

Characterization of 56 Soybean Accessions on Yield Components and Maturity-related Traits

(Karakterisasi 56 Aksesori Kedelai untuk Karakter Komponen Hasil dan Umur)

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ABSTRAK

Peningkatan produktivitas kedelai nasional dapat dilakukan dengan penggunaan varietas produktivitas tinggi dan manipulasi indeks panen menggunakan varietas genjah. Pembentukan varietas di atas memerlukan plasma nutfah dengan potensi hasil tinggi dan berumur genjah. Tujuan dari penelitian ini adalah untuk mengidentifikasi aksesori kedelai yang mempunyai potensi hasil tinggi dan aksesori kedelai berumur genjah. Sebanyak 56 aksesori kedelai terdiri atas varietas elit dan introduksi, aksesori lokal dan galur-galur persilangan ditanam di Kebun Percobaan Cikeumeuh (250 m dpl) dan Pacet (1.200 m dpl) menggunakan Rancangan Acak Kelompok dengan tiga ulangan. Pengamatan dilakukan terhadap karakter morfologi, komponen hasil dan karakter reproduktif yang meliputi umur berbunga (fase R1, R3, R7, dan R8). Hasil penelitian menunjukkan 28 aksesori (50%) diuji di Cikeumeuh dan 43 aksesori (76,79%) diuji di Pacet menunjukkan jumlah polong/tanaman lebih dari 50. Sekitar 35,71% aksesori di Cikeumeuh dan 41,07% aksesori di Pacet menghasilkan biji/tanaman lebih dari 10 g/tanaman. Aksesori kedelai yang menunjukkan komponen hasil tinggi hanya di KP Cikeumeuh adalah B2981, B3517, dan B3628. Aksesori kedelai yang menunjukkan komponen hasil tinggi hanya di KP Pacet adalah B4441, B3628, B382, B4334, dan B3414. Aksesori yang menunjukkan komponen hasil tinggi di kedua lokasi (Cikeumeuh dan Pacet) adalah B3417. Aksesori B3417 diklasifikasikan sebagai aksesori dengan adaptasi luas karena berkeragaan komponen hasil tinggi di dataran rendah dan di dataran tinggi. Aksesori dengan umur panen genjah ditunjukkan oleh B2973 (74 hari setelah tanam, hst) yang tidak berbeda nyata dengan aksesori B1430 (75 hst), B3611 (76 hst), B4433 (77 hst), dan B4439 (80 hst) berdasarkan uji DMRT ($p < 0,05$). Berdasarkan karakter morfologi, sebagian besar plasma nutfah kedelai terbagi dalam tiga kelompok termasuk *landraces* tanpa mempertimbangkan asal daerahnya. Analisis klaster berdasarkan karakter agronomi mendukung analisis DMRT bahwa aksesori kedelai dengan hasil biji tinggi dan umur genjah dapat dibedakan. Aksesori kedelai dengan jumlah polong banyak, hasil biji tinggi, umur genjah potensial digunakan dalam program pemuliaan kedelai produktivitas tinggi dengan umur genjah.

Kata kunci: komponen hasil, umur genjah, plasma nutfah, aksesori, kedelai.

ABSTRACT

One effort to improve soybean production in Indonesia is by using high yielding and manipulating harvest index by using early maturing varieties. Such variety development requires the availability of soybean germplasm with high yield potential and early maturity. The objective of this study was to identify soybean genotypes showing high yield potential and early maturity. A total of 56 soybean accessions consisting of elite and introducing varieties, landraces, and breeding lines were characterized in the field with different altitudes i.e. Cikeumeuh (250 m above sea level) and Pacet (1.200 m asl). The experiments were arranged in a randomized block design using three replications. Characters observed were morphological characters, yield components and maturity-related traits (days to R1, R3, R7, and R8). Results showed that 28 accessions (50%) tested at Cikeumeuh and 43 accessions (76.79%) tested at Pacet demonstrated pod number/plant more than 50. About 35.71% at Cikeumeuh and 41.07% at Pacet showed seed yield more than 10 g/plant. Soybean accessions demonstrating high yield components only at Cikeumeuh were B2981, B3517, and B3628. Soybean accessions demonstrating high yield components only at Pacet were B4441, B3628, B382, B4334, and B3414. The accession demonstrating high yield component performance at both locations (Cikeumeuh and Pacet) was shown by B3417. Accession B3417 is then classified as a broad adapting soybean genotype. The early pod maturing accession was demonstrated by B2973 (74 dap) that was not significantly different from accessions B1430 (75 dap), B3611 (76 dap), B4433 (77 dap), and B4439 (80 dap) based on DMRT at $p = 0.05$. Three distinct clades were generated based on morpho-agronomical variables on both locations (Cikeumeuh dan Pacet). Cluster analysis of agronomical characters was able to distinguish accessions with high yield components in either one or both locations (B3417, B3628, and B2981), and accessions with early maturity and least pod number (B4439 and B4433). Cluster analysis results were in well-agreement with the results based on DMRT. Soybean accessions having high pod number, high seed yield and early in maturity are potentially used for developing high yielding soybean varieties with early in maturity.

Keywords: yield component, maturity, germplasm, accession, soybean.

INTRODUCTION

Soybean (*Glycine max*), an economical legume crop, is one of alternative source of protein (Hanafie, 2004; Vuong *et al.*, 2007). In the last 20 years, Indonesian soybean plantations showed significant decreases both in total areas and production with a total national area of 1.6 millions ha and total production of 1.87 million tons in 1992 to become only 0.551 million ha and 0.780 million tons in 2013. The national soybean consumption in 2013, however, reached 2.51 million tons. Eventhough there is a high potency of soybean to be a superior commodity, the deficit of 1.73 million tons (69%) was fullfilled through import (BPS, 2014).

A number of improved soybean varieties with targeted characters have been released. Many local accessions of soybean have also been found to be well cultivated in the local regions. However, the main constrains of the Indonesian soybean cultivation is the low productivity with the national average of only 1.3 ton/ha, much lower than that shown by the main soybean produsers such as the USA, Brazil, and Argentine with national productivity could reach up to 3.0 tons/ha (Marwoto *et al.*, 2005).

In Indonesia, soybean self-sufficiency should be acheived to fullfill national demand through several approaches such as by increasing soybean productivity, plantation expansion outside the Java island and manipulation of harvest index (HI). Selection of parents having high yield potentials and varied in yield components will facilitate breeding programs for inreased yield. The seed yield of soybean consists of several components, including the number of plants per unit area, pod number per plant, seeds per pod, and seed size (Liu and Herbert, 2002). Yield and yield components are quantative traits and controlled by several to many genes and are the product of interaction between genotypes and environment (Liu and Herbert, 2002). There is a differential response of yield components to changes in environmental conditions (Kang, 1998; Liu *et al.*, 2010).

Increasing HI can be done by increasing planting frequency within a year of cultivation

cycle. This can be done by planting early maturity soybean cultivars. Earliness level of a soybean genotype is determined by the quickness of that particular genotype to initiate flowers and shows early in maturity compared to that of the late maturing genotypes. The reproductive-related traits in soybean are controlled by eight maturity genes known as the *E* gene series (*E1-E8*) (Bonato and Vello, 1999; Cober *et al.*, 2010). These *E* loci show differential sensitivity to light quality and photoperiod, and dominant *E* alleles are involved to determine late flowering and maturity in soybean (Cober *et al.*, 2010). The genes were found to interact with day length (McBlain *et al.*, 1987) that determines when the right time to flower. In addition, a gene controlling the soybean growth habit (*Dt1*) also affects the time of flowering and maturity in soybean (Foley *et al.*, 1986).

Plant breeding activities are the way to manipulate superior genes to be integrated into a superior cultivar. The development of the biotechnology techniques will optimise the capitalization of good alleles into a single plant. Both classical and modern breeding techniques demand excellent genetic materials to be manipulated for development of high yielding cultivars in a breeding program.

Increasing HI should be supported by the use of very early maturity varieties so that more than two planting seasons can be accomplished within a year. Early maturing soybean cultivars will also be very useful in dry season as the water availability is limited. In Indonesia, utilization of irrigated paddy field is still not optimal yet, most of the land is allowed fallow after rice harvest in the cropping pattern of rice-rice-fallow. Another cropping system, rice-rice-rice, are done but it has a high risk of increasing of pests and plant diseases. It is highly recommended on irrigated field to cultivate crops or lowland vegetables after rice harvest. Early maturing soybean also could be a promising alternative to increase its productivity by planting on paddy field. Thus, developing a very early maturing soybean varieties with productivity similar to the ones available at present will be a challenging task and will be very crucial to support the national soybean self sufficiency goal.

The objectives of this study were to identify soybean genotypes showing the high yielding potential and early pod maturity. The accessions with high yield potential and the ones showing early maturity traits can be used to develop high productivity soybean cultivars with early in pod maturity.

MATERIALS AND METHODS

Plant Materials

Fifty six soybean accessions of the Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development (ICABIOGRAD) soybean collections were characterized for their yield, yield components, and maturity-related characters. The total accessions consisted of 27 landraces, 12 plant introductions (PI) of different country origins, 11 breeding lines, and 6 elite varieties (Table 1). Characterization of total accessions were conducted in the fields at West Java that have different environment condition and altitude.

Characterization of 56 Soybean Accessions on Yield and Yield Components at Two West Java Locations

The experiments were conducted at the ICABIOGRAD's Cikeumeuh Experimental Station Bogor (250 m above sea level, asl) and Pacet Experimental Station Cianjur (1.200 asl), from February to June, 2009. The experiments were carried out using a randomized block design with three replications. Each accession was planted in a 1.5 m long row, three rows per accession. Individual soybean accessions were planted using spacing of 0.4 m (between lanes) x 0.2 m (within lanes) planted with two seeds per hill. Plants were fertilized with dung manure (2 tons/ha), 50 kg urea, 100 kg SP-36, and 150 KCl per hectare. To control insect attacks, plants were sprayed weekly with insecticide Decis.

Characters observed included plant height, branch number/plant, pod number/plant, and seed weight/plant. Data of the above characters were obtained based on observations of five individual

plants per accession per replication. Other characters observed included flower color, seed coat color, and pubescent color.

Characterization of 56 Soybean Accessions on Maturity-related Traits at Cikeumeuh Experimental Station

The study was conducted at the ICABIOGRAD Cikeumeuh Experimental Station, Bogor, West Java (250 m asl). The experiment was in paralel with that of the yield component characterization and evaluation studies. Due to intensive field observations required in this study and limited number of observers available, this study was only conducted at one location of the Cikeumeuh Research Station.

Characters observed in this maturity-related trait study included days to R1, days to R3, days to R7, and days to R8 (Fehr and Caviness, 1977). Days to R1 is defined as the day after emergence when 50% of the plants within a plot had presented an open flower at one of the top nodes with a fully expanded leaf. Days to R3 is the number of days after emergence when 50% of plants in a plot had presented the first 5 mm pod at one of the top four nodes with fully expanded leaf. Days to R7 is the number of days after emergence when 50% of pods within a plot had mature pod color. Days to R8 is the number of days after emergence when 100% of pods within a plot had mature pod color (Fehr and Caviness, 1977; Fehr, 1987). The earliest genotypes, should show days to R7 as close as 70 days (70–80) after planting (dap) the seeds as our original objectives were to obtain the ones with days to R7 approached 70 days. The late maturity was determined where the genotypes showed days to R7 approached 20 days latter than that demonstrated by the early maturing genotypes. This is because of the effects of the dominant allele of the maturity gene *E1*. The dominant allele *E1* delayed days to R7 14–20 days compared to the early allele *e1*.

Table 1. Accession name, type, and morphological characteristics of 56 soybean accessions tested at the Cikeumeuh and Pacet Experimental Stations, February-June 2009.

Accession name	Accession type ^a	Flower color	Pubescent color ^b	Seed coat color
B2981	Landrace	Purple	Grey	Black
B3293	Elite variety	Purple	Tawney	Black
B3414	Landrace	Purple	Tawney	Green
B3417	Breeding line	Purple	Tawney	Green
B3562	PI	Purple	Tawney	Yellow
B3611	Landrace	Purple	Grey	Brown
B3626	Landrace	Purple	Tawney	Yellow
B3628	PI	Purple	Tawney	Yellow
B3633	Landrace	Purple	Tawney	Green
B3753	Landrace	Purple	Tawney	Black
B3897	PI	Purple	Tawney	Black
B4176	Breeding line	Purple	Tawney	Yellow
B4182	Breeding line	White	Tawney	Yellow
B4229	Landrace	White	Tawney	Yellow
B4334	Landrace	White	Tawney	Yellow
B4334	Landrace	Purple	Tawney	Black
B4395	PI	White	Tawney	Yellow
B4439	PI	White	Tawney	Yellow
B4125	PI	White	Tawney	Yellow
B4433	Elite variety	Purple	Tawney	Yellow
B4440	Landrace	Purple	Grey	Yellow
B4441	Landrace	Purple	Grey	Yellow
B4432	Elite variety	Purple	Tawney	Green
B4431	Elite variety	Purple	Tawney	Yellow
B4429	Elite variety	Purple	Tawney	Black
B3492	Elite variety	Purple	Tawney	Yellow
B1312	Breeding line	Purple	Tawney	Yellow
B1593B	Landrace	Purple	Tawney	Green
B1635	PI	Purple	Grey	Yellow
B1658	Landrace	Purple	Grey	Yellow
B1958	PI	Purple	Tawney	Yellow
B3185	Landrace	White	Tawney	Yellow
B3193	Landrace	Purple	Grey	Green
B3367	Landrace	White	Tawney	Yellow
B3391	Landrace	White	Tawney	Yellow
B3442	Landrace	Purple	Tawney	Green
B3498	Landrace	Purple	Grey	Yellow
B3517	Breeding line	Purple	Tawney	Green
B3558	Breeding line	Purple	Grey	Yellow
B3570	Breeding line	Purple	Grey	Yellow
B3625	Landrace	Purple	Tawney	Yellow
B3648	Landrace	Brown	Tawney	Yellow
B3686	Landrace	Purple	Tawney	Yellow
B3778	Landrace	White	Tawney	Black
B3787	Landrace	Purple	Tawney	Green
B3799	PI	Purple	Tawney	Black
B3802	PI	Purple	Tawney	Black
B3841	Landrace	Purple	Tawney	Green
B3898	Breeding line	Purple	Tawney	Green
B3907	Breeding line	White	Tawney	Yellow
B3918	PI	Purple	Tawney	Black
B4304	Breeding line	White	Grey	Yellow
B4309	Landrace	Purple	Tawney	Yellow
B4311	Landrace	Purple	Tawney	Black
B4214	Breeding line	Purple	Tawney	Green
B3284	PI	Purple	Tawney	Black

^aPI, Plant Introduction; ^bPubescent color is a well-known marker for the maturity gene *E1* and *E7* located on chromosome C2 of the soybean molecular genetic map (Creagan *et al.*, 1999; Song *et al.*, 2004).

Data Analysis

Both yield and yield component data and the maturity-related trait data were subjected to the analysis of variance (ANOVA) using a SAS PROC GLM procedure (SAS, 1990). Significant differences between the mean values of a particular trait was determined using a Duncan Multiple Range Test (DMRT) (Steel and Torrie, 1980; Sudjana, 1989).

Each observation in the randomized block design can be described by equation that is made up of a number of components. The mathematical model expressed in term of sample statistics is as the following:

$$Y_{ij} = \mu + \tau_i + \beta_j + \varepsilon_{ij}$$

Where Y_{ij} = the observation in the j^{th} block receiving the i^{th} treatment; μ = overall mean; τ_i = the effect of the i^{th} treatment; β_j = the effect of the j^{th} block; ε_{ij} = random error.

Morphological (qualitative data) and agronomical data were separately analyzed to produce dendrogram in clade with Unweighted Pair-Group (UPGMA) Method using Power Marker 3.25 package (Liu and Muse, 2005) based on Nei coefficient (Nei, 1983).

RESULTS AND DISCUSSION

Morphological Character Performances of 56 Soybean Accessions Tested at Two West Java Locations

The majority of the accessions tested (75.7%) demonstrated purple flower color and the remaining 24.3% showed white flower color (Table 1). Flower color is a morphological marker that is oftenly used to differentiate soybean accessions purity as well as used for monitoring the crossing outcomes (Palmer *et al.*, 2004). A total of 73.3% of the accessions showed tawney pubescent color and the remaining 26.7% demonstrated grey pubescent color (Table 1). Pubescent color gene, *T*, is a good marker for the *E*-series maturity genes (Cober *et al.*, 2010; Palmer *et al.*, 2004; Song *et al.*, 2004). Crossing two accessions having different pubescent colors will facilitate the identification of progenies related to time of flowering and pod maturity.

Of the 56 accessions tested, 31 accessions (55.4%) demonstrated yellow seed color, 13 accessions (23.2%) were black, and 12 (21.4%) were green (Table 1). The variety of seed coat and flower colors of soybean accessions observed in this study could complement previous study in respect to genetic analysis of genes controlling natural variation of the traits in a soybean population (Yang *et al.*, 2010). The brown seed coat color shown in Table 1 is actually the imperfect black and, therefore, is classified as the black seed coat color. This phenomenon is due the action of gene *R* causing the variation of seed hylum color and the action of gene *T* for brown pubescent color. Allelic combination, *RT* demonstrated black seed coat color and combination of *rT* showed the brown seed coat color (Bernard and Weiss, 1973).

Yield and Yield Components Performances of 56 Soybean Accessions at Cikeumeuh Experimental Station

F test of the analysis of variance (ANOVA) showed that genotypes tested in this study demonstrated high significant differences on plant height, branch number per plant, pod number per plant, and seed weight per plant (Table 2). This indicates that enough variability available among the genotypes on yield and yield components. Plant height ranges from 20.0 cm to 90.5 cm. The tallest plant was shown by the accession B3628 (90.5 cm) and the shortest plant was shown by B4439 (20.0 cm). The branch numbers per plant among the genotypes tested range from 1.7 to 6.0. The highest branch number was shown by accession B3367 and B3841 (6.0) and the smallest one was shown by B4439 (1.7).

Pod number per plant and seed yield per plant are two most important traits of the soybean breeder interests and were addressed in this study. This is because the two yield component traits demonstrated the most significant effects in determining soybean seed yield based on the previous path analysis studies of the soybean yield components and seed yield (Faisal *et al.*, 2007; Liu and Herbert, 2002; Rezaizad *et al.*, 2001).

Table 2. Yield and yield component performances of the 56 soybean accessions evaluated at the Cikeumeuh Experimental Station, February-June 2009.

Accession	Plant height (cm)	Branch number per plant	Pod number per plant	Seed yield per plant (g)
B2981	70.833 c-i	5.67 ab	99.00 ab	19.667 a
B3293	53.600 j-p	3.67 a-d	41.67 d-i	6.583 e-i
B3414	61.000 e-o	4.00 a-d	68.67 a-d	7.667 e-i
B3417	66.200 c-n	5.33 a-c	101.53 a	22.110 a
B3562	72.733 b-g	4.00 a-d	33.33 d-i	8.000 c-i
B3611	49.667 n-p	4.67 a-d	41.00 c-i	9.417 b-i
B3626	88.667 ab	5.67 ab	55.67 c-g	5.333 f-i
B3628	90.500 a	4.00 a-d	71.33 a-d	17.110 a-c
B3633	55.767 g-p	3.67 a-d	47.00 c-i	7.223 d-i
B3753	69.667 c-i	4.67 a-d	47.67 c-i	8.443 c-i
B3897	69.167 c-k	3.33 b-d	41.67 c-i	9.417 b-i
B4176	55.600 g-p	5.00 a-d	57.67 c-g	10.277 c-h
B4182	55.667 g-p	2.67 d	30.67 d-i	7.667 d-i
B4229	71.500 b-g	3.33 b-d	40.00 c-i	8.110 c-i
B4334	51.400 l-p	4.00 a-d	30.00 d-i	4.417 hi
B4381	71.333 b-g	3.00 cd	56.00 c-g	6.583 e-i
B4395	67.233 c-m	4.67 a-d	46.67 d-h	7.333 d-i
B4439	20.000 r	1.67 e	5.33 i	2.000 i
B4125	72.200 b-g	3.67 a-d	47.67 c-h	11.233 c-h
B4433	30.333 qr	2.67 d	24.33 e-h	12.667 c-f
B4440	62.933 d-o	4.00 a-d	49.67 c-h	12.667 b-e
B4441	64.000 c-o	3.67 a-d	50.67 c-g	10.333 c-g
B4432	53.867 i-p	3.67 a-d	54.00 c-h	9.623 c-g
B4431	53.100 k-p	4.33 a-d	68.00 a-d	9.833 c-g
B4429	51.433 l-p	4.33 a-d	58.00 c-g	10.333 c-g
B3492	61.000 e-o	3.33 b-d	45.33 c-I	9.223 c-i
B1312	88.667 ab	5.00 a-d	64.33 a-e	6.610 e-i
B1593B	76.400 a-e	4.33 a-d	45.33 c-i	8.117 c-i
B1635	68.033 c-m	4.00 a-d	50.33 e-h	11.233 c-h
B1658	69.333 c-k	5.00 a-d	64.33 a-d	10.24 c-h
B1958	61.000 e-o	4.33 a-d	45.67 c-i	9.873 c-h
B3185	47.433 op	5.00 a-d	53.33 c-h	15.167 a-c
B3193	70.433 c-j	5.33 a-c	48.00 c-h	16.360 ab
B3367	79.967 a-c	6.00 a	57.33 c-g	14.333 a-d
B3391	57.500 f-p	4.33 a-d	64.33 a-e	10.333 c-g
B3442	40.900 pq	3.00 cd	55.33 c-g	6.140 e-i
B3498	73.200 b-f	4.00 a-d	57.00 c-g	5.010 f-i
B3517	68.533 c-k	4.33 a-d	71.67 a-d	17.367 a-c
B3558	70.867 c-i	5.00 a-d	69.00 a-d	10.610 d-h
B3570	66.833 c-l	3.67 a-d	39.67 c-I	6.000 e-i
B3625	59.633 e-o	4.67 a-d	65.00 a-e	13.000 c-e
B3648	76.300 a-e	4.33 a-d	54.00 c-h	10.333 c-g
B3686	76.667 a-e	4.00 a-d	04.67 c-i	7.890 c-i
B3778	61.733 d-o	4.00 a-d	53.33 c-h	7.417 d-i
B3787	78.733 a-d	4.67 a-d	61.67 a-f	7.917 c-i
B3799	69.067 c-k	3.67 a-d	49.00 c-h	10.610 d-h
B3802	68.167 c-l	4.00 a-d	56.67 c-f	7.553 d-i
B3841	70.533 c-i	6.00 a	53.33 c-h	11.233 c-h
B3898	75.600 a-e	5.00 a-d	60.33 a-f	6.860 d-i
B3907	51.000 m-p	4.33 a-d	39.67 c-I	8.333 c-i
B3918	75.100 a-e	4.00 a-d	64.00 a-e	9.000 c-i
B4304	67.600 c-m	4.00 a-d	38.00 d-i	7.610 d-i
B4309	68.500 c-k	3.33 b-d	12.33 hi	10.223 c-h
B4311	75.900 a-e	4.67 a-d	20.33 f-i	8.117 c-i
B4214	75.200 a-e	4.67 a-d	17.00 g-i	10.143 c-h
B3284	73.533 b-f	3.00 cd	15.33 g-I	8.973 c-i

Numbers followed by the same letters in each column are not significantly different at $p>0.05$ using Duncan's Multiple Range Test.

Among the accessions, only 4 accessions (7.14%) showed pod number per plant more than 70; 10 accessions (17.86%) showed pod number per plant more than 60 but less than 70 pods; 14 accessions (25%) demonstrated pod number per plant more than 50 but less than 60 pods per plant. Nineteen accessions (33.93%) showed medium pod number per plant of more than 30 but less than 50 pods/plant; and 9 accessions (16.07%) showed low pod number per plant of less than 30 pods per plant. Among those, 5 accessions (8.9%) showed pod number per plant less than 20.

The best pod number was shown by accession B3417 (101.5 pods/plant) that was not significantly different from accessions B2981 (99.0), B3517 (71.7), and B3628 (71.3) based on DMRT ($p < 0.05$). The least pod number was shown by accession B3686 (4.7 pods/plant) that was not significantly different from the accessions B4439 (5.3), B4309 (12.3), B4214 (17.0) and B3284 (15.3) based on DMRT ($p < 0.05$). This wide range of per plant pod number observed among the accessions tested in this study indicated the wide variation of yield components among the accessions tested. In parallel with pod number, the accessions showing the highest pod number (B3417) also showed the highest seed yield per plant (Table 2). The highest seed yield per plant was shown by B3417 (22.11g) that was not significantly different from accessions B2981 (19.67g), B3517 (17.37g), and B3628 (17.11g) based on DMRT ($p < 0.05$). Similarly, the accession showing the least pod number (B3686) also demonstrated the lowest seed yield per plant (Table 2). The lowest seed yield shown by accession B3686 was not significantly different from many other accessions (e.g., B3778, B3787, B3802, B3907, B4304, B4214, and B4439) based on DMRT ($p < 0.05$). This is in good agreement with the previous studies indicating that seed weight per plant is mostly determined by seed number as the plant with more pod numbers showed more seed number, and therefore, demonstrated higher seed yield per plant (Faisal *et al.*, 2007; Liu and Herbert, 2002; Rezaizad *et al.*, 2001.). This is in consistent with the path analysis results reported by Rezaizad *et al.* (2001) indicating that seed number showed

the highest correlation on soybean seed yield ($r = 0.92$) followed by pod number per plant ($r = 0.67$).

As the objectives of this study were to identify soybean accession showing high seed yield potential, we concluded that accessions B3417, B2981, B3517, and B3628 can be selected to represent the best yield performances at Cikeumeuh as the four accessions demonstrated the best performances for both pod number and seed yield per plant, and therefore, the four accessions showed highest seed yield potential at lower altitude environments of Cikeumeuh.

Yield and Yield Components Performances of 56 Soybean Accessions at Pacet Experimental Station

F test of the ANOVA showed that genotypes tested at the Pacet Experimental Station demonstrated high significant differences on plant height, branch number per plant, pod number per plant, and seed weight per plant (Table 3). This indicates enough variability among the soybean genotypes tested on yield and yield components, supporting field test at Cikeumeuh.

Plant height at Pacet ranges from 42.7 cm to 104.3 cm (Table 3). This observed plant height range is higher than that shown by the same set of soybean genotypes tested at the Cikeumeuh Experimental Station (ranges from 20.0–90.7 cm). The shortest plant height was shown by B4125 (42.7 cm) and the highest plant was shown by B3517 (104.7 cm). The branch number per plant observed at Pacet Experimental Station ranges from 3.0–7.3. This observation trend is very similar to that of the plant height data trend.

As previously described, pod number per plant and seed yield per plant are two traits of soybean breeder's interests. The two traits are emphasized their discussions in this study as the two yield components demonstrated the most significant effects in determining soybean seed yield based on the previous path analysis studies of seed yield (Faisal *et al.*, 2007; Liu and Herbert, 2002; Rezaizad *et al.*, 2001). Among the accessions tested 23 accessions (41.07%) showed pod number per plant more than 70; 10 accessions (17.86%) showed pod number per plant more than

60 but less than 70 pods; 10 accessions (17.86%) demonstrated pod number per plant more than 50 but less than 60. The remaining 13 accessions

(23.21%) demonstrated pod number per plant less than 50. Among those, only 2 accessions (3.57%) showed pod number per plant less than 30.

Table 3. Yield and yield component performances of 56 soybean accessions evaluated at the Pacet Experimental Station, February-June 2009.

Accession	Plant height (cm)	Branch number per plant	Pod number per plant	Seed yield per plant (g)
B2981	63.6 c-i	5.33 a-e	80.67 ab	9.74 a-i
B3293	54.1 j-p	4.33 c-f	59.33 d-i	6.55 c-j
B3414	66.3 e-o	5.00 b-f	85.67 c-h	8.39 b-j
B3417	66.5 c-n	5.67 a-e	89.33 a	12.19 a-d
B3562	64.5 b-g	3.66 e-f	51.67 c-i	7.55 c-j
B3611	46.0 n-p	4.33 c-f	47.67 c-i	9.417 b-i
B3626	91.8 ab	6.33 a-d	79.00 c-h	10.38 a-i
B3628	90.500 a	5.33 a-e	94.67 a-d	11.110 b-h
B3633	95.2 g-p	5.67 a-e	81.33 c-i	10.38 a-i
B3753	59.3 c-i	4.33 c-f	54.67 c-i	8.443 c-i
B3897	58.2 c-k	5.33 a-e	67.33 c-g	7.97 c-k
B4176	56.5 g-p	5.67 a-e	67.33 c-g	8.67 a-j
B4182	99.3 g-p	5.33 a-e	65.87 d-i	11.77 a-g
B4229	75.7 b-g	5.67 a-e	70.00 c-i	8.51 b-j
B4334	56.9 l-p	5.33 a-e	81.33 c-i	9.99 a-i
B4381	87.9 b-g	5.00 b-f	88.00 c-g	9.74 a-i
B4395	87.9 c-m	5.33 a-e	71.53 d-h	7.55 c-j
B4439	59.2 r	4.33 c-f	6.43 i	2.56 i
B4125	42.7 b-g	3.00 f	47.67 c-h	9.74 a-i
B4433	70.0 qr	5.00 b-f	24.33 e-h	9.24 a-j
B4440	67.0 d-o	5.33 a-e	64.00 c-h	9.99 a-i
B4441	78.2 c-o	36.00 a-e	104.67 c-g	11.87 a-f
B4432	76.5 i-p	5.67 a-e	78.00 c-h	7.65 c-j
B4431	71.0 k-p	5.67 a-e	57.33 a-d	11.91 a-e
B4429	57.5 l-p	4.66 c-f	61.67 c-g	12.18 a-d
B3492	104.4 e-o	3.33 b-d	45.33 c-l	12.73 a-c
B1312	85.8 a-e	5.67 a-e	67.33 a-e	9.99 a-i
B1593B	89.3 a-e	4.33 a-d	76.00 a-d	8.15 b-j
B1635	87.7 c-m	4.33 c-f	47.67 c-i	11.63 c-h
B1658	75.2 c-k	6.00 a-e	76.00 a-d	11.74 a-h
B1958	52.7 e-o	5.00 b-f	57.33 a-d	8.39 b-j
B3185	92.5 op	7.33 a	53.33 c-h	8.99 a-j
B3193	85.8 c-j	5.33 a-e	77.17 c-h	12.06 a-e
B3367	72.9 a-c	3.00 f	57.33 c-g	10.38 a-i
B3391	83.3 f-p	7.00 ab	75.33 a-e	6.55 c-j
B3442	96.1 pq	4.00 d-f	48.33 c-g	6.140 e-i
B3498	86.7 b-f	6.00 a-e	78.33 c-g	11.31 a-h
B3517	104.3 c-k	4.33 c-f	80.53 a-d	8.51 b-j
B3558	70.867 c-i	5.67 a-e	76.33 a-d	10.84 a-i
B3570	79.0 c-l	6.00 a-e	78.67 c-i	14.66 ab
B3625	77.5 e-o	6.00 a-e	75.33 a-e	11.02 a-h
B3648	89.0 a-e	6.67a-c	85.67 c-h	11.86 a-f
B3686	80.6 a-e	4.66 c-f	52.33 g-j	7.890 c-i
B3778	108.300 d-o	6.00 a-e	53.33 c-h	8.51 b-j
B3787	76.5 a-d	4.33 c-f	61.67 a-f	6.55 c-j
B3799	78.4 c-k	5.33 a-e	65.87 d-i	10.610 d-h
B3802	103.2 c-l	7.00 ab	56.67 c-f	8.51 b-j
B3841	95.7 c-i	7.00 ab	53.33 c-h	12.85 a-c
B3898	79.7 a-e	6.00 a-e	70.00 c-i	6.860 d-i
B3907	52.2 m-p	4.00 d-f	39.67 c-l	8.333 c-i
B3918	69.7 a-e	5.33 a-e	60.67 a-e	8.51 b-j
B4304	67.0 c-m	3.66 e-f	48.33 c-g	8.67 a-j
B4309	59.0 c-k	4.66 c-f	68.53 c-h	10.223 c-h
B4311	87.2 a-e	6.00 a-e	20.33 f-i	8.39 b-j
B4214	75.200 a-e	4.00 d-f	80.33 c-h	10.07 a-i
B4382	80.8 b-f	5.00 b-f	92.20 g-i	11.95 a-e

Numbers followed by the same letters in each column are not significantly different at $p > 0.05$.

The best pod number was shown by accession B4441 (104.67 pods/plant) and the least was shown by B4439 (6.43 pods/plant). The following best pod number per plant were shown by accessions B3628 (94.7) that were not significantly different from B4382 (92.2), B3417 (89.3), B4334 (88.0), and B3414 (85.7) based on DMRT ($p < 0.05$). The accessions showing the least pod number per plant include B4433 (24.3), B4311 (20.3), and B4439 (6.4) (Table 3). This wide range of per plant pod number observed among the accessions indicated the their wide variation of yield components.

The highest seed yield was demonstrated by B3841 (12.85 g/plant) that was not significantly different from B3492 (12.73 g), B3417 (12.19 g), B4429 (12.18 g), B3193 (12.06 g), B4382 (11.95 g), B4441 (11.87 g), and B3648 (11.86 g) based on DMRT at $p = 0.05$ (Table 3).

Result at the Cikeumeuh showed that accession showing highest pod number and highest seed yield demonstrated by the same accession (B4417). Similarly, accession showing the highest pod number at Pacet also demonstrated seed yield at the highest category (Table 3). The most per plant pod number at Pacet was shown by accession B4441 (104.67) that was not significantly different from that demonstrated by accessions B3628 (94.7), B4382 (92.2), B3417 (89.3), B4334 (88.0), and B3414 (85.7) based on DMRT ($p < 0.05$). The highest seed yield at Pacet was shown by accession B3841 (12.85 g/plant) that was not significantly different from B3492 (12.73 g), B3417 (12.19 g), B4429 (12.18 g), B3193 (12.06 g), B4382 (11.95 g), B4441 (11.87 g), and B3648 (11.86 g) based on DMRT at $p = 0.05$ (Table 3).

The highest pod number and seed yield per plant at Cikeumeuh was demonstrated by B3417 (101.5 pods/plant; seed yield of 22.11 g). The highest pod number (including seed yield that is still classified within the highest category) at Pacet was demonstrated by B4441 (pod number of 104.67; seed yield of 11.87 g) that was not significantly different from the pod number and seed yield demonstrated by accession B3417 (pod number of 89.30; per plant seed yield of 12.19 g) based on DMRT ($p < 0.05$). Therefore, accession

3417 demonstrated highest yield at a lower altitude (Cikeumeuh) still showed at the superior highest category of yield component performances at a higher altitude (Pacet) indicating that the yield stability performance of accession B3417 was demonstrated across different altitudes. Other members of accessions showing high yield at Cikeumeuh were different from those showing high yield performance at Pacet. The accessions that only showed high yield component performances at Cikeumeuh included B2981, B3517, and B3628; and the accessions that only showed high yield component performances at Pacet included B3841, B3492, B4429, B3193, B4382, B4441, and B3648. These findings indicate that the accessions showing high pod number or seed yield in one location do not always demonstrate high pod number or seed yield per plant at other locations. This suggests that a particular soybean genotype could adapt well only in a particular location but not in other locations.

Both data (Cikeumeuh and Pacet) showed similar number of pods/plant for genotypes showing highest number of pod/plant in both locations. However, the soybean accession showing highest seed yield at the Cikeumeuh demonstrated much higher seed yield per plant than that showing highest seed yield at Pacet. This is most likely due to much more empty pods were observed at Pacet than those observed at Cikeumeuh causing the seed yield per plant is much lower at Pacet compared to those grown at the Cikeumeuh. More empty pods mean that less seeds were obtained per plant even though the number of pod per plant were relatively similar between accessions grown at the two locations. The environments, therefore, affect the pod productivity and then affect the seed yield per plant for the soybean accessions tested. Further more, the yield variation is not only influenced by external factors which mostly determined by different environmental conditions but also it also is influenced by internal factors especially the genetic make-up of the soybean accessions (Liu *et al.*, 2006) as clearly demonstrated by this study.

Table 4. Performances of the maturity-related traits of the 56 soybean accessions evaluated at the Cikeumeuh Experimental Station, February-June 2009.

Accession	Days to R1	Days to R3	Days to R7	Days to R8
B1306	45.333 a-d	50.333 a-g	83.667 g-p	86.333 k-p
B1430	37.333 p-v	44.000 i-q	75.000 t	82.000 rs
B2973	37.000 q-v	41.667 n-q	75.000 t	82.667 rs
B2981	39.667 k-r	48.333 b-i	82.333 k-q	85.000 m-s
B3293	37.667 0-v	42.667 m-q	82.000 k-q	85.667 k-r
B3414	38.333 n-v	42.667 m-q	82.667 j-q	85.000 m-s
B3417	38.333 n-v	43.667 j-q	80.667 m-q	83.667 p-s
B3562	39.333 l-s	43.667 j-q	83.000 i-p	87.667 i-o
B3611	35.333 vw	42.333 m-q	76.000 st	91.333 c-g
B3626	47.667 ab	52.000 a-c	87.333 a-g	91.667 c-h
B3628	39.333 l-s	44.667 i-p	87.667 a-f	86.333 k-p
B3633	46.007 a-d	51.000 a-e	81.333 m-q	91.667 c-f
B3753	38.667 m-t	43.667 j-q	80.667 m-q	83.667 p-s
B3897	38.333 n-v	43.000 l-q	79.000 q-s	84.333 o-s
B4176	36.000 t-v	43.000 l-q	80.000 p-r	80.000 q-s
B4182	35.667 u-w	45.333 h-o	81.667 l-q	85.000 m-s
B4229	43.000 e-i	50.667 a-f	85.000 c-m	90.333 c-j
B4334	39.667 k-r	44.333 i-p	83.667 g-p	86.333 k-p
B4334	44.000 c-f	49.333 a-h	86.667 b-i	89.000 e-l
B4395	40.333 i-p	46.333 f-m	83.000 i-p	88.333 g-m
B4439	33.000 vwz	40.667 q	80.333 q-t	82.667 rs
B4125	41.667 g-m	47.667 c-j	87.333 a-g	90.667 c-i
B4433	32.000 vx	35.667 r	77.000 r-t	82.000 s
B4440	36.667 r-v	45.333 h-o	82.333 k-q	86.000 k-r
B4441	37.667 o-v	43.000 l-q	84.333 e-n	88.333 g-m
B4432	39.667 k-r	47.667 c-j	82.667 j-q	85.667 k-r
B4431	36.667 r-v	43.000 l-q	81.333 m-q	85.333 l-s
B4429	36.333 s-v	43.000 l-q	84.667 e-m	90.333 c-j
B3492	39.333 l-s	44.000 i-q	87.667 a-f	92.667 b-d
B1312	44.000 c-f	52.000 a-c	88.000 a-e	91.333 c-h
B1593B	40.333 i-p	45.333 h-o	83.667 g-p	88.333 g-m
B1635	47.000 a-c	53.000 a	86.333 b-j	92.000 c-f
B1658	42.667 f-k	49.333 a-h	87.667 a-f	91.667 c-f
B1958	39.000 l-t	43.667 j-q	84.667 e-m	90.333 c-j
B3185	38.667 m-t	43.667 j-q	84.333 e-n	88.667 f-m
B3193	46.667 a-d	45.000 h-p	85.000 c-m	90.333 c-j
B3367	39.000 l-t	44.333 i-p	83.333 h-p	88.000 h-o
B3391	40.667 h-n	44.333 i-p	88.667 a-c	97.000 a
B3442	43.333 e-i	47.667 c-j	88.333 a-d	93.333 bc
B3498	37.000 q-v	51.667 a-d	87.333 a-g	95.667 ab
B3517	49.000 a	53.000 a	90.667 a	98.000 a
B3558	48.333 ab	53.000 a	88.000 a-e	92.667 b-d
B3570	40.667 h-n	41.000 n-q	86.667 b-i	91.667 c-f
B3625	42.000 f-k	47.333 c-l	90.000 ab	91.667 c-f
B3648	43.667 d-h	46.667 e-m	87.000 a-h	92.333 c-e
B3686	47.667 ab	53.000 a	86.667 b-i	93.000 bc
B3778	39.000 l-t	46.667 e-m	84.000 f-o	87.667 i-o
B3787	39.333 l-s	46.667 e-m	83.000 i-p	86.333 k-p
B3799	41.333 g-n	46.333 f-m	83.333 h-p	87.667 i-o
B3802	41.333 g-n	45.667 h-n	82.667 j-q	86.333 k-p
B3841	47.333 ab	52.333 ab	85.333 c-l	90.667 c-i
B3898	43.667 d-h	49.333 a-h	85.667 c-k	92.667 b-d
B3907	43.333 e-i	48.333 b-i	83.333 h-p	87.000 j-p
B3918	39.000 l-t	46.000 g-n	84.500 e-m	87.500 i-o
B4304	38.333 n-v	44.333 i-p	82.333 k-q	86.000 k-r
B4309	36.667 r-v	42.667 m-q	82.667 j-q	86.000 k-r

Numbers followed by the same letters in each column are not significantly different at $p>0.05$.

Maturity-Related Trait Performances of 56 Soybean Accessions Based on Study at The Cikeumeuh Experimental Station

F test of the ANOVA showed that genotypes tested in this study demonstrated significant differences on days to R1, days to R3, days to R7, and days to R8 (Table 4). The results indicated that the genotypes tested are well represented by variable alleles related to the soybean time of flowering and maturity.

Nine accessions (16.07%) demonstrated early maturity (pod maturity of 75–80 days after planting); 35 accessions (62.5%) showed medium seed maturity (pod maturity of 81–85 dap); and 16 accessions (28.57%) showed late maturity (pod maturity of >85 dap). The earliest flowering time was demonstrated by accession B4433 (32 dap) that are not significantly different from B4439 (33 dap), B3611 (35.3 dap), B2973 (37 dap), and B1430 (37.3 dap) based on DMRT at $p = 0.05$ (Table 4). However, the earliest seed maturing

(days to R7) genotypes was shown by B2973 (75 dap) that were not significantly different from B1430 (75 dap), B3611 (76 dap), B4433 (77 dap), and B4439 (80.33 dap) based on DMRT at $p = 0.05$ (Table 4).

The maturity related traits (days to R1, R3, R7, and R8) observed in this study indicated the trend of a normal distribution across the genotypes tested. This indicated the multigenic nature controlling the maturity-related traits.

The results also indicated that the reproductive-related traits observed in this study are controlled by more than two loci. A similar normal distribution trend was also reported in the previous studies based on studies using different populations and tested at several different locations and years (Yamanaka *et al.*, 2000; Tasma *et al.*, 2001). The results of this study also support the study outcomes derived from model plant *Arabidopsis thaliana* indicating that the transition from vegetative phase to flowering phase is complex and is controlled by many genes and by

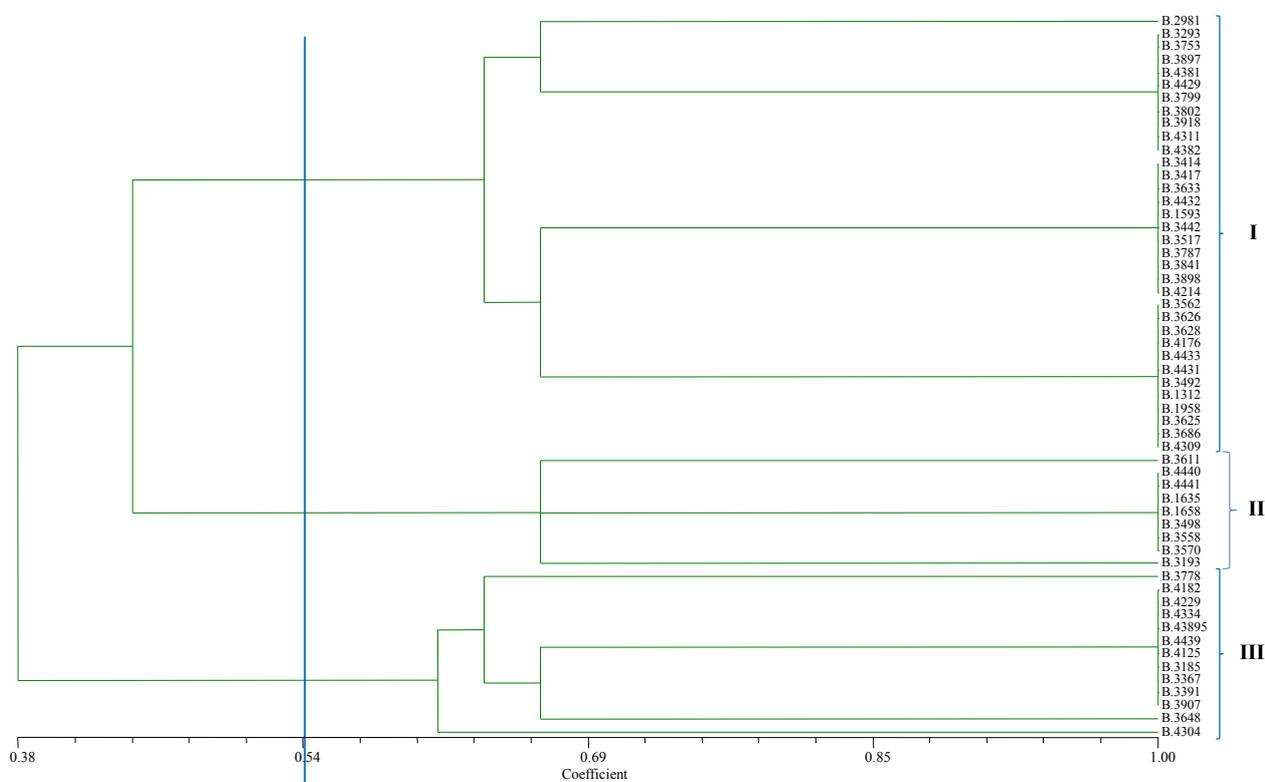


Figure 1. Dendrogram depicting genetic relationship between the 56 soybean accessions based on morphological characters using UPGMA method. I, II, and III represents different clade.

several genetic pathways (Koorneef *et al.*, 1998; Levy and Dean, 1998).

Genetic Relationship of Soybean Accessions Based on Morpho-Agronomical Traits

UPGMA analysis generated three distinct clades based on morpho-agronomical variables on both locations, Cikeumeuh and Pacet. According to morphological characters, most of breeding status of the soybean germplasm tested were distributed among three clades including landraces without considering their local origin (Figure 1). All elite varieties which possessed more uniform flower and pubescent colors (purple and tawny) were preferentially in the same clade (clade I). The separated group of breeding lines observed in this study represents their different genetic background. Most introducing lines also tended to be grouped in the same clade, suggesting their genetical close relationship but far distance from the remaining PI accessions (such as B1635, B3897, B4439, and

B4125). This morphological data could complement agronomical data of total soybean accessions tested in this study.

Similarities among soybean accessions were also established based on agronomical properties. A dendrogram (UPGMA) grouped accessions that shared similar agronomic features in respect to yield and yield components and maturity-related traits, and revealed three main clades (Figure 2). In particular first clade is distinguished by a group of accessions with high seed yield and pod number in either in one and/or both locations (B3417, B3628, and B2981). The second main clade grouped most accessions with diverse agronomical characters, consisting of 49 accessions. The third clade grouped only four accessions which have the least pod number (B4439, B4433, B3686, and B4311), but of those, the two showed early flowering and maturity (B4439 and B4433) as shown according to DMRT analysis. These phylogeny demonstrated that soybean accessions with early maturity and

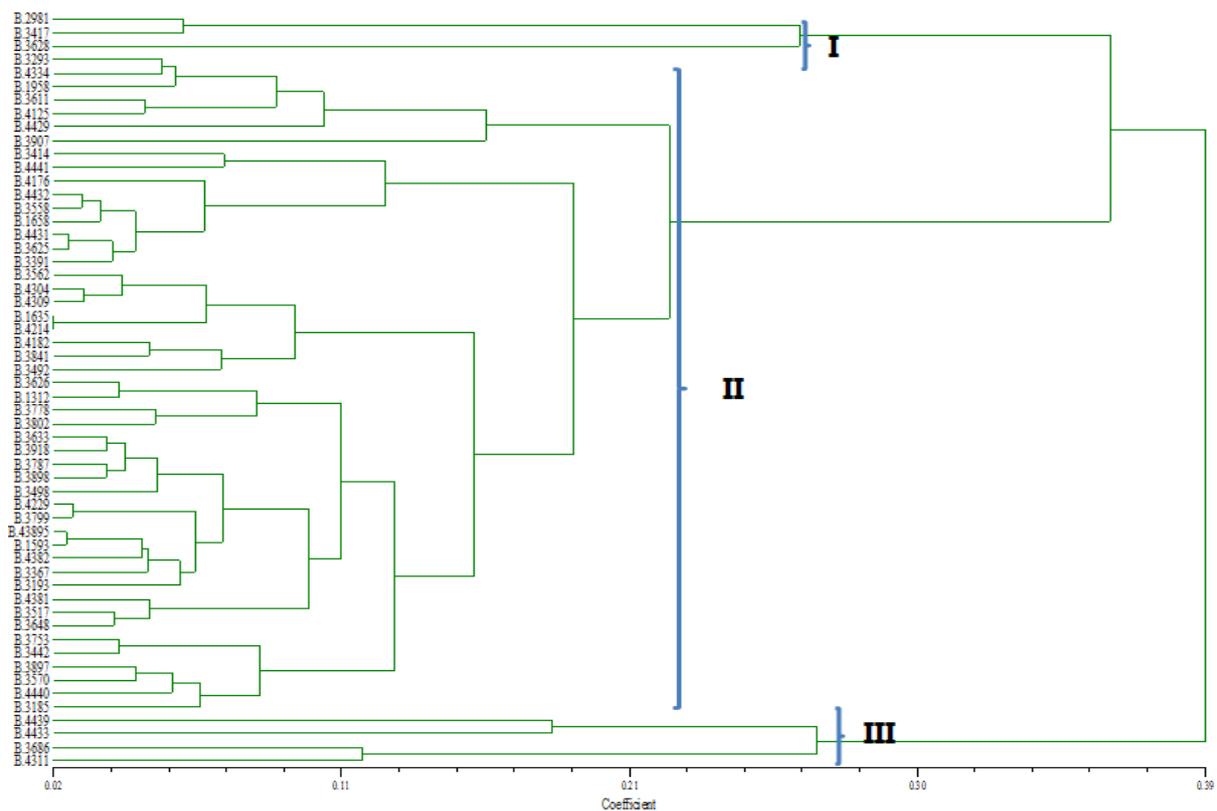


Figure 2. Dendrogram depicting genetic relationship between the 56 soybean accessions based on yield and yield components, and maturity related traits on both locations, Pacet and Cikeumeuh using UPGMA method. I,II, and III represents different clade.

low seed yield were grouped in the same clade, indicating their close relationship. Notably, these cluster analyses on the basis of agronomical characters support and is in good agreement with the DMRT analysis as discussed above that soybean accession with high yield and early flowering/ maturity were able to be differentiated.

Overall, the phenotypic data further indicated that the genotypes tested represent well the allelic variations among the genotypes tested suggesting an excellent selection of the plant genetic materials used in this study. The phenotypic data obtained from this study should be very useful for genetic analysis including the genomic-based association studies for yield and yield component and maturity-related traits of soybean.

CONCLUSION

Soybean accessions demonstrating high yield components only at Cikeumeuh Experimental Station were B2981, B3517, and B3628. Soybean accessions that demonstrated high yield components only at Pacet Experimental Station included B4441, B3628, B382, B4334, and B3414. The accession that demonstrated high yield component performance at both locations (Cikeumeuh and Pacet Experimental Stations) was shown by only one accession, B3417. Accession B3417, therefore is classified as a broad adapting soybean genotype as this genotype can perform well at both low and high altitudes of cultivation.

The early pod maturing accession was demonstrated by B2973 (74 dap) that was not significantly different from accessions B1430 (75 dap), B3611 (76 dap), B4433 (77 dap), and B4439 (80 dap) based on DMRT at $p = 0.05$.

Three distinct clades were generated based on morpho-agronomical variables on both locations, Cikeumeuh dan Pacet Experimental Stations. The cluster analysis of agronomical properties was able to distinguish a group of accessions with high seed yield and high pod number in either in one and/or both locations (B3417, B3628, and B2981), and the other groups of accessions with early flowering and maturity and the least pod number (B4439 and B4433). The

cluster analysis results were in well agreement with those analyzed based on DMRT.

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REFERENCES

- Badan Pusat Statistik. 2014. Produksi kedelai 2013. Badan Pusat Statistik Jakarta.
- Bernard, R.L. and M.G. Weiss. 1973. Qualitative genetics of soybean. In: B.E. Caldwell, editor, Soybeans: Improvement, Production, and Uses. The American Society of Agronomy, Madison, Wisconsin, USA. p. 117–154.
- Bonato, E.R. and N.A. Vello. 1999. *E₆*, a dominant gene conditioning early flowering and maturity in soybeans. *Genet. Mol. Biol.* 22:229–232.
- Cober, E.R., S.J. Molnar, M. Charette, and H.D. Voldeng. 2010. A new locus for early maturity in soybean. *Crop Sci.* 50:524–527.
- Cregan, P.B., T. Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, T.T. van Toai, D.G. Lohnes, J. Chung, and J.E. Specht. 1999. An integrated genetic linkage map of the soybean genome. *Crop Sci.* 39:1464–1490.
- Faisal, M., A. Malik, M. Ashraf, A.S. Qureshi, and A. Ghafoor. 2007. Assessment of genetic variability, correlation, and path analysis for yield and its components in soybean. *Pak. J. Bot.* 39(2):405–413.
- Fehr, W.R. 1987. Principles of cultivar development. Volume 1: Theory and techniques. MacMillan Publishing Co., New York.
- Fehr, W.R. and C.E. Caviness. 1977. Stages of soybean development. Special report 80, agricultural and home economic experimental station. Iowa State University, Ames, IA, USA.
- Foley, T.C., J.H. Orf, and J.W. Lambert. 1986. Performance of related determinate and indeterminate soybean lines. *Crop Sci.* 26:5–8.
- Hanafie, R. 2004. Tingkat konsumsi kacang-kacangan dan umbi-umbian sebagai pendukung ketahanan pangan. Dalam: A.K. Makarim, Marwoto, M.M. Adie, A.A. Rahmianna, Heriyanto, dan I.K. Tastra, editor. Kinerja Penelitian Mendukung Agribisnis Kacang-kacangan dan Umbi-umbian, Badan Penelitian dan Pengembangan Pertanian, Pusat

- Penelitian dan Pengembangan Tanaman Pangan, Bogor. hlm. 592–602.
- Kang, M.S. 1998. Using genotype-by-environment interaction for crop cultivar development. *Adv. Agron.* 35:199–240.
- Koorneef, M., C. Alosa-Blanco, A.J.M. Peters, and W. Soppe. 1998. Genetic control of flowering time in *Arabidopsis*. *Annu. Rev. Plant Physiol. Plant Mol. Biol.* 49:345–370.
- Levy, Y.Y. and C. Dean. 1998. The transition to flowering. *Plant Cell* 10:1973–1989.
- Liu, X.B. and S.J. Herbert. 2002. Fifteen years of research examining cultivation of continuous soybean in Northeast China. *Field Crops Res.* 79:1–7.
- Liu, K. and S. Muse. 2005. Power Marker: An integrated analysis environment for genetic marker analysis. *Bioinformatics* 21:2128–2129.
- Liu, X.B., S.J. Herbert, Q.Y. Zhang, and A.M. Hashemi. 2006. Yield density relation of glyphosate-soya beans and their responses to light enrichment in north-eastern USA. *J. Agron. Crop Sci.* 193:55–62.
- Liu, B., X.B. Liu, C. Wang, Y.S. Li, J. Jin, and S.J. Herbert. 2010. Soybean yield and yield component distribution across the main axis in response to light enrichment and shading under different densities. *Plant Soil Environ.* 56:384–392.
- Marwoto, D.K.S. Swastika, dan P. Simatupang. 2005. Pengembangan kedelai dan kebijakan penelitian di Indonesia. Lokakarya pengembangan kedelai di lahan sub-optimal, 26 Juli 2005. Balai Penelitian Kacang-kacangan dan Umbi-umbian, Malang.
- McBlain, B.A., R.L. Bernard, C.R. Cremeens, and J.F. Korczak. 1987. A procedure to identify genes affecting maturity using soybean isoline testers. *Crop Sci.* 27:1127–1132.
- Nei, M. and N. Takazaki. 1983. Estimation of genetic distances and phylogenetic trees from DNA analysis. *Proc 5th World Cong. Genet. Appl. Livestock Prod.* 21:405–412.
- Palmer, R.D., T.W. Pfeiffer, G.R. Buss, and T.C. Kilen. 2004. Qualitative genetics. In: Boerma, H.R. and J.E. Specht, editors, *Soybeans: Improvement, production, and uses*, Third Edition, Number 16 in the series of *Agronomy*, American Society of Agronomy, USA. p. 137-234.
- Rezaizad, A., B.Y. Samadi, M.R. Ahmadi, and H. Zeinali. 2001. Relationships between yield and yield components in soybean using path analysis. *JCPP* 5(3):107–115.
- SAS Institute, Inc. 1990. SAS/stat user's guide. Version 6, 4th ed., Vol 2, SAS Institute, Inc., Cary, NC.
- Song, Q.J., L.F. Marek, R.C. Shoemaker, K.G. Lark, V.C. Concibido, X. Delannay, J.E. Specht, and P.B. Cregan. 2004. A new integrated genetic linkage map of the soybean. *Theor. Appl. Genet.* 109:122–128.
- Steel, R.G.D. and J.H. Torrie. 1980. Principles and procedures of statistics: A biometrical approach. 2nd ed. McGraw-Hill Book Co., New York.
- Sudjana. 1989. Desain dan analisis eksperimen. Edisi III. Tarsito Bandung.
- Tasma, I.M., L.L. Lorenzen, D.E. Green, and R.C. Shoemaker. 2001. Mapping genetic loci for flowering time, maturity, and photoperiod insensitivity in soybean. *Mol. Breed.* 8:25–35.
- Vuong, T.D., X. Wu, M.D.S. Pathan, B. Valliyodan, and H.T. Nguyen. 2007. Genomics approaches to soybean improvement. In: R.K. Varshney and R. Tuberosa, editors, *Genomics Assisted Crop Improvement*, Vol. 2. (= Dordrecht: Genomics Application in Crops. p. 243–279. doi:10.1007/978-1-4020-6297-1_11.
- Yamanaka, N., Y. Nagamura, Y. Tsubokura, K. Yamamoto, R. Takahashi, H. Kouchi, M. Yano, T. Sasaki, and K. Harada. 2000. Quantitative trait locus analysis of flowering time in soybean using a RFLP linkage map. *Breed. Sci.* 50:109–118.
- Yang, K., N. Jeong, J.K. Moon, Y.H. Lee, S.H. Lee, H.M. Kim, C.H. Hwang, K. Back, R.G. Palmer, and S.C. Jeong. 2010. Genetic analysis of genes controlling natural variation of seed coat and flower colors in soybean. *J. Heredity.* 101(6):757-768. doi:10.1093/jhered/esq07.
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