EXPRESSION AND INHERITANCE OF AGRONOMIC TRAITS IN F_2 POPULATION OF MUNGBEAN

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ABSTRACT

The expression and inheritance of various agronomic traits were studied inF_2 mungbean population from the cross Berken/DX92-1 and its parents. Segregations were observed in all measured traits in F_2 population. Qualitative traits including morphological and visual seed traits exhibited single or two gene models depending on circumstances. Single gene model included leaf color, flower color, seed color, hilum color, seed shinness, and pod shape; two gene model included seed shape, pod color, and stem color. There were no significant differences in phenological traits between parents, resulting in low variation in F_2 progeny. The growth duration of F_2 progeny was in the range of 71 - 76 days, indicating short growth duration. For most quantitative traits, the means of morphological, vegetative and yield related traits were higher than parents. There were transgressive segregations for leaf size, pod size, seed yield, and pod dry mass. The coefficients of variation varied from 0.9 - 40.5%. Low broad-sense heritability estimates, 2.2 - 59.8%, for most traits indicated large environmental effects on trait expression. The exceptional traits included leaflet and pod width with high broad-sense heritability of 90.4% and 97%, respectively while individual seed yield and standing dry biomass with average broad-sense heritability of 64.9% and 66.8%, respectively. Average seed yield of F_2 population was similar to Berken but some individuals exhibited higher seed yield than Berken which could be further advanced and studied.

Keywords: Expression, F_2-population, inheritance, mungbean, qualitative and quantitative traits.

Sự biểu hiện và di truyền các tính trạng ở quần thể F_2 đậu xanh

TÓM TẮT

Quần thể F_2 của tổ hợp lai giữa Berken và ĐX92-1 và bố mẹ được trồng trên đồng ruộng, đánh giá và nghiên cứu sự biểu hiện và di truyền các tính trạng chất lượng và số lượng. Các tính trạng đánh giá đều phân ly. Các tính trạng chất lượng liên quan đến hình thái, quả và hạt được xác định do 1 hay 2 gen quy định, như màu sắc lá, hoa, hạt và rốn hạt, và độ bóng của hạt được do 1 gen điều khiển; hình dạng hạt, màu sắc quả, màu sắc thân do 2 gen điều khiển. Các đặc điểm về thời gian sinh trưởng không có sự biến động lớn ở F_2. Tổng thời gian sinh trưởng của quần thể F_2 dao động từ 71 - 76 ngày, chứng tỏ thời gian sinh trưởng ngắn. Giá trị trung bình đối với hầu hết các tính trạng số lượng về sinh trưởng, phát triển và năng suất cao hơn trung bình của bố mẹ. Một số cá thể có sự phân ly tăng tiến vượt ra ngoài khoảng của bố mẹ như kích thước lá, kích thước quả, năng suất cá thể, tổng khối lượng quả. CV% biến động từ 0.9 - 40.5%. Hệ số di truyền nghĩa rộng cho hầu hết các tính trạng thấp, 2.2 - 59.8%, cho thấy môi trường có ảnh hưởng lớn. Một số trường hợp đặc biệt bao gồm chiều rộng lá và quả có hệ số di truyền nghĩa rộng cao tương ứng với 90.4% và 97%; năng suất cá thể và khối lượng sinh khối khô có hệ số di truyền nghĩa rộng ở mức trung bình tương ứng với 64.9% và 66.8%. Năng suất cá thể trung bình của F_2 tương đương với Berken. Một số cá thể có năng suất cao hơn Berken có thể được lựa chọn để nhân thế hệ và đánh giá tiếp.

Từ khóa: Biểu hiện và phân ly, đậu xanh, quần thể F_2, tính trạng số lượng và chất lượng.

1. INTRODUCTION

Mungbean (*Vigna radiata* (L.) Wilczek) is an ancient legume crop with respect to production, trade, and consumption. Mungbean is an important grain legume, particularly in Asia, where it is widely used for starch, flour, noodles, and bean sprouts. Besides nourishing people, the cultivation of mungbean can sustain the soil by adding nitrogen through rhizobial symbiosis. Availability of early maturing cultivars had made mungbean cultivation possible into different cropping systems.With a cultivation area of about 6 million hectares, the largest mungbean cultivation occurs in Asian countries where India, China, Myanmar, and Indonesia account for ~90% of world production (Nair *et al.,* 2014). India is the world's largest mungbean producer with 3.72 million ha at around 60% of world's area (Abdel-Haleem, 2007). However, India consumed almost the of production (about 54%) (Nair *et al.*, 2013). Currently, mungbean is considered to be a major cash crop and mungbean research programs are being conducted globally.

In Vietnam, mungbean as a pulse crop is widely grown in the South. Traditionally, mungbean is grown in a low yield environment with little attention to the yield input compared to other crops. Future strategies should be directed toward improving high yield in farmer's fields. Utilization of the mungbean's early maturity as an intercrop or as a short season crop in a multiple cropping systems would increase profitability of thiscrop (Yaqub *et al.,* 2010; Kumar and Kumar, 2014)

The yield of mungbean remains rather low. The main reason for low productivity is the lack of high yielding and disease resistant mungbean varieties adaptable to different regions, seasons, cropping systems and agronomic conditions. Thus, there are urgent needs of high yielding, disease resistant varieties suited to different situations (Kumar and Kumar, 2014; Nair *et al.,* 2014).

Understanding the genetic inheritance of traits is very important for breeders in variety improvement. The inheritance of various traits in mungbean were reported in several studies, such as vines (Sen and Ghosh, 1959; Pathak and Singh, 1963), leaf size, leaf shape (Yimram*et al.*, 2009), lobed leaves (Sen and Ghosh, 1959; Nguyen, 2012; Vu, 2013), the traits related to seed coat (Nguyen, 2012; Vu, 2013) and type of growth (Iqbal *et al.*, 2015). Similarly, there has been a variety of studies on the genetics of agronomic traits such as weight of 100 seeds (Rohman*et al.*, 2003; Khattak*et al.*, 2004; Iqbal *et al.*, 2015; Shrinkhala *et al.*, 2016), number of seeds/pod (Marlik and Singh, 1983), number of branches/main stem (Singh and Singh, 1996; Khattak *et al.*, 2002) and biomass (Rehman *et al.*, 2009;Khan *et al.*, 2016; Nguyen *et al.*, 2016).

To develop a new variety with desirable combination of qualitative and quantitative traits, commprehensive information on the genetic mechanism controlling various traits is considereda pre-requisite for initiating an efficient breeding program.

This study aimed to dissect genetic expression and control of various traits in F_2 mungbean and to provide useful information for mungbean improvement.

2. MATERIALS AND METHODS

2.1. Plant materials

F_2 mungbean population consisting of 236 individual plants and parental plants were used in this study (Table 1). The cross was made in 2014 summer from crossing of DX92-1 and Berken and advanced to F_2 in 2016 summer.

2.2. Experimental design

Plants were grown in the experimental field of Faculty of Agronomy, Vietnam National University of Agriculture in 2016 summer season. The F_2 population and parental plants were grown in 1.5 m^2 plots with density of 35 plants/m^2. This spacing was large enough for plants to fully express traits.

2.3. Data collection and measurement

Measurements were made on individual F_2 and parental plants including morphology, seed traits, phenology and agronomic traits (Table 2, 3).

Table 1. The number of individual plants sown for each generation in parents and F_2 population

Population	Number of plants	Origin and main characteristics
DX92-1	37	Plant Resources Center; early flowering, short growth duration (65-60 days); large, dull green seed.
Berken	30	Cultivated variety form USA; early flowering (68- 97 d), annual; erect stem, large shiny green seed.
F_2	236	Berken/ĐX92-1 cross

Table 2. Measurement of morphological characteristics on parental plants and F_2 population

Traits	Expression
Stem and leaf	
Hypocotyl color	1- Greenish purple; 2-Green; 3-Purple
Stem color	1-Green; 2-Dark green
Leaf color	1-Green; 3-Dark green;
Density of stem pubescence	1-Scatter; 2-Dense;
Flower colour	1-Light yellow; 2-Yellow
Pod and seed traits	
Pod color	1-Greenish black; 2-Grey; 3-Brown; 4-Black
Pod curvature	1-Least curved; 2-Medium; 3-Most curved
Seed color	1-Yellow; 2-Yellowish green; 3-Light green; 4-Dark green;
Seed shape	1-Round; 2-Oval; 3-Other shape
Testa color	1-Green; 2-Yellow; 3-Other color
Seed shining	1-Shiny; 2-Dull
Hilum color	1-White; 2-Tan

Table 3. Measurement of quantitative traits on parental plantsand F_2 population

Traits	Definition/ Measurement
Plant height	cm; from the ground to the furthest point of the main stem
Leaflet size	cm; length & width of terminal leaflet of 5^{th} and 6^{th} trifoliate leaves
Petiole length	cm; petiole length of 5^{th} and 6^{th} leaves
Internode length	cm; the average node length between the 5^{th} and 7^{th} leaves
Stem diameter	cm; diameter; average of measures below the node 5^{th} and 6^{th} fully-expanded trifoliolate leaves
Number of leaves on stem	All leaves on main stem
Number of nodes on stem	Nodes on main stem
Number of primary branches on stem	All primary branches on main stem
Total number of pods/plant	Number of pods/plant at harvest
Pod traits	
- Number of seeds per pods	- 10 first collected pods for each plant
- Pod size	- Length and width (mm) of 5 pods/plant
- Seed size	- Weight of 100 seeds (g)
Pod dry weight (including seed)	g/plant; Pods harvested, dried and weighed for individual plants
Individual seed yield	g/plant; Cleaned seeds of each plant were weighed
Standing dry biomass	g/plant; the standing biomass was removed, dried and weighed
Harvest index (HI)	HI = Individual seed yield/(Pod mass + Standing dry biomass)

Hypocotyl color was observed at five days after emergence. Other quantitative traits including stem color, leaf color, flower color… were recorded during plant growth. Pod and seed traits were observed after drying and cleaning the seeds.

Quantitative traits were observed weekly on plant height, number of leaves on main stem, number of leaves per plant, and branches per plant. After harvest, yield and yield components were recorded on pod length, pod width, number of seeds per pod, number of pods per plant, 100-seed weight, and seed yield per plant (Table 3).

2.4. Data analysis

Initially, frequency distribution for each trait was used separately for qualitative traits with discrete distribution and for quantitative traits with continuous distribution.

2.4.1. Qualitative traits analysis

For traits that appeared to be qualitatively inherited, the standard chi- square (X^2) test was used to test hypotheses related to categorical data such as would be collected from inheritance studies. The chi- square was computed to test the goodness of fit of the observed data to genetic models of single and digenic inheritance at $p \leq 0.05$ using the following formula:

$$X^2 = \sum\left[\left(f_0 - f_e \right)^2 / f_e \right]$$

Where:

f_0: Observed sample frequency

f_e: Expected frequency based on Mendelian ratios.

The segregation ratios of F2 population were tested for 1 or 2 gene control according to expected Mendelian ratios (Table 4) (Acquaah, 2007).

2.4.2. Quantitative trait analysis

For quantitative traits, several analyses were undertaken to explore the expression of the traits and assess their variability and heritability.

For each trait, analysis of variance was used to test for differences in the expression of traits in the parental and progeny generation. The values of individual plants were used to estimate variances for the parental and progeny generations. In turn, these variance estimates were used to calculate environmental, phenotypic, and total genetic variances for each trait. These variance estimates were then used to estimate broad sense heritability for each trait, using the variance ratios method (Acquaah, 2007). These entities were defined as per the following formulas (Acquaah, 2007):

$$\bar{X} = \frac{X_i}{n}$$

$$CV\% = \frac{S.D \times 100}{\bar{X}}$$

$$Ve = \frac{V_{F1} + V_{P1} + V_{P2}}{3}$$

$$H_b^2(\%) = \frac{V_{F2} - Ve}{V_{F2}} \times 100$$

Where:

$\bar{X}$: Mean value of the trait

n: Observed sample size

CV%: Coefficient of variation

S.D: Phenotypic standard deviation

V_{P1} and V_{P2}: Phenotypic variance of parent 1 and parent 2, respectively

Ve: Environmental variance

X_i: Observed phenotypic value in individual i (i from 1, 2,... n)

V_{F2}: Phenotypic variance in F_2

H_b^2: Broad-sense heritability (%)

The formula given by Acquaah (2007) was used to calculate phenotypic correlation coefficient (r):

$$r = \frac{N * \sum(X * Y) - \left(\sum X\right) * \left(\sum Y\right)}{\sqrt{N * \sum X^2 \left(\sum X\right)^2} * \sqrt{N * \sum Y^2 - \left(\sum Y\right)^2}}$$

Where:

N: population size

X, Y: measured values of the traits X, and Y, respectively

The data were analyzed using Microsoft Excel 2010.

Table 4. Expected phenotypic ratios in F_2 according to Mendel's segregation

Gene	Type of gene interaction	Phenotypicratio in F_2
One gene	Complete dominance	1: 3
	Incomplete dominance	1:2:1
Two genes	Independent segregation	1: 1: 1: 1
	Duplicate dominant genes	9: 7
	Two dominant genes with additive effect	9: 6: 1
	Dominant epitasis	12: 3: 1
	Dominant and recessive interaction	13: 3
	Recessive epitasis	9: 3: 4
	Duplicate dominant gene action	15: 1

3. RESULTS

3.1.Qualitatively inherited traits

- Morphological traits

Segregation were observed for all qualitative inherited traits, viz. hypocotyl color, stem color, leaf color, leaf pubescence, and flower color (Table 5).In general, most F_2 plants segregated closer to DX92-1.

Hypocotyl colour is one of the traits that can be used to differentiate the varieties in early stage of germination. Whereas Berken had purple hypocotyl color, DX92-1 had light green hypocotyl color. The F_2 segregation ratio was 9:6:1 which indicated digenic model of inheritance ($P > 0.05$) (Table 5).The F_2 segregation ratio for stem color was consistent with a 3:1 ratio for green: dark green. The traits were conditioned by a single gene with green being dominant over dark green.

The parents showed two leaf colors, green (DX92-1) and dark green (Berken). The segregation of F_2 population fitted to 3:1 ratio (P-value = 0.45), indicating that the leaf color was conditioned by a single gene, and green was dominant over dark green.

The F_2 generation segregated for density of stem pubescence into scatter and dense categories, consistent with a ratio 3:13. This result was consistent with digenic model of inheritance for stem pubescence with suppressive epitasis action.

The F_2 segregation for flower colour ratio fitted to 1 yellow: 1 light yellow. This result was consistent with single gene model of inheritance.

- Visual pod and seed traits

Visual appearances of pods and seeds affect commercial values in mungbean. The F_2 population segregated for brown and black color in pod color (Figure 1a) and fitted to the ratio of 3 brown: 13 black. The simplest most likely inheritance model was two dominant genes with suppressive action for black color (Table 6).

More plants were segregated for least curved than medium curved. F_2 ratio was close to 3:1 least curved: medium curved, conditioned by one gene with complete dominance.

The parental plants were in contrast in seed color and shininess. DX92-1 showed the dull and dark green seed color, whereas Berken exhibited shiny and yellowish green seeds (Figure 1b). The F_2 plants segregated in both traits in reasonable fit to 1:3 ratio. This ratio fitted to a model for one dominant gene with complete dominance (Table 6).

Most of observed seeds in F_2 population were of drum shape; few of them were oval shaped. The F_2 plants segregated for oval: other shape in reasonable fit to a 1:15 ratio, which might be assumed to control by two genes with duplicate action for other shapes (Table 6).

Table 5. Qualitative traits for which differences were observed in F_2 generation, the observed category frequencies, the chi-square (χ^2) values and probabilities for the goodness-of-fit to putative ratios

Traits	Observed distribution for rating categories			Expected segregation ratio	χ^2	P-value
Hypocotyl color(Berken: purple; DX92-1: green)						
	Purple	Greenish purple	Green			
	80	14	142	6:1:9	1.499	0.47
Stem color (Berken, purple; DX92-1: green)						
	Green	Dark green				
	183	52		3:1	1.034	0.31
Leaf color (Berken: dark green; DX92-1: green)						
	Green	Dark green				
	182	54		3:1	0.565	0.45
Density of stem pubescence (Berken and DX92-1: dense)						
	Scatter	Dense				
	42	194		3:13	0.141	0.71
Flower color (Berken: yellow; DX92-1: light yellow)						
	Yellow	Light yellow				
	126	110		1:1	1.099	0.29

(a) Pod color

Black pods

Brown pods

(b) Visual seed traits

Shiny, yellowish green (Berken)

Dull, dark green (DX92-1)

Dull, yellowish green (F_2)

Shiny, yellowish green (F_2)

Figure 1. Representative examples illustrating the degree of expression in mungbean for (a) pod color; (b) visual seed traits

Table 6. Qualitative traits for which differences were observed in F_2 generation, the observed category frequencies, the chi-square (χ^2) values and probabilities for the goodness-of-fit to putative ratios crossing

Traits	Observed distribution for rating categories		Expected segregation ratio	χ^2	P-value
Pod color (Berken: brown; DX92-1: black)					
	Brown	Black			
	38	198	3:13	1.086	0.30
Pod shape (Berken: medium curved; DX92-1: least curved)					
	Least curved	Medium curved			
	178	58	3:1	0.023	0.88
Seed color (Berken: yellowish green; DX92-1: dark green)					
	Yellowish green	Dark green			
	68	168	1:3	1.831	0.55
Seed shining (Berken: shiny; DX92-1: dull)					
	Shiny	Dull			
	68	168	1:3	1.831	0.55
Seed shape (Berken; DX92-1: other shape)					
	Oval shape	Other shape			
	17	219	1:15	0.343	0.55
Hilum color (Berken: white; DX92-1: tan)					
	White	Tan			
	69	167	1:3	2.260	0.13

DX92-1 had tan hilum color while Berken had white hilum. The F_2 generation segregated into 1:3 ratio, indicated that hilum color was conditioned by one gene with complete dominance.

3.2. Expression and inheritance of phenological traits in F_2 population

There seemed to be no significant differences between the parents and individuals of F_2 population in days to flowering, the duration of flowering and growth duration. Both parents and F_2 flowered less than five weeks after sowing and matured their first pod about 13 - 14 days later. Both CV% and broad-sense heritability for days to flowering were low (Table 7).

In terms of flowering duration, F_2 progeny was closed to Berken. As with time to flowering, the range for this trait in F_2 progeny (46 - 40 days) was wider than parents (Table 7).

The average of days to first pod maturity of F2 progeny(58.7 days) was slightly shorter than DX92-1 (59.4 days) and Berken (58.8 days), but the range was wider (Table 7).

Generally, the growth duration of DX92-1, Berken and F_2 population were non-significant difference, ranged from 70 - 76 days after showing and average of 73.7 days (Table 7d). Frequency distribution for growth duration indicated additive genetic affects and transgressive segregation with several F_2 individual plants outside the parental ranges (Figure 2a). CV% was low in LMB5, indicating there were not many variations (0.9%). Broad-sense heritability was low indicating that environment affected strongly this trait.

3.3. Expression and inheritance of vegetative and morphological traits in F_2 population

There were differences among parents and F_2 progeny in various vegetative and morphological traits. Size related traits including plant height, leaflet size, petiole length, internode length and

stem diameter were generally greater in average magnitude in the F_2 progeny than in parents (Table 8). Within F_2 population, there was a wide range among individuals for most traits (Table 8). While most individuals were intermediate between the parents, transgressive segregations were observed in some individuals with regard to plant height, internode length or number of primary branches.

The plant height of F_2progeny was significantly greater than DX92-1 and Berken (Table 8). F_2 plants segregated in range of 40.2 - 73.8 cm in plant height. Several individuals were less than 45 cm and above 70 cm in height, which were outside parental ranges of 46.7 - 64.0 cm (Figure 2). CV% was low (8.3%) while broad-sense heritability was high (83.0%), showing the strong effect of genotype on this trait.

F_2 generation was transgressive outside parental ranges of 8.5 - 13.0 cm in leaf length and 6.9 - 12.6 cm in leaf width (Table 8). CV% and broad-sense heritability of leaf length were low (8.8% and 13.0%, respectively), while CV% and broad-sense of heritability of leaf width were higher (33.5% and 90.4% respectively).

F_2 generation had the longest petiole length with the average 15.1 cm. F_2 segregated with a range of 13.0 - 18.1 cm (Table 8). Coefficient of variation and heritability were low at 5.6% and 2.2%, respectively.

Other traits including internode length, stem diameter, number of leaves, number of nodes per plant, and number of primary branches also showed apparent segregation in F_2 population (Table 8). The means of these traits in F_2 population were higher than those in the parents. Low CV% (10.2 - 30.1) and broad-sense heritability (2.7 - 16.5%) were found for these traits, except CV% for number of primary branches was significantly higher (40.5%).

3.4. Expression and inheritance of pod and seed traits in F_2 population

The means for the F_2 generation were slightly higher than parents with some evidence of transgressive segregation at the upper end of the range, such as for pod length, total number of pods per plant, number of seeds per pod and weight of 100 seeds (Table 9).

Table 7. Average, range, coefficient of variation (CV%) and broad-sense heritability (H^2_b) of phenological traits in parents and F_2 population

Phenological traits		DX92-1	Berken	F_2 population
Days to flowering (days)	Average	38.0	37.8	37.7
	Range	38 - 39	37 - 39	36 - 40
	CV%			2.0
	H^2 (%)			18.4
Days to first pod (days)	Average	42.3	41.8	41.9
	Range	42 - 43	41 - 43	40 - 45
	CV%			1.8
	H^2 (%)			59.8
Days to first pod maturity (days)	Average	59.4	58.8	58.7
	Range	58 - 61	57 - 61	55 - 62
	CV%			2.6
	H^2 (%)			41.3
Growth duration (days)	Average	73.7	73.7	73.7
	Range	70 - 75	73 - 74	71 - 76
	CV%			0.9
	H^2 (%)			10.1

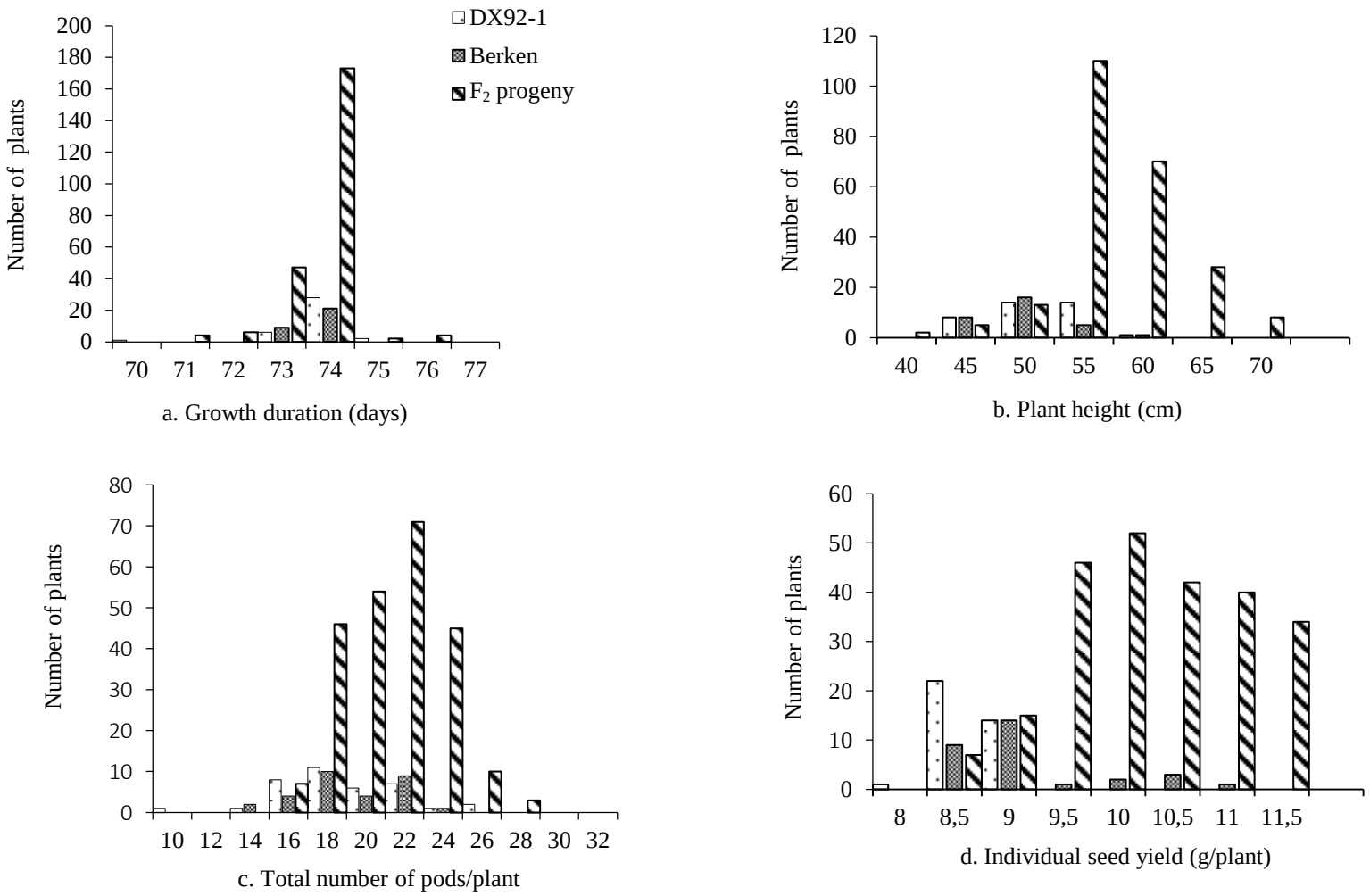

Figure 2. Frequency distribution for (a) growth duration (days), (b)plant height (cm), (c) total number of pods/plant and (d) individual seed yield (g/plant)in parents and F_2 population

Table 8. Average, range, coefficients of variation (CV%) and broad-sense heritability (H^2_b) for vegetative and morphological traits in the parents and F_2population

Traits		DX92-1	Berken	F_2 population
Plant height (cm)	Average	53.4	52.3	60.2
	Range	46.8 - 60.0	46.7 - 64.0	40.2 - 73.8
	CV%			8.3
	H^2%			83.4
Leaf length (cm)	Average	10.8	10.5	11.4
	Range	8.5 - 12.6	8.9 - 13.0	7.5 - 14.5
	CV%			8.8
	H^2%			13.0
Leaf width(cm)	Average	10.0	9.9	10.5
	Range	7.7 - 11.5	6.9 - 12.6	6.6 - 14.2
	CV%			33.5
	H^2%			90.4
Petiole length (cm)	Average	13.9	13.7	15.1
	Range	11.8 - 15.3	12.3 - 15.1	13.0 - 18.1
	CV%			5.6
	H^2%			2.2
Length of internode (cm)	Average	3.4	3.8	5.0
	Range	2.0 - 4.6	2.2 - 5.2	3.5 - 7.0
	CV%			13.1
	H^2%			16.5
Stem diameter (cm)	Average	0.7	0.7	0.8
	Range	0.5 - 0.9	0.5 - 0.8	0.6 - 1.1
	CV%			12.1
	H^2%			15.4
No.of leaves/plant	Average	9.4	9,2	9,2
	Range	8.0 - 11.0	7.0 - 11.0	6.0 - 12.0
	CV%			13.0
	H^2%			39.5
No. of nodes/plant	Average	10.0	9.8	10.1
	Range	8.0 - 13.0	8.0 - 11.0	8.0 - 14.0
	CV%			10.2
	H^2%			2.7
Number of primary branches	Average	2.5	2.5	2.8
	Range	0.0 - 6.0	1.0 - 4.0	1.0 - 6.0
	CV%			40.5
	H^2%			15.1

Variation among the individuals in F_2 progeny as indicated by CV% was generally not high for all pod and seed traits, except pod width of 30.1%. Other traits had CV% in the range of 4.6 - 13.9%.

Pod length, for example, had wider range in F_2 progeny (7.4 - 10.6 cm) than in the parents with mean of 9.3 cm. Both CV% and broad-sense heritability were low with 4.9% and 36.8%, respectively.

The number of pods per plant of F_2 population was greater than parents with wide range of 15.0 - 36.0 (Figure 2c). CV% and broad-sense heritability were low at 13.9% and 6.1%, respectively (Table 9c).

The average number of seeds per pod was greater in the F_2 population than parents (Table 9). There were transgressive segregations outside parental ranges of 9.1 - 12.3 for F_2 compared with 9.0 - 11.6 for parents. CV% and broad-sense heritability in F_2 population were low.

The 100 seeds weight of F_2 was around 5.8 g (Table 9), which was slightly higher than parents. Both CV% and broad-sense heritability were low, 4.6% and 24.9%, respectively.

3.5. Expression and inheritance of yield related traits in F_2 population

Analysis of variance showed that there were significant differences between parents and F_2 progeny means for all yield related traits, except HI (Table 10). In general, pod dry mass, seed yield, standing dry biomass were greater in Berken than those of DX92-1. Only HI was similar in the parents and F_2 progeny (Table 10).

The means of F_2 population were mostly intermediate, except pod dry mass (15.5 $g.plant^{-1}$ in F_2 population compared with parental range of 11.3 - 15.0 $g.plant^{-1}$ (Table 10). Transgressive segregants were higher than the higher parent in most traits, except HI.

CV% were low to moderate for yield related traits (5.7 - 11.0%), indicating moderate variation of these traits among individuals in F_2 population. Broad-sense heritability for yield related traits was low to moderate (27.5 - 66.8%), indicating large environment effects for these traits.

As with pod dry biomass, the differences in total pod dry mass between F_2 population and parents were generally small although significant (Table 10). In F_2 population, several segregants expressed higher pod dry mass than parents, 17.0 g/plant compared with 15.0 g/plant and 14.9 g/plant. Both CV% and broad-sense heritability were low with 5.7%, and 27.5%, respectively.

Individual seed yield per plant tended to be higher in the F_2 population than parents. There were also some segregants with higher yields than highest parents (Figure 2d). CV% was low (10.2%) while the broad-sense heritability was moderate (64.9%), suggestingthe effect of both genotype and environment onindividual seed yield.

3.6. Phenotypic correlations between quantitative traits in F_2 population

There was a positive correlation between growth duration and several traits such as plant height (r = 0.05), number of primary branches per plant (r = 0.03), leaf size and seeds per pod (r = 0.03), but these were nonsignificant. Number of pods per plant were negatively correlated, but nonsignificant, with all vegetative traits such as plant height (r = -0.13), number of nodes per plant (r = -0.21) and stem diameter (r = -0.09).

Among the morphological traits, there were significant positive correlations, such as between plant height and number of nodes per plant (r = 0.32), number of leaves per plant (r = 0.21), and stem diameter (r = 0.32), reflecting that higher stem produced more number of nodes and leaves per plant and larger stem diameter (Table 11).

Table 9. Average, range, coefficients of variation (CV%) and broad-sense heritability (H^2_b) for pod and seed traits in the parents and F_2population

Traits		DX92-1	Berken	F_2 population
Pod length(cm)	Average	8.8	8.9	9.3
	Range	7.8 - 9.9	8.5 - 9.4	7.4 - 10.6
	CV%			4.9
	H^2%			36.8
Pod width(cm)	Average	0.5	0.5	0.5
	Range	0.4 - 0.5	0.4 - 0.5	0.4 - 0.7
	CV%			30.1
	H^2%			97.0
Total number of pods per plant	Average	18.5	18.8	21.1
	Range	10.0 - 26.0	13.0 - 23.0	15.0 - 36.0
	CV%			13.9
	H^2%			6.1
No.of seeds/pod	Average	9.6	10.6	10.7
	Range	9.0 - 10.3	9.5 - 11.6	9.1 - 12.3
	CV%			5.0
	H^2%			21.1
Weight of 100 seeds (g)	Average	5.4	5.7	5.8
	Range	5.0 - 5.8	5.0 - 6.2	4.9 - 6.5
	CV%			4.6
	H^2%			24.9

Table 10. Average, range, coefficients of variation (CV%) and broad-sense heritability (H^2_b) for yield related traits in the parents and F_2population

Traits		DX92-1	Berken	LMB5
Pod dry mass(g/plant)	Average	13.0	13.6	15.5
	Range	11.3 - 15.0	12.2 - 14.9	14.0 - 17.0
	CV%			5.7
	H^2%			27.5
Individual seed yield (g/plant)	Average	8.9	9.4	10.4
	Range	8.4 - 9.3	8.7 - 11.0	8.5 - 11.9
	CV%			8.1
	H^2%			64.9
Standing dry biomass (g/plant)	Average	13.3	14.2	15.6
	Range	11.3 - 15.8	13.1 - 15.4	13.0 - 23.5
	CV%			11.0
	H^2%			66.8
Harvest index	Average	0.3	0.3	0.3
	Range	0.3 - 0.4	0.3 - 0.4	0.3 - 0.4
	CV%			10.2
	H^2%			52.1

Table 11. Pairwise phenotypic correlations (*r*) of quantitative traits observed in F_2 population

	PH	NoP	NL	PB	SD	LL	LW	PP	SP	GD	SY	HI
NoP	0.32	1										
NL	0.21	0.55	1									
PB	0.30	0.35	0.18	1								
SD	0.32	0.55	0.76	0.69	1							
LL	0.50	0.36	0.20	0.34	0.33	1						
LW	0.27	0.33	0.20	0.27	0.29	0.44	1					
PP	-0.13	-0.21	-0.14	-0.01	-0.09	-0.11	-0.17	1				
SP	-0.06	0.001	-0.09	-0.02	-0.04	-0.13	-0.06	-0.06	1			
GD	0.05	-0.03	0.001	0.03	0.01	0.09	0.04	0.01	0.03	1		
SY	0.005	0.03	0.02	-0.07	-0.06	0.006	-0.03	0.01	0.03	-0.01	1	
HI	-0.009	0.04	-0.008	-0.06	-0.06	0.002	-0.02	-0.01	0.02	-0.05	0.80	1
SW	-0.07	-0.10	-0.09	-0.02	-0.04	-0.14	-0.14	0.015	0.16	0.019	-0.06	-0.11

Note: PH: Plant height; Nop: Number of node per plant; NL: Number of leaves per plant; PB: Number of primary branches per plant; SD: stem diameter; LL: Leaf length; LW: Leaf width; PP: Number of pods per plant; SP: Number of seeds per pod; GD: Growth duration; SY: Seed yield per plant; HI: Harvest index; SW: 100 seed weight

4. DISCUSSION AND CONCLUSIONS

Generally, segregations were observed in all measured traits in cross population of DX92-1 and Berken. Qualitative traits including morphological and visual seed traits exhibited single or two gene models depending on circumstances, such as single gene for leaf color, flower color, seed color, hilum color, seed shinning, and pod shape, and two gene models for seed shape, pod color, stem color.

The findings for those traits in this study were quite consistent with previous studies in terms of trait expression and genetic models such as single gene for flower colour, hilum colour (Nguyen 2012, Vu 2013).

However, some traits indicated different models. For example, the pubescence density on the stem in F_2 progeny segregated in dense or scatter pattern with two gene control. Murty and Patel (1973) and Vu (2013) found that one gene regulates the pubescence density. Similarly, while some studies indicated several genes controlled flower colour (Murty and Patel, 1973), this study and Vu (2013) suggested single gene inheritance. These differences can be explained by differences of parental genotypes involved in hybridization.

There were no significant differences in phenological traits between parents, resulting in low variation in F_2 progeny. F_2progeny had growth duration in the range of 71-76 days, indicating short growth duration.

For most quantitative traits, the means of morphological, vegetative and yield related traits were higher than parents. There were also transgressive segregations outside parent ranges, such as leaf size, pod size, seed yield, pod dry mass. Especially, seed yields of F_2 were similar to Berken, a cultivated variety from USA. Even some individuals exhibited higher seed yield than Berken.

Frequency distributions for agronomical traits in this study were continuous, indicating additive genetic effects. Some studies even estimated gene effects of additive, dominant and non-allelic interactions. For instance, both additive and dominant effects contributed to days to maturity in mungbean (Shrinkhala *et al.*, 2016). Plant height in four mungbean crosses was found to be non-allelic gene

interaction of duplicate or complementary (Khan *et al.*, 2016). Non-allelic gene interactions and/or linkage disequilibrium in their inheritance also suggested for branches per plant, pod length and seeds per pod (Shrinkhala *et al.*, 2016).

Low CV% and broad-sense heritability estimates for most traits suggested large environmental effects on trait expression. Broad-sense heritability estimates in the study were also in the ranges of heritability identified in various studies, viz. Murty et al., 1976, Mehandi *et al.*, 2013, Iqbal *et al.*, 2015, Khan *et al.*, 2016, Shrinkhala *et al.*, 2016, Nguyen *et al.*, 2016.

Flowering time had broad-sense heritability in the range of 39.5 - 99%, indicating additive effects. However, dominant x dominant interaction was also determined by Murty et al., (1976).Heritability of plant height varied significantly from 7.9-96.9% and the number of branches/stem varied from 31.0 to 85.2%. Heritability for weight of seed was high, from 51.2 - 98.6%. Heritability for yield component traits ranged from 8.6 - 92.6% (Mehandi et al., 2013; Iqbal et al., 2015). Number of pods/plant was correlated with yield, and the average range from 12.4 - 30.5 pods/plant and. Heritability of number of pods/plant could be ranged from 21.7 - 99.1%. Some yield component traits had medium to high heritabilities such as number of pod clusters/plant (95.5%), number of seeds/plant (58.8%) (Mehandi et al., 2013).

The differences in heritability estimates from various studies are due to different plant materials/populations as well as effects of environment, genetic factors, and genotype x environment interaction. The findings in this study suggested some traits with moderate to high heritability, such as plant height and individual seed yield, which could be considered as significant selection criteria for mungbean improvement. Especially, some individual segregants positively exceeded parental ranges for growth duration and seed yield that should be selected for and advanced further.

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