)	1.24±1.65 ab	0.68±0.59 b
Bragg (S23)	-1.19±1.67abc	0.12±0.32 bc
BS-13 (S25)	1.67±1.80 ab	-0.45±0.95 bc
H1H5-W1H5 (S26)	0.82±0.27 ab	-1.65±1.71 bc
Tainans (S38)	-2.11±1.21 bc	0.82±1.95 b



**Figure 8.** Biplot for shoot and root traits of ten soybean genotypes; PH= Plant height, GA= Ground area, L/P= Leaves per plant, LL/P= Leaflets per plant, LAI= Leaf area index, N/P= Nodules per plant, NFW= Nodules fresh weight, NDW= Nodules dry weight, RFW= Root fresh weight, RDW= Root dry weight, SFW= Shoot fresh weight, SDW= Shoot dry weight, PRL= Primary root length, MLRL= Maximum lateral root length, LR/P= Lateral roots per plant, P/P= Pods per plant, 100-SW= Hundred seeds weight, Y/P= Yield per plant. Here, S3= Lokon, S4= Acc-1222, S5= Shohag, S10= Santarosa, S13= PM-78-6-3-13, S20= Davis, S23= Bragg, S25= BS-13, S26= H1H5-W1H5, S38= Tainans

For measuring the mutual relationship between different shoot and root traits, correlation coefficient analysis was conducted. In the present study, correlation analysis revealed that hundred seeds weight showed a significant positive correlation with plant height, nodules per plant, nodule fresh weight, nodule dry weight, shoot fresh weight, shoot dry weight and lateral roots per plant (Table 5). Pods per plant also showed a significant positive correlation with shoot fresh weight and shoot dry weight (Table 5). A similar result was also made by Jin et al. (2010) who found that

high yielding soybean genotypes have greater root biomass and root length. Another study showed that, the correlations between the degree of nodulation and plant growth and seed yield were significant (Corbin et al., 1977). By contrast, no significant correlation between seed yield and nodule number or weight was also reported (Bhuiyan et al., 2008). However, from the current study, it was obvious that nodulation and root traits might have an effect on the yield contributing characters in soybean.

**Table 5.** Correlation coefficients among shoot and root traits of ten soybean genotypes

Traits	PH	GA	L/P	LL/P	LAI	N/P	NFW	NDW	RFW	RDW	SFW	SDW	PRL	MLRL	LR/P	P/P	100-SW	Y/P	
PH	1																		
GA	0.523**	1																	
L/P	0.441*	0.595***	1																
LL/P	0.413*	0.606***	0.995***	1															
LAI	0.689***	0.492**	0.230	0.174	1														
N/P	0.369*	0.154	-0.135	-0.143	0.222	1													
NFW	0.623***	0.072	0.011	-0.014	0.346	0.800***	1												
NDW	0.564***	0.151	-0.062	-0.079	0.387*	0.879***	0.942***	1											
RFW	0.735***	0.380*	0.287	0.267	0.524**	0.583***	0.701**	0.674***	1										
RDW	0.679***	0.429*	0.230	0.200	0.604***	0.620***	0.675***	0.743***	0.894***	1									
SFW	0.617***	0.152	0.244	0.205	0.357	0.283	0.543**	0.470**	0.548**	0.607***	1								
SDW	0.570***	0.224	0.253	0.221	0.379*	0.247	0.445**	0.433*	0.528**	0.549***	0.936***	1							
PRL	-0.050***	0.132	0.179	0.186	-0.273	0.095	0.013	0.067	-0.040	0.153	0.245	0.387*	1						
MLRL	0.545**	0.360	0.199	0.189	0.315	0.256	0.382**	0.363	0.581***	0.580***	0.439*	0.438*	0.147	1					
LR/P	0.470**	0.1	0.006	-0.003	0.400*	0.376*	0.659***	0.625***	0.395**	0.339	0.380*	0.270	-0.192	0.083	1				
P/P	0.131	0.036	0.346	0.300	0.061	-0.118	0.050	-0.054	0.018	0.065	0.482**	0.371**	0.165	-0.194	-0.029	1			
100-SW	0.411*	-0.002	-0.13	-0.140	0.300	0.495**	0.615***	0.608***	0.203	0.303	0.446*	0.398*	0.051	0.124	0.570***	-0.062	1		
Y/P	0.316	0.146	0.168	0.167	0.297	-0.191	0.084	0.032	0.266	0.183	0.314	0.336	-0.170	0.334	0.279	-0.105	0.069	1	

Here \*, \*\* and \*\*\* = significant at  $\leq 5\%$ ,  $\leq 1\%$  and  $\leq 0.1\%$  level of probability, PH= Plant height, GA= Ground area, L/P= Leaves per plant, LL/P= Leaflets per plant, LAI= Leaf area index, N/P= Nodules per plant, NFW= Nodules fresh weight, NDW= Nodules dry weight, RFW= Root fresh weight, RDW= Root dry weight, SFW= Shoot fresh weight, SDW= Shoot dry weight, PRL= Primary root length, MLRL= Maximum lateral root length, LR/P= Lateral roots per plant, P/P= Pods per plant, 100-SW= Hundred seeds weight, Y/P= Yield per plant.

## Conclusion

Soybean is one of the most important legume crops for Bangladesh. The current study was the first attempt to conduct in depth research on root and nodulation traits of soybean. The goal of this study was to investigate the genetic variability and heritability of root morphological traits including nodulation and also to find out the relationship of those traits with the yield contributing characters of soybean. Significant level of genetic variability was observed between ten soybean genotypes for the studied traits. Several traits including plant height, ground area, leaves per plant, leaflets per plant, leaf area index, nodules per plant, hundred seed weight, and yield/plant showed high heritability whereas other traits showed low to medium heritability. Finally, it was found that root and nodulation related traits have a significant effect on yield for all the ten genotypes of soybean. So, in the stress breeding or for yield improvement of soybean, root and nodulation traits should be taken under consideration.

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