Genetic variance and heritability estimation of hybridized pepper plants (*Capsicum annuum* L.) F$_2$ progeny for begomovirus resistance in growth stage

E Kesumawati$^{1, *}$, Sabaruddin$^1$, E Hayati$^1$, N Hadisah$^2$, R Hayati$^2$, Y Haidar$^2$, N S Pohan$^2$, R Jannah$^2$, A Ardika$^3$, M Khalil$^2$, M Jalil$^3$, Fitrizal$^4$

$^1$Department of Agrotechnology, Faculty of Agriculture, Universitas Syiah Kuala, Darussalam-Banda Aceh 23111, Indonesia
$^2$Bachelor Program of Agrotechnology Department of Agrotechnology, Faculty of Agriculture, Universitas Syiah Kuala, Darussalam-Banda Aceh, 23111, Indonesia
$^3$Department of Agrotechnology, Faculty of Agriculture, Universitas Teuku Umar, West Aceh 23615, Indonesia
$^4$Agricultural Extension Training Centre, Saree, Aceh Besar 23952, Indonesia

*Email: ellykesumawati@unsyiah.ac.id

**Abstract.** Pepper is widely cultivated as a condiment and cash crop in Indonesia. However, Pepper yellow leaf curl disease (PepYLCD) caused by begomovirus is currently seriously affect the domestic pepper production. Breeding for begomovirus resistance material by crossing is currently necessary to overcome the constraint. The present study is aimed to determine the resistance of pepper (*C. annuum*) plants F$_2$ progenies to begomovirus infection in the growth stage. Two local *C. annuum* accessions, BaPep-5 as a resistance donor for pepy-1 begomovirus resistance gene (locally called Perintis) and BaPep-4 as a susceptible parent (locally called Kencana) were crossed to generate F$_2$ progenies. The research was conducted in Agricultural Extension Training Centre (BLPP) Saree and Horticulture Laboratory of Syiah Kuala University from February to July 2020. 500 F$_2$ progenies were transplanted to the field along with 15 plants of each parent as control. The result suggested that plant height and crown width had the highest broad sense heritability value, whereas the dichotomous height, stem diameter, secondary branch, and tertiary branch had the lowest broad sense heritability value. Coefficient of genetic variance and coefficient of phenotypic variance from overall characteristics were relatively low which suggest the narrow sense to slightly narrow sense heritability.

**1. Introduction**

Pepper (*C. annuum*) is an important versatile condiment and cash crop in Indonesia. In 2019, 2.7 M tonnes of fresh market pepper was produced to meet high demand of the domestic market [1]. Pepper production is occupying 155,000 hectares land and involving more than 500,000 local farmers [2]. Pepper is vulnerable to various abiotic and biotic stress [3]. Currently pepper yellow leaf curl disease (PepYLCD) is one of the most serious threat for pepper production in Indonesia that cause substantial yield loss up to 100% [4]. In 1999, PepYLCD was firstly noted in West Java and followed by subsequent incidence report from Central Java in 2003 [5]. PepYLCD has extensively spread to Sumatra in 2005.
In addition, PepYLCD was also observed in five pepper cultivation fields in Aceh Province, Indonesia with more than 81% plants exhibiting the typical symptoms and symptoms reaching 100% at four out of five fields [7]. PepYLCD is caused by viruses belonging to the genus of begomovirus of the Geminiviridae family [8]. The genus comprises 445 species composed of a circular single-stranded DNA component and its transmission depends on the insect vector *Bemisia tabaci* Genn. [9]. PepYLCD symptom is recognized by distinct vein yellowing, mosaic, severe leaf curl, failure of flower and fruit formation followed by significant yield-loss [10].

Current management for begomovirus caused disease in pepper rely on vector population control which is less effective [11]. As the most efficient and effective method, breeding of resistance material is urgently required. One of the ways to breed for resistance is by crossing. Crossing is aimed to combine all attractive traits into a newly generated genotype with broad genetic diversity, increase the hybrid vigour, and examine the potential of parent or progeny test [12]. Essential information in breeding newly attractive cultivar includes the fulfilled assumption for determined inheritance pattern of a desired trait where genes between parent spread equally, thereby to determine the inheritance pattern of desired trait, groups of genotypes representing the tolerance response is chosen as parent [13]. Consequently, genotype with high potential can be used as parent in the breeding of PepYLCD resistance cultivars [14].

BaPep-5 is a locally grown *C. annuum* accession in Aceh Province, Indonesia. In our preliminary study, a pepper yellow leaf curl disease virus resistance-1 (*pepy-1*) gene has been identified from BaPep-5 [15] after the challenge inoculation of prevalent isolates in Aceh, pepper yellow leaf curl Indonesia virus (PepYLCIV) and Pepper yellow leaf curl Aceh virus (PepYLCAV) [16]. Therefore, BaPep-5 is currently essential germplasm for begomovirus resistance. Because estimation of genetic parameters is an essential process for plant breeding, notably in obtaining heritability and genetic variability information [17], in this present study we evaluate the begomovirus resistance response in BaPep-5 by estimating the genetic variance and heritability value related to growth stage.

2. Materials and methods

2.1. Experiment place and time

The experiment was conducted at the Agricultural Extension Training Centre (BLPP) Saree, Lembah Seulawah, Aceh Besar (458 m asl approximate temperature ± 24°C - 28°C, Soil type: Andisol). Analysis of growth was conducted at the Horticulture Laboratory of Agrotechnology Department, Faculty of Agriculture, Universitas Syiah Kuala, Darussalam Banda Aceh. The study was started from February to July 2020.

2.2. Plants materials

500 *F₂* progenies (*C. annuum*) derived from a cross between BaPep-5 and the begomovirus susceptible accession BaPep-4 was used as the plant material. 15 plants of the respective parent were included as control.

2.3. Cultivation

Pepper plants were sown in a 87 m x 1 m plot, a total of 6 plots were formed and covered with plastic mulch. A 30 cm depth of drainage was implemented with a 50 cm distance of each plot. Plants were transplanted with 40 cm x 50 cm plant-to-plant distance. Initial fertilizer application was conducted by applying 20 tons ha⁻¹ of organic fertilizer, the application of dolomite lime 1.4 tonnes ha⁻¹ and 50 kg ha⁻¹ anorganic fertilizer NPK Mutiara (16:16:16). Irrigation was maintained for every morning. Pest and disease management was applied with chemical pesticides every 10 days from 7 days post transplanting (DPT) to 90 DPT.
2.4 Genetic variance estimation

2.4.1 Phenotypic variance

\[ \sigma^2_p = \sigma^2_{F2} \]  

\text{annotation:}
\sigma^2_p : \text{phenotypic variance}
\sigma^2_{F2} : \text{F}_2 \text{ population variance}

2.4.2 Environmental variance

\[ \sigma^2_e = \sqrt{(\sigma^2_{P1})(\sigma^2_{P2})} \]  

\text{annotation:}
\sigma^2_e : \text{environment variance}
\sigma^2_{P1} : \text{P}_1 \text{ population variance}
\sigma^2_{P2} : \text{P}_2 \text{ population variance}

2.4.3 Genotypic variance

\[ \sigma^2_g = \sigma^2_p - \sigma^2_e \]  

\text{annotation:}
\sigma^2_g : \text{genotypic variance}
\sigma^2_p : \text{phenotypic variance}
\sigma^2_e : \text{environment variance}

2.4.4 Heritability in a broad sense \((h^2_{bs})\) using Mahmud Kramer Method

\[ h^2_{bs} = \frac{\sigma^2_{F2} - \sqrt{(\sigma^2_{P1})(\sigma^2_{P2})}}{\sigma^2_{F2}} \times 100\% \]  

\text{annotation:}
h^2_{bs} : \text{heritability in a broad sense}
\sigma^2_{F2} : \text{F}_2 \text{ population variance}
\sigma^2_{P1} : \text{P}_1 \text{ population variance}
\sigma^2_{P2} : \text{P}_2 \text{ population variance}

Heritability criteria (%) by [18]
0 < \text{h}_{2bs} < 20 \quad \text{low}
20 \leq \text{h}_{2bs} < 50 \quad \text{moderate}
50 \leq \text{h}_{2bs} \quad \text{high}

2.4.5 Genotypic coefficient of variance (GCV)

\[ \text{GCV} = \frac{\sqrt{\sigma^2_g}}{x} \times 100\% \]  

\text{annotation:}
\sigma^2_g : \text{genetic variance}
x : \text{grand mean}
The criteria of genotypic coefficient of variance (GCV) by [19]

0 < X ≤ 10.94, narrow
10.94 < X ≤ 21.88, moderately narrow
21.88 < X ≤ 32.83, moderately broad
32.83 < X ≤ 43.77, broad
43.77 < X, highly broad

2.4.6 Phenotypic coefficient of variance (PCV)

\[ PCV = \sqrt{\frac{\sigma^2_p}{x}} \times 100\% \]  

(6)

annotation:

\( \sigma^2_p \) : phenotypic variance
\( x \) : grand mean

The criteria of phenotypic coefficient of variance (PCV) by [19]

0 < X ≤ 24.94, narrow
24.94 < X ≤ 49.71, moderately narrow
49.71 < X ≤ 74.71, moderately broad
74.71 < X ≤ 99.65, broad
99.65 < X, highly broad

3. Result and discussion

3.1. Begomovirus infection typical symptoms

Various symptom can be caused by begomovirus infection, this depends on the virus strain and the infected host plants. The typical symptom caused by begomovirus can be observed in leaf, for instance curlying, vein swelling, yellowing, mosaic, and dwarf. Begomovirus infect the host plants at the very early stage and inhibit the growth. Leaves of the infected plants will curled and swelled consequently it will reduce in size [20].

Begomovirus which infect pepper plants usually caused the symptoms such as blanching of the leaf vein which continue to develop as yellowing, vein swelling, and curled leaves. Heavier infection of begomovirus lead to reduced size of leaves with bright yellowing, and dwarf phenotype of plant. In the field, symptom caused by begomovirus is various. Several plants will exhibit complete yellowing leaves, stripped green and yellow, and yellowing leaves with curled edges, this typical symptoms spread is generally occur evenly [6].

3.2. Begomovirus transmission

Virus transmission in the field is highly dependent on the vector. Begomovirus which originated from pepper plants is not capable of being transmitted mechanically by extracted liquid from the infected plants, yet it can only transmit by the insect vector \( B. tabaci \) and side grafting. The efficiency of infection by insect vector is higher compared to that of grafting, therefore to conduct experiment related to begomovirus infection, the insect vector transmission is commonly implemented [14].

Several terms are frequently used to highlight the relationship between plant, virus, and vector particularly from the insect group such acquisition access period (AAP), inoculation access period (IAP), latent period, and persistency. AAP is a period for insect vector to obtain liquid from plant cell. Whereas IAP is an important period for vector to absorb the plants cell liquid and transfer it to the healthy plants. Latent periods occur between AAP and IAP. Persistency is period for the insect vector to be sustainably fit to run further IAP after its previous infection. Three categories of persistency; non-persistent, semi persistent, dan persistent [21]. Begomovirus is transmitted in a persistent or circulative manner. Virus will be able to maintain its life cycle inside vector body at least one week and the vector
can transmit virus for its entire life cycle [22]. Gaswanto et al., [23] stated that minimal AAP and IAP for B. tabaci is 15 minutes, respectively.

3.3 Genetic parameter estimation
Phenotypic expression of a plant is determined by genetic factor, environment, and interaction of both factors. The phenotypic variation in F$_2$ population could be expressed due to the segregation of first filial (F$_1$) which enables a crossing over at certain period allowing more quantity and more variation of gamete formation affected by multiple genes. Genetic factor become the most concerned since it is inherited from parents to its progeny. Heritability value is the principle in determining selection character. Heritability will create precise visualization of characters affected by genetic or environment which can be further used for examining the genetic relationship between two parents and the derived progenies. Heritability is classified according to several criteria from low to high. Heritability is classified as high if the value is higher than 50%, quite high if the value is 20-50%, and low if the value is less than 20% [24]. The result of general mean, phenotypic variance, environmental variance, genotypic variance, and heritability are shown in Table 1.

Table 1. Mean, heritability, phenotypic variance, environmental variance, genotypic variance calculated from vegetative stage parameters.

| Agronomic trait      | Mean | $\sigma^2p$ | $\sigma^2e$ | $\sigma^2g$ | $h^2_{bs}$ (%) | Criteria |
|----------------------|------|-------------|-------------|-------------|----------------|----------|
| Plant height         | 70.25| 275.07      | 121.65      | 72.17       | 230.84         | high     |
| Dichotomous height   | 35.07| 45.64       | 23.17       | 0           | 0              | low      |
| Stem diameter        | 7.22 | 1.74        | 1.17        | 0.31        | 0              | low      |
| Secondary branch     | 4.49 | 0.74        | 0           | 0           | 0.74           | low      |
| Tertiary branch      | 8.96 | 2.92        | 0           | 0           | 2.92           | low      |
| Crown width          | 65.49| 316.74      | 291.50      | 194.24      | 224.71         | high     |

Note: $\sigma^2p$: phenotypic variance; $\sigma^2e$: environment variance; $\sigma^2g$: genotypic variance; $h^2_{bs}$: heritability in a broad sense. Heritability criteria: low ($h^2_{bs} < 20$), moderate ($20 \leq h^2_{bs} < 50$) and, high ($h^2_{bs} \geq 50$) [18]

Variance in a population is affected by the value of genotypic variance and phenotypic variance observed in the evaluated trait. A higher genotypic variance suggesting that the trait is predominantly influenced by its genotypic factor, whereas a higher phenotypic variance suggesting that the trait is predominantly influenced by its environmental factor. In Table 1, all the observed traits had higher phenotypic variance compared to genotypic variance which demonstrated a high influence of environmental factor on phenotypic expression.

The broad sense heritability values shown in Table 1 indicates that plant height (230.84%) and crown width (224.71%) have high heritability values whereas dichotomous height (0%), stem diameter (0%), secondary branches (0.74%) and tertiary branches (2.92%) had low heritability values. Mahmud-Kramer equation for heritability analysis was established using P1 and P2 population data as a pure accession to determine the heritability and the results suggests that high heritability in several trait was contributed by the ability of genetic trait in particular individual to inherit the trait to its offspring.

The heritability value for the character of plant height is relatively high (230.84%) indicating that the expression of genes holds an important role in plant height which more influenced by genetic factors, whereas environmental factors slightly affect the character of plant height such as Begomoviral disease which causes plants to grow abnormally. The heritability value of the crown width character (224.71%) also had a high heritability value which indicated that the genes from the parents influenced or dominated the character of the width of the crown more than the experimental environmental conditions.
According to [12], quantitative characters in plants are controlled by many genes, each of which has a small effect on quantitative characters; these characters are heavily influenced by environmental factors. Characters that have high heritability values indicate that genotype variety plays a more important role than environmental variety. The low heritability value suggests that environmental factors affect the character more. According to [25], the heritability value of quantitative characters which is relatively high indicates the phenotypic diversity in that generation is the diversity that can be passed on to their offspring.

The relationship between plant height and production is very close, it is suspected that there is a relationship with the formation of the number of productive branches, the taller the plant, the more opportunities for the emergence of productive branches, and with the number of productive branches, presumably the more flowers will be formed [26]. According to [27], in addition to having many productive branches, tall plants are more favoured by farmers because taller plants can prepare better vegetative organs, this affects the amount of photosynthesis so that many produce flowers which later become fruit.

### Table 2. Genotypic coefficient of variability (GCV) and phenotypic coefficient of variability (PCV) calculated from vegetative stage parameters.

| Agronomic trait        | Mean | GCV (%) | Criteria          | PCV (%) | Criteria          |
|------------------------|------|---------|--------------------|---------|--------------------|
| Plant height           | 70.25| 12.09   | Moderately narrow  | 23.61   | Narrow             |
| Dichotomous height     | 35.07| 0       | Narrow             | 19.26   | Narrow             |
| Stem diameter          | 7.22 | 7.75    | Narrow             | 18.25   | Narrow             |
| Secondary branch       | 4.49 | 0       | Narrow             | 19.15   | Narrow             |
| Tertiary branch        | 8.96 | 0       | Narrow             | 19.07   | Narrow             |
| Crown width            | 65.49| 21.28   | Moderately narrow  | 27.17   | Moderately narrow  |

Note: Criteria GCV: narrow (x ≤ 10.94), moderately narrow (10.94 < x ≤ 21.88), moderately broad (21.88 < x ≤ 32.83), broad (32.83 < x ≤ 43.77), highly broad (x ≥ 43.77) Criteria PCV: narrow (x ≤ 24.94), moderately narrow (24.94 < x ≤ 49.71), moderately broad (49.71 < x ≤ 74.71), broad (74.71 < x ≤ 99.65), highly broad (x ≥ 99.65)

Generally, a reduction in plant height is common in plants that are infected by viruses because the chlorophyll was hijacked by virus component and resulted in reduced efficiency of photosynthesis. Very high viral activity is thought to affect plant metabolic processes, thereby reducing primary metabolites and plant growth. The main metabolism is the process of photosynthesis which is connected with the pigment chlorophyll. Plants infected with the virus are thought to reduce their growth in both the vegetative and generative phases [4].

Diversity can be determined by the coefficient of genetic diversity (GCV), there are various coefficients of genetic diversity in Table 2 ranging from 0-21.28%. The value of the coefficient of genetic diversity is influenced by the experimental environment where the more heterogeneous the experimental environment, the greater the coefficient of diversity. The overall agronomic characters of plant height, dichotomous height, stem diameter, secondary branches, tertiary branches, and crown widths had criteria for GCV and PCV which are moderately narrow to narrow. The low GCV and PCV values indicate that environmental influences influence these characters more. Selection of characters with narrow coefficient of genetic diversity is difficult to increase their genetic potential. If the diversity is high then there is an opportunity to expect for genetic improvements and will presumably resulted in well-established selection [28].

According to [29], the GCV and PCV values which almost coincide with these characters indicate that the diversity of a character is caused by genetic factors. Stating the existence of a high criterion on
the GCV value can indicate a wide level of genetic diversity so that the selection process can be carried out more easily and efficiently [23]. The more diverse the individual traits in the population, the higher the frequency of the desired gene, therefore the opportunity to obtain an individual with attractive phenotype through selection is higher [30].

4. Conclusion
According to the result of the experiments, below are the conclusion points:
1. The coefficient of genetic diversity in the F2 population derived from crossing BaPep-5 and BaPep-4 was highly diverse with the coefficient of genetic variance ranging from 0% - 21.28% narrow to moderately narrow criteria for all characters.
2. The broad sense heritability based on the Mahmud-Kramer method varied, the character of plant height (230.84%) and crown width (224.71%) had high broad sense heritability values. Characters of dichotomous height (0%), stem diameter (0%), secondary branches (0.74%), and tertiary branches (2.92%) had low broad sense heritability values.

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References
[1] Badan Pusat Statistik 2017 Badan Pusat Statistik 335–58
[2] Ali M 2006 Chili (Capsicum spp.) food chain analysis: Setting research priorities in asia
[3] Devendran R, Kumar M, Ghosh D, Yogindran S, Karim M J and Chakraborty S 2021 Capsicum-infecting begomoviruses as global pathogens: host–virus interplay, pathogenesis, and management Trends Microbiol.
[4] Setiawati W, Udiarto B and Soetiarso T 2008 Pengaruh Varietas Dan Sistem Tanam Cabai Merah Terhadap Penekanan Populasi Hama Kutu Kebul J. Hortik. 18
[5] Sumardiyo Y B. S S and S H 2003 Epidemi Penyakit Daun Keriting Kunang Cabai J. Perlindungan Tanam. Indones. 9
[6] Sulandari S R I, Suseno R, Hidayat S H, Harjosudarmo J and Sosromarsono S 2006 Detection and Host Range Study of Virus Associated with Pepper Yellow Leaf Curl Disease HAYATI J. Biosci. 13
[7] Koeda S, Kesumawati E, Tanaka Y, Hosokawa M, Doi M and Kitajima A 2016 Mixed infection of begomoviruses on pepper plants at northern Sumatra, Indonesia Trop. Agric. Dev. 60 59–64
[8] Malathi V G, Renukadevi P, Chakraborty S, Biswas K K, Roy A, Sivalingam P N, Venkataravanappa V and Mandal B 2017 Begomoviruses and their satellites occurring in India: Distribution, diversity and pathogenesis A Century of Plant Virology in India
[9] Walker P J, Siddell S G, Lefkowitz E J, Mushegian A R, Adriaenssens E M, Dempsey D M, Duttilh B E, Harrach B, Harrison R L, Hendrickson R C and others 2020 Changes to virus taxonomy and the Statutes ratified by the International Committee on Taxonomy of Viruses (2020)
[10] Rojas M R, Macedo M A, Maliano M R, Soto-Aguilar M, Souza J O, Briddon R W, Kenyon L, Rivera Bustamante R F, Zerbini F M, Adkins S, Legg J P, Kvarnheden A, Wintermantel W M, Sudarshana M R, Peterschmitt M, Lapidot M, Martin D P, Moriones E, Inoue-Nagata A K and Gilbertson R L 2018 World Management of Geminiviruses Annu. Rev. Phytopathol. 56
[11] Borah B K and Dasgupta I 2012 Begomovirus research in India: A critical appraisal and the way ahead J. Biosci. 37
[12] Arif A Bin, Sujiprihati S, Syukur D M, Penelitian B B, Pengembangan D, Pertanian P and
Pelajar J T 2012 Estimation of Several Genetic Parameter on Quantitative Characters of Hybridization between Big and Curly Chilli (Capsicum annuum L.) *Indonesia* **40**

[13] Singh R J and Jauhar P P 2006 *Genetic resources, chromosome engineering, and crop improvement* vol 2

[14] Ganefianti D W, Sujiprihati S, Hidayat S H and Syukur M 2008 Metode penularan dan uji kestabilitan genotipe cabai (Capsicum spp.) terhadap Begomovirus *Aka Agrostosia* **11**

[15] Koeda S, Onouchi M, Mori N, Pohan N S, Nagano A J and Kesumawati E 2021 A recessive gene pepy-1 encoding Pelota confers resistance to begomovirus isolates of PepYLCSV and PepYLCAV in Capsicum annuum *Theor. Appl. Genet.*** 134

[16] Kesumawati E, Okabe S, Homma K, Fujiwara I, Zakaria S, Kanzaki S and Koeda S 2019 Pepper yellow leaf curl Ach virus: a novel bipartite begomovirus isolated from chili pepper, tomato, and tobacco plants in Indonesia *Arch. Virol.* **164**

[17] Yunendra, Syukur M and Maharjaya D A 2017 Seleksi dan Kemajuan Seleksi Karakter Komponen Hasil pada Persilangan Cabai Keriting dan Cabai Besar *J. Agron. Indones. (Indonesian J. Agron.*** **45**

[18] Zen S and Bahar H 1996 Penampilan dan pendugaan parameter genetik tanaman jagung *Agric. J* **3** 1–9

[19] Qosim W A, Karuniawan A, Marwoto B and Badriah D S 2000 Stabilitas parameter genetik mutan-mutan krisis generasi VM3 *Lap. Has. Penelit. Lemb. Penelit. Univ. Padajajaran***

[20] Torres-Pacheco I, Garzón-Tiznado J A, Brown J K, Becerra-Flora A and Rivera-Bustamante R F 1996 Detection and distribution of geminiviruses in Mexico and the southern United States *Phytopathology*** **86**

[21] Wahyuni W S 2005 Dasar-dasar virologi tumbuhan *Univ. Jember UGM Press***

[22] Frankham R 1996 *Introduction to quantitative genetics* (4th edn) *Trends Genet.* **12**

[23] Hidayat dan, Penelitian Tanaman Sayuran B, Agronomi dan Hortikultura D and Proteksi Tanaman D 2015 Metode Penularan Massal untuk Uji Penapisan Kestabilan Cabai Mutan terhadap Begomovirus (The Mass Transfer Method for Resistance Screening Test of Chilli Mutant to Begomovirus) *J. Hort*** 25 246–56

[24] Fajar Sidiq A R, Syukur M and Marwiyah S 2017 Pendugaan Parameter Genetik dan Seleksi Karakter Kuantitatif Cabai Rawit (Capsicum annuum L.) Populasi F3 *Bul. Agrohorti*** 5

[25] Jambormias E and others 2014 Analisis genetik dan segregasi transgresif berbasis informasi kekerabatan untuk potensi hasil dan panen serempak kacang hijau

[26] Noor A, Sri H H, Rusmilah S and Soemartono S 2002 Transmission of an Indonesian Isolate of Tobacco leaf curl virus (Geminivirus) by Bemisia tabaci Genn. (Hemiptera: Aleyrodidae) *Plant Pathol. J.* **18**

[27] Duriat A, Gunaneti N and Wulandari A 2007 *Penyakit Penting Tanaman Cabai dan Pengendaliannya***

[28] Rachmadi M 2000 Pengantar pemuliaan tanaman membiak vegetatif *Univ. Padjajaran Bandung*** 159

[29] Trustinah R and Hapsari R T 2017 Seleksi Galur Kacang Hijau Berbiji Kecil *Bul. Palawija*** **15** 24–31

[30] Hapsari R T 2016 Pendugaan Keragaman Genetik dan Korelasi Antara Komponen Hasil Kacang Hijau Berumur Genjah *Bul. Plasma Nutfah*** **20**