

# Diversity of twenty-three sweet corn (*Zea mays* L. *saccharata*) varieties in Indonesia

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**Abstract.** Heryanto FSS, Wirnas D, Ritonga AW. 2022. Diversity of twenty-three sweet corn (*Zea mays* L. *saccharata*) varieties in Indonesia. *Biodiversitas* 23: 6075-6081. One of the most well-known vegetables in Asian countries, including Indonesia. Improving superior sweet corn varieties is important in the face of increasing biotic or abiotic stresses and consumer preferences for agricultural products. Plant breeding programs rely on genetic variability and heritability information. Therefore, this study aimed to quantify the genetic diversity and heritability of 23 commercial sweet corn varieties in Indonesia. The study was conducted at the Leuwikoppo experimental field of the Department of Agronomy, Faculty of Agriculture, IPB University, Bogor, West Java, Indonesia, from August to November 2021. Twenty-three commercial sweet corn varieties (hybrid and open-pollinated) from Indonesia were planted in the field employing a randomized complete block design with 3 replications. Ear shelf life and green ear yield had a high genotypic coefficient of variation (GCV), whereas plant height, ear height, stalk length, 100-grain weight, total soluble solids, green ear shelf life, green ear weight, and ear weight had a moderate GCV. Stem diameter, leaf number, leaf length, leaf width, 50% days to tasseling and silking, anthesis, silking interval, ear length, ear diameter, ear length with the kernel, ear length percent with the kernel, kernel length, and kernel width had a low GCV. High genetic diversity was present among the trialed varieties, indicating their high potential for improvement.

**Keywords:** Clustering, genetic diversity, heritability, *Zea mays* L. *saccharata*

## INTRODUCTION

Sweet corn (*Zea mays* L. var. *saccharata*) is characterized by a high kernel sugar content when harvested at the fresh, or R3, stage (Chouhan et al. 2021). Sweet corn kernels have a higher sugar content (9 to 30% at the milk stage) than normal corn kernels (2 to 5% at the milk stage) (Seshu et al. 2015). The higher sugar content in sweet corn is caused by a gene mutation that prevents the conversion of sugar to starch in the seed endosperm. Eight recessive monogenic genes control the sweetness of sweet corn: shrunken-1 (sh1), shrunken-2 (sh2), shrunken-4 (sh4), brittle-1 (bt1), brittle-2 (bt2), amylose extender (ae), dull (du), sugary2 (su2), and waxy (ex) (Vanipraveena et al. 2022). However, only four genes are commonly used in sweet corn breeding: sh2 and bt2, which are categorized as 'super sweet' corn, and sugary-1 (su1) and sugary enhancer (se), which are categorized as general sweet corn (Santos et al. 2014; Ojo et al. 2020). Recessive sh2-based sweet corn genotypes, also known as 'extra sweet corn' or 'super sweet,' accumulate six times more sugar than normal corn at the milky ripe stage (Chhabra et al. 2022).

Sweet corn is one of the most famous vegetables in Asian countries like Indonesia (Dermail et al. 2022), as it can be consumed fresh or processed as an ingredient for the food industry (Alan et al. 2013). Sweet corn has the third-largest planted area of a vegetable in Indonesia, after chili peppers and shallots. Product quality is critical for a horticultural crop (Bulgari et al. 2019) like sweet corn

because it is frequently consumed fresh and has high economic value (Becerra-Sanchez and Taylor 2021). Consumers consider shelf life, ear size and shape, and kernel sweetness and color when selecting sweet corn, making these traits key breeding targets (Alan et al. 2013). Additionally, tropical conditions in Indonesia are characterized by high disease incidence, pest pressure, and high temperatures (Abe and Adelegan 2019; Bisbis et al. 2019). As biotic and abiotic stresses increase, high productivity and stress resistance will be important traits for sweet corn growers to consider when purchasing seeds (Chouhan et al. 2021).

Plant breeding programs are initially determined by the genetic variability present in the base populations (Kumar et al. 2019b). Information on genetic variability can be used to determine the parents and breeding methods of a plant breeding program (Lopes et al. 2015; Hemavathy et al. 2020) and the ideotypes consumers favor. The success of a plant breeding program is also determined by the presence of information on the inheritance of the traits to improve (Bello et al. 2012), such as yield and kernel sweetness, which have traditionally been the focus of commercial sweet corn breeding programs. Broad sense heritability (H<sub>b</sub>) provides information about the heritability of a trait because it describes the proportion of phenotypic variability caused by genetic variability. For example, a high H<sub>b</sub> value indicates that genetic components play a more important role than environmental components in the phenotypic variability of a trait (Taneva

et al. 2019). Heritability can also be quantified as the difference between the genotypic (GCV) and phenotypic (PCV) coefficients of variation. Information about genetic variability and heritability helps breeders determine the selection criteria for improving yield and other traits (Niji et al. 2018). Therefore, this study aimed to determine the genetic diversity and heritability of 23 commercial sweet corn varieties in Indonesia.

## MATERIALS AND METHODS

### Study area

This study was conducted at the Leuwikoppo experimental field of the Department of Agronomy, within the IPB University Faculty of Agriculture, in Bogor, West Java, Indonesia (6°33'48" S 106°43'34" E, 250 m elevation, Latosol type soil). The study was conducted from August to November 2021 (rainy season), with rainfall ranging from 309 to 321 mm per month and daily mean air temperature ranging from 26 to 27°C.

### Site management

Twenty-three varieties of commercial sweet corn (hybrid and open-pollinated) from Indonesia (Table 1) were trialed in a randomized complete block design with 3 replications. Each experimental plot contained 20 plants, with 10 plants used as samples.

**Table 1.** Commercial sweet corn varieties used in a West Java, Indonesia field study from August to November 2021

Variety	Type
Glory	Hybrid
Top Green SL 307	Hybrid
Golden Boy	Hybrid
Prima	Hybrid
Super Sweet Corn	Open-pollinated
Maestro	Open-pollinated
King Sweet	Open-pollinated
Gulaku	Open-pollinated
Paragon	Hybrid
Jambore	Hybrid
Exotic	Hybrid
Magenta	Hybrid
Soneta	Hybrid
Manise	Hybrid
Baruna	Open-pollinated
Bimmo	Hybrid
Secada F1	Hybrid
New Lorenza F1	Hybrid
Bonanza 9 F1	Hybrid
BN 44	Open-pollinated
Sweet Boy	Hybrid
Sweet Lady	Hybrid
Talenta	Hybrid

The field was prepared by plowing, loosening, and weeding 2 weeks before planting. In addition, 10 tons per hectare of manure and 1 ton per hectare of dolomite were applied 1 week before planting. An 80 cm x 10 cm spacing was used, with one seed planted per hole. The field was sprinkler irrigated every morning and evening when it was not raining. The field was initially fertilized with 90 kg per hectare of N, 120 kg per hectare of K<sub>2</sub>O, 72 kg per hectare of P<sub>2</sub>O<sub>5</sub> 10 days after planting, and again with 200 kg per hectare of urea 4 weeks after planting. An insecticide, with the active ingredient abamectin (concentration 0.5 - 1.0 mL L<sup>-1</sup>), and a fungicide, with the active ingredient mancozeb 80% (concentration 1- 2 g L<sup>-1</sup>), were applied 3 and 5 weeks after planting, respectively. Weeding and hoarding were carried out at 1, 3, and 6 weeks after planting. Sweet corn was harvested fresh, or at the R3 stage, with the criteria that the corn cob hair was dry and the kernels were fully enlarged.

### Data collection

Observations were made when the tassel and ear bloomed and were repeated after harvesting. The plant height, stem diameter, leaf number, leaf length, leaf width, days to 50% tasseling and silking, and anthesis silking interval (ASI) were measured when the tassel and ear bloomed. Postharvest measurements consisted of ear length, stalk length, ear diameter, length of the ear with the kernel, percent length of the ear with the kernel (length of the ear with the kernel/ear length x 100%), kernel length, kernel width, 100-grain weight, total soluble solids (TSS), ear and green ear shelf life at room temperature (26-27°C), ear weight, green ear weight, and green ear yield. Ear shelf life was observed from the day of harvest until 50% kernel of the ear wrinkled, whereas the green ear shelf life was observed from the day of harvest until the corn husks turned brown. TSS was determined using a DR102 Digital Brix Refractometer with a 0 to 90% measurement range. Three to four kernels from the center of each ear of corn were carefully removed and hand-pressed. Several drops were then transferred to the surface of the instrument for measurement. TSS observations used kernels from corn ears from selfing. The yield was calculated using green ear weight per plot.

### Data analysis

An analysis of variance for quantitative data was performed using PKBT STAT 3.1 at a 5% significant level. A cluster analysis using different agglomerative hierarchical clustering based on Euclidean distance was conducted to identify the similarities and dissimilarities of the trialed varieties (Figure 1). Several metrics, including Euclidean, Manhattan, Mahalanobis, and the Gower coefficient, are frequently employed in the dissimilarity analysis of individuals using phenotypic attributes (Darkwa et al. 2020). GCV and PCV were computed for all traits using the following equations (Mia et al. 2020):

$$\text{Phenotypic coefficient of variation (PCV)} = \frac{\sqrt{\delta^2_p}}{X} \times 100$$

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\sqrt{\delta^2_g}}{X} \times 100$$

Hbs, expressed as the percentage of the ratio of genotypic variance ( $\delta^2g$ ) to phenotypic variance ( $\delta^2p$ ), was calculated with the following equation (Allard 1960):

$$\text{Broad sense heritability (Hbs)} = \delta^2g / \delta^2p \times 100\%$$

The phenotypic, genotypic, and environmental variances, as well as the coefficient of variation, were calculated according to the following equations (Burton and Devane 1953):

$$\text{Environmental variance: } (\delta^2e) = \text{MSE}$$

$$\text{Genotypic variance } (\delta^2g) = \frac{(\text{MSG} - \text{MSE})}{r}$$

$$\text{Phenotypic variance } (\delta^2p): \delta^2p = \delta^2g + \delta^2e$$

Where: MSG represents the mean square due to genotype, MSE represents the mean square error (environmental variance), and  $r$  is the number of replications.

## RESULTS AND DISCUSSION

### Varietal effect on agronomic traits

The ANOVA results revealed a significant effect of variety on most observed traits, providing an early

indication of the genetic diversity of the trialed varieties. In addition, the genotypic variance was highly significant for all traits studied, indicating that the trialed genotypes were genetically different (Saravanan et al. 2019). This variation should provide ample scope for breeders to select superior genotypes for crop improvement (Sujatha and Pushpavalli et al. 2017; Mia et al. 2020).

### Statistical metrics of agronomic traits

The GCV ranged from 0.00 to 26.71, with high GCV for ear shelf life and green ear yield (Table 2). Plant height, ear height, stalk length, 100-grain weight, total soluble solids, green ear shelf life, green ear weight, and ear weight had moderate GCV. Stem diameter, leaf number, leaf length, leaf width, 50% days to tasseling and silking, ASI, ear length, ear diameter, ear length with the kernel, percent length of the ear with the kernel, kernel length, and kernel width had low GCV. The present study results are in agreement with the results of Niji et al. (2018), but differ from those of Abe and Adelegan (2019) and Chavan et al. (2020) due to differences in the sweet corn population used in each study. Niji et al. (2018) used hybrid populations with various types of sweetness genes, while Abe and Adelegan (2019) used only sh-2 populations and Chavan et al. (2020) used a population of inbred lines so that each genotype had low average productivity due to high inbreeding depression in sweet corn (Badr et al. 2016).

**Table 1.** Analysis of variance (mean square) results for 23 traits measured across 23 varieties of sweet corn in West Java, Indonesia in 2021

Character	Replication		Variety		Error	CV
Plant height	940.67	**	1332.25	**	111.49	6.26
Ear height	109.23	ns	378.48	**	77.79	9.92
Stem diameter	2.71	**	0.10	ns	0.05	13.79
Leaf number	4.84	**	1.46	**	0.58	6.58
Leaf length	25.05	*	180.98	**	6.28	2.55
Leaf width	0.99	**	2.30	**	0.16	4.21
Days to 50% tasseling	20.19	ns	14.66	ns	9.70	5.73
Days to 50% silking	13.32	ns	17.91	**	6.52	3.75
Anthesis silking interval	0.75	ns	8.08	**	3.41	13.37
Ear length	1.89	ns	6.13	**	2.55	7.65
Stalk length	3.01	ns	4.20	*	2.21	20.66
Ear diameter	0.85	ns	0.60	ns	0.44	13.77
Ear length with kernel	4.19	ns	4.20	ns	4.42	11.86
Percent ear length with kernel	50.38	ns	78.45	ns	64.80	9.46
Kernel length	0.01	ns	0.03	**	0.01	9.40
Kernel width	0.00	ns	0.02	ns	0.02	13.26
100-grain weight	21.10	**	15.60	**	0.07	1.83
Total soluble solids	0.62	ns	9.80	**	0.27	4.13
Ear shelf life	5.23	**	4.18	**	0.99	21.45
Green ear shelf life	0.75	ns	6.36	**	2.10	21.84
Green ear weight	20638.23	**	8867.81	**	3349.32	17.25
Ear weight	837.72	ns	4802.12	**	1377.10	15.47
Green ear yield	17.96	*	27.27	**	4.27	19.92

Note: \*: significant differences ( $p \leq 0.05$ ) according to Tukey's HSD, \*\*: significant differences ( $p \leq 0.01$ ) according to Tukey's HSD, ns: not significant differences ( $p \leq 0.05$ ) according to Tukey's HSD

The GCV indicates a trait's genetic variability level (i.e., a high GCV indicates high genetic variability). Trait improvement is generally more effective for traits with high genetic variability than low genetic variability (Gao 2021). Therefore, increasing the genetic variability of low genetic variability traits can increase the efficacy of trait improvement. Hybridization, mutation induction, gene transfer, and genome editing can increase plant genetic diversity (Kumar et al. 2019a; Graham et al. 2020; Zhang et al. 2020). Sweet corn genotypes used in this study were commercial varieties in Indonesia, so the low GCV traits are likely to be favored by Indonesian consumers. Therefore, Indonesian consumers likely prefer sweet corn varieties with a maximum ASI of 7 days, ears with full kernels, ear lengths ranging from 18 to 24 cm, and ear diameters from 4 to 7 cm. Therefore, these traits can serve as an idiomorph for sweet corn breeding in Indonesia.

The PCV was higher than the GCV for all studied traits, suggesting an environmental influence on trait variation (Behera et al. 2018; Buthelezi et al. 2019; Bayisa et al. 2020) as reported in other studies (Niji et al. 2018; Abe and Adelegan 2019; Chavan et al. 2020). The higher PCV is because the observed traits were quantitative characters easily influenced by the environment (Rosmaina et al. 2021). A smaller difference between the PCV and GCV was observed for plant height, ear height, leaf number, leaf length, leaf width, days to 50% silking, ASI, ear length, kernel length, 100-grain weight, TSS, ear shelf life, green ear shelf life, ear weight, and green ear yield, suggesting there was less of an environmental effect on the phenotypic expression of these traits. Meanwhile, a larger difference between the PCV and GCV was obtained for days to 50%

tasseling, stalk length, ear diameter, ear length with kernels, ear length with the kernel, and kernel width, suggesting there was more of an environmental influence on the phenotypic expression of these traits. Phenotypic selection is more effective when the genetic influence on the variability of a trait is greater than the environmental influence (Niji et al. 2018; Shweta et al. 2020).

#### Broad sense heritability and genetic advance

A high Hbs indicates that genetic components play a more important role than environmental components in the phenotypic variability of a trait (Tanefa et al. 2019). The Hbs of the observed traits ranged from low to high. Plant height, ear height, leaf length, leaf width, 100-grain weight, total soluble solids, ear shelf life, and green ear yield showed a moderate to high Hbs, indicating that the variability of these traits was influenced by genetic factors more than environmental factors (Table 3). High heritability of plant height, ear height, TSS, and green ear yield characters was also reported previously (Niji et al. 2018; Abe and Adelegan 2019; Vanipraveena et al. 2022).

Stem diameter, leaf number, days to 50% tasseling, days to 50% silking, ASI, ear length, stalk length, ear diameter, length of the ear length with the kernel, percent length of the ear with the kernel, kernel width, and green ear weight had low heritability, indicating that their variability was influenced by environmental factors more than genetic factors. In contrast, Abe and Adelegan (2019) reported high heritability for days to 50% tasseling and days to 50% silking.

**Table 2.** Mean, minimum, and maximum performance, standard error, and coefficients of variation for 23 characters measured across 23 varieties of sweet corn in West Java, Indonesia in 2021

Character	Mean	Range		SE	CV	GCV	PCV
		Min.	Max.				
Plant height (cm)	168.76	127.80	208.05	0.90	6.26	11.95	13.49
Ear height (cm)	88.87	71.98	104.82	0.48	9.92	11.27	15.01
Stem diameter (cm)	1.70	1.51	2.03	0.01	13.79	7.60	15.20
Leaf number	11.55	10.13	13.02	0.03	6.58	4.69	8.09
Leaf length (cm)	98.35	80.72	114.66	0.33	2.55	7.76	8.17
Leaf width (cm)	9.65	6.95	10.77	0.04	4.21	8.76	9.69
Days to 50% tasseling (days)	54.36	51.33	60.33	0.09	5.73	2.37	6.20
Days to 50% silking (days)	68.16	62.67	75.67	0.10	3.75	2.86	4.71
Anthesis silking interval (days)	13.80	7.33	15.00	0.07	13.37	9.04	16.15
Ear length (cm)	20.85	18.65	23.69	0.06	7.65	5.24	9.28
Stalk length (cm)	7.19	4.77	9.17	0.05	20.66	11.32	23.57
Ear diameter (cm)	4.79	4.09	6.10	0.02	13.77	4.82	14.65
Length of the ear with kernel (cm)	17.72	16.22	19.48	0.05	11.86	0.00	11.87
Percent ear length with the kernel (%)	85.13	72.86	94.45	0.22	9.46	2.51	9.78
Kernel length (cm)	1.13	1.00	1.50	0.00	9.40	7.20	11.38
Kernel width (cm)	0.97	0.84	1.34	0.00	13.26	0.00	14.60
100-grain weight (g)	14.61	10.00	21.00	0.10	1.83	15.57	15.68
Total soluble solids (% Brix)	12.68	8.00	15.33	0.08	4.13	14.05	14.64
Ear shelf life (days after harvest)	4.64	3.33	7.33	0.05	21.45	22.23	30.90
Green ear shelf life (days after harvest)	6.64	4.67	10.00	0.06	21.84	17.95	28.27
Green ear weight (g)	335.41	283.03	283.03	2.31	17.25	12.79	21.48
Ear weight (g)	239.94	179.78	305.97	1.70	15.47	14.08	20.92
Green ear yield (metric tons per ha)	10.37	4.37	14.87	0.13	19.92	26.71	33.33

Note: SE: standard error, CV: coefficient of variation, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation

**Table 3.** Broad sense heritability (Hbs) and genetic advance (GA) for 23 characters measured across 23 varieties of sweet corn in West Java, Indonesia in 2021

Character	Hbs (%)	Category	GA (%)	Category
Plant height	78.49	Moderately high	21.91	High
Ear height	56.30	Moderately high	17.19	Moderate
Stem diameter	25.00	Low	11.53	Moderate
Leaf number	33.59	Low	5.91	Low
Leaf length	90.27	Very high	14.94	Moderate
Leaf width	81.68	Very high	16.25	Moderate
Days to 50% tasseling	14.56	Low	1.87	Low
Days to 50% silking	36.80	Low	3.56	Low
Anthesis silking interval	31.34	Low	10.22	Moderate
Ear length	31.88	Low	6.00	Low
Stalk length	23.09	Low	11.13	Moderate
Ear diameter	10.81	Low	3.27	Low
Ear length with kernel	0.00	Low	0.00	Low
Percent ear length with kernel	6.56	Low	1.31	Low
Kernel length	40.00	Medium	9.92	Low
Kernel width	0.00	Low	0.00	Low
100-grain weight	98.67	Very high	31.97	High
Total soluble solids	92.17	Very high	27.27	High
Ear shelf life	51.79	Moderately high	33.45	High
Green ear shelf life	40.34	Medium	23.05	High
Green ear weight	35.45	Low	16.24	Moderate
Ear weight	45.33	Medium	19.20	Moderate
Green ear yield	64.23	Moderately high	44.10	High

The influence of genetic factors greater than environmental factors on most of the characters could have occurred because these characters are controlled by genetically different genes in the tested sweet corn varieties. On the other hand, the environmental factor's effect that was greater than that of the genetic factor in several characters may have occurred because, genetically, these characters were not significantly different among the commercial varieties of the sweet corn used in this study, and the observed variability was mainly due to the environmental effect. Direct selection is more effective on traits with high heritability than low heritability (Ghasolia et al. 2021), making a direct selection of low heritability traits potentially misleading (Ritonga et al. 2018).

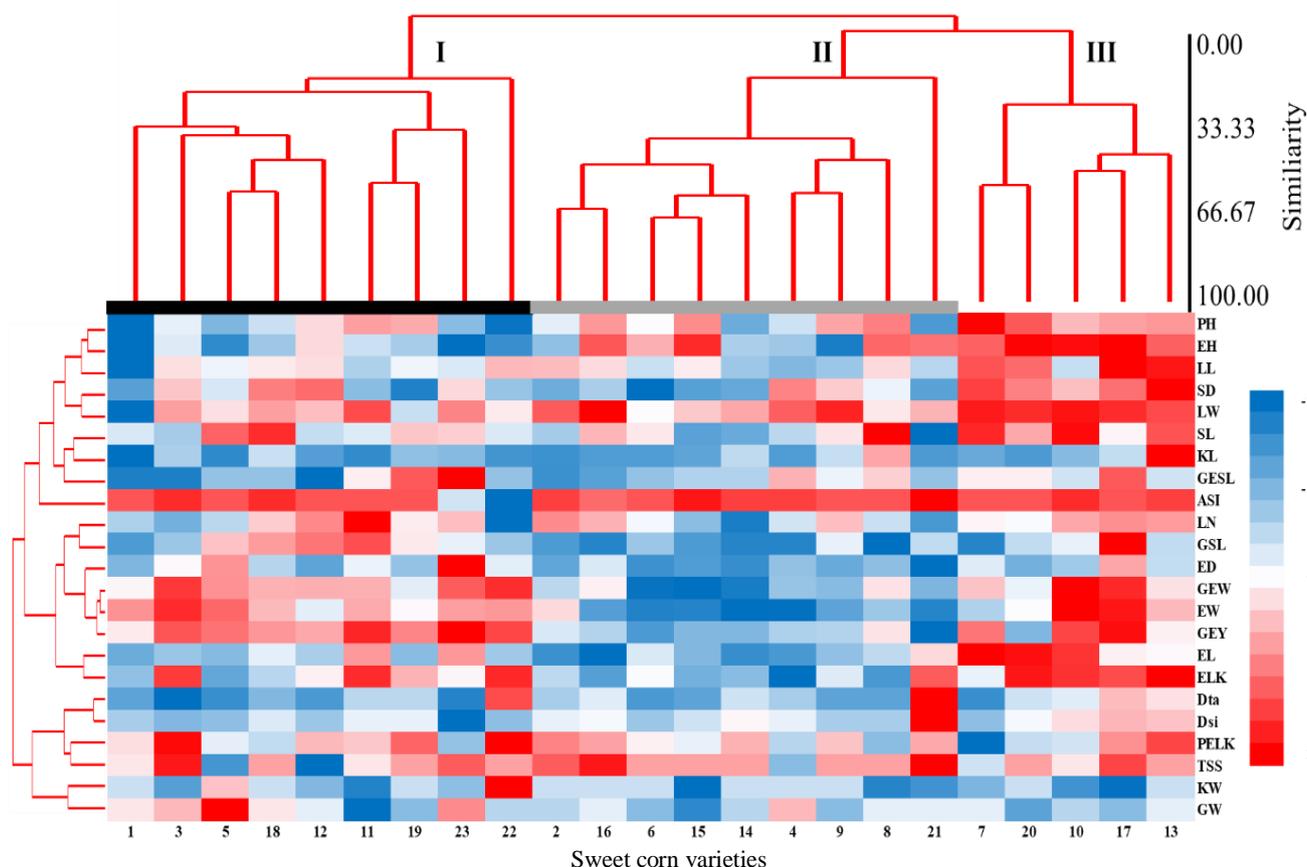
The percent genetic advance ranged from low to high. Plant height, 100-grain weight, total soluble solids, ear shelf life, green ear shelf life, and green ear yield had a high genetic advance. Traits with high GCV and heritability will generally also have high genetic advances (Bartaula et al. 2019), indicating that crop improvement on these traits is effective.

### Hierarchical cluster analysis

Cluster analysis based on the 23 observed traits divided the 23 varieties into three main groups. Cluster 1 and cluster 2 each consisted of nine varieties, with a similarity level of 21.41 to 59.29% in cluster 1 and 20.83 to 68.24% in cluster 2. Meanwhile, cluster 3 consisted of five varieties with a similarity level of 30.07 to 57.26%. The diversity of sweet corn in this study was higher than the diversity

reported by Stansluos et al. (2019), who divided 11 hybrid and non-hybrid varieties into four clusters with a similarity level of 75 to 97%, and Yuwono et al. (2017), who divided eight inbred lines into three clusters with a similarity level of 62.5%. Stansluos et al. (2019) and Yuwono et al. (2017) used agronomic traits for clustering. The diversity of sweet corn in this study is similar to Roy et al. (2015), who divided 30 genotypes into several clusters with 25 to 66% similarity using molecular markers. Differences in diversity and clustering are likely caused by differences in the number and type of characters and the number and background of genotypes used in each study. Low similarity, and thus high genetic diversity, is ideal for sweet corn breeding (Bello et al. 2012; Hemavathy et al. 2019).

The main traits that distinguished the three clusters were green ear yield, green ear weight, ear weight, plant height, and ear height, indicating the high potential improvement of yield and yield component traits of this population. Similarly, Mahato et al. (2018) reported that plant height, ear height, and green ear weight were the main traits in grouping 39 sweet corn inbred lines. Improvements can be made with hybridization between high-yielding genotypes from different clusters, with genetic diversity present in the available genotypes holding immense value for crop improvement in traits of interest (Lahane et al. 2016). Cluster differences in cluster analysis indicate a high diversity among plant genotypes (Jumaa and Madab 2018). A high heterotic level is also paramount for sweet corn improvements (Mahato et al. 2018).



**Figure 1.** Hierarchical cluster showing similarities among 23 sweet corn varieties based on agronomic traits using the complete linkage method based on Euclidean distance. ESL: ear shelf life, EY: green ear yield, PH: plant height, EH: ear height, SL: stalk length, GW: 100-grain weight, TSS: total soluble solids, GESL: green ear shelf life, GEW: green ear weight, EW: ear weight, SD: stem diameter, LN: leaf number, LL: leaf length, LW: leaf width, Dta: 50% days to tasseling, Dsi: 50% days to silking, ASI: anthesis silking interval, EL: ear length, ED: ear diameter, ELK: ear length with the kernel, PELK: ear length percent with the kernel, KL: kernel length, and KW: kernel width.

In conclusion, plant height, ear height, stalk length, 100-grain weight, total soluble solids, green ear shelf life, green ear weight, ear weight, ear shelf life, and green ear yield resulted in a moderate to high GCV. There is high genetic diversity among the 23 Indonesian sweet corn varieties trialed in this study based on 23 agronomic traits, indicating high potential for improvement of these varieties.

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