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Genetic Parameters Estimation of Unipa Red Waxy Corn Intercropped with Peanuts in Susweni Land, East Manokwari District

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A R T I C L E I N F O

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A B S T R A C T

Corn is the second staple food after rice in Indonesia. The productivity of dry corn kernels with a water content of 14 percent in West Papua was 6,481 tons in 2022 and decreased to 4,623 tons in 2023. Estimating genetic parameters is essential before improving any trait. Genetic parameters in plants typically include the genetic diversity coefficient, heritability, and correlation between plant traits. Observation data were statistically analyzed using analysis of variance (ANOVA). The ANOVA results were used to obtain values for the Variance Partition, Genetic Coefficient of Variation (GCV), Phenotype Coefficient of Variation (PCV), and Heritability. The correlation between traits was analyzed using the Costat program version 6.311. The observations revealed that the PCV was higher than the GCV in corn plants, indicating that environmental factors more dominantly influence visual character diversity (phenotype). Some narrow sense heritability values were negative for several traits of the Unipa glutinous red corn plants. The weight of corn cob showed a very high correlation without the husk and with the husk (r=0.93), while a very low correlation was observed between the width of the leaves at 7 WAP and the diameter of the stem at 1 WAP (r=-0.38)

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INTRODUCTION

Corn (*Zea mays* L.) is a beneficial food crop for human and animal consumption. In Indonesia, it ranks as the second most important staple food after rice. Globally, corn holds the third position among staple foods following wheat and rice (Utari, 2023; Prakoso, 2017). Corn is a significant commodity that contributes substantially to the country's foreign exchange, and the export market for corn can boost economic resources for the people of Indonesia.

Based on data from the Central Statistics Agency of Indonesia (2023), the harvest area of shelled corn was 2.49 million hectares in 2023, which is estimated to decrease by 0.28 million hectares or equivalent to 10.03 percent compared to the harvest area in 2022, which was 2.76 million hectares. Consequently, the productivity of dry-shelled corn with a 14 percent water content in 2023 was 14.46 million tons, a decrease of 2.07 million tons or 12.50 percent compared to the 16.53 million tons of corn production in 2022.

The productivity of dry corn kernels with a water content of 14 percent in West Papua was 6,481 tons in 2022 and decreased by 4,623 tons in 2023 (Central Statistics Agency of Indonesia, 2023). Based on these data, several efforts can be made to achieve high corn plant productivity in West Papua. These include the use of adequate agricultural tools, proper application of fertilizers, effective use of pesticides or pest and disease control, and the use of superior seeds. According to Yuwariah *et al*. (2022), the opportunity to increased corn productivity can be optimized by expanding the planting area, increasing productivity through superior varieties, changing planting patterns, controlling plant pest attacks, and improving post-harvest handling.

Genetic variation in a plant significantly aids in streamlining selection activities. A relatively large genetic variation in a population indicates that individuals within the population are highly diverse and have a greater chance of obtaining the desired genotype. The estimation of genetic parameters needs to be done before improving a trait to increase plant yield. Genetic parameters in plants usually include estimating the value of the genetic diversity coefficient, heritability and correlation between traits (Mustakim, 2019).

In selection activities on plants, the estimation of genetic parameters plays a very important role. By estimating genetic parameters, genetic variability can be determined, which includes genetic variability values, genotype, phenotype and environmental variations, heritability values, genetic progress, phenotype and genotype correlation values. These components are essentials as basic information for plant breeders in their efforts to improve plant characters through subsequent plant breeding activities.

The phenotypic appearance of a plant character is influenced by genetic factors, environmental factors and the interactions between genetic and environmental factors. Through genetic parameter estimation, the values of genotype, phenotype, and environmental variations can be separated and estimated between individually, facilitating the measurement of genetic variability, heritability and genetic progress in a plant. Additionally, genetic parameter estimation related to the characterization of plant traits is a major component to allign with desired outcomes (Saefudin and Wardiana, 2011).

Efforts to increase corn productivity play a crucial role in the development of food crops. One promising variety is local corn, which hold great potential for cultivation due to the growing demand and consumption of local corn as a food ingredient. Besides being a staple food for human consumption, local corn is also a main raw material in the production of poultry feed in Indonesia. According to Tarigan (2021), the types of corn commonly used by people in several areas of West Papua Province to meet their food needs include local orange and white corn, as well as red corn. Several areas in West Papua that possess red corn germplasm with development potential are Anggi District, Kebar District, Prafi District and several other areas. Unipa glutinous red corn has been developed by Mawikere *et al*. (2014), but its yield has not been tested in various locations. This study aims to analyze the genetic parameters of Unipa glutinous red corn intercropped with peanuts and monocultures which include the genetic diversity coefficient, phenotypic diversity coefficient, heritability, and correlation between characters.

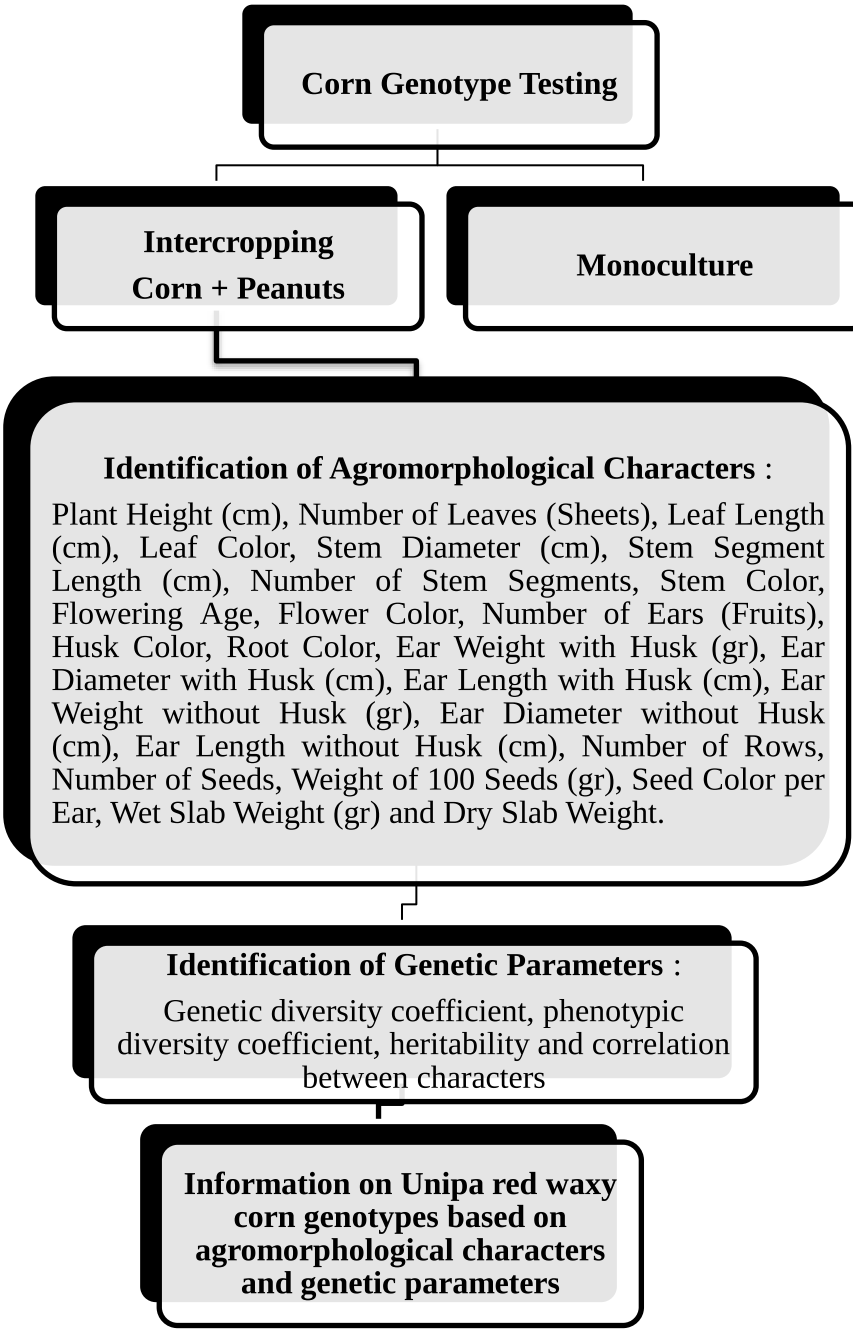
LITERATURE REVIEW

Research Hypothesis

H0 : There is no difference in the genetic parameters of the four genotypes of UNIPA glutinous red corn when intercropped with peanuts versus grown in monoculture.

H1 : There are differences in the genetic parameters of the four genotypes of UNIPA glutinous red corn when intercropped with peanuts versus grown in monoculture.

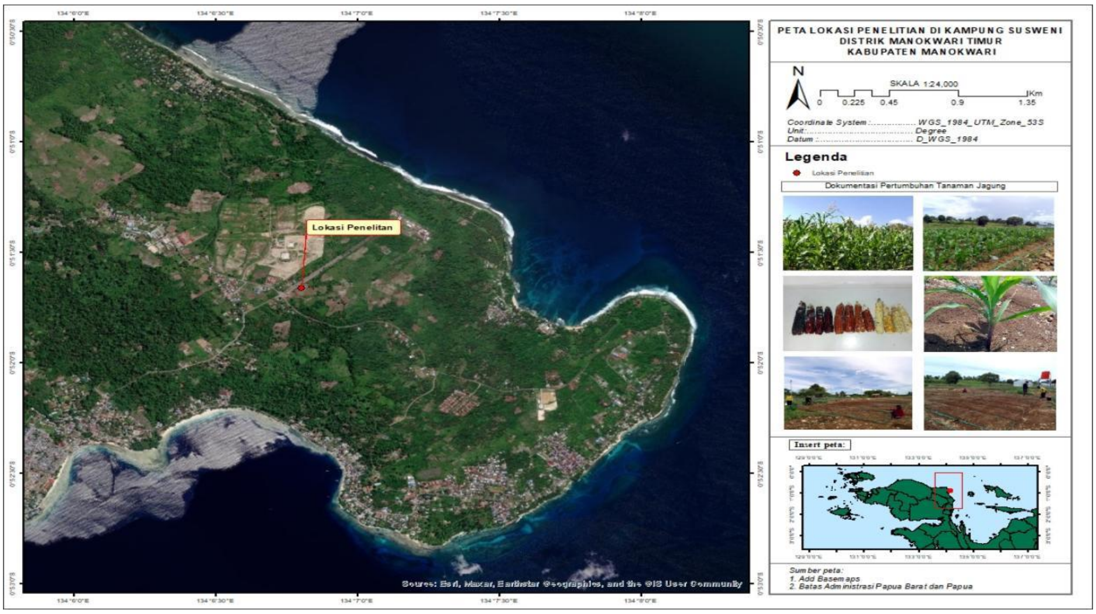
Research Framework



Picture 1. Conceptual Framework

METHODOLOGY

This research was conducted in Susweni land, spesifically in Susweni Village, East Manokwari District, Manokwari Regency. The research was carried out from August 2023 to January 2024.



Picture 2. Map of research location

The materials used in this study were the local corn seeds of Genotype 1 (G1), Genotype 2 (G2), Genotype 3 (G3), and Genotype 4 (G4), NPK fertilizer, organic fertilizer (compost), and furadan.

This study employed an experimental method and was designed using a Factorial Randomized Block Design with 2 factors. The first factor was the UNIPA glutinous red corn genotype, which includes Genotype I (G_1), Genotype II (G_2), Genotype III (G_3) and Genotype IV (G_4). The second factor consisted of two levels: (a) Intercropping pattern between four genotypes of UNIPA glutinous red corn and peanuts, and (b) Corn monoculture. The combination of treatments used is as follows:

- G_1M : Genotype 1 in Corn Monoculture
- G_1TS : Intercropping Genotype 1 Corn with Peanuts
- G_2M : Genotype 2 in Corn Monoculture
- G_2TS : Intercropping Genotype 2 Corn with Peanuts
- G_3M : Genotype 3 in Corn Monoculture
- G_3TS : Intercropping Genotype 3 Corn with Peanuts
- G_4M : Genotype 4 in Corn Monoculture
- G_4TS : Intercropping Genotype 4 Corn with Peanuts

Each treatment was repeated 3 times, resulting in 24 experimental units.

The research implementation commenced with land clearing, soil cultivation, plot creation, labeling, planting, fertilizer application, maintenance, harvesting, and observation. The size of the land used for the research was 25.5 m x 9 m (229.5 m²). Basic compost fertilizer was applied after soil cultivation at a rate of 12.5 kg per plot, followed by a resting period of one week before planting. NPK fertilizer was applied twice: the first application was given one week after planting the corn, and the second application was given in the fourth week after planting.

Peanut seeds were planted one week after the corn seeds. For each plot, 26 planting holes for corn and 24 planting holes for peanuts were prepared, with a planting distance of 60 cm x 50 cm. Three corn seeds were placed in each hole, with one plant removed after 1 WAP, leaving two plants per hole. Similarly, two peanut seeds were placed in each hole. Consequently, each plot contained 52 corn plants and 48 peanut plants.

Watering was carried out 1-2 times daily, in the morning and evening. Replanting of corn was done by removing three plants from each hole and transferring them to the holes of dead or non-growing plants. Replanting of peanut plants took place one week after the initial planting. Weeding involves removing and clearing unwanted plants (weeds) from the land.

Observation data were analyzed statistically using analysis of variance (ANOVA), presented in Table 1. If the treatment had a significant effect, it was continued with the Duncan Multiple Range Test (DMRT) with a 95% confidence level using the Costat version 6.311 program. The results of the ANOVA analysis were used to obtain the values of the Variance Partition, Genetic Coefficient of Variation (GCV), Phenotype Coefficient of Variation (PCV), and Heritability. The correlation between characters was also analyzed using the Costat version 6.311 program.

Table 1. Components of Variance Analysis

Source of Variation	**Degrees of Freedom**	**Sum of Squares**	**Mean Square**	**Middle Square of Expectations**
Group	r-1	SS 3		
Genotype (G)	v-1	SS 2	MS 2	$\sigma^2e + \sigma^2g$
Planting Pattern (PP)				
G x PP Interaction				
Error	(r-1)(v-1)	SS 1	MS 1	σ^2e
Total				

Based on the variant component, the variance partition values, which include genetic variance, environmental variance, and phenotypic variance, can be determined using the formula provided by Hartoko (2005) as follows:

- **Genetic Variance** : $\boldsymbol{\sigma}^2 g = \frac{M_2 - M_1}{r}$
- **Environmental Variance** : $\boldsymbol{\sigma}^2 e = M_1$
- **Phenotypic Variance** : $\boldsymbol{\sigma}^2 p = \boldsymbol{\sigma}^2 e + \boldsymbol{\sigma}^2 g$

Information:
$\sigma^2 p$: phenotypic variance
$\sigma^2 e$: environmental variance
$\sigma^2 g$: genetic variance
M_1 : mean square error
M_2 : mid-square of variety
r : number of repetitions

- **Genetic Coefficient of Variation:**
  The genetic coefficient of variation (GCV) is determined by the formula:

$$\boldsymbol{GCV} = \frac{\sqrt{\boldsymbol{\sigma}^2 g}}{\mu}\ \boldsymbol{x}\ \mathbf{100}\%$$

Information **:**
GCV : Coefficient Of Genetic Variation
μ : General Average
$\Sigma^2 g$: Genotypic Variance

The absolute value of the Genetic Coefficient of Variation Criteria according to Hartoko (2005) is low (0%-13.58%), rather low (13.58% - 31.68%), quite high (31.68% - 40.70%), and high (40.70% - 80.75%).

- **Phenotypic Diversity Coefficient**
  The Phenotypic Coefficient of Variation (PCV) is determined using the formula:

$$\boldsymbol{PCV} = \frac{\sqrt{\boldsymbol{\sigma}^2 \boldsymbol{p}}}{\mu}\ \boldsymbol{x}\ \mathbf{100}\%$$

Information:
PCV : Phenotypic Coefficient Of Variation
μ : General Average
$\Sigma^2 P$: Phenotypic Variation

The absolute value of the Phenotype Coefficient of Variation criteria according to Hartoko (2005) is low (0% - 10.64%), rather low (10.64 - 32.74%), quite high (32.74% - 40.64%) and high (40.64% - 87.40%).

- **Heritability**
  Heritability in a broad sense can be calculated by:

$$h^2(bs) : \frac{\boldsymbol{\sigma}^2 g}{\boldsymbol{\sigma}^2 p}$$

Information:
$h^2(bs)$: heritability in the broad sense
σ^2g : genetic variance
σ^2p : phenotypic variance

The heritability value criteria according to Pinaria *et al*. (1995) are high ($h^2 > 50\%$), medium ($20\% < h^2 < 50\%$), low ($h^2 < 20\%$).

- **Correlation between characters**

The correlation between plant characters is calculated using the following formula:

$$r(xy) = \frac{n\,(\sum xy) - (\sum x).(\sum y)}{\sqrt{n(\sum_X 2) - (\sum_X)2}\ .\ \sqrt{n\,(\sum y2) - (\sum y)2}}$$

Information:
R(xy) : Correlation Between Character X And Character Y
x : Character Value X
y : Character Value Y
n : Number of Characters

RESULTS

1. ***Genetic Coefficient of Variation and Phenotypic Coefficient of Variation***

The estimated variance values obtained from the analysis of variance can be partitioned into genetic variance, environmental variance, and phenotypic variance. Table 2 presents the values of genetic variance, environmental variance, phenotypic variance, genetic variance coefficient, and phenotypic variance coefficient for the four analyzed corn genotypes.

Table 2. Genetic Variation Values (Σ^2g), Environmental Variation (Σ^2e), Phenotype Variation (Σ^2f), Genetic Coefficient of Variation (GCV), and Phenotype Coefficient of Variation (PCV)

	σ^2g	**σ^2e**	**σ^2f**	**GCV (%)**	**PCV (%)**
Plant Height 1 WAP	0.02	0.03	0.05	0.08	0.23
Plant Height 3 WAP	0.25	0.86	1.11	0.26	1.16
Plant Height 5 WAP	-8.64	44.94	36.30	-2.11	8.88
Plant Height 7 WAP	-52.79	216.16	163.36	-4.07	12.59
Number of Leaves 1 WAP	0.00	0.02	0.02	0.00	0.07
Number of Leaves 3 WAP	-0.04	0.27	0.23	-0.07	0.40
Number of Leaves 5 WAP	-0.04	0.26	0.22	-0.05	0.24
Number of Leaves 7 WAP	0.02	0.07	0.08	0.02	0.09
Stem Diameter 1 WAP	2.83	0.00	2.83	98.65	98.72
Stem Diameter 3 WAP	0.00	0.01	0.01	-0.02	0.15
Stem Diameter 5 WAP	-0.01	0.04	0.03	-0.05	0.16
Stem Diameter 7 WAP	1.34	0.01	1.35	6.76	6.80
Leaf Length 1 WAP	0.16	0.22	0.38	0.28	0.65
Leaf Length 3 WAP	3.85	9.46	13.31	1.43	4.93
Leaf Length 5 WAP	-2.49	10.53	8.04	-0.43	1.40

Leaf Length 7 WAP	-0.83	9.69	8.87	-0.14	1.48
Leaf Width 1 WAP	0.00	0.01	0.01	0.03	0.09
Leaf Width 3 WAP	0.03	0.12	0.15	0.10	0.51
Leaf Width 5 WAP	-0.01	0.16	0.15	-0.01	0.24
Leaf Width 7 WAP	0.00	0.11	0.10	0.00	0.15
Segment Length	0.25	2.09	2.34	0.27	2.59
Number of Sections	-0.19	0.59	0.40	-0.22	0.47
Male Flowering Age	0.27	1.01	1.28	0.07	0.32
Female Flowering Age	-4.08	20.83	16.75	-0.79	3.23
Number of Cobs	-0.01	0.09	0.08	-0.08	0.63
Weight of Corncob with Husk	-0.54	223.97	223.43	-0.09	38.16
Diameter of Cob with Husk	2.03	42.70	44.73	0.47	10.42
Length of Corn Cob with Husk	-2.30	17.01	14.71	-0.84	5.35
Weight of Corncob Without Husk	-11.37	172.62	161.26	-2.79	39.58
Length of Corn Cob Without Husk	-1.84	6.83	4.99	-1.31	3.55
Diameter of Corn Cob Without Husk	-5.00	28.81	23.81	-1.46	6.97
Number of Rows of Seeds/Cobs	-0.08	0.34	0.26	-0.09	0.31
Number of Seeds/Cob	-217.29	1477.65	1260.36	-10.72	62.17
Weight 100 Seeds	0.64	3.00	3.64	0.37	2.14
Weight of Seed/Cob	-17.72	115.82	98.10	-4.09	22.66
Seed Weight/Plot	0.00	0.12	0.12	0.02	1.21
Seed Weight/Ha	0.00	0.18	0.19	0.03	1.51
Wet Plant Sludge Weight	-957.64	3579.01	2621.36	-42.80	117.14
Dry Weight of Plant Waste	-85.85	377.34	291.49	-11.32	38.42

Description: GCV: Genetic Coefficient of Variation (Hartoko, 2005): low: (0%-13.58%), rather low (13.58%-31.68%), quite high (31.68%-40.70%) and high (40.70%-80.75%); PCV: Phenotypic Coefficient of Variation (Hartoko, 2005): low (0%-10.64%), rather low (10.64%'-32.74%), quite high (32.74%-40.64%), high (40.64%-87.40%); and WAP: Week After Planting

2. ***Heritability Value***

The observation results indicated that the heritability values for each observed character ranged from -46.78% to 99.93%, with varying criteria from low to high based on Pinaria *et al*. (1995). The Unipa red waxy corn character with the lowest heritability value was the number of internodes (-46.78%), while the character with the highest heritability value was the stem diameter at 1 WAP

(99.93%). Table 3 presents the estimated heritability values for each character of the four analyzed corn genotypes.

Table 3. Heritability Estimate Value (%)

	h^2 (%)	**Criteria**
Plant Height 1 WAP	35.44	Currently
Plant Height 3 WAP	22.60	Currently
Plant Height 5 WAP	0	Low
Plant Height 7 WAP	0	Low
Number of Leaves 1 WAP	0	Low
Number of Leaves 3 WAP	0	Low
Number of Leaves 5 WAP	0	Low
Number of Leaves 7 WAP	18.95	Low
Stem Diameter 1 WAP	99.93	Tall
Stem Diameter 3 WAP	0	Low
Stem Diameter 5 WAP	0	Low
Stem Diameter 7 WAP	99.41	Tall
Leaf Length 1 WAP	42.82	Currently
Leaf Length 3 WAP	28.94	Currently
Leaf Length 5 WAP	0	Low
Leaf Length 7 WAP	0	Low
Leaf Width 1 WAP	37.50	Currently
Leaf Width 3 WAP	20.57	Currently
Leaf Width 5 WAP	0	Low
Leaf Width 7 WAP	0	Low
Segment Length	10.59	Low
Number of Sections	0	Low
Male Flowering Age	21.30	Currently
Female Flowering Age	0	Low
Number of Cobs	0	Low
Weight of Corncob with Husk	0	Low
Diameter of Cob with Husk	4.55	Low
Length of Corn Cob with Husk	0	Low
Weight of Corncob Without Husk	0	Low
Length of Corncob Without Husk	0	Low
Diameter of Corn Cob Without Husk	0	Low
Number of Rows of Seeds/Cobs	0	Low
Number of Seeds/Cob	0	Low
Weight 100 Seeds	17.50	Low
Weight of Seed/Cob	0	Low
Seed Weight/Plot	1.94	Low
Seed Weight/Ha	1.95	Low
Wet Plant Sludge Weight	0	Low
Dry Weight of Plant Waste	0	Low

Description: The h^2 criteria according to Pinaria et al. (1995) are: high ($h^2 > 50\%$), medium ($20\% < h^2 < 50\%$), and low ($h^2 < 20\%$); and WAP: Week After Planting.

3. *Correlation Analysis*

Correlation analysis between characters is used to determine the closeness of their relationship. Characters that are positively correlated with other characters exhibit directional growth; that is, as the value of one character increases, the value of the other character also increases, and vice versa.

The correlation between plant characters can be either positive or negative. Positive values indicate that the relationship between characters is in the same direction, while negative values indicate that the relationship is in the opposite direction. The correlation coefficient ranges from -1 to 1. A coefficient of 0 means there is no correlation between the characters. Coefficients close to -1 or 1 indicate a strong correlation. The criteria for the degree of closeness based on the correlation coefficient are as follows: 0: no correlation between two variables, 0 - 0.25: very low correlation, 0.25 - 0.5: moderate correlation, 0.5 - 0.75: high correlation, 0.75 - 0.99: very high correlation, while 1: perfect correlation (Sarwono, 2009).

Table 4. Correlation Between Plant Characters

	Y1	Y2	Y3	Y4	Y5	Y6	Y7	Y8	Y9	Y10	Y11	Y12	Y13	Y14	Y15	Y16	Y17	Y18	Y19	Y20	Y21	Y22	Y23	Y24	Y25	Y26	Y27	Y28	Y29	Y30	Y31	Y32	Y33	Y34	Y35	Y36	Y37
Y1-TT1MST	1																																				
Y2-TT3MST	0.24	1																																			
Y3-TT 5 MS	0.13	0.64***	1																																		
Y4-TT 7 MS	0.19	0.36	0.82***	1																																	
Y5-JD 1 MS	0.27	-0.03	-0.23	-0.09	1																																
Y6-JD 3 MS	-0.29	0.29	-0.14	-0.09	0.12	1																															
Y7-JD 5 MS	0.23	0.45*	0.64***	0.42*	-0.12	-0.29	1																														
Y8-JD 7 MS	0.14	-0.09	0.48*	0.47*	-0.11	0.34	0.44*	1																													
Y9-DB 1 MS	-0.12	0.10	-0.13	-0.08	-0.17	0.60**	0.46*	0.49*	1																												
Y10-DB 3 M	0.22	0.50*	0.70***	0.72***	-0.03	-0.18	0.52**	0.60**	-0.23	1																											
Y11-DB 5 MS	0.21	0.56**	0.80***	0.83***	-0.09	-0.06	0.50*	0.46*	-0.14	0.73***	1																										
Y12-DB 7 M	0.37	0.49*	0.57**	0.41*	0.14	-0.28	0.71***	-0.30	-0.33	0.42*	0.55**	1																									
Y13-PD 1 MS	0.58**	0.27	-0.04	-0.002	0.28	-0.17	0.14	0.01	-0.10	0.41*	-0.02	0.10	1																								
Y14-PD 3 M	0.21	0.74***	0.62**	0.56**	-0.08	0.18	0.43*	-0.12	0.18	0.64***	0.57**	0.32	0.48*	1																							
Y15-PD 5 M	0.3	0.43*	0.75***	0.63***	0.02	-0.37	0.52**	0.55**	0.43*	0.63***	0.56**	0.57**	0.12	0.29	1																						
Y16-PD 7 M	0.38	0.60**	0.78***	0.66***	-0.02	-0.31	0.57**	-0.38	-0.36	0.54**	0.62**	0.59**	0.14	0.45*	0.90***	1																					
Y17-LD 1 MS	0.27	0.15	-0.01	0.05	0.19	0.29	0.001	-0.08	0.21	0.25	-0.01	-0.18	0.53**	0.40	-0.08	-0.11	1																				
Y18-LD 3 MS	0.18	0.73***	0.54**	0.41*	-0.08	0.39	0.37	-0.12	0.32	0.51*	0.46*	0.29	0.31	0.77***	0.36	0.42*	0.38	1																			
Y19-LD 5 MS	0.3	0.69***	0.80***	0.63***	-0.23	-0.21	0.58**	-0.33	-0.19	0.70***	0.66***	0.57**	0.35	0.70***	0.70***	0.72***	0.09	0.60**	1																		
Y20-LD 7 M	0.45*	0.57**	0.67***	0.54**	-0.25	-0.33	0.69***	-0.29	-0.38	0.65***	0.69***	0.66***	0.21	0.42*	0.67***	0.71***	-0.02	0.41*	0.76***	1																	
Y21-PR	0.12	0.39	0.73***	0.68***	-0.27	0.01	0.45*	-0.26	0.02	0.58**	0.66***	0.34	-0.19	0.45*	0.48*	0.51*	0.07	0.40	0.39	0.55**	1																
Y22-JR	-0.43	0.16	0.17	0.23	-0.03	0.48*	0.01	0.05	0.37	0.17	0.24	-0.19	-0.02	0.42*	-0.21	-0.15	0.45*	0.28	-0.06	-0.09	0.51**	1															
Y23-JT	-0.04	-0.18	0.06	0.09	-0.18	-0.01	0.22	0.19	0.13	0.05	-0.001	-0.09	-0.14	0.05	-0.22	-0.18	0.13	-0.05	-0.12	0.03	0.26	0.16	1														
Y24-BTK	-0.04	0.35	0.56**	0.57**	-0.13	0.17	0.22	-0.36	0.07	0.42*	0.46*	0.13	-0.11	0.44*	0.40	0.40	0.32	0.34	0.25	0.32	0.66***	0.55**	-0.04	1													
Y25-DTK	0.11	0.52**	0.48*	0.33	0.17	0.29	0.03	-0.10	0.11	0.32	0.23	0.17	0.08	0.38	0.41*	0.34	0.30	0.37	0.36	0.16	0.34	0.11	-0.14	0.50*	1												
Y26-PTK	-0.17	0.02	0.08	0.08	-0.09	0.03	-0.07	-0.05	0.20	0.01	-0.02	-0.06	0.17	0.33	-0.24	-0.22	0.21	-0.01	0.10	-0.23	-0.05	0.39	-0.24	0.29	0.18	1											
Y27-BTT	-0.07	0.35	0.61**	0.65***	-0.11	0.16	0.20	-0.36	0.10	0.49*	0.59**	0.16	-0.10	0.53**	0.38	0.37	0.30	0.44*	0.34	0.33	0.63***	0.55**	-0.05	0.93***	0.50*	0.37	1										
Y28-PTT	0.13	0.24	0.21	0.25	-0.06	0.16	-0.08	-0.13	0.18	0.26	0.24	-0.19	0.17	0.31	0.08	0.08	0.45*	0.18	0.05	0.11	0.28	0.53**	-0.21	0.76***	0.43*	0.43*	0.74***	1									
Y29-DTT	0.02	0.17	0.33	0.44*	-0.10	0.09	0.10	-0.24	0.07	0.32	0.31	-0.06	0.07	0.39	0.18	0.17	0.43*	0.19	0.16	0.14	0.34	0.50*	-0.10	0.84***	0.44*	0.50*	0.84***	0.89***	1								
Y30-JB	0.14	0.36	0.38	0.38	-0.06	0.10	0.10	-0.11	0.05	0.37	0.46*	-0.08	-0.002	0.27	0.40	0.44*	0.05	0.42*	0.26	0.34	0.43*	0.27	-0.04	0.45*	0.25	-0.2	0.53**	0.44*	0.38	1							
Y31-JBiT	-0.05	0.35	0.64***	0.73***	0.01	0.27	0.21	0.43*	0.22	0.45*	0.56**	0.09	-0.15	0.50*	0.33	0.37	0.33	0.42*	0.33	0.17	0.63***	0.51*	0.12	0.75***	0.53**	0.31	0.77***	0.45*	0.58**	0.44*	1						
Y32-100 Bi	-0.17	0.01	0.04	0.18	-0.33	0.55**	-0.11	0.21	0.53**	-0.11	0.06	-0.33	-0.31	0.11	-0.24	-0.19	0.07	0.26	-0.24	-0.19	0.28	0.51*	0.10	0.28	-0	0.04	0.26	0.32	0.30	0.1	0.24	1					
Y33-BBT	-0.13	0.31	0.53**	0.65***	-0.17	0.46*	0.14	-0.24	0.42*	0.31	0.47*	-0.06	-0.26	0.46*	0.16	0.21	0.29	0.47*	0.17	0.07	0.62**	0.62**	0.14	0.72***	0.39	0.26	0.73***	0.51*	0.60**	0.41*	0.89***	0.66***	1				
Y34-BBP	-0.08	0.12	0.44*	0.52**	-0.21	0.29	0.27	-0.04	0.36	0.26	0.34	-0.04	-0.26	0.36	0.01	0.07	0.25	0.29	0.07	0.10	0.61**	0.52**	0.73***	0.46*	0.18	0.01	0.45*	0.19	0.32	0.2	0.68***	0.50*	0.77***	1			
Y35-BBHa	-0.08	0.12	0.44*	0.52**	-0.21	0.29	0.27	-0.04	0.36	0.26	0.35	-0.04	-0.26	0.36	0.01	0.07	0.26	0.29	0.07	0.10	0.62**	0.52**	0.73***	0.46*	0.18	0.01	0.45*	0.20	0.33	0.2	0.68***	0.50*	0.77***	0.99***	1		
Y36-BBB	0.51*	0.40	0.53**	0.48*	-0.09	-0.39	0.59**	-0.22	-0.34	0.67***	0.62**	0.64***	0.33	0.42*	0.60**	0.58**	0.01	0.32	0.65***	0.84***	0.52**	-0.03	0.08	0.16	0.04	-0.3	0.18	-0.002	0.03	0.2	-0.02	-0.17	-0.08	0.06	0.06	1	
Y37-BBK	0.53**	0.30	0.49*	0.51*	0.05	-0.24	0.41*	-0.16	-0.22	0.52**	0.60**	0.58**	0.27	0.40*	0.54**	0.53**	0.10	0.45*	0.54**	0.66***	0.49*	0.07	-0.01	0.13	0.03	-0.3	0.23	-0.03	-0.01	0.1	0.04	0.01	0.03	0.07	0.07	0.85***	1

Description: TT: Plant Height, JD: Number of Leaves, DB: Stem Diameter, PD: Leaf Length, LB: Leaf Width, PR: Internode Length, JR: Number of Internodes, JT: Number of Ears/Plant, BTK: Ear Weight with Husk, DTK: Ear Diameter with Husk, PTK: Ear Length with Husk, BTT: Ear Weight without Husk, PTT: Ear Length without Husk, DTT: Ear Diameter without Husk, JB: Number of Seed Rows per Ear, JBiT: Number of Seeds per Ear, 100 Bi: Weight of 100 Seeds, BBT: Seed Weight per Ear, BBP: Seed Weight per Plot, BBHa: Seed Weight per Ha, BBB: Wet Sludge Weight, BBK: Dry Sludge Weight, WAP: Week After Planting, "*" Closely Related, "**" Very Closely Related, "-" Negatively Related.

DISCUSSION

The results of the GCV analysis in Table 4 show that the genetic diversity in four corn genotypes ranges from -42.80% to 98.65%, while the PCV value ranges from 0.07% to 117.14%. A high phenotypic diversity value in a plant character indicates that the character is more influenced by environmental factors than by the plant's genetic factors. The coefficient of genotype diversity in corn plants demonstrates that environmental influences are more dominant in the diversity of observed plant characteristics. Suliartini *et al*. (2023) noted that the high or low value of a plant's phenotypic diversity coefficient visually represents the diversity of a plant character. A low diversity coefficient value indicates that individuals in a plant population tend to be uniform, whereas a high diversity coefficient indicates high levels of diversity in the tested plants. The higher the phenotypic diversity coefficient value in a plant, the greater the chance of obtaining a good new generation. Conversely, a lower phenotypic coefficient value suggests a narrower chance of producing a good new generation from the plant.

Moderate value of the genotype diversity coefficient in corn plants shows that there is an influence of genetic and environmental factors that have the same proportion in influencing plant characteristics. Meanwhile, the value of the genotype diversity coefficient and the phenotype diversity coefficient in plants that are almost similar or close together indicate that the diversity in plant characters is more dominated by genetic factors originating from within the plant (Widyaningtyas *et al*., 2023). The value of the phenotype diversity coefficient that is higher than the genotype diversity coefficient in corn plants indicates that there is a visual character diversity (phenotype) in plants that is displayed more dominantly by environmental factors. If the degree of diversity in a population is greater, the effectiveness of selection for selecting a plant character that is the same as the will is greater, and the success in obtaining the desired character. However, this selection is very precarious because high environmental factors influence it. Therefore, it is necessary to analyze genetic parameter estimation in plants further using heritability values (Syukur *et al*., 2010).

In several observed traits of UNIPA glutinous red corn plants, there were several narrow sense heritability values that had negative values, namely plant height 5 WAP, plant height 7 WAP, number of leaves 3 WAP, number of leaves 5 WAP, stem diameter 3 WAP, stem diameter 5 WAP, leaf length 5 WAP, leaf length 7 WAP, leaf width 5 WAP, leaf width 7 WAP, number of segments, number of cobs, cob weight with husk, cob length with husk, cob weight without husk, cob length without husk, cob diameter without husk, number of seed rows per cob, number of seeds per cob, seed weight per cob, wet stalk weight, dry stalk weight and germination percentage. Anugrah (2018) added that this was caused by several influencing factors so that the heritability value in corn plants was negative, including the diversity of the growing environment which was different from the variety analyzed as well as the imbalance of research data and the statistical methods used were not appropriate so that they could not separate genetic and environmental variations effectively.

Heritability is a measure commonly used to show the proportion of genetic factors to environmental factors shown by a plant character. Heritability is also a genetic benchmark in plants that is used as a description of the ability of a plant genotype in a population to pass on the characters it has in its offspring. The value of heritability is a genetic component that shows how much a trait is passed down from a plant to its offspring (Sa'diyah *et al.*, 2013).

Genetic diversity and heritability in plants are crucial during the selection process. Heritability values can be used to guide plant selection, which will be more effective if a population exhibits wide genetic diversity and high heritability values. Plant characters with low to moderate heritability values should be selected first by the next generation to ensure the additive genes are well-fixed. It is important to estimate the heritability value of a plant's character to determine the progress of selection and whether the trait is primarily influenced by genetic factors within the plant or by environmental factors (Ansari *et al.*, 2004).

The selection of a desired plant character is more meaningful if the trait is easily inherited. The ease or difficulty of inheriting a plant character can be determined by its heritability value. The gene action of a plant trait resulting from a cross can be understood through its potential ratio, which shows the effect of gene action from the cross between the two parents on their offspring. The heritability value of a plant trait depends on the gene action controlling the trait. If the heritability of a trait in the narrow sense is high, the trait is typically controlled by additive gene action to a great extent. Conversely, if the narrow-sense heritability value is low, the trait is usually controlled by non-additive gene action (dominance or epistasis) to a significant extent. These plant characters are generally not easily inherited from the parents to their offspring (Sa'diyah *et al.*, 2016).

Based on research conducted by Anti (2023) on several genotypes of Unipa glutinous red corn planted in Nabire Regency, it was found that the morphological characteristics of the corn genotypes exhibited quite high variations. The corn similarity analysis results also showed high similarities, with a yield test ranging from 5.73 tons/ha to 6.76 tons/ha. The genetic parameter test results indicated that the heritability values of the corn plants varied from low to medium to high. A correlation coefficient test revealed that several planted genotypes had a fairly strong correlation (significantly positive) with values between 0.5-0.75 and a very strong correlation (very significant positive) with values between 0.76-0.99. These findings suggest that the UNIPA glutinous red corn genotype has great potential for development in Nabire Regency and other areas.

Kilala (2023) also noted that Unipa glutinous red corn planted in North Manokwari District, Manokwari Regency showed the most consistent results in both vegetative and generative plant growth. Additionally, Tarigan (2021) reported that the Unipa glutinous red corn planted in Moyang SP 2 Dusun Preparation Village, Prafi District, Manokwari, West Papua, exhibited high heritability values, with several characters positively correlated. Furthermore, research conducted by Pertiwi (2022) on Unipa glutinous red corn planted in

Oransbari District, South Manokwari Regency, demonstrated high corn productivity, ranging from 4.52 tons/ha to 6.46 tons/ha, with varying genetic parameter characteristics.

The highly correlated growth components include plant height at 7 WAP and plant height at 5 WAP (0.82), stem diameter at 5 WAP and plant height at 5 WAP (0.80), leaf length at 5 WAP and plant height at 5 WAP (0.75), leaf length at 7 WAP and plant height at 5 WAP (0.78), leaf width at 5 WAP and plant height at 5 WAP (0.80), stem diameter at 5 WAP and plant height at 7 WAP (0.83), leaf width at 3 WAP and leaf length at 3 WAP (0.77), leaf width at 7 WAP and leaf width at 5 WAP (0.76), and wet stalk weight and leaf width at 7 WAP (0.84).

Meanwhile, the highly correlated production components include cob length without husk and cob weight with husk (0.76), cob diameter without husk and cob weight with husk (0.84), weight of cob without husk and weight of cob with husk (0.93), number of seeds per cob and weight of cob with husk (0.75), diameter of cob without husk and weight of seed per cob (0.84), number of seeds per cob and weight of seed per cob (0.77), weight of seed per cob and number of seeds per cob (0.83), weight of seed per plot and weight of seed per cob (0.77), and weight of seed per hectare and weight of seed per cob (0.77) (Table 2). In general, positive correlations in plant growth indicate that an increase in growth trait components in corn plants will enhance their yield components. Plants with strong growth characteristics, such as plant height, number of leaves, stem diameter, leaf length, leaf width, length of internodes, number of internodes, wet stalk weight, and dry stalk weight, are better at increasing production. Plants that exhibit vigorous growth will grow taller and larger, allowing them to store more food reserves beyond their roots, which can help boost crop production (Pennita *et al*., 2020).

The growth components that are highly correlated include plant height 7 WAP and plant height 5 WAP (0.82); stem diameter 5 WAP and plant height 5 WAP (0.80); leaf length 5 WAP and plant height 5 WAP (0.75); leaf length 7 WAP and plant height 5 WAP (0.78); leaf width 5 WAP and plant height 5 WAP (0.80); stem diameter 5 WAP and plant height 7 WAP (0.83); leaf width 3 WAP and leaf length 3 WAP (0.77); leaf width 7 WAP and leaf width 5 WAP (0.76); wet stalk weight and leaf width 7 WAP (0.84). Meanwhile, the production components that are highly correlated are cob length without husk and cob weight with husk (0.76); cob diameter without husk and cob weight with husk (0.84); weight of cob without husk and weight of cob with husk (0.93); number of seeds per cob and weight of cob with husk (0.75); diameter of cob without husk and weight of seed per cob (0.84); number of seeds per cob and weight of seed per cob (0.77); weight of seed per cob and number of seeds per cob (0.83); weight of seed per plot and weight of seed per cob (0.77); weight of seed per ha and weight of seed per cob (0.77) (Table 4). In general, positively correlated plant growth can explain that an increase in the growth trait components in corn plants will increase the yield components of corn plants. Plants that have good growth components such as plant height, number of leaves, stem diameter, leaf length, leaf width, length of internodes, number of internodes, wet stalk weight, and dry stalk weight will be better in increasing production. Plants that have good growth will grow very well and become taller and bigger, so they can store more food reserves other than in the roots of the plant so that these plants can help increase crop production (Pennita *et al*., 2020).

Some growth components that are moderately correlated include the number of leaves at 5 WAP and plant height at 5 WAP (0.64), stem diameter at 3 WAP and plant height at 3 WAP (0.50), leaf length at 7 WAP and plant height at 7 WAP (0.66), and leaf length at 7 WAP and stem diameter at 7 WAP (0.59). Meanwhile, some moderately correlated production components are the weight of the cob with husk and the length of the segment (0.66), cob diameter without husk and cob length with husk (0.50), and the number of seeds per cob and cob diameter without husk (0.58).

Increasing plant height can lead to better absorption of sunlight, enhancing photosynthesis, which can then be translocated for seed formation in the plant's generative phase, thus increasing seed production (Herawati *et al*., 2018). Oktarina (2016) stated that plant height showing a positive correlation with yield has a relationship that ranges from quite close to very close in terms of weight, in a positive direction. This indicates that the higher the value of the growth and yield components, the higher the results obtained (Surtinah, 2018).

Improve the sentences: Furthermore, several growth components that have very low correlation are plant height 3 WAP and plant height 1 WAP (0.24); stem diameter 1 WAP and plant height 3 WAP (0.10); stem diameter 7 WAP and several leaves 1 WAP (0.14); leaf width 1 WAP and number of leaves 1 WAP (0.19); leaf width 1 WAP and stem diameter 1 WAP (0.21); length of segment and width of leaf 1 WAP (0.07). Meanwhile, several production components that have very low correlation are the weight of cob without husk and number of leaves 5 WAP (0.20); diameter of cob without husk and width of leaf 5 WAP (0.16); weight of 100 seeds and number of rows (0.14); diameter of cob with husk and number of segments (0.11); number of seeds per cob and number of cobs (0.12); seed weight per cob and leaf width 5 WAP (0.17).

Furthermore, several growth components have very low correlations: plant height at 3 WAP and plant height at 1 WAP (0.24), stem diameter at 1 WAP and plant height at 3 WAP (0.10), stem diameter at 7 WAP and number of leaves at 1 WAP (0.14), leaf width at 1 WAP and number of leaves at 1 WAP (0.19), leaf width at 1 WAP and stem diameter at 1 WAP (0.21), and length of segment and leaf width at 1 WAP (0.07).

Meanwhile, several production components have very low correlations: the weight of cob without husk and number of leaves at 5 WAP (0.20), cob diameter without husk and leaf width at 5 WAP (0.16), weight of 100 seeds and number of rows (0.14), cob diameter with husk and number of segments (0.11), number of seeds per cob and number of cobs (0.12), and seed weight per cob and leaf width at 5 WAP (0.17).

Seed weight is a key indicator in assessing growth and production capacity. Correlation results show that seed weight is correlated with plant height and stem internode length. These results indicate that taller corn plants and longer stem internodes produce higher seed weights per plot and per hectare, consistent with findings by Ariyanti *et al*. (2018).

This is due to several factors:

1) Taller plants usually have more biomass stored in the stem, which can produce more seeds per plant per hectare (Proulx, 2021);
2) Taller plants can capture more sunlight, which is important for photosynthesis and overall plant growth (Anten, 2005).

In selecting the highest-yielding genotypes, studying correlations provides reliable information about the nature, extent, and direction of crop selection. Understanding the correlation between yield attributes and their components is very helpful in understanding the relationship between traits used to obtain better yields. Correlation analysis can be used to determine the pattern of the relationship between production and quantitative characteristics in plants (Pennita *et al*., 2020).

CONCLUSION AND RECOMMENDATION

The coefficient of genotype diversity in corn plants shows that the influence of the growing environment is more dominant in the diversity of observed plant characteristics. The character of Unipa glutinous red corn that has the lowest heritability value is the number of internodes (-46.78%) and the character with the highest heritability value is the stem diameter 1 WAP (99.93%). In several traits of Unipa red waxy corn plants observed, several narrow sense heritability values are negative. This is due to the occurrence of several influencing factors so that the heritability value in corn plants is negative, including the diversity of the growing environment that is different from the variety analyzed and the imbalance of research data and the statistical methods used are not appropriate so that they cannot separate genetic and environmental variations effectively. The weight of the cob shows a very high correlation without the husk and the weight of the cob with husk (r = 0.93) and a very low correlation is the correlation between the width of the leaf 7 WAP with the diameter of the stem 1 WAP (r = -0.38).

FURTHER STUDY

Further study is required to examine the morphology and yield of four Unipa red waxy corn genotypes intercropped with peanuts in various regions.

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