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Screening for Resistance in New Hybrid Maize (*Zea mays* L.) Genotypes to Downy Mildew (*Peronosclerospora spp.*)

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Abstract

Downy mildew in maize plants (*Peronosclerospora* spp.) is a major disease that reduces maize productivity. The use of resistant varieties is a sustainable solution for managing the development of this disease. This research seeks to evaluate the resistance of hybrid maize genotypes to downy mildew under strong natural infection pressure in an endemic field environment. The study was conducted from July to October 2024 in an area endemic to maize downy mildew, namely Rambai Village, South Pariaman District, Pariaman City, West Sumatra Province. This study used a Randomized Block Design (RBD) with three replications. A total of 22 maize genotypes were used in this study, comprising 20 test genotypes and 2 comparison varieties: the P32 maize hybrid and the Sukmaraga composite. Downy mildew screening was performed using spreader rows as the inoculum source. Data were analyzed using analysis of variance (ANOVA) based on a randomized block design, and mean comparisons were performed using Tukey's Honestly Significant Difference (HSD) test at the 5% level when genotype effects were significant. The results showed that genotype effects on disease incidence and severity were significant at 21 and 35 days after planting, but not significant at 28 and 42 days after planting. Nine test genotypes were classified as very resistant, while the remaining eleven test genotypes and the two check varieties were classified as resistant. Genotype G8 was classified as very resistant, with the lowest incidence (19.67%) and severity (5.96%). Other genotypes classified as very resistant were HUA18 (G18), HUA1 (G1), HUA15 (G15), HUA9 (G9), HUA2 (G2), HUA19 (G19), HUA16 (G16), and HUA6 (G6). These findings suggest that genotypes classified as very resistant and resistant should be further evaluated, particularly through preliminary yield trials to assess plant performance and yield potential.

Keywords: Disease Resistance, Incidence, Plant Breeding, Selection, Severity

1. Introduction

Maize (*Zea mays* L.) is among the most significant grain crops worldwide, contributing substantially to global food supplies and agricultural-based economies (Saijo, 2022). According to the United States Department of Agriculture (USDA) (2025), total world maize production reached 1.23 billion metric tons in the 2024/2025 planting season. This confirms its strategic role in the food, feed, and industrial systems, as well as its connection to food security and sustainable development (Kulsum et al., 2024). In Indonesia, maize serves as a strategic food commodity with yields of 5-7 tons per hectare. It is a major source of feed, carbohydrates, and protein (Makmur & Sainuddin, 2020). The growth in maize consumption in Indonesia is expected to continue, driven by population growth and the development of the nutrition and livestock feed sectors. This underscores the need for sustainable innovation to meet national maize targets (Kalqutny & Pakki, 2020).

Despite its importance, maize production is frequently constrained by biotic stresses, particularly plant diseases, which cause substantial yield losses and reduce production stability. One of the most destructive diseases affecting

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maize in Indonesia is downy mildew caused by *Peronosclerospora* spp. Yield losses due to downy mildew may reach 50–80% in major maize-producing regions such as East Java, South Sulawesi, and West Kalimantan (Pakki, 2017; Saijo, 2022). Three major species, namely *Peronosclerospora maydis, P. philippinensis, and P. sorghi*, have been identified in Indonesia, each showing distinct regional distributions (Ginting et al., 2020; Muis et al., 2023). Among these, *P. maydis* is considered the most aggressive and may cause complete crop failure if not properly managed (Muis et al., 2013).

Plant diseases remain a fundamental challenge in crop production systems, particularly in tropical environments where climatic conditions favor pathogen development. Disease incidence and severity are strongly influenced by interactions among host, pathogen, and environment, especially in endemic areas. Consequently, plant disease control efforts are generally directed toward suppressing pathogen development and reducing inoculum sources, while managing host and environmental factors to keep losses below economic thresholds. However, many control measures, including chemical and cultural practices, often provide inconsistent results and raise economic and environmental concerns. Therefore, the development of effective, efficient, and sustainable disease management strategies remains a critical priority. Among available approaches, the use of resistant varieties is regarded as the most strategic, economical, and environmentally friendly option (Mirsam et al., 2023; Ulhaq & Masnilah, 2019).

Given the economic importance of maize and the persistent threat of downy mildew in endemic regions, evaluating resistance in newly developed hybrid genotypes is highly relevant.

This study is a continuation of previous breeding stages that generated 20 single-cross maize hybrid combinations from five inbred lines (Hidayatullah et al., 2023, 2025). However, the resistance level of these hybrid combinations to downy mildew under natural infection pressure in an endemic field has not been specifically evaluated. Therefore, this study aimed to assess the resistance level of new hybrid maize genotypes to downy mildew under endemic field conditions in Pariaman City, West Sumatra. The results are expected to provide a scientific basis for selecting resistant hybrid genotypes and identifying promising candidates for further yield evaluation and maize breeding programs targeting downy mildew resistance.

2. Material and Methods

The research was carried out between July and October 2024 within a region affected by maize downy mildew (Dewi et al., 2021, 2022), located in Rambai Village, South Pariaman District, Pariaman City, West Sumatra Province (0°37'18.9 "S, 100°10'04.3" E; 7 m above sea level). According to data from the Meteorology, Climatology, and Geophysical Agency of Indonesia (BMKG) from the Jalan Baru rainfall station (July-October 2024), total rainfall reached 1882 mm across 57 rainy days, with the highest monthly precipitation in August (935 mm). These conditions provided a favorable environment for the natural development of downy mildew.

The research site is presented in Figure 1.

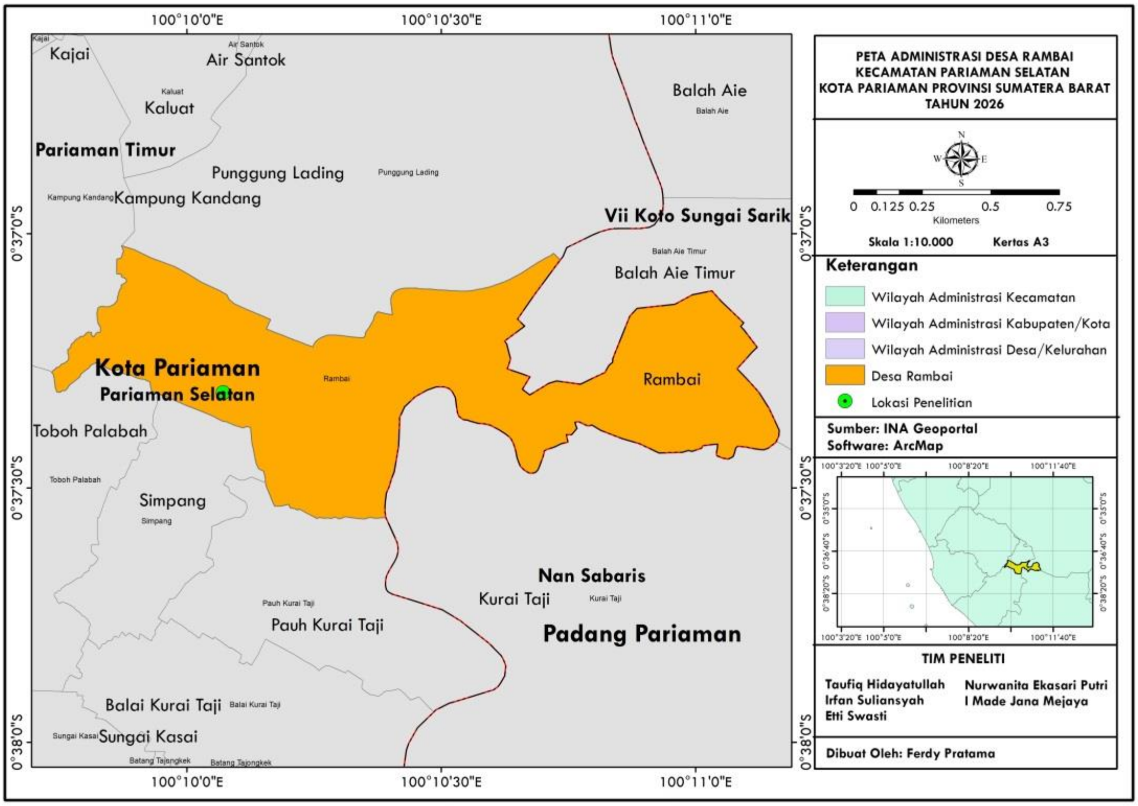


Figure 1. Research location in Rambai Village, South Pariaman District, Pariaman City

This study employed a Randomized Block Design (RBD) with a single factor, genotype, comprising 22 treatments and three replications.

A total of 22 maize genotypes were evaluated, comprising 20 candidate single-cross hybrid genotypes and 2 check varieties: the hybrid maize variety P32 and the composite variety Sukmaraga. The description of the test genotypes used is presented in Table 1.

Table 1. Description of maize genotypes tested

Genotype Code	Hybrid Code	Crossing		Description
		Female	Male	
G1	HUA1	Mz2	Mz1	Single-Cross Hybrid
G2	HUA2	Mz3	Mz1	Single-Cross Hybrid
G3	HUA3	Mz4	Mz1	Single-Cross Hybrid
G4	HUA4	Mz5	Mz1	Single-Cross Hybrid
G5	HUA5	Mz3	Mz2	Single-Cross Hybrid
G6	HUA6	Mz4	Mz2	Single-Cross Hybrid
G7	HUA7	Mz5	Mz2	Single-Cross Hybrid
G8	HUA8	Mz4	Mz3	Single-Cross Hybrid
G9	HUA9	Mz5	Mz3	Single-Cross Hybrid
G10	HUA10	Mz5	Mz4	Single-Cross Hybrid
G11	HUA11	Mz4	Mz5	Single-Cross Hybrid
G12	HUA12	Mz3	Mz5	Single-Cross Hybrid
G13	HUA13	Mz2	Mz5	Single-Cross Hybrid
G14	HUA14	Mz1	Mz5	Single-Cross Hybrid
G15	HUA15	Mz3	Mz4	Single-Cross Hybrid
G16	HUA16	Mz2	Mz4	Single-Cross Hybrid
G17	HUA17	Mz1	Mz4	Single-Cross Hybrid
G18	HUA18	Mz2	Mz3	Single-Cross Hybrid
G19	HUA19	Mz1	Mz3	Single-Cross Hybrid
G20	HUA20	Mz1	Mz2	Single-Cross Hybrid
G21	P32	-	-	National Hybrid Maize (Check Variety)

G22	Sukmaraga	-	-	National Composite Maize (Check Variety)

Description: G: Genotype; HUA: Andalas University Hybrid; Mz: Maize (1: parent 1; 2: parent 2; 3: parent 3; 4: parent 4; 5: parent 5)

Each experimental plot, measuring 3.75 m × 2 m, was prepared using complete tillage. Each plot was considered as an experimental unit. Each plot consists of 5 (five) rows with a planting distance of 75 cm between rows and 20 cm between holes. Each plot contained 50 test plants, for a total of 3,300.

Sweet corn seeds were planted 2 weeks earlier as inoculum sources and arranged around the test plots at a 2 m spacing. Planting was carried out with the rows perpendicular to the test genotype rows. The plants were allowed to grow until they exhibited characteristic symptoms of downy mildew, thus serving as natural hosts for the tested genotypes.

The evaluated genotypes were planted when the severity of downy mildew on the spreader rows reached approximately 70%. The tested plants were planted in plots with two seeds per hole. Thinning was carried out at 14 days after planting (DAP) before the first fertilization, leaving one plant per hill. Fertilization was carried out at 14 DAP with NPK fertilizer (350 kg/ha) and urea (250 kg/ha), and at 30 DAP with urea fertilizer (100 kg/ha) (Azrai et al., 2016).

Plant maintenance was carried out mechanically, with pest control using insecticides as needed, but without fungicide application. This was done to ensure that genotype responses to natural *Peronosclerospora* spp. Infection could be observed without chemical disease control intervention. To assess the resistance of hybrid maize genotypes to *Peronosclerospora* spp. Infection: observations were made on the incidence rate and the level of damage (severity) of downy mildew in the test genotypes. Observations were made every week, starting at 21, 28, 35, and 42 DAP. The overall experimental procedure is summarized in the research flow diagram (Figure 2).

Observations of downy mildew incidence were conducted visually in the field, based on characteristic symptoms observed on the tested genotypes. The symptoms observed included systemic chlorosis on young leaves, stunted growth, and discolored leaves from the early vegetative phase. Incidence was calculated from infected plants using the equation reported by Setyawan et al.

$$\boldsymbol{I = \frac{a}{b} x \; 100\%}$$

I = Incidence;
a = number of infected plants;
b = number of plants observed.

The incidence values presented in this study represent the percentage of plants showing downy mildew symptoms at each observation time, not cumulative incidence over the entire observation period.

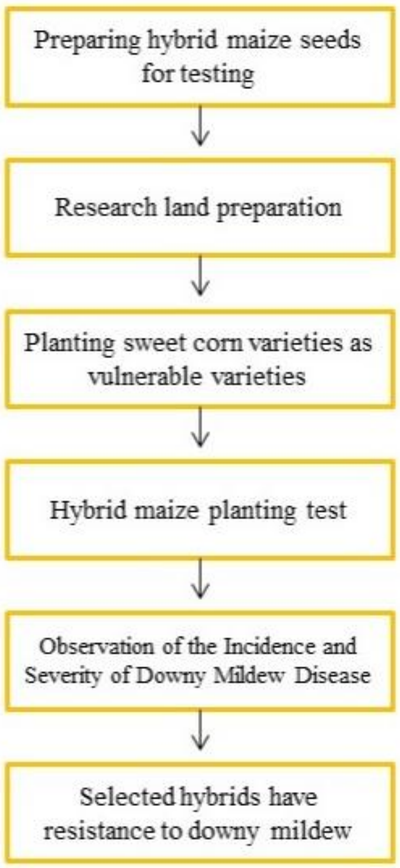


Figure 2. Research flow diagram

Disease severity is assessed based on a score of the level of downy mildew symptom damage on leaves. The scale for downy mildew disease assessment follows Matruti et al. (2013), as presented in Table 2.

Table 2. Downy Mildew Severity Scale

Scale	Description of symptoms
0	No symptoms
1	Leaf symptom area 1–25%
2	Leaf symptom area 26–50%
3	Leaf symptom area 51–75%
4	Leaf symptom area 76–100%

Severity was calculated for each category according to Ulhaq and Masnilah (2019):

$$DS = \frac{\sum(ni \; x \; vi)}{V \; x \; z} x \; 100\%$$

DS : Disease Severity;
Ni : Number of diseased leaves in category i;
vi : Scale value (0-4) of category i;
V : Highest scale value;
Z : Total number of leaves observed.

The resistance category of each evaluated genotype was determined descriptively based on the overall mean disease severity value according to Pajrin et al. (2013), as follows:

Very resistant (VR) = ≤ 10%
Resistant (R) = > 10–20%
Moderately resistant (MR) = > 20–40%
Susceptible (S) = > 40–60%
Very susceptible (VS) = > 60%

Data on disease incidence and severity were subjected to analysis of variance (ANOVA) based on a Randomized Block Design (RBD) with genotype as the single factor. The analysis was conducted on data from each observation time, namely 21, 28, 35, and 42 days after planting (DAP), to evaluate genotype responses to disease development over time. When the ANOVA indicated significant genotype effects, mean comparisons were performed using Tukey's Honestly Significant Difference (HSD) test at the 5% significance level. All data analyses were performed using Statistix 8.0 software.

3. Results and Discussion

3.1. Hybrid Maize Genotypes Resistance to Downy Mildew

The analysis of variance showed that maize genotypes' responses to downy mildew infection varied across observation time and disease parameters. Genotype effects on disease incidence and severity were significant at 21 and 35 days after planting (DAP), but not significant at 28 and 42 DAP. These results indicate that differences among genotypes were more clearly expressed during specific stages of disease development.

Based on the overall mean values across the four observation times, genotype HUA8 (G8) showed the lowest disease incidence (19.67%) and severity (5.96%) and was therefore categorized as very resistant. These values were lower than those of the reference genotypes, Sukmaraga (G22) and P32 (G21), which had the same incidence value of 31.33% and severity values of 14.29% and 18.71%, respectively. The highest disease incidence was recorded in HUA13 (G13) (41.67%), while the highest disease severity was recorded in P32 (G21) (18.71%). Complete data on the resistance responses of maize genotypes to downy mildew are presented in Table 3.

3.2. Disease incidence of downy mildew

The results of disease incidence (Table 4) show that eleven test genotypes (HUA8 (G8), HUA18 (G18), HUA1 (G1), HUA2 (G2), HUA15 (G15), HUA9 (G9), HUA6 (G6), HUA3 (G3), HUA16 (G16), HUA19 (G19), and HUA20 (G20)) showed lower incidence values compared to the two check varieties (P32 and Sukmaraga), which each had an incidence value of 31.33%. The incidence values of the eleven genotypes ranged from 19.67% to 30.83%. In addition, ten (10) of the eleven (11) genotypes also showed lower severity values compared to Sukmaraga (14.29%) and P32 (18.71%), except for genotype HUA3 (G3), which had a severity value of 16.08%, higher than Sukmaraga (G22) and lower than P32 (G21). The severity value range for these ten genotypes ranged from 5.96% to 11.17%.

Table 3. Percentage incidence and severity of downy mildew (*Peronosclerospora* spp.)

Genotype Code	Hybrid Code	Incidence (%)	Severity (%)	Resistance Category
G8	HUA8	19.67	5.96	VR
G18	HUA18	20.33	6.88	VR
G1	HUA1	20.67	7.13	VR
G15	HUA15	22.50	7.38	VR
G9	HUA9	25.50	7.63	VR
G2	HUA2	22.33	8.33	VR
G19	HUA19	30.17	9.00	VR
G16	HUA16	29.67	9.04	VR
G6	HUA6	27.33	9.58	VR
G12	HUA12	32.00	10.71	R
G7	HUA7	34.00	10.75	R
G5	HUA5	33.17	11.08	R
G20	HUA20	30.83	11.17	R
G10	HUA10	36.00	12.42	R
G4	HUA4	32.67	13.25	R
G13	HUA13	41.67	13.38	R
G11	HUA11	33.83	13.42	R
G14	HUA14	33.33	14.08	R
G22	Sukmaraga	31.33	14.29	R
G17	HUA17	38.33	14.54	R
G3	HUA3	27.33	16.08	R
G21	P32	31.33	18.71	R

Note: The overall average disease severity determines the resistance category.

Variations in the incidence and severity of downy mildew indicate that the pathogen in the experimental plot infected all test genotypes equally. Differences in infection intensity among genotypes indicate an interaction between varietal resistance and the pathogen's virulence, which helps determine the level of infection in the field (Kalqutny & Pakki, 2020). Differences in resistance responses among the 22 test genotypes are thought to be influenced by genetic variation, with resistant varieties harboring horizontal or vertical resistance genes (Mirsam et al., 2021). In addition to genetic factors, agroecosystem conditions that support pathogen development and the presence of abundant inoculum sources can also reduce resistance levels (Mirsam et al., 2023).

Overall, all test genotypes exhibit good resistance to *Peronosclerospora* spp. downy mildew disease, which is divided into two classifications: 9 genotypes are classified as "Very Resistant" (HUA8 (G8), HUA18 (G18), HUA1 (G1), HUA15 (G15), HUA9 (G9), HUA2 (G2), HUA19 (G19), HUA16 (G16), and HUA6 (G6)), and 13 genotypes classified as "Resistant" (HUA12 (G12), HUA7 (G7), HUA5 (G5), HUA20 (G20), HUA10 (G10), HUA4 (G4), HUA13 (G13), HUA11 (G11), HUA14 (G14), HUA17 (G17), HUA3 (G3), P32 (G21) and Sukmaraga (G22)). Although genotype effects were not significant at all observation times, the ANOVA indicated significant genotype effects at 21 and 35 DAP, suggesting that genotypic responses to downy mildew were expressed during specific stages of disease development. These findings suggest that most genotypes had good resistance potential and are suitable for further evaluation in maize breeding programs for downy mildew resistance.

The development of disease incidence and severity in maize genotypes infected with downy mildew is shown in Tables 4 and 5. Generally, disease symptoms were visible from 21 days after planting (DAP). Observations of twenty-two (22) maize genotypes up to 42 days after planting showed a fluctuating pattern with an increasing trend in the early weeks and a sharp decline in the fourth week.

In the first week, the initial incidence of disease was already apparent in most of the test genotypes. The highest value was recorded in HUA4 (G4) (60.67%), followed by HUA13 (G13) (58.67%) and HUA10 (G10)-HUA11 (G11) (54.67%). Conversely, the genotypes with the lowest values were HUA3 (G3) and HUA6 (G6) (22%), indicating a slower onset of infection. In the second week, most genotypes showed a decrease in incidence compared to the first week, such as HUA1 (G1) and HUA2 (G2). However, some genotypes, such as HUA6 (G6) and HUA17 (G17), experienced an increase in incidence. Entering the third week, there was a spike in incidence in certain genotypes, such as HUA3 (G3), HUA17 (G17), and HUA13 (G13), indicating a peak in disease development. This indicates that in the third week, there was an epidemic phase of downy mildew, during which infection and disease spread reached their peak. However, in the fourth week, most genotypes experienced a drastic decline in incidence. The most significant decline was seen in genotypes HUA1 (G1) and HUA2 (G2). This decline likely reflects the final phase of the disease cycle.

Table 4. The average percentage of downy mildew incidence at 21, 28, 35, and 42 DAP

Genotype Code	Hybrid Code	Observation 1 (21 DAP)	Observation 2 (28 DAP)	Observation 3 (35 DAP)	Observation 4 (42 DAP)
G1	HUA1	37.33^{a}	18.00	24.67^{b}	2.67
G2	HUA2	43.33^{a}	17.33	23.33^{b}	5.33
G3	HUA3	22.00^{a}	31.33	46.67^{ab}	9.33
G4	HUA4	60.67^{a}	30.00	34.67^{ab}	5.33
G5	HUA5	51.33^{a}	32.00	39.33^{ab}	10.00
G6	HUA6	22.00^{a}	35.33	40.67^{ab}	11.33
G7	HUA7	38.00^{a}	32.67	48.00^{ab}	17.33
G8	HUA8	40.00^{a}	15.33	20.00^{b}	3.33
G9	HUA9	34.00^{a}	28.67	35.33^{ab}	4.00
G10	HUA10	54.67^{a}	31.33	48.00^{ab}	10.00
G11	HUA11	54.67^{a}	29.33	39.33^{ab}	12.00
G12	HUA12	47.33^{a}	32.67	41.33^{ab}	6.67
G13	HUA13	58.67^{a}	36.00	63.33^{a}	8.67
G14	HUA14	47.33^{a}	32.67	42.67^{ab}	10.67
G15	HUA15	36.67^{a}	22.00	25.33^{b}	6.00
G16	HUA16	52.67^{a}	26.00	33.33^{ab}	6.67
G17	HUA17	46.67^{a}	40.00	55.33^{ab}	11.33
G18	HUA18	27.33^{a}	22.67	22.00^{b}	9.33
G19	HUA19	32.67^{a}	30.67	46.00^{ab}	11.33
G20	HUA20	45.33^{a}	26.00	29.33^{ab}	22.67
G21	P32	42.00^{a}	40.67	36.67^{ab}	6.00
G22	Sukmaraga	49.33^{a}	26.67	39.33^{ab}	10.00

Note**:** Means followed by the same letter in the same column are not significantly different according to Tukey's HSD test at the 5% level. Mean separation was performed only for observation times showing significant genotype effects in the ANOVA.

In general, HUA8 (G8) showed the lowest overall mean incidence across the four observation times, although its incidence varied among individual observation times. This indicates a tendency toward greater resistance to downy mildew. In contrast, genotypes such as HUA13 (G13) and HUA17 (G17) showed higher incidence values during the middle observation period, indicating a relatively weaker response to disease development.

3.3. Disease severity of downy mildew

Analysis of variance showed that genotype significantly affected downy mildew severity at 21 and 35 DAP, but not at 28 and 42 DAP. This indicates that genotypic differences in disease severity were more clearly expressed during the early and middle stages of disease development.

Furthermore, observations of downy mildew severity in 22 test genotypes (Table 5) up to 42 DAP showed varying patterns of development, with some genotypes experiencing a consistent decline in value, while others showed an increase in certain weeks.

In the first week, initial severity scores were high across several genotypes, including G22 (Sukmaraga), HUA4 (G4), and HUA11 (G11). In contrast, genotypes HUA6 (G6) and HUA3 (G3) showed the lowest initial scores, suggesting a relatively resistant initial response to infection. However, in the second week, there was a drastic increase in severity across several genotypes, including HUA3 (G3), HUA17 (G17), and P32 (G21). This shows that in the second week, some genotypes entered a critical phase of symptom development, coinciding with the pathogen's systemic infection phase. Conversely, genotypes HUA8 (G8) and HUA1 (G1) showed a significant decrease, indicating a greater ability to suppress symptom development. In the third week, severity decreased in many genotypes, except for a few that experienced a recurrence of increase, such as HUA13 (G13) and HUA3 (G3). Meanwhile, the fourth week showed a general downward trend in severity across almost all genotypes.

Several genotypes with low severity values in the fourth week were HUA8 (G8), HUA1 (G1), HUA15 (G15), and HUA16 (G16), indicating that these genotypes tended to maintain relatively low severity values until the end of the observation phase. These low-severity values contributed to their classification as very resistant. In contrast, the check variety G21 (P32) continued to show high values in the fourth week, despite a drastic decline from the second week. This indicates that P32 experienced early infection and maintained relatively high symptom levels throughout the observation period.

Table 5. The average percentage of downy mildew severity at 21, 28, 35, and 42 DAP

Genotype Code	Hybrid Code	Observation 1 (21 DAP)	Observation 2 (28 DAP)	Observation 3 (35 DAP)	Observation 4 (42 DAP)
G1	HUA1	15.67^{a}	4.50	7.00^{b}	1.33
G2	HUA2	14.50^{a}	8.33	5.83^{b}	4.67
G3	HUA3	6.50^{a}	31.17	13.67^{ab}	13.00
G4	HUA4	24.50^{a}	16.67	8.67^{ab}	3.17
G5	HUA5	20.50^{a}	9.67	9.83^{ab}	4.33
G6	HUA6	6.33^{a}	17.67	10.33^{ab}	4.00
G7	HUA7	12.83^{a}	12.67	12.17^{ab}	5.33
G8	HUA8	14.17^{a}	3.83	5.00^{b}	0.83
G9	HUA9	10.00^{a}	8.50	9.17^{ab}	2.83
G10	HUA10	19.50^{a}	13.67	12.50^{ab}	4.00
G11	HUA11	22.00^{a}	10.33	12.00^{ab}	9.33
G12	HUA12	18.67^{a}	10.17	10.33^{ab}	3.67
G13	HUA13	18.83^{a}	11.00	18.83^{a}	4.83
G14	HUA14	20.17^{a}	15.17	10.83^{ab}	10.17
G15	HUA15	13.00^{a}	7.17	6.83^{b}	2.50
G16	HUA16	17.00^{a}	8.00	8.67^{ab}	2.50
G17	HUA17	15.17^{a}	25.33	14.33^{ab}	3.33
G18	HUA18	8.17^{a}	7.50	7.83^{b}	4.00
G19	HUA19	10.17^{a}	8.33	11.50^{ab}	6.00
G20	HUA20	15.00^{a}	8.67	11.83^{ab}	9.17
G21	P32	18.33^{a}	40.83	9.33^{ab}	6.33
G22	Sukmaraga	26.67^{a}	9.83	9.83^{ab}	10.83

Description : 0-10 = Very resistant (VR), 10-20% = Resistant (R), 20 – 40% = Moderately resistant (MR), 40-60% = Susceptible (S), >60% = Very susceptible (VS). Means followed by the same letter in the same column are not significantly different according to Tukey's HSD test at the 5% level. Mean separation was performed only for observation times showing significant genotype effects in the ANOVA.

Fluctuations in downy mildew severity across observation times illustrate the dynamic development of the disease and indicate the period when symptom intensity was highest. Tables 4 and 5 show that symptoms were already visible at 21 DAP and increased in several genotypes at 28 and 35 DAP, indicating that the pathogen was actively developing during the early vegetative phase. Mirsam et al. (2023) reported that downy mildew incidence in maize genotypes may increase up to around 35 DAP, reflecting the period of active disease development. In addition, Sulfitri et al. (2024) showed that infection by *Peronosclerospora philippinensis* in maize can develop unevenly depending on environmental conditions and host susceptibility. Therefore, the fluctuation in incidence and severity observed in this study reflects the interaction among pathogen pressure, host genotype, and environmental conditions.

Weather factors also support the development of the disease. Weather conditions, particularly rainfall, appeared to support the development of downy mildew at the research site. This was reflected in the disease development pattern, which increased during August, when the highest rainfall was recorded at 935 mm (Figure 3). Mirsam et al. (2023) reported that humid conditions and high rainfall during certain periods favor sporulation and infection by Peronosclerospora maydis, thereby increasing disease severity. According to Hooda et al. (2018), all types of *Peronosclerospora* spp. require surface moisture for conidia germination and infection. Moderate rainfall was found to be most conducive to downy mildew development in maize. High rainfall and humidity are essential weather elements for the progression of epidemics. Conversely, in September and October, with lower rainfall (412 and 439 mm), disease development tended to decline.

Symptoms of *Peronosclerospora* spp. Disease incidence generally begins at 21 days after planting, with a mild category. Characteristic visual symptoms included systemic chlorosis ranging from pale yellow to silvery white, starting in young leaves and spreading symmetrically along the leaf veins due to systemic infection by *Peronosclerospora* spp. On the underside of the leaves, especially in the morning, fine grayish-white mycelium growth is visible, indicating the presence of the pathogen. This is consistent with what numerous previous researchers have reported: the initial symptom of downy mildew is the appearance of yellowish lines (chlorosis) parallel to the leaf veins, which then spreads to the entire leaf surface (Mirsam et al., 2023; Ulhaq & Masnilah, 2019). Previous microscopic descriptions have reported that *Peronosclerospora* spp. has conidiophores resembling stalks with round conidia at their tips (Mirsam et al., 2023).

The use of disease-resistant hybrid maize varieties is regarded as an affordable, eco-sustainable approach to managing major maize diseases. Genetic resistance represents one of the most cost-effective and efficient approaches to disease management in maize. Thus, genotypes showing low overall incidence and severity values, particularly HUA8 (G8) and HUA18 (G18), can be recommended as promising candidates for further evaluation as downy mildew-resistant hybrid maize genotypes adaptable to West Sumatra conditions.

This study provides important insights into downy mildew resistance; however, the findings are limited to a single location and season. Therefore, further evaluation of agronomic performance and yield potential across multiple locations is required.

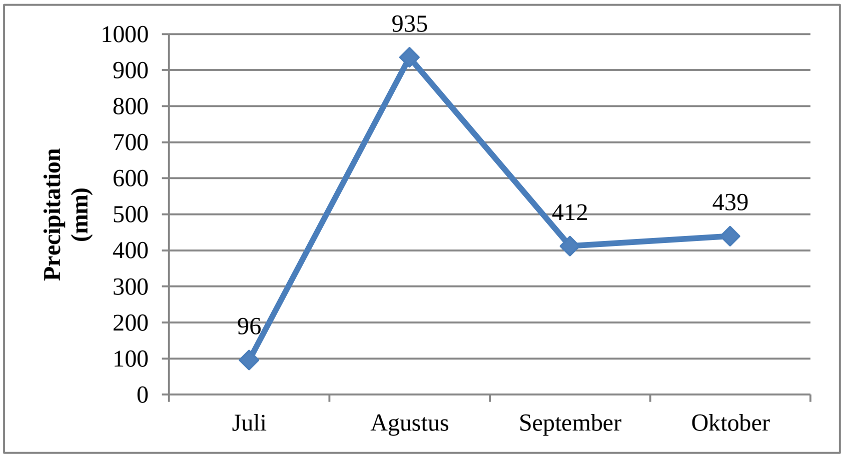
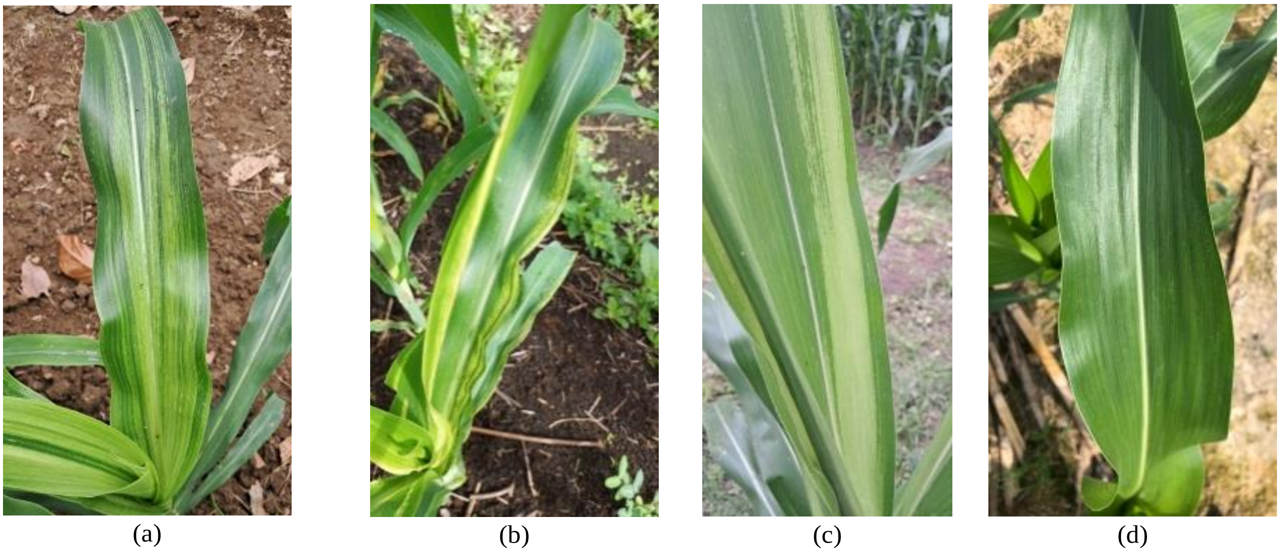


Figure 3. Precipitation at the research site from July to October 2024



(a) (b) (c) (d)

Figure 4. Comparison of maize leaf appearance between plants infected with downy mildew and healthy plants. (a–c) Leaves showing chlorotic streak symptoms caused by *Peronosclerospora* spp.; (d) healthy leaf.

4. Conclusion

All tested maize hybrid genotypes showed resistance responses to downy mildew under endemic field conditions. Genotypic differences were more clearly expressed at certain observation times, indicating that resistance response depended on the stage of disease development. Based on overall incidence and severity, HUA8 (G8) and HUA18 (G18) showed the lowest disease levels and were classified as very resistant. These genotypes are recommended as promising candidates for preliminary and advanced yield testing, multi-location evaluation, and as potential genetic sources in maize breeding programs to develop high-yielding, downy mildew-resistant hybrids.

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