

Genetic and morphological diversity of various corn lines for the determination of waxy corn (*Zea mays* var. *ceratina*) parents

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²Department of Agronomy and Horticulture, Faculty of Agriculture, Institut Pertanian Bogor. Jl. Meranti, Bogor 16680, West Java, Indonesia. Tel.: +62-251-8629354, Fax.: +62-251-8629352, ✉✉email: surjonoagh@apps.ipb.ac.id

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Abstract. Pangestu DA, Sutjahjo SH, Ritonga AW. 2023. Genetic and morphological diversity of various corn lines for the determination of waxy corn (*Zea mays* var. *ceratina*) parents. *Biodiversitas* 24: 5643-5652. Genetic diversity is the first step in plant breeding programs. Information about genetic diversity is essential for commodity development to run well, and crop improvement can be more focused. This study aimed to evaluate the genetic diversity and performance of various genotypes of waxy corn. A total of 18 genotypes of waxy corn were grown using a randomized complete block design with three replications. Analysis of variance, estimation of the genetic parameters, broad-sense heritability, genotypic and phenotypic coefficient of variances, and cluster analysis were carried out in this study. The results showed differences in qualitative and quantitative characters between the genotypes of the tested waxy corn. The characters of plant height, ear height, stem diameter, number of leaves, tassel length, ear weight, and number of seeds per row had a high heritability and genetic coefficient of variance. This result indicates that those traits have a high variability among genotypes. Cluster analysis based on qualitative and quantitative characters divided 18 genotypes of waxy corn into three main clusters with similarity 18.34%. The main characteristics that divide the 3 clusters include ear weight with husk, ear length, ear length with kernels, stem diameter, plant height, and ear height. Based on the cluster analysis results, it was suspected that the F1 hybrid resulting from crossing genotypes JPM-1-5-9 with JPS-13-6-5-5 was a hybrid that could produce the best ear character.

Keywords: Cluster analysis, GCV, heritability, PCV, yield component

Abbreviations: Hbs: Heritability broad sense, GCV: Genotypic coefficient of variation, PCV: Phenotypic coefficient of variation, CV: Coefficient of variation, ASI: Anthesis silking interval

INTRODUCTION

Eastern Indonesia, such as Sulawesi, Maluku, and East Nusa Tenggara, has a variety of local waxy corn germplasm (Sinay and Karuwal 2018; Syaiful et al. 2020). Waxy corn is a type of specialty corn characterized by its high stickiness due to the high proportion of amylopectin and thin pericarp (Xiaoyang et al. 2017), which usually consumed in the form of fresh ears, and the seeds can also be processed into flour (Ketthaisong et al. 2015). Amylopectin is a property that makes corn taste fluffier. The higher the amylopectin content, the softer, fluffier, and tastier the texture and taste of corn. The higher the amylopectin content, the softer, fluffier, and more flavorful the texture and taste of corn become. The waxy gene (*wx*) expresses the fluffier and more pleasant taste of waxy corn. When this gene is in a homozygous recessive state (*wxwx*), it results in a very high amylopectin content (Xiaoyang et al. 2017). Visually, the characteristics of waxy corn are easy to recognize. Waxy corn grains are round and dense; the outside is smoothly textured. The endosperm is hard, like dent corn, and it has various color (Harakotr et al. 2015; Sukto et al. 2021), but in Indonesia, local waxy corn has a pallid color. Another way to identify waxy corn is by

using iodine, which reacts with amylopectin endosperm and produces a reddish-brown color (Cengiz 2022).

The development of waxy corn for food has a problem, concerning in low productivity. Therefore there is a need for genetic improvement of glutinous corn to increase the quantity and quality of yields. These improvements can be made through plant breeding activities by assembling hybrid varieties. Waxy corn has the potential to be developed into hybrid varieties as industrial raw materials, especially for starch production (Ja et al. 2022). The advantage of hybrid varieties is that they can provide the best results from crosses between pure lines (Sorsa et al. 2023).

The diversity of waxy corn must be done as a first step to improve quality and productivity in supporting plant breeding programs to assemble new superior varieties. The success of plant breeding will depend on a high level of genetic diversity, which enables the selection of desired genotypes (Begna et al. 2021). Therefore, it is necessary to provide information about the genetic diversity of waxy corn, such as the inheritance of traits that want to be improved, such as seed size, ear size, and amylopectin content (Simla et al. 2016; Dermail et al. 2020). With that information, the development of this commodity can run well, and crop improvement can be more focused (Lu et al. 2016).

The acquired genetic information is subsequently categorized through cluster analysis. The cluster analysis method showed phenotypic differences among the tested genotypes. Describing and identifying plant phenotypes is the most basic method of grouping germplasm. Classifying variable genotypes in homogeneous groups based on their genetic relationships and similarities increase the efficiency in planning crosses for a breeding program (Laude and Carena 2015). The cluster analysis method can reflect significant differences in phenotypic traits between plants and can be an important and comprehensive reference in selecting plants based on characters (Tan et al. 2022). The criteria for determining the parents for a waxy corn hybrid is heterosis. A high heterosis level shows that the hybrid performs better than the parent. One of the ways to identify high heterosis levels in corn plants is by choosing a significant genetic distance, which can be demonstrated by cluster differences (Mahato et al. 2021). This study aims to evaluate the genetic diversity and performance of various parental genotypes (pure lines) of waxy corn so that potential parents can be obtained for forming F1 hybrids of waxy corn with high-yield characteristics.

MATERIALS AND METHODS

Study area

This research was conducted in Pasir Kuda Experimental Field of IPB University, Bogor, Indonesia (6°36'8.98"S, 106°45'55.12"E), elevation 222 m, alluvial soil type). The research was conducted from November 2022 to February 2023 (rainy season), with monthly rainfall ranging from 312-323 mm and average daily temperatures ranging from 25-27°C.

Procedures

Field experiment

The 18 genotypes of waxy corn used in the study (Table 1) were tested using a randomized complete block design

with three replications. Each experimental unit consisted of 20 plants, with ten plants used as sample plants.

Land preparation is conducted through meticulous tillage, followed by the application of organic fertilizer. Each genotype is then planted in a single row, with a spacing of 70×20 cm and one seed per planting hole. The planted seeds were treated with an insecticide containing the active ingredient carbofuran, as well as a fungicide containing dimethomorph 80%. Replanting is performed at 1 MST. Fertilizer application is conducted twice: first, seven days after planting, using 150 kg ha⁻¹ of urea, 200 kg ha⁻¹ of SP-36, and 100 kg ha⁻¹ of KCl; and the second application involves a dose of 150 kg ha⁻¹ of urea fertilizer, applied 30 days after planting. Weed control was carried out twice manually at 14-20 days after planting together with hilling and at six weeks after planting. Control of plant-disturbing organisms in the form of pests and diseases uses insecticides with the active ingredient carbofuran at a dose of 5 kg ha⁻¹ and profenofos 500 g L⁻¹ and a fungicide with the active ingredient mancozeb 80% at a concentration of 3 g L⁻¹

Data collection

Observations were made on the quantitative and qualitative characters of 10 sample plants for each genotype in each replication (UPOV 2009). Quantitative characters observed included plant height, ear height, stem diameter, leaf length, leaf width, tassel length, number of tassel branch, anthesis date 50%, silking date 50%, anthesis silking interval, ear weight husk, weight ear unhusked, ear diameter, ear length, ear length with kernels, number of kernel rows, and number of kernels per row. The qualitative characteristics observed were leaf tip shape, leaf curvature, leaf angle, anthocyanin on leaf, anthocyanin on internode, anthocyanin on silk, anthocyanin on tassel, anthocyanin on root, and tassel angel.

Table 1. Genetic materials of 18 genotype waxy corn

Genotype	Code	Type	Color		Origin
			Kernel	Husk	
JPS-13-16-12-10	G1	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JP-30-2-5K-5	G2	Inbreed	Yellow (RHS 10B)	Green (RHS 144A)	Southeast Sulawesi
JPS-13-16-12-7	G3	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JPM-1-6P-3	G4	Inbreed	White (RHS 155B)	Green (RHS 144A)	West Java
JPS-13-16-12-12	G5	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JPS-13-6-5-5	G6	Inbreed	White (RHS 155B)	Green (RHS 144A)	East Nusa Tenggara
JPS-13-6-1P-10	G7	Inbreed	White (RHS 155B)	Green (RHS 144A)	East Nusa Tenggara
JPS-13-16-12-13	G8	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JPM-1-5-19	G9	Inbreed	White (RHS 155B)	Green (RHS 144A)	West Java
JPS-13-6-1P-20	G10	Inbreed	White (RHS 155B)	Green (RHS 144A)	Southeast Sulawesi
JPM-1-2P-3	G11	Inbreed	White (RHS 155B)	Green (RHS 144A)	West Java
JPS-13-6-1K-1	G12	Inbreed	Yellow (RHS 16A)	Green (RHS 144A)	East Nusa Tenggara
JPS-13-6-1P-15	G13	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JPM-1-6P-4	G14	Inbreed	White (RHS 155B)	Green (RHS 144A)	West Java
JPS-13-16-12-3	G15	Inbreed	White (RHS 155A)	Green (RHS 144A)	East Nusa Tenggara
JPM-1-6K-1	G16	Inbreed	Yellow (RHS 10C)	Green (RHS 144A)	West Java
JPS-13-6-1K-17	G17	Inbreed	Yellow (RHS 16A)	Green (RHS 144A)	East Nusa Tenggara
JPS-13-16-12-20	G18	Inbreed	White (RHS 155B)	Green (RHS 144A)	East Nusa Tenggara

Data analysis

Analysis of variance was carried out on quantitative character data followed by a follow-up test of HSD at the α level of 5% using PKBT STAT 3.1 (<http://pbstat.com/pkbt-stat/>). Estimation of genetic parameters and heritability follows the method of Magar et al. (2021):

$$\sigma_e^2 = \text{MSE} = \text{Environment variance}$$

$$\sigma_g^2 = \text{MSG} - \text{MSE} / r = \text{Genetic variance}$$

$$\sigma_p^2 = \sigma_g^2 + \sigma_e^2 = \text{Phenotypic variance}$$

MSG is the mean square of the genotype, MSE is the mean square of error, R is the number of replicates and x is the general average of the population

$\text{GCV} = \sqrt{(\sigma_g^2/x \times 100\%)} = \text{Genotypic coefficient of variation}$

$\text{PCV} = \sqrt{(\sigma_p^2/x \times 100\%)} = \text{Phenotypic coefficient of variation}$

$$\text{Hbs} = \sigma_g^2 / \sigma_p^2 \times 100\% = \text{Broad sense heritability}$$

Qualitative character data are presented descriptively Cluster analysis was carried out based on "Euclidian dissimilarity" and "Complete linkage clustering method" using Microsoft excel and Minitab 18 software.

RESULTS AND DISCUSSION

Qualitative characters of various pure lines of waxy corn

The diversity of qualitative characteristics of waxy corn leaves is presented in Table 2. The tested waxy corn leaf curvature showed moderate character except for the genotype JPS-13-16-12-3, which had a strong leaf curvature character. All genotypes of waxy corn did not show any variation in leaf tip shape and leaf surface anthocyanins. All genotypes of waxy corn showed a

character with a sharp leaf tip shape and produced very weak leaf surface anthocyanins.

All waxy corn genotypes tested had various leaf angles: small, medium, and large. A smaller leaf angle indicates the leaves are more upright, making them more effective in utilizing sunlight and can be planted more densely to increase plant productivity. This shows that the greater the leaf angle, the lower the seed yield. Corn plants with wider leaf angles absorb more heat from the sun, so they tend to be more stressed by drought than corn plants with more upright leaf angles (Al-Naggar et al. 2016).

Variations in the qualitative characters of waxy corn were also produced in the angle between the main tassel stalk and the lateral tassel branches (very small, small, medium, large, and very large) (Table 3). Anthocyanins in ear hair (silk and tassels show various appearances (weak, weak, medium, strong, and strong). In addition, the anthocyanin in the internode and roots showed a very weak and moderate appearance. Genetic factors of waxy corn influence the presence of anthocyanins in ear hairs, internodes, and tassels. Morphological diversity of corn plants grown under the same conditions can occur because differences in genetic sequences are one of the factors causing plant diversity (Selvi et al. 2013; Gupta et al. 2016).

Agronomic characters of waxy corn lines

The analysis of variance showed that the genotype had a significant effect on most of the characters observed (Table 4). This indicated an indication of the genetic diversity of the genotypes tested. The diversity in genotypes can provide a wide space for choosing superior genotypes in waxy corn breeding programs (Ja et al. 2019). The coefficient of variance value <20% shows good data collection (Ritonga et al. 2018).

Table 2. Description of various qualitative characters of leaves and stems of 18 genotypes of waxy corn

Genotype	LTS	LC	LA	AL	AI
JPS-13-16-12-10	Sharp	Moderate	Medium	Very weak	Very weak
JP-30-2-5K-5	Sharp	Moderate	Medium	Very weak	Very weak
JPS-13-16-12-7	Sharp	Moderate	Medium	Very weak	Very weak
JPM-1-6P-3	Sharp	Moderate	Medium	Very weak	Very weak
JPS-13-16-12-12	Sharp	Moderate	Large	Very weak	Medium
JPS-13-6-5-5	Sharp	Moderate	Large	Very weak	Medium
JPS-13-6-1P-10	Sharp	Moderate	Small	Very weak	Very weak
JPS-13-16-12-13	Sharp	Moderate	Medium	Very weak	Medium
JPM-1-5-19	Sharp	Moderate	Small	Very weak	Very weak
JPS-13-6-1P-20	Sharp	Moderate	Small	Very weak	Very weak
JPM-1-2P-3	Sharp	Moderate	Medium	Very weak	Very weak
JPS-13-6-1K-1	Sharp	Moderate	Medium	Very weak	Very weak
JPS-13-6-1P-15	Sharp	Moderate	Small	Very weak	Very weak
JPM-1-6P-4	Sharp	Moderate	Medium	Very weak	Very weak
JPS-13-16-12-3	Sharp	Strong	Small	Very weak	Medium
JPM-1-6K-1	Sharp	Moderate	Small	Very weak	Very weak
JPS-13-6-1K-17	Sharp	Moderate	Small	Very weak	Very weak
JPS-13-16-12-20	Sharp	Moderate	Medium	Very weak	Very weak

Note: LTS: Leaf tip shape, LC: Leaf curvature, LA: Leaf angle, AL: Anthocyanin on leaf, AI: Anthocyanin on internode

Table 3. Description of various qualitative characteristics of ear silk, roots, and tassels

Genotype	AS	AT	AR	TA
JPS-13-16-12-10	Strong	Very weak	Medium	Very large
JP-30-2-5K-5	Medium	Medium	Very weak	Small
JP-S-13-16-12-7	Medium	Very weak	Very weak	Medium
JPM-1-6P-3	Very weak	Very weak	Very weak	Very small
JPS-13-16-12-12	Medium	Medium	Medium	Large
JPS-13-6-5-5	Sangat Strong	Weak	Medium	Large
JPS-13-6-1P-10	Strong	Weak	Very weak	Very small
JPS-13-16-12-13	Strong	Medium	Medium	Medium
JPM-1-5-19	Very weak	Very weak	Very weak	Very small
JPS-13-6-1P-20	Strong	Weak	Medium	Very small
JPM-1-2P-3	Strong	Very weak	Very weak	Very small
JPS-13-6-1K-1	Very weak	Very weak	Very weak	Very small
JPS-13-6-1P-15	Strong	Medium	Medium	Very small
JPM-1-6P-4	Very weak	Very weak	Very weak	Very small
JPS-13-16-12-3	Strong	Weak	Medium	Large
JPM-1-6K-1	Very weak	Very weak	Very weak	Very small
JPS-13-6-1K-17	Very weak	Very weak	Very weak	Medium
JPS-13-16-12-20	Strong	Very weak	Very weak	Medium

Note: AS: Anthocyanin on silk, AT: Anthocyanin on tassel, AR: Anthocyanin on root, TA: tassel angel

Table 4. Estimation of the mean square for 18 characters in 18 genotypes of the waxy corn

Characters	Range	Mean square		CV (%)
		Reply	Genotype	
Plant height (cm)	114.00-221.00	3094.75**	929.62**	11.55
Ear height (cm)	36.50-106.80	435.3 ^{ns}	601.56**	19.23
Diameter of stem (cm)	1.55-2.50	0.02 ^{ns}	1.59**	7.83
Number of leaf	8.80-13.00	0.46 ^{ns}	1.59**	4.51
Leaf length (cm)	48.50-95.00	3324.4**	69.3*	6.83
Leaf width (cm)	6.38-11.60	5.19**	2.15**	5.85
Anthesis date 50% (day)	40-56	21.62**	16.18**	3.81
Silking date 50% (day)	44-45	6.74**	8.08**	2.92
Anthesis-silking interval (day)	0-4	1.40 ^{ns}	1.78*	52.40
Tassel length (cm)	23.00-42.00	44.81 ^{ns}	30.06 ^{ns}	11.98
number of tassel branches	9.20-17.00	1.27 ^{ns}	8.94**	9.81
Ear weight with husk (g)	72.94-197.82	667.61 ^{ns}	1557.07**	15.23
Ear weight unhusked (g)	29.83-130.39	95.47 ^{ns}	997.41**	23.17
Ear length (cm)	9.17-17.90	0.58 ^{ns}	11.9**	8.21
Ear length with kernel (cm)	7.30-15.17	1.75 ^{ns}	7.93**	9.49
Ear diameter (cm)	3.03-4.75	0.04 ^{ns}	1.98*	8.73
Number row of ear	10.00-15.00	0.03 ^{ns}	1.29**	4.01
Number kernel of row	9.00-30.00	1.31 ^{ns}	48.4**	10.25

Note: ns: not significant, *: significant on alpha 5%, **: significant on alpha 1%

The height of waxy corn plants ranged from 129.33 cm to 196.73 cm, and the ear height of waxy corn in this study ranged from 44.70 cm to 97.40 cm (Table 5). Genotype had a significant effect on stem diameter. The diameter of the waxy corn stalks tested had values ranging from 1.78-2.33 cm. The diameter of the stem between genotypes is different. Stem diameter is essential in supporting plants and growing corn plants. Genotypes with large stem diameters are indicated to have higher productivity than genotypes with smaller stem diameters (Chen et al. 2014). The length and width of the leaves range from 65.23-83.60 cm and 7.55-10.55 cm. Tassel length in waxy corn ranged from 28.17-39.35 cm, but this result was not significantly different between the genotypes tested. The number of tassel branches ranges from 9.87-16.02 panicles.

Characteristics of the flowering date are presented in Table 6. Among all the genotypes tested, Genotype JPS-13-16-12-7 exhibited the earliest anthesis date at 45.00 days. Meanwhile, the JPM-1-6P-4 genotype had the longest flowering date, 64.57 days. Genotype JPS-13-16-12-7 exhibited the quickest silk flowering date character, specifically at 47.67 days, while the genotype that demonstrated the longest time was JPM-1-6K-1, at 54.33 days. The JPS-13-6-1P-10 genotype had the shortest silking interval of 0 days, and the longest JPM-1-6P-4 genotype had 3.33 days. The flowering date trait characteristic is early maturity, with an ASI value close to zero. The pollination rate of the male parent, the receptive time of the female parent's ear hair, and the interaction among these factors can impact seed formation in hybrid seed

production. Anthesis silking interval values that are close to zero are considered relatively desirable as they enhance pollination optimization. The corn silk on female flowers remains optimally receptive for up to seven days after emergence, and seed formation decreases as it transitions into the senescent phase (Shen et al. 2018).

Observation of yield characters and yield components showed ear length and ear length with kernels ranged from 10.56-17.30 cm and 8.12-14.63 cm (Table 7). Based on the results of the variance analysis, none of the tested waxy corn genotypes showed diversity of ear diameter. The diameter of the corn ear ranges from 3.16-4.05 cm. The ear weights with husk and ear weight unhusked tested ranged between 76.17-160.20 g and 32.33-96.63 g. These results are lower than the study of Ja et al. (2019) which showed ear weight with husk and ear weight unhusked ranging from 241-374 g and 192-252 g. The number of rows of kernels and kernels per row of waxy corn ranged from 11.67-14.50 rows and 12.33-27.00 kernels. This result is lower than that of Santoso et al. (2014), which produced the number of kernel rows, and the number of kernels per row ranged from 8-15 rows and 11.5-25.5 kernels. These differences are caused by differences in the waxy corn populations used between the trials. The maize population in this study used population the same inbred lines as Santoso et al. (2014) but different from Ja et al. (2019) using a population of hybrid waxy corn.

Waxy corn lines typically exhibit inferior characteristics, such as shorter plant height or smaller ear size, when compared to hybrid waxy corn populations. This is primarily due to the significant inbreeding depression present in waxy corn during self-pollination. Self-pollination on corn plants will change their genetic constitution to become homozygous. Selfing is an inbreeding method that can reduce heterozygosity in offspring. There was a decrease in plant height and yield of maize due to

inbreeding depression from the S1 (first selfing generation) maize population which was still heterozygous to S5 (fifth selfing generation) which had high homozygosity (Ali et al. 2019). The percentage of genomic homozygosity among different S7 individu was 99.6 to 99.7% (Han et al. 2021). Inbreeding depression causes a decrease in fitness so that the plant's appearance looks unattractive, especially for the lower plant height, and the ears become smaller due to increased genomic homozygosity (Pekkala et al. 2014).

Table 6 Flowering date characteristics of various lines of waxy corn

Genotype	AD	SD	ASI
JPS-13-16-12-10	52.00 ^a	54.00 ^a	-2.00 ^b
JP-30-2-5K-5	52.33 ^a	53.00 ^a	-0.67 ^{ab}
JP-S-13-16-12-7	45.00 ^b	47.67 ^b	-2.67 ^b
JPM-1-6P-3	52.67 ^a	53.00 ^a	-0.33 ^{ab}
JPS-13-16-12-12	50.67 ^{ab}	52.00 ^{ab}	-1.33 ^b
JPS-13-6-5-5	51.00 ^{ab}	53.33 ^a	-2.33 ^b
JPS-13-6-1P-10	53.67 ^a	53.67 ^a	0.00 ^{ab}
JPS-13-16-12-13	53.00 ^a	54.00 ^a	-1.00 ^b
JPM-1-5-19	54.33 ^a	54.00 ^a	0.33 ^{ab}
JPS-13-6-1P-20	51.33 ^a	53.67 ^a	-2.33 ^b
JPM-1-2P-3	51.67 ^a	51.67 ^{ab}	0.00 ^{ab}
JPS-13-6-1K-1	53.67 ^a	53.33 ^a	0.33 ^{ab}
JPS-13-6-1P-15	54.33 ^a	54.33 ^a	0.00 ^{ab}
JPM-1-6P-4	54.67 ^a	51.33 ^{ab}	3.33 ^a
JPS-13-16-12-3	48.67 ^{ab}	51.33 ^{ab}	-2.67 ^b
JPM-1-6K-1	53.67 ^a	54.33 ^a	-0.67 ^{ab}
JPS-13-6-1K-17	52.33 ^a	54.00 ^a	-1.67 ^b
JPS-13-16-12-20	52.67 ^a	52.00 ^{ab}	0.67 ^{ab}

Note: AD: Anthesis date 50% (day), SD: Silking date 50% (day), ASI: Anthesis silking interval (day). Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

Table 5. Morphological traits of various lines of waxy corn

Genotype	PH	EH	DS	NL	LL	LW	LT	NTB
JPS-13-16-12-10	165.87 ^{ab}	88.27 ^{ab}	1.96 ^{ab}	11.53 ^{abc}	71.47 ^{ab}	8.45 ^{bcd}	34.93	13.20 ^{abcd}
JP-30-2-5K-5	129.33 ^b	44.70 ^b	1.75 ^b	11.77 ^{ab}	68.20 ^{ab}	8.58 ^{bcd}	28.17	11.87 ^{bcd}
JP-S-13-16-12-7	145.20 ^{ab}	54.73 ^{ab}	2.01 ^{ab}	10.00 ^c	71.23 ^{ab}	7.55 ^e	41.00	14.00 ^{abc}
JPM-1-6P-3	169.88 ^{ab}	78.78 ^{ab}	2.07 ^{ab}	12.22 ^a	81.55 ^{ab}	7.84 ^{cde}	30.67	16.02 ^a
JPS-13-16-12-12	180.93 ^{ab}	97.40 ^a	1.90 ^{ab}	12.20 ^a	77.17 ^{ab}	7.39 ^e	33.60	11.47 ^{bcd}
JPS-13-6-5-5	196.73 ^a	94.53 ^a	1.96 ^{ab}	11.33 ^{abc}	78.70 ^{ab}	8.39 ^{bcd}	37.07	12.27 ^{abcd}
JPS-13-6-1P-10	162.80 ^{ab}	71.43 ^{ab}	2.24 ^{ab}	11.27 ^{abc}	79.33 ^{ab}	9.63 ^{ab}	37.17	9.87 ^d
JPS-13-16-12-13	167.53 ^{ab}	81.80 ^{ab}	2.03 ^{ab}	12.40 ^a	83.60 ^a	7.65 ^{de}	33.77	13.73 ^{abcd}
JPM-1-5-19	181.95 ^{ab}	71.85 ^{ab}	2.08 ^{ab}	10.00 ^c	78.66 ^{ab}	10.55 ^a	39.35	13.00 ^{abcd}
JPS-13-6-1P-20	165.67 ^{ab}	76.10 ^{ab}	2.38 ^a	11.17 ^{abc}	81.50 ^{ab}	9.12 ^{abcd}	34.83	10.70 ^{cd}
JPM-1-2P-3	160.13 ^{ab}	64.58 ^{ab}	2.01 ^{ab}	11.20 ^{abc}	65.23 ^b	7.60 ^{de}	33.81	10.89 ^{cd}
JPS-13-6-1K-1	144.47 ^{ab}	54.20 ^{ab}	2.30 ^a	11.40 ^{abc}	78.77 ^{ab}	8.77 ^{bcd}	32.18	12.88 ^{abcd}
JPS-13-6-1P-15	152.87 ^{ab}	56.93 ^{ab}	2.33 ^a	10.20 ^{bc}	77.00 ^{ab}	9.28 ^{abc}	39.33	10.53 ^{cd}
JPM-1-6P-4	146.73 ^{ab}	82.77 ^{ab}	2.09 ^{ab}	12.27 ^a	78.07 ^{ab}	8.57 ^{bcd}	32.80	14.93 ^{ab}
JPS-13-16-12-3	174.40 ^{ab}	72.80 ^{ab}	2.04 ^{ab}	10.87 ^{abc}	76.53 ^{ab}	7.83 ^{cde}	34.83	14.13 ^{abc}
JPM-1-6K-1	147.44 ^{ab}	75.94 ^{ab}	2.05 ^{ab}	11.67 ^{ab}	78.17 ^{ab}	9.31 ^{abc}	35.00	14.00 ^{abc}
JPS-13-6-1K-17	134.90 ^b	66.13 ^{ab}	2.32 ^a	11.20 ^{abc}	80.13 ^{ab}	8.44 ^{bcd}	36.83	12.13 ^{abcd}
JPS-13-16-12-20	173.00 ^{ab}	77.97 ^{ab}	2.22 ^{ab}	11.47 ^{abc}	78.40 ^{ab}	7.89 ^{cde}	33.93	15.00 ^{ab}

Note: PH: Plant height (cm), EH: Ear height (cm), DS: Diameter of stem (cm), NL: Number of leaf, LL: Leaf length (cm), LW: Leaf width (cm), LT: Length of tassel (cm), NTB: Number tassel of branch. Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

Table 7 Yield characters and yield components of various lines of waxy corn

Genotype	EL	ELK	ED	EWH	EWUH	NR	NSR
JPS-13-16-12-10	11.75 ^{cde}	9.52 ^{cde}	3.16 ^a	92.89 ^{cd}	43.20 ^{cd}	12.00 ^b	16.67 ^{cdefg}
JP-30-2-5K-5	12.70 ^{bcde}	10.60 ^{bcde}	4.05 ^a	150.43 ^{abc}	87.40 ^{ab}	12.00 ^b	19.00 ^{bcde}
JPS-13-16-12-7	10.12 ^e	9.75 ^{bcde}	3.50 ^a	96.21 ^{bcd}	46.14 ^{bcd}	11.67 ^b	12.00 ^g
JPM-1-6P-3	13.38 ^{bcde}	10.15 ^{bcde}	3.84 ^a	124.74 ^{abcd}	68.83 ^{abcd}	12.00 ^b	17.00 ^{cdefg}
JPS-13-16-12-12	10.40 ^e	8.79 ^{de}	3.18 ^a	76.17 ^d	32.33 ^d	12.00 ^b	12.33 ^{fg}
JPS-13-6-5-5	15.52 ^{ab}	12.82 ^{ab}	3.77 ^a	152.71 ^{ab}	74.42 ^{abcd}	12.00 ^b	23.50 ^{ab}
JPS-13-6-1P-10	14.98 ^{abc}	12.91 ^{ab}	3.28 ^a	133.60 ^{abcd}	64.21 ^{abcd}	12.00 ^b	22.00 ^{abc}
JPS-13-16-12-13	10.56 ^e	9.84 ^{bcde}	3.39 ^a	109.28 ^{abcd}	37.73 ^{cd}	12.00 ^b	14.00 ^{efg}
JPM-1-5-19	17.30 ^a	14.63 ^a	3.73 ^a	160.20 ^a	96.63 ^a	14.50 ^a	27.00 ^a
JPS-13-6-1P-20	12.97 ^{bcde}	10.87 ^{bcde}	3.20 ^a	125.36 ^{abcd}	55.29 ^{abcd}	12.50 ^b	21.50 ^{abcd}
JPM-1-2P-3	12.66 ^{bcde}	10.56 ^{bcde}	3.29 ^a	127.68 ^{abcd}	61.11 ^{abcd}	12.00 ^b	22.00 ^{abc}
JPS-13-6-1K-1	14.54 ^{abcd}	11.89 ^{abcd}	3.46 ^a	129.67 ^{abcd}	68.16 ^{abcd}	13.00 ^{ab}	18.00 ^{bcdef}
JPS-13-6-1P-15	12.30 ^{bcde}	12.00 ^{abc}	3.36 ^a	121.69 ^{abcd}	56.25 ^{abcd}	12.00 ^b	18.50 ^{bcde}
JPM-1-6P-4	12.75 ^{bcde}	10.33 ^{bcde}	3.41 ^a	107.62 ^{abcd}	56.53 ^{abcd}	12.00 ^b	19.00 ^{bcde}
JPS-13-16-12-3	10.28 ^e	8.12 ^e	3.30 ^a	93.09 ^{cd}	35.57 ^{cd}	12.00 ^b	16.00 ^{defg}
JPM-1-6K-1	14.03 ^{abcd}	11.13 ^{bcde}	3.66 ^a	128.52 ^{abcd}	76.26 ^{abc}	11.50 ^b	16.50 ^{cdefg}
JPS-13-6-1K-17	14.62 ^{abcd}	11.12 ^{bcde}	3.45 ^a	144.55 ^{abc}	55.19 ^{abcd}	12.00 ^b	14.67 ^{efg}
JPS-13-16-12-20	11.62 ^{de}	9.00 ^{cde}	3.57 ^a	122.10 ^{abcd}	36.24 ^{cd}	12.00 ^b	14.50 ^{efg}

Note: EL: Ear length (cm), ELK: Ear length with kernel (cm), ED: Ear diameter (cm), EWH: Ear weight with husk (g), EWUH: Ear weight unhusked (g), NR: Number row on ear, NSR: Number kernel of row. Numbers followed by the same letter in the same column are not significantly different based on the HSD test at a 5% level

**Figure 1.** Diversity of ear shape of genotype waxy corn

The appearance of waxy corn ears is presented in Figure 1. All genotypes showed the appearance of various corn ear shapes and grain row characters. Ear shape genotypes JPS-13-16-12-10 (G1), JPS-13-16-12-7 (3), JPM-1-6P-3(G4), JPM-1-5-19(G9), JPS-13-6-1P-20(G10), JPM-1-2P-3(G11), JPS-13-6-1P-15 (G13), JPM-1-6P-4 (G14), JPS -13-16-12-

20(G18) has a cylindrical ear shape. Genotypes JP-30-2-5K-5 (G2), JPS-13-6-5-5 (G6), JPS-13-6-1P-10 (G7), JPS-13-6-1K-1 (G12), JPS-13-16-12-3 (G15), JPS-13-6-1K-17 (G17) has a conical-cylindrical ear shape. Genotype JPS 13-16-12-13 (G8), JPM-1-6K-1 (G16) has a conical ear shape.

Estimation of genetic parameters of various characters of waxy corn

The estimated values for variance and heritability are presented in Table 8. The majority of the traits displayed high broad-sense heritability values, with the exception of tassel length (0.58). This shows that the diversity of most of the characters in this study was caused by genetic rather than environmental factors. GCV showed values that varied from low to high (9.03-50.38%) in this study. The characters of plant height, ear height, stem diameter, number of leaves, tassel length, ear weight with husk, and number of kernels per row produced high GCV values. The characters of leaf length, number of tassels, ear weight unhusked, ear diameter, and number of kernel rows had GCV values classified as medium.

The GCV values for the characters of leaf width, ear length, and seed ear length were low. This result is in line with the research of Bartaula et al. (2019) on the observed characteristics. However, it is better than the research of Julianto et al. (2017) which showed that all genotypes tested had low GCV values for plant height characteristics (4.69%), ear height (6.05%), number of seed rows (4.39%) and ear diameter (4.78%). The PCV value is higher than the GCV value for all observed characters. The GCV value indicates a high variation in a character, while a low GCV value indicates low genetic diversity.

Based on Table 8, the majority of the characters had high Hbs values except for silking date and anthesis silking intervals. Both of these characters have broad-sense heritability values which are classified as moderate. Characters with high heritability values indicate that the diversity of these traits within the population is primarily influenced by genetic factors. Quantitative character is controlled by many genes and is influenced by environmental factors. Estimating heritability values is

utilized to ascertain the contribution of genetic factors to the observed phenotype (Ketthaisong et al. 2014). Broad-sense heritability (h^2_{bs}) is the value of the results of comparing the total genotypic variance and the phenotypic variance. Heritability can indicate whether a trait is more influenced by genetic factors or environmental (non-genetic factors) (Hallauer et al. 2010). By combining the coefficients of genetic diversity, phenotypic diversity, and heritability values, an overview of the selection program to be implemented can be obtained. Magar et al. (2021) explained that a heritability value greater than zero indicates that parental variables are more easily passed on to their offspring and predicts the progress of selection.

Cluster analysis of various lines of waxy corn

Cluster analysis aims to group observational objects or variables based on their characteristics, and each variable has similar properties and is closest in similarity to grouping in the same cluster. The euclidean distance shows the distance between one genotype and another. The smaller the euclidean distance, the closer or more similar a genotype is to another genotype (Tan et al. 2022).

Cluster analysis based on qualitative and quantitative characters divided 18 genotypes of waxy corn into three main clusters (similarity 18.34%) showed on Figure 2. The main characteristics that distinguish the 3 clusters include ear weight with husk, ear length, ear length with kernels, stem diameter, plant height, and ear height. Cluster 1 consists of five genotypes, namely JPS-13-16-12-10 (G1), JPS-13-16-12-12 (G5), JPS-13-16-12-13 (G8), JPS-13-16-12-3 (G15), and JPS-13-6-5-5 (G6) with a similarity level of 38.29 to 72.10%. Genotypes belonging to cluster 1 had low ear weight with husk, short ear length, small stem diameter, plant height and high ear height.

Table 8. Genetic parameters of various lines of waxy corn

Characters	Means	S.E	σ^2_e	σ^2_g	σ^2_p	Hbs	GCV	PCV
Plant height	161.10	25.01	346.32	814.18	1160.50	0.70	31.10	34.67
Ear height	72.83	18.14	196.07	536.20	732.27	0.73	52.38	57.28
Diameter of stem	2.10	0.21	0.03	0.08	0.11	0.73	26.29	27.54
Number of leaf	11.34	0.83	0.26	1.50	1.76	0.85	25.54	27.25
Leaf length	76.87	12.74	27.60	60.10	87.70	0.69	11.14	14.08
Leaf width	8.49	1.01	0.25	2.07	2.32	0.89	9.03	9.89
Anthesis date	52.29	2.92	3.94	4.08	8.02	0.51	3.88	5.44
Silking date	52.81	2.09	2.39	1.90	4.29	0.44	2.61	3.92
Anthesis-silking interval	1.69	1.06	0.78	0.33	1.11	0.30	34.32	62.64
Tassel length	34.96	4.71	17.54	24.21	41.75	0.58	38.17	39.53
number of tassel branches	12.81	1.96	1.58	8.41	9.99	0.84	17.71	21.15
Ear weight husk	122.03	27.11	349.60	1440.54	1790.14	0.80	31.80	37.16
Ear weight unhusked	58.42	20.81	183.19	936.35	1119.54	0.84	13.49	15.81
Ear length	12.91	2.12	1.12	11.53	12.65	0.91	10.81	11.71
Ear length with kernel	10.78	1.79	1.05	7.58	8.63	0.88	10.08	12.18
Ear diameter	3.48	0.34	0.09	0.15	0.24	0.63	16.93	17.93
Number row of ear	12.18	0.75	0.24	1.21	1.45	0.83	14.08	18.48
Number kernel of row	18.01	4.17	3.41	47.26	50.67	0.93	22.64	24.67

Note: SE: standard error, σ^2_e : Environment variance, σ^2_g : Genetic variance, σ^2_p : Phenotypic variance, Hbs: Heritability broad sense, GCV: genotypic coefficient of variation, PCV: phenotypic coefficient of variation, CV: coefficient of variation

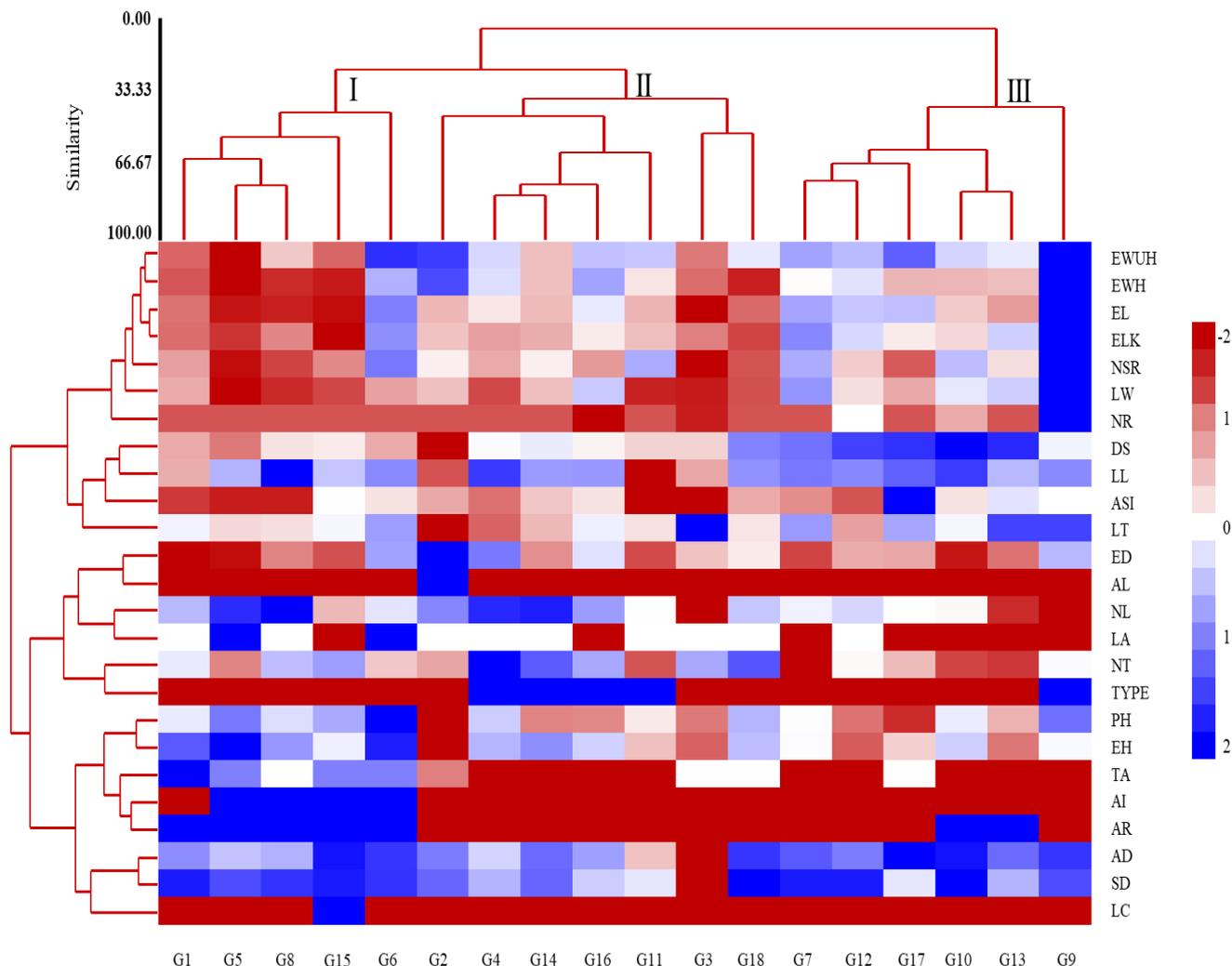


Figure 2. Hierarchical clusters showing similarities between 18 genotypes of waxy corn based on agronomic characteristics using the complete linkage method based on the euclidean method. EWUH: Ear weight unhusked, EWH: Ear weight husk, EL: Ear length, ELK: Ear length with kernel, NSR: Number kernel of row, LW: Leaf width, NR: Number of row kernel on ear, DS: Diameter of stem, LL: Leaf length, ASI: Anthesis silking interval, LT: Length of tassel, ED: Ear diameter, AL: Anthocyanin on leaf, NL: Number of leaf, LA: Leaf angle, NT: Number of tassel branch, TYPE: Type shape of kernel, PH: Plant height, EH: Ear height, TA: Tassel of angel, AI: Anthocyanin on internode, AT: Anthocyanin on tassel, AR: Anthocyanin on root, AD: Anthesis date, SD: Silking date, LC: Leaf curvature

Cluster 2 consisted of seven genotypes namely JP-30-2-5K-5 (G2), JPM-1-6P-3 (G4), JPM-1-6P-4 (G14), JPM-1-6K-1 (G16), JPM-1-2P-3 (G11), JPS-13-16-12-7 (G3), and JPS-13-16-12-20 (G18) with a similarity rate of 31.94% to 76.76%. Genotypic characters from cluster 2 exhibited relatively large ear weight with husk, relatively low ear length, sufficiently large stem diameter, a maximum number of tassel branches, and relatively high plant height and ear height. Cluster 3 consists of six genotypes, namely JPS-13-6-1P-10 (G7), JPS-13-6-1K-1 (G12), JPS-13-6-1K-17 (G17), JPS-13-6-1P-20 (G10), JPS-13-6-1P-15 (G13), and JPM-1-5-19 (G9) with a similarity level of 35.89% to 74.77%. Genotypes in cluster 3 exhibited the most substantial ear weight and stem diameter among all clusters. The ear length was relatively long, while both the plant height and ear height were the shortest.

The cluster analysis method showed phenotypic differences among the tested genotypes. Plant phenotype is the result of the interaction between genotype and environmental factors. When environmental factors have a large influence, grouping according to plant phenotypes cannot properly reflect genotypic differences between plant germplasm (Islam et al. 2020). Based on the cluster analysis results of all genotypes, most of the variability in the various characters observed was influenced by genetic factors. The wide genetic diversity between these inbred lines can increase the genetic potential of the characters from the crosses so that they can be utilized for hybrid corn breeding programs (Maruthi and Rani 2015).

Based on the cluster analysis results, it was suspected that the F1 hybrid resulting from crossing genotypes JPM-1-5-9 with JPS13-6-5-5 was a hybrid that could produce

the best ear character. The parental genotype JPM.1.5.9 comes from a different cluster from JPS-13-6-5-5 (Figure 2) but both have the same characteristics of ear weight with husk, ear weight unhusked, number of rows of kernel, number of kernel per row, ear length the largest (Table 5). Crosses between genotypes with large genetic distances based on cluster differences can produce high yields (Dermail et al. 2020) In addition, high yields are also largely determined by the high yields of the two parents selected (Devi et al. 2017)

In conclusion, there were differences in qualitative and quantitative characters between the tested waxy corn genotypes. The characters of plant height, ear height, stem diameter, number of leaves, tassel length, ear weight husk, and number of kernels per row had broad heritability values and high coefficients of genetic diversity. In all traits tested, PCV is larger than GCV, indicating that there was an environmental influence. The 18 waxy corn genotypes can be used as breeding populations to improve ear character and production. We recommend that parents for waxy corn hybrids should be selected from different clusters/groups. By utilizing different genetic backgrounds, it is hoped that a superior waxy corn hybrid will be obtained.

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