

# Resistance Assessment of Hybrid Corn Genotypes to Major Corn Diseases and Its Effects on Disease Epidemic Components in South Sulawesi, Indonesia

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**Abstract.** The use of resistant varieties is one of approach that can be used in the management of the pathogen development. This study aimed to examine the resistance level of hybrid corn genotypes to the corn major diseases and to determine its effect on the components of the disease epidemic. Testing for the three major diseases was carried out using spreader row plants as an inoculum source. Parameters observed in this study were disease incidence for downy mildew (DM), disease severity for maydis leaf blight (MLB) and leaf rust (LR), disease development model, infection rate, area under the disease progress curve (AUDPC), protection index, and path analysis. The results showed that the HBC01 genotype had the lowest attack intensity to DM, MLB, and LR, namely 35.55%, 37.33%, and 25.33%, respectively. The disease epidemic components also showed that the HCB01 genotype has the lowest AUDPC value and infection rate with the highest protection index against DM, MLB, and LR. Furthermore, relative humidity, temperature, rainfall, and wind velocity were correlated in influencing the development of DM, MLB, and LR. The conclusion is that the hybrid corn genotype greatly influences the development of epidemics of DM, MLB, and LR.

Keywords: *Bipolaris*, disease epidemic, *Peronosclerospora*, *Puccinia*

## 1 Introduction

Corn is one of the most important food crops in the world, besides wheat and rice [1]. World demand for corn is estimated to increase to 3.3 billion tonnes by 2050 [2] and corn will become the largest producing crop globally in 2025. In Indonesia, corn is one of the most strategic food commoditie to be developed because it is one of the main sources of

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feed, carbohydrates, and protein [3] with productivity ranging from 5-7 tons/ha. The demand for corn in Indonesia is projected to always increase in line with population growth and the development of the food and feed industry. This encourages the fulfillment of corn needs to continue to be carried out through various innovative corn seed production activities [4].

One of the obstacles that become a limiting factor in efforts to meet the national target is plant pathogen infection. Plant pathogens can affect the quality and quantity of plants causing yield losses of around 11% of the total production. Corn plants have many types of diseases, especially those caused by pathogenic fungi [5; 6]. Several researchers reported that there are at least three major diseases of corn which can cause significantly reduce production, low product quality, and even cause crop failure in susceptible varieties, namely downy mildew (DM), maydis leaf blight (MLB), and leaf rust (LR). DM disease caused by *Peronosclerospora* is one of the main problems in increasing corn production in corn centers in Indonesia [7]. In Indonesia, DM causes yield loss of up to 80% in East Java, Gorontalo, South Sulawesi, Lampung and West Kalimantan. Three pathogenic species of DM were found, namely *P. maydis* which spread on the islands of Java, Lampung, West Kalimantan, South Kalimantan, Central Sulawesi, and Gorontalo; *P. philippinensis* found on the island of South Sulawesi and North Sulawesi; *P. sorghi* has only been reported in the highlands of Aceh, North Sumatra, Lampung, Southeast Sulawesi, and Java [8, 9].

Other major diseases found in corn cultivation are MLB caused by the *Bipolaris maydis* and LR by the fungus *Puccinia polysora* with low to high attack intensity, so that it can affect the decline in corn yields [10]. Symptoms of LR disease generally appear after the formation of male flowers (generative phase), while MLB begins to appear after corn plants are about 2 weeks after planting. Both of these diseases, namely rust and leaf spot, need to be watched out for because in climatic conditions, especially humidity and temperature under their development, these diseases will be able to infect corn crops, especially if the varieties planted are susceptible.

Disease control efforts are basically carried out through controlling the pathogen development, reduce the source of the pathogen inoculum by modifying the host and environment so that the economic injury level and the economic threshold are negligible. Therefore, it is necessary to continue to strive for the development of effective and efficient control methods for these diseases. One approach to effective control is the use of resistant varieties and understanding the disease epidemic component. Developments in epidemiology have led to various analyses of disease development models according to changes in host, pathogenic, and environmental conditions. Host conditions are related to the ability of plants to protect themselves from pathogen attacks. In this case, resistant varieties are believed to be more profitable and genetic because more stable resistance, economical, and environmentally friendly.

Determining the appropriate disease development model requires a comparison of disease epidemic models [11]. Plant disease epidemics in nature are complex and dynamic interactions of three main factors, namely pathogen, host, and environment. Epidemics of plant diseases develop on a dynamic scale of space and time. A complex understanding of the factors that influence the scale of space and time will be the basis for predicting the occurrence of disease epidemics in supporting the success of disease management [12, 13]. Therefore, it is necessary to continue to strive for the development of effective and efficient control methods for this disease.

Data related to the effect of hybrid corn on the main disease epidemic components of corn such as disease incidence, disease distribution patterns, and disease development models in corn main diseases need to be studied further. This study aimed to examine the

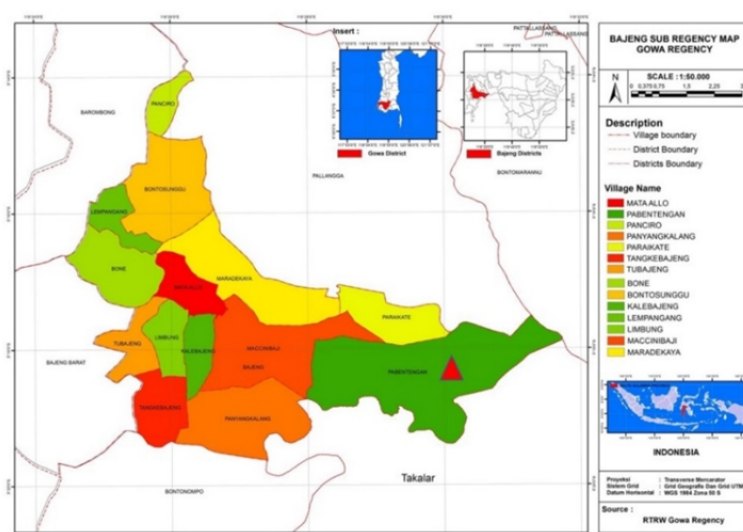
resistance level of hybrid corn genotypes to the corn major diseases and to determine its effect on the components of the disease epidemic.

## 2 Material and methods

### 2.1 Description of test locations and preparation of test materials

Genotype testing of hybrid corn against DM, MLB, and LR was done at a farmer's field in Bajeng District, Gowa Regency, South Sulawesi. Bajeng sub-district is one part of the territory of Gowa Regency which is located to the north of the capital city of Gowa Regency and is located at  $-5^{\circ}18'23''$  S and  $119^{\circ}30'20''$  E (Figure 1). As with other regions in Indonesia, Gowa Regency has two seasons, namely the dry season in June - September and the rainy season in December - March. Weather changes occur in the middle of the year after going through transitional periods, namely April – May and October – November. The Gowa Regency area has a rainfall of 237.75 mm with a temperature of around 25 - 27 °C. Several observation stations in Gowa Regency reported that the highest average rainfall occurred in December of 676 mm, while the lowest average rainfall occurred from July to September, even in those months there was almost no rain [14].

A total of five hybrid corn genotypes were tested, namely HCB01, HCB02, HCB03, HCB04, and HCB05. While the comparison varieties used were P36, PAC339, BISI18, Anoman, and Pulut varieties. The Anoman variety was used as a comparison variety and spreader rows for testing DM, while the Pulut variety was used for testing MLB and LR.



**Fig. 1.** Administrative map of the location for testing hybrid corn genotypes against major corn diseases in Bajeng District, Gowa District, South Sulawesi, Indonesia. The symbol represents the test location point in Pabentengan village.

### 2.2 Resistance assessment of hybrid corn varieties to corn major diseases

#### 2.2.1 Testing for downy mildew

DM testing was carried out in June – August 2022. The corn seeds of the Anoman variety as a source of DM inoculum (spreader row plants) were planted in three rows around the test plots and blocks. Planting of spreader row plant was carried out 3 to 4 weeks before

planting the tested genotype. Suspension of *Peronosclerospora* spp. conidia was inoculated on 10-day-old spreader row plants. Inoculation was carried out in the morning and conditions of high humidity.

The tested genotypes were planted when the intensity of DM disease on the inoculum source plants reached 70%. A total of two tested genotype seeds were planted with a spacing of 75 cm x 20 cm in 4 rows of 5 meters long. Fertilization of the tested genotypes was carried out twice using urea. The first fertilization using 300 kg/ha of urea at 10 DAP while the second fertilization uses urea of 150 kg/ha of urea at 30 DAP. DM was observed at the age of 14, 21, 28, 35, and 42 DAP. The percentage of DM pathogen attack is calculated by the formula:

$$DI (\%) = \frac{N}{n} \times 100\% \quad (1)$$

where DI, disease incidence (%); N, the number of plants with DM symptoms; and n, the number of plants observed in each genotype.

### 2.2.2 Testing for maydis leaf blight (MLB) and leaf rust (LR).

Tests for MLB and LR were carried out in November 2022 – January 2023. The testing unit for MLB and LR made in separate fields. The MLB and LR spreader row plants were planted in three rows around the test plots and blocks. The spreader row plants using the anoman variety for the MLB test and the pulut variety for the LR test. Suspension of conidia of *B. maydis* causing MLB and *P. polysora* causing LR were inoculated on a 28-day-old spreader row plants. Conidial suspension with a density concentration of  $6 \times 10^4$  conidia/ml was sprayed on the spreader row plants in the afternoon. The *B. maydis* isolate used in this study from the collection of the Diseases Laboratory, Indonesian Cereals Research Institute. Meanwhile, corn leaves with LR symptom were collected and incubated overnight by soaking the base of the leaf in a sugar solution and covering it with plastic. After incubating overnight, the leaves were rinsed with distilled water to harvest the urediniospores. Furthermore, planting of tested geotypes was carried out after the intensity of MLB disease on spreader row plants reached 70%. Planting and fertilizing of the tested genotypes followed the method of Mirsam et al [10]. MLB disease severity was observed at the 45, 60, and 75 DAP using the disease scoring modified by the Hooda et al. [15] scale, namely:

**Table 1.** MLB disease scoring

Scale	Description
0	No disease symptoms
1	Very low infection, blight symptoms spread on the lower leaves by 1% - 5%
2	Low infection, blight symptoms on the lower leaves by 6% - 20%
3	Moderate infections, blight symptoms on the lower and middle leaves by 21% - 50%
4	High infection, blight symptoms reach >50% on the middle , < 25% on upper leaves, and lower leaves die
5	Very high infection. There are many blight symptoms on all the leaves which caused the leaves to dry out

The scoring of rust-infected plant was carried out at the 50, 60, and 70 DAP. The score for the attack of LR was determined following the method of the Directorate of Maize Research India [15] as follows :

**Table 2.** LR disease scoring

Scale	Description
0	No disease symptoms
1	Very low infection. There are two or more pustules on the lower leaves
2	Low infection. There are few pustules spread on the lower leaves
3	Moderate infection. Many pustules on the lower leaves and a few on the middle leaves
4	High infection. Many pustules on lower and middle leaves and started spreading to upper leaves
5	Very high infection. There are many pustules spread on all the leaves, the leaves dry out prematurely and die

The disease scale was tabulated into the disease severity percentage formula below:

$$DS (\%) = \frac{\sum(n \times v)}{(Z \times N)} \times 100\% \quad (2)$$

where DS, disease severity; n, the number of affected plants in each category; v, Scale value on each affected plant; Z, the highest scale value; and N, the number of plants observed in each attack.

### 2.2.3 Determination of hybrid corn genotype resistance criteria.

The average disease intensity data in the last observation was used as a standard of resistance level of the hybrid corn genotype. Determination of the level of resistance of the corn genotype against these three diseases was based on the Directorate of Maize Research India's resistance criteria [15] which was modified according to the Indonesian Food Crop Varieties Release Procedures standards:

Very resistant (VR) =  $\leq 5\%$   
 Resistant (R) =  $> 5\% - 20\%$   
 Moderately resistant (MR) =  $>20\% - 40\%$   
 Susceptible (S) =  $>40\% - 60\%$   
 Very susceptible (VS) =  $>60\%$

### 2.2.4 Data analysis.

This study was arranged using a randomized block design consisting of 9 treatments (5 tested genotypes and 4 comparison varieties) and repeated 3 times as experimental blocks. Observational data were analyzed statistically, then continued with the least significant difference test at the 5% level ( $\alpha=0.005$ ).

## 2.3 Analysis of disease development model and infection rate

Analysis of DM, MLB, and LR disease development in the field was done based on model fit test using three disease development models, namely monomolecular, logistic, and Gompertz. Disease intensity data was transformed through the three formulas of the disease development model. The data obtained was then regressed linearly related to disease intensity (DI) and time (t) of disease development. The model fit test was carried out by looking at the highest coefficient of determination and the lowest mean square of error. In addition, these data were also used to calculate the infection rate. The calculation of the infection rate is based on the results of the selection of the disease development model using the formula [16]:

Molecular model:

$$r_m = \frac{1}{t} \left( \ln \frac{1}{1-X_t} - \ln \frac{1}{1-X_0} \right) \text{ per unit of time} \quad (3)$$

Logistic model:

$$r_l = \frac{1}{t} \left( \ln \frac{X_t}{1-X_t} - \ln \frac{X_0}{1-X_0} \right) \text{ per unit of time} \quad (4)$$

Gompertz model

$$r_g = \frac{1}{t} - \ln \left\{ -\ln \ln (X_t) \right\} + \ln \ln (-\ln \ln (X_0)) \text{ per unit of time} \quad (5)$$

where  $x_t$ , the disease proportion at time  $r$ ;  $x_0$ , the disease proportion at the initial observation ( $t = 0$ );  $t$ , time;  $r$ , disease infection rate.

## 2.4 Analysis of the value of the area under the disease progress curve (AUDPC) and the protection index

The intensity of pathogen attack in a certain observation period was calculated based on the AUDPC. The disease development level during a certain period was described by the AUDPC value obtained through the equation [17]:

$$AUDPC = \sum_{i=1}^{n-1} \left( \frac{X_i + X_{i+1}}{2} \right) (t_{i+1} - t_i) \quad (6)$$

where,  $n$  is the number of observations;  $x$ , DM intensity, and  $(t_{i+1}-t_i)$  is the time interval between observations. While the protection index is calculated based on the AUDPC value using Formula 4 [18].

$$\text{Protection index (\%)} = \left( 1 + \frac{\text{AUDPC of hybrid corn genotypes as treatment}}{\text{AUDPC of Anoman variety as control}} \right) \times 100\% \quad (7)$$

## 2.5 Effect of weather factors on the major diseases of corn-based on path analysis

The weather factors effect on the major corn diseases development was tested by path analysis. This analysis can describe the direct and indirect effects of weather factors on disease development and can determine the most influential weather factors on disease development [19]. In this analysis, the incidence and severity of disease are dependent variables (Y) while weather factors are independent variables (X). The analyzed weather data includes relative humidity (RH), temperature (T), rainfall (RF), and wind velocity (WV) taken from the Indonesian Agency for Meteorology, Climatology and Geophysics.

## 3 Results



### 3.1 Corn genotype resistance to downy mildew

Observation of DM disease showed that the incidence of DM at the age of 14 DAP was generally still low in all entries with the percentage of attacks between 9.37% - 21.35%. A significant increase in the incidence of DM disease was seen at the age of 28 DAP, where the test genotypes HCB03 and HCB04, as well as the comparison Anoman, showed susceptible reactions with attack intensities of 41.85%, 45.46%, and 49.04%, respectively. The last observation (45 DAP) showed that the incidence of DM disease in Anoman and P21 varieties was very high with a percentage of 63.81% (very susceptible) and 55.80 (susceptible), while P36 and BISI 18 showed a relatively low incidence of DM disease of 28.62% and 37.90% with the moderately resistant reaction. There was one of the five test hybrid corn genotypes that showed a moderately resistant reaction to DM, namely the HCB01 genotype. DM intensity in the HCB01 genotype was 35.55% significantly lower than the PAC339 and Anoman at the 5% level of LSD test ( $\alpha=0.005$ ) (Table 3).

**Table 3.** DM incidence in hybrid corn genotype

Genotype	Disease incidence (%) at (DAP)									Resistance Reaction
	14	21		28		35		42		
HCB01	10.29	16.81	bd	22.80	bd	31.62	bd	35.55	bd	MR
HCB 02	17.29	27.34	d	36.13	d	42.80	d	47.32	d	S
HCB 03	13.93	28.00	d	41.85		48.69		52.98		S
HCB 04	16.50	24.22	d	36.10	d	45.27	d	51.41		S
HCB 05	21.35	29.01	d	45.46		59.39		62.81		VS
P36 (a)	13.56	17.14		22.35		26.41		28.62		MR
PAC339 (b)	9.37	27.34		38.84		47.57		55.80		S
BISI18 (c)	15.78	20.88		25.49		33.37		37.90		MR
Anoman (d)	13.69	38.92		49.04		57.31		63.76		VS
Means	14.64	25.52		35.34		43.60		48.46		
CV	35.35	16.43		17.41		15.49		14.82		
LSD 5%	-	7.25		10.65		11.69		12.43		

Notes: a: the disease incidence rate was significantly lower than the P36 at the 5% LSD test level; b: the disease incidence rate was significantly lower than the PAC339 at the 5% LSD test level; c: the disease incidence rate was significantly lower than the BISI18 at the 5% LSD test level; d: the disease incidence rate was significantly lower than the Anoman at the 5% LSD test level.

### 3.2 Corn genotype resistance to maydis leaf blight

Observations of the MLB severity in the attack category were quite high, in the range between 11.33% - 40.67% at the first observation at 45 DAP. Increased observations at the age of 60 DAT showed a significant increase in attack where the HCB04 genotype reacted susceptible to MLB with an attacking intensity of 41.33%. The increase in attack continued until the plant was 75 DAP, where only 2 test genotypes showed a somewhat resistant reaction to MLB. The genotypes HCB01 and HCB05 showed significantly lower disease severity than the BISI18 and Anoman varieties at the 5% level of LSD test ( $\alpha=0.005$ ) with attack intensity of 37.33% and 36%, respectively (Table 4).

**Table 4.** MLB severity in hybrid corn genotype

Genotype	Disease severity (%) at (DAP)						Resistance Reaction
	45		60		75		

HCB01	14.00	b d	36.67	d	37.33	cd	MR
HCB02	14.67	d	31.33	d	46.67	d	S
HCB03	18.67	d	31.33	d	45.33	d	S
HCB04	11.33	b d	41.33	d	45.33	d	S
HCB05	23.33	d	32.00	d	36.00	cd	MR
P36 (a)	14.67		30.67		37.33		MR
PAC339 (b)	21.33		31.33		39.33		MR
BISI18 (c)	11.33		33.33		53.33		S
Anoman (d)	40.67		61.33		63.33		VS
Average	18.89		36.59		44.89		
LSD 5%	7.13		16.16		13.27		
CV (%)	21.79		25.51		17.08		

Notes: a: the disease severity rate was significantly lower than the P36 at the 5% LSD test level; b: the disease severity rate was significantly lower than the PAC339 at the 5% LSD test level; c: the disease severity rate was significantly lower than the BISI18 at the 5% LSD test level; d: the disease severity rate was significantly lower than the Anoman at the 5% LSD test level.

### 3.3 Corn genotype resistance to leaf rust

Observation of the severity of LR on the test material at 50 DAP showed a fairly high intensity of attack with a range of 10.00% to 16.67%. The increasing intensity of LR disease continued until the last observation. At the age of 60 DAP, the Pulut variety showed a susceptible reaction with an attacking intensity of 43.33% and a P36 variety with a moderately resistant reaction of 26%. At 70 DAP, the disease severity of four candidate hybrid corn varieties namely HCB01, HCB02, HCB03, and HCB4 were significantly lower than the Pulut variety, where the Pulut variety reacted very susceptible (VS) to LR with a disease severity rate of 62.00%. The four candidate hybrid corn varieties reacted somewhat resistant to LR with a low disease severity level of below 30%. (Table 5).

**Table 5.** LR severity in hybrid corn genotype

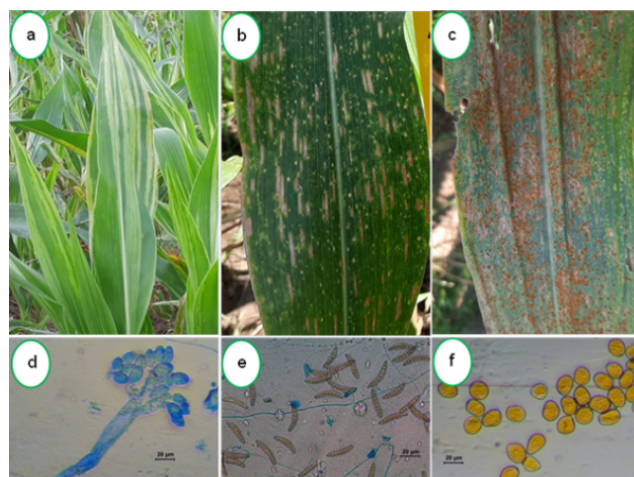
Genotype	Disease severity (%) at (DAP)						Resistance Reaction
	50		60		70		
HCB01	11.33	cd	18.67	cd	30.67	d	MR
HCB02	16.00		18.67	cd	25.33	d	MR
HCB03	15.33		28.00	d	28.67	d	MR
HCB04	12.00	d	16.00	abcd	26.67	d	MR
HCB05	16.67		30.00	d	42.67	d	S
P36 (a)	14.00		26.00		28.67		MR
PAC339 (b)	10.00		26.00		34.67		MR
BISI18 (c)	14.67		33.33		36.67		MR
Pulut (d)	15.33		43.33		62.00		VS
Average	13.93		26.67		35.11		
LSD 5%	3.14		7.66		14.97		
CV (%)	27.69		35.18		24.61		

Notes: a: the disease severity rate was significantly lower than the P36 at the 5% LSD test level; b: the disease severity rate was significantly lower than the PAC339 at the 5% LSD test level; c: the disease severity rate was significantly lower than the BISI18 at the 5% LSD test level; d: the disease severity rate was significantly lower than the Anoman at the 5% LSD test level.





**Fig. 2.** The resistance level of the hybrid corn genotype to the corn major disease. A, DM disease; B, MLB disease; C, LR disease.



**Fig. 3.** Symptoms and signs of the major diseases in corn. a: DM symptom; b, MLB symptom; c, LR symptom; d, conidia of *Peronosclerospora* spp. observed under a compound microscope; e, macroconidia of *B. maydis* observed under a compound microscope; f, conidia of *P. polysora* observed under the compound microscope.

### 3.4 Disease development model and infection rate value

DM development in 5 hybrid corn genotypes had different models. In the HCB01, HCB02, HCB3, and HCB04 genotypes, the disease developed according to a monomolecular model, while in the HCB05 genotype the disease developed according to the Gompertz model (Table 2). The analysis of the disease incidence development data on the HCB01, HCB02, HCB3, HCB04, and HCB05 genotypes that were observed obtained different infection rate values ( $r$ ), which were 0.013, 0.016, 0.022, 0.020, and 0.030 respectively (Table 6).

The developmental model of MLB on 5 hybrid corn genotypes showed a more diverse model than DM. Disease development in the HCB01, HCB04, and HCB05 genotypes showed a monomolecular model with infection rates of 0.011, 0.016, and 0.006,

respectively. Meanwhile, in the HCB02 and HCB03 genotypes, the development of MLB followed the Gompertz and Logistics models with infection rates of 0.031 and 0.042, respectively (Table 7).

The development of LR disease in 5 genotypes of hybrid corn followed the Logistics and Gompertz model. LR disease in genotypes HCB01, HCB02, and HCB04 showed a logistic disease development model with infection rates of 0.065, 0.028, and 0.050, respectively. While the genotypes HCB03 and HCB05 followed the Gompertz model with infection rates of 0.021 and 0.037, respectively (Table 8).

**Table 6.** The developmental model of DM disease on hybrid corn genotype

Genotype	Disease development model	Infection rate	Regression equation	R <sup>2</sup>
HCB01	Monomolecular	0.013	$Y=0.013x-0.076$	0.991
HCB02	Monomolecular	0.016	$Y=0.016x-0.029$	0.990
HCB03	Monomolecular	0.022	$Y=0.022x-0.131$	0.973
HCB04	Monomolecular	0.020	$Y=0.020x-0.107$	0.991
HCB05	Gompertz	0.030	$Y=0.050x-1.119$	0.975

**Table 7.** The developmental model of MLB on hybrid corn genotypes

Genotype	Disease development model	Infection rate	Regression equation	R <sup>2</sup>
HCB01	Monomolecular	0.011	$Y=0.011x-0.274$	0.773
HCB02	Gompertz	0.031	$Y=0.031x-2.015$	0.999
HCB03	Logistic	0.042	$Y=0.042x-3.316$	0.999
HCB04	Monomolecular	0.016	$Y=0.016x-0.549$	0.857
HCB05	Monomolecular	0.006	$Y=0.006x-0.005$	0.962

**Table 8.** The developmental model of LR disease in hybrid corn genotypes

Genotype	Disease development model	Infection rate	Regression equation	R <sup>2</sup>
HCB01	Logistic	0.065	$Y=0.065x-5.319$	1.000
HCB02	Logistic	0.028	$Y=0.028x-3.081$	0.979
HCB03	Gompertz	0.021	$Y=0.021x-1.646$	0.799
HCB04	Logistic	0.050	$Y=0.050x-4.542$	0.965
HCB05	Gompertz	0.037	$Y=0.037x-2.421$	0.999

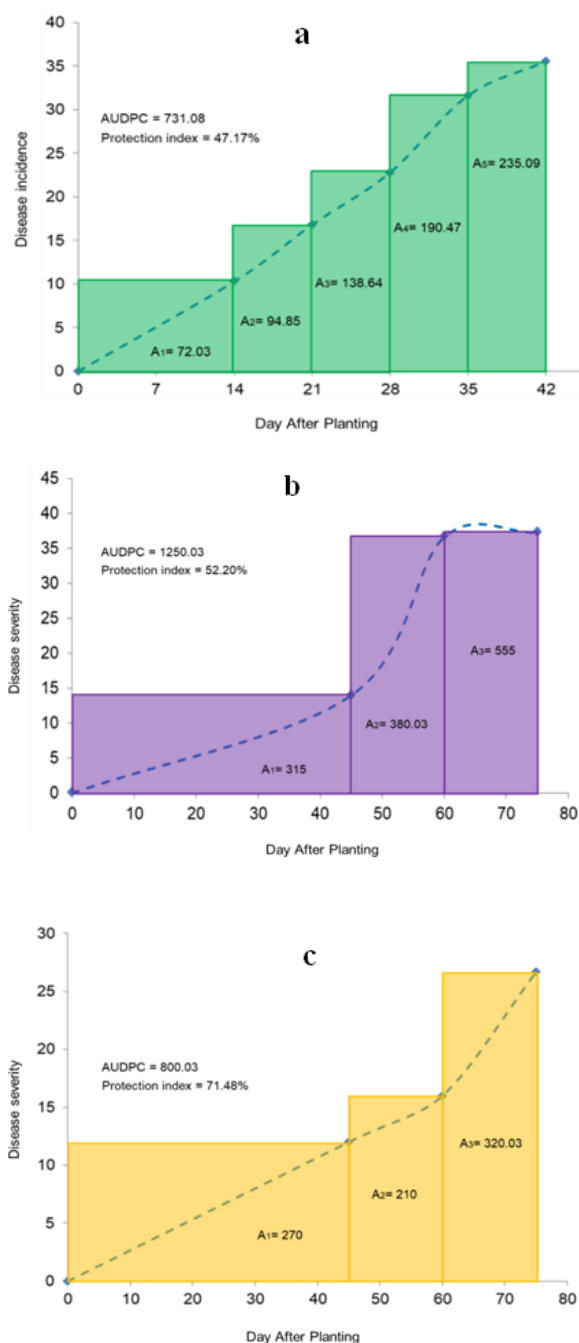
### 3.5 AUDPC value and protection index

Based on the data on the incidence of DM, the HCB01 hybrid corn genotype tested was able to suppress the development of this disease incidence over time (Figure 4a). This indicates that disease development in the HCB01 hybrid corn genotype is the slowest compared to other test genotypes. In total, the assessment of the incidence of DM based on the AUDPC value showed the HCB01 genotype had the lowest score of 731.08 and the highest protection index value of 47.17% (Table 9). Similar to DM, the HCB01 genotype also showed its ability to suppress the development of the severity of MLB the best among other genotypes (Figure 4b). The HCB01 genotype was also able to suppress the severity of MLB based on the lowest AUDPC value of 1250.03 and the highest level of resistance with a protection index value of 52.20%. In contrast to DM and MLB, the slowest development of LR was shown in the HCB04 genotype with an AUDPC value of 653.35 and the highest resistance level with a protection index value of 73.40% (Table 9).

**Table 9.** Effect of hybrid corn genotype on the AUDPC and protection index

Genotype	DM		MLB		LR	
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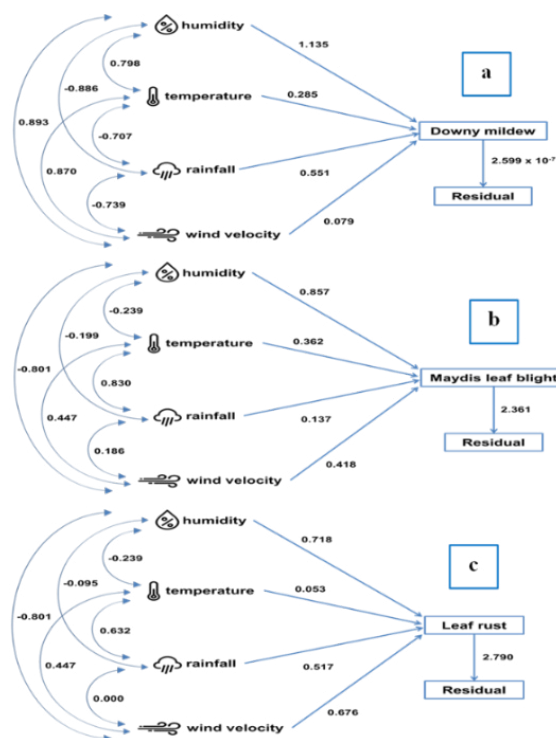
	AUDPC	Protection index (%)	AUDPC	Protection index (%)	AUDPC	Protection index (%)
HCB01	731.08	47.17	1250.03	52.20	679.95	72.32
HCB02	1091.06	21.15	1260.08	51.82	793.35	67.70
HCB03	1161.48	16.07	1370.03	47.61	883.25	64.04
HCB04	1092.32	21.06	1299.83	50.29	653.35	73.40
HCB05	1381.03	0.20	1449.90	44.56	1013.45	53.74
Anoman (control)	1383.80	-	2615.03	-	2456.50	-



**Fig. 4.** The AUDPC graphics of corn major diseases in hybrid corn genotype. a: DM in HCB01; b, MLB in HCB01; c, LR in HCB04; A<sub>1</sub>, AUDPC of the 1st time interval; A<sub>2</sub>, AUDPC of the 2nd time interval; A<sub>3</sub>, AUDPC the 3rd time interval; A<sub>4</sub>, AUDPC of the 4th time interval; A<sub>5</sub>, AUDPC of the 5th time interval.

### 3.5 The influence of weather factors on corn major disease

The results of path analysis of the relationship between weather and disease development indicated that weather conditions affect disease development either directly or indirectly. The RH, T, RF, and WV significantly influence the development of DM, MLB, and LR. The path coefficient values for RH, T, RF, and WV were 1.135, 0.285, 0.551, and 0.079 for DM, respectively; 0.857, 0.362, 0.137, and 0.418 for MLB; and 0.718, 0.053, 0.517, and 0.676 for LR (Figure 5).



**Fig. 5.** Diagram of the results of path analysis of weather factors influence on the development of the main corn disease. The value on the path that connects the weather factor and the type of corn disease is the path coefficient. The value on the path that connects RH, T, RF, and WV is a correlation coefficient.

The results of the path analysis also show that there was a correlation between weather factors in influencing the development of the main corn disease, both positive (+) and negative (-) correlations. Weather factors that showed a positive correlation in influencing the development of DM could be seen in the correlation between RH↔T, RH↔WV, and T↔WV with correlation coefficient values of 0.798, 0.893, and 0.870, respectively. While the negative correlation between weather factors could be seen in the correlation between RH↔RF, T↔RF, and RF↔WV with correlation coefficient values of (-0.886), (-0.707), and (-0.739) respectively. (Figure 5a).

The correlation between weather factors that showed a positive correlation in supporting the development of MLB could be seen in the correlation between T↔RF, T↔WV, and RF↔WV with correlation coefficient values of 0.830, 0.447, and 0.186, respectively. Weather factors that showed a negative correlation to MLB were RH↔T, RH↔RF, and RH↔WV with correlation coefficient values of (-0.239), (-0.199), and (-0.199) respectively. (-0.801). The correlation results showed that RH did not affect each other with T, RF, and WV in accelerating the development of the severity of MLB (Figure 5b).

The correlation of weather factors in influencing the development of LR disease was the same as that of MLB with the correlation coefficient between different weather factors.

Weather factors that showed a positive correlation to LR disease were the correlation between  $T \leftrightarrow RF$ ,  $T \leftrightarrow WV$ , and  $RF \leftrightarrow WV$  with correlation coefficient values of 0.632, 0.447, and 0.000, respectively. Meanwhile, weather factors that showed a negative correlation to LR disease, namely  $RH \leftrightarrow T$ ,  $RH \leftrightarrow RF$ , and  $RH \leftrightarrow WV$  with correlation coefficient values of (-0.239), (-0.0.95), and (-0.801) (Figure 5c).

## 4 Discussion

DM testing showed that only the HCB01 hybrid corn genotype reacted moderately to DM with a disease incidence of 35.55%. Meanwhile, the incidence of disease in the comparison varieties Anoman and PAC339 in all experimental blocks showed a very susceptible and susceptible reaction with attack intensities of 63.76% and 55.80%, respectively. This indicates that DM stress around the test plot is optimal and is assumed to infect evenly. The difference in the intensity of transmission of DM in the test genotypes showed that there was a relationship between the resistance level of the variety and the virulence level of the pathogens that invaded plants, in terms of producing phytoalexins, causing early infection in plants in the field [7]. In addition, the differences in the resistance of the five hybrid corn genotypes were caused by several factors including plant genetic differences. Resistant variety was suspected to have horizontal or vertical resistance gene [10]. In addition to genetic factors, supportive agroecosystem conditions and abundant sources of inoculum cause changes in the level of resistance from previously resistant to susceptible. Changes in the level of resistance can also occur if the same variety is grown in different locations. Apart from these factors, the high and low incidence of DM in the tested strains also depended on the source of DM.

The diagnosis of DM can mainly be made by direct observation of the symptoms and signs of the pathogen using a hand lens and a microscope [20]. Based on field observations of the pathogen *Peronosclerospora* spp. obtained from corn plants that were attacked by DM with white lines parallel to the leaf bones, besides that there was a white flour-like layer under the leaf surface and caused chlorosis (Figure 3a). Microscopically *Peronosclerospora* spp. has conidiophores resembling rods, then at the ends of the stems, there are round conidia (Figure 3d). This is following what was reported by several researchers that the initial symptoms of DM were the appearance of yellowish lines (chlorosis) parallel to the leaf bones and then the chlorosis spread over the entire leaf surface. There are conidiophores shaped like stems, then on the branches at the ends, there are spores or round conidia [21]. The conidia structure is like sporangiophores, sporangia, and zoospores because it is related to their survival and distribution [22].

In general, the severity of MLB was high in all test genotypes. The HCB01 and HCB05 genotypes showed the lowest severity of MLB compared to the other test genotypes. The high intensity of MLB is strongly influenced by environmental conditions, especially T and RH during the study, namely the rainy season with fairly high intensity (September-December 2020). The optimum temperature for the development of the fungus *B. maydis* is between 20°-30°C with RH >90%. In addition, MLB occur in corn plants with different intensity also due to the level of resistance of a plant [23]. It was previously reported that the worst blight attacks were observed at 63.67 to 79 DAP. MLB, like most other leaf diseases of corn, is a late-season disease in which the development of the disease is most severe during postanthesis [24].

Symptoms of MLB were observed in the field, namely the presence of brownish spots with an oval and elliptical shape which are getting bigger day by day and cause the leaves to dry up in very severe symptoms (Figure 3b). Hussain et al. [1] explained the same thing that



the MLB symptoms at the infection initiation are marked by the appearance of greenish-brown spots that were small and elongated in shape, then the spots became increasingly elongated of an ellipse and merge with other spots. The appearance of symptoms of this disease starts from the lower leaves and continues to increase to the upper leaves. Furthermore, explained that the spots will expand and some spots can coalesce, causing the leaf necrosis. The fungus *B. maydis* observed under a compound microscope showed about 7 insulated conidia, rounded ends, and elongated and curved (Figure 3e). These characteristics are also similar to those reported by several researchers that the conidia of *B. maydis* began to be seen after 6 days and increased by 12 days. Conidia slightly curved shape, blunt ends, insulated 3-10 pieces [24].

The severity of LR disease in the tested genotype showed conditions similar to MLB where the intensity of the attack was quite high. The test results showed that there were 4 genotypes of hybrid corn (HBC01, HBC02, HBC03, HBC04) which showed low disease severity with moderately resistant criteria. This indicates that MLB and LR have a similar trend towards infection strategies, and those resistant hybrids have a broad spectrum of resistance to several pathogens. Plants that have good resistance to MLB tend to also have good resistance to LR, and vice versa. This phenomenon may be related to the existence of a quantitative resistance mechanism which is the result of a combination of several genes (multigenic) which are non-specific to certain pathogens and have a wide spectrum [25]. LR disease identified in the field showed symptoms such as Southern Corn Rust caused by *P. polysora*, namely pustules formed on the upper leaves surface and only a few on the lower leaves surface. The pustules were circular to round and orange to brown (Figure 3e). The morphological characteristics of *P. polysora* were similar to reported by Sun et al. [26] that the upper and lower surfaces of symptomatic corn leaves have small or pustule-like spots, round to oval in shape, and reddish-brown in size 2 mm. These spots produce spores called teliospores.

The difference in the increase in AUDPC value in a certain period compared to other periods could describe the dynamics of disease attacks and determine the period in which the intensity of the attacks is the highest. In Figure 4, it could be seen that the highest increase in AUDPC values was in the age range of 0-35 DAP for DM and 45-70 DAP for MLB and LR. This indicates that the highest DM development rate occurred in that period. This is following several previous reports where it is known that the incubation phase from infiltration to the appearance of early DM disease ranges from 11 to 14 days, while MLB and LR from 45 to 60 days [27].

The hybrid corn genotype showed the ability to protect itself from these three diseases. This could be seen from the relatively high protection index value of the hybrid corn genotype. The HCB01 genotype showed the highest protection index value against DM and MLB, which were 47.17% and 52.20%, respectively, while HCB04 had the highest protection index value against LR disease at 71.48% (Table 4 and Figure 4). Overall test results showed that the HCB01 hybrid corn genotype had better and more consistent resistance to the three diseases. This could be seen from the low AUDPC value and high protection index value. The protection index shown by each genotype of hybrid corn varies. According to Azrai et al. [28], corn resistance to pathogens is quite diverse, depending on genetic variability, phenotypic variability, and the interaction between genetics and the environment. Knowledge of this variability is very important, especially in the application of the right selection program to obtain the desired plant character. In addition, the resistance reaction that appears depends on infection rate and timing and the development of pathogenic conidia in corn.



The results of the analysis of the major disease development models in the five hybrid corn genotypes that were observed obtained three different disease development models, namely monomolecular, logistic, and Gompertz models (Tables 5, 6, and 7). The HCB01 genotype had the lowest DM and MLB infection rate by following the monomolecular model, while the HCB03 genotype had the lowest LR infection rate by following the logistic model. Looking at the developmental models of DM, MLB, and LR that are different in each hybrid corn genotype, the effort to delay infection at the beginning of planting has a very important role in suppressing the intensity of the disease. Delaying infection to 2 MST caused only low levels of damage. Control efforts by setting the planting time can delay the occurrence of disease epidemics.

The results of path analysis between weather conditions and disease development showed that weather conditions in the form of RH, T, RF, and WV had a positive effect on DM, MLB, and LR indicated by path coefficients which were positive for all components. In addition, the correlation between weather factors shows that RH, T, RF, and WV influence each other in accelerating the severity of DM, MLB, and LR. The components of RH, T, and WV have a positive correlation in influencing DM. Meanwhile, in MLB and LR, the components of T, RF, and WV were positively correlated in accelerating the disease development.

DM testing was done in the transition season, namely the rainy season to dry season, where in the dry season the WV was higher than the rainy season so that it could be the main trigger for the release of conidia. In addition, the conditions of WV and RH were high enough at the time of the test so that the conidia could be forcibly released from their supports and then dispersed. *Peronosclerospora* spp. produced conidia with a clear release periodicity and had a close relationship with weather factors such as RH, T, RF, and WV. According to Hooda et al. [15], all types of *Peronosclerospora* spp. requires surface moisture for conidia germination and infection as well as high RH for conidia production. Temperatures ranging from 20oC to 30oC, RH above 90%, and moderate RF were found to be most conducive to DM development in corn. Furthermore explained that RF and high RH were critical weather factors for the development of an epidemic.

In addition to DM, this study clearly illustrated the relationship between weather factors such as RH, T, RF, and WV with the development of MLB on corn. MLB testing was carried out in the rainy season where the RH was high and the temperature was relatively low. In conditions of high RF and RH, it is suspected that the fungus causing MLB and LR develops and initiated contact with the host plant, penetrates, and becomes infected. The optimal temperature for the development of this disease ranges from 17 to 26°C. Under these conditions, the conidia will pass through the germination phase and will penetrate the host plant within 6 hours. Ye et al. [29] also reported that relatively low-temperature conditions of 16 - 20°C and high annual rainfall were favorable for infection, colonization, reproduction, and spread of *Bipolaris* species, thus greatly influencing the development of the MLB epidemic [30].

Similar to MLB, LR disease testing was also carried out under conditions of high RF, where the RH was high and the temperature was moderate to low. The T and RH were the important factor affecting germination, penetration, formation, and dispersion of *P. polysora* spores. *P. polysora* optimally at high RH and moderate to low temperature. Urediniospore germination and disease development occur at optimal temperatures of 25–29 °C and 25-28 °C, respectively. Li et al. [31] reported that temperatures >27°C and duration of sunlight were negatively correlated with the urediniospores density in the air. In addition, the mean daily temperature is positively correlated with the epidemic LR rate, but when the RH is >90%, the epidemic LR rate is negatively correlated with hours of sunshine.

The use of resistant hybrid corn varieties to the management of major corn diseases is believed to be a more cost-effective and environmentally safe alternative control. Genetic resistance is considered one of the most economical and effective preventive methods for the management of major diseases in corn. Breeding resistance to DM, MLB, and LR on corn in the tropics, especially in Indonesia, continues to be developed and has been widely reported by researchers [32]. In addition, knowledge of the epidemic component of a disease is important basic information for formulating efforts to control the disease in question.

## 5 Conclusion

The HCB01 consistently showed a fairly low attack intensity to the corn major disease, where this genotype was somewhat resistant to DM, MLB, and LR, namely 35.55%, 37.33%, and 25.33%, respectively, so it can be recommended as new superior variety.

The hybrid corn genotype greatly influences the development of epidemics of DM, MLB, and LR. This can be seen from the value of the epidemiological component in each genotype of hybrid corn for each type of disease:

1. The highest protection index was shown in the HCB01 genotype for DM (47.17%) and MLB (47.17%) and the HCB04 genotype for LR (73.40%)
2. The lowest AUDPC values were shown in the HCB01 genotype for DM (731.08) and MLB (1250.03) and the HCB04 genotype for LR (653.35).
3. The lowest infection rate values were shown in the genotypes HCB01 for DM (0.013), HCB05 for MLB (0.006), and HCB03 for LR (0.021).
4. Disease development in the five genotypes of hybrid corn had different models, depending on the type of disease and the level of resistance of the hybrid corn genotype.
5. Weather factors such as RH, T, RF, and WV had a positive effect on DM, MLB, and LR.

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