



Genetic analysis of Maize crop resistance to Polysora Rust: A comprehensive investigation

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ABSTRACT

This study investigates the inheritance pattern of *Puccinia polysora* rust resistance in maize, focusing on a segregating F2 population derived from a cross between the susceptible inbred line CM 202 and the resistant inbred line MAI 105. Disease severity was assessed using the Percent Leaf Area Covered (PLAC) method, revealing a spectrum of resistance within the population. Genetic analysis confirmed a single dominant gene controlling rust resistance, aligning with previous research indicating monogenic inheritance in maize. The identification of this dominant gene offers significant implications for breeding programs, enabling the development of rust-resistant varieties through marker-assisted selection and gene pyramiding. Additionally, the presence of moderate resistance and susceptibility suggests the involvement of modifiers or quantitative trait loci. Understanding these mechanisms is crucial for comprehensive rust resistance elucidation. Overall, this study provides valuable insights into the genetic basis of polysora rust resistance, informing breeding strategies to enhance maize productivity and resilience against rust diseases.

KEY WORDS: Maize; *Puccinia polysora*; Disease resistance; Inheritance pattern; Genetic analysis

1. Introduction

Maize (*Zea mays* L.) is a fundamental crop globally, serving as a staple food for millions of people and playing a crucial role in various industries. Its versatility extends beyond dietary consumption, encompassing applications in livestock feed, biofuels, and industrial production. This cereal crop's adaptability to diverse climates and soil conditions underscores its significance in ensuring food security and economic stability worldwide. However, maize production faces formidable challenges, with diseases posing a significant threat to yields and food security. Among these pathogens, Polysora rust, caused by the fungus *Puccinia polysora*, emerges as a

prominent adversary. This biotrophic fungus primarily targets maize leaves, manifesting as rust-like lesions that compromise photosynthetic efficiency and weaken the plant's overall vigor, ultimately leading to yield losses.

Understanding the genetic basis of resistance to Polysora rust is paramount for developing effective management strategies to mitigate its impact. Previous research endeavors have made notable progress in unraveling the genetic mechanisms underlying resistance, shedding light on the intricate interplay between host genetics and pathogen virulence. Studies have highlighted the existence of genetic diversity among maize

genotypes concerning Polysora rust resistance. Chungu *et al.* (2007) conducted research on tropical maize inbred lines, revealing substantial variation in resistance levels. This diversity provides a valuable resource for breeding programs aimed at enhancing resistance in maize cultivars, thereby bolstering resilience against Polysora rust.

Furthermore, investigations into the resistance of maize hybrids and inbred lines have yielded insights into the genetic architecture of resistance traits. Munkvold and Mengistu (1998) evaluated various maize genotypes for their resistance to northern leaf blight and Polysora rust, identifying promising candidates with durable resistance. These findings underscore the importance of genotype-specific responses to pathogen challenges and emphasize the need for tailored breeding strategies to enhance resistance in maize cultivars. Characterization studies have contributed to elucidating the mechanisms underlying resistance to Polysora rust in maize. Takan *et al.* (1998) conducted comprehensive analyses to delineate the genetic basis of resistance traits, identifying key genomic regions associated with resistance. By dissecting the molecular pathways involved in host-pathogen interactions, such studies provide a foundation for targeted breeding efforts aimed at developing maize cultivars with enhanced resistance to Polysora rust.

Moreover, advances in molecular genetics and genomic technologies have facilitated the identification of candidate genes and markers linked to Polysora rust resistance in maize. These molecular tools offer valuable resources for marker-assisted selection (MAS) programs, enabling breeders to expedite the development of

rust-resistant maize cultivars with improved agronomic traits.

In summary, maize stands as a cornerstone crop in global agriculture, but its productivity is threatened by diseases such as Polysora rust. Understanding the genetic basis of resistance to this pathogen is crucial for developing sustainable management strategies and ensuring food security. Through genetic diversity studies, characterization of resistance mechanisms, and leveraging molecular tools, researchers are making significant strides towards enhancing maize resilience to Polysora rust. Continued interdisciplinary efforts will be essential for harnessing the full potential of genetic resistance and safeguarding maize production against emerging challenges in the agricultural landscape.

2. Materials and Methods

The materials utilized, experimental procedures employed, and data analysis methods are comprehensively detailed below.

2.1 Selection of plant material

The base material for experimentation comprised one polysora rust-resistant inbred, MAI 105, and one susceptible inbred, CM 202. These lines were maintained through successive generations by selfing.

2.2 Crossing programme

The two selected inbred lines were planted during the late rainy season. The crossing procedure involved uniform silk cutting the previous evening, followed by crossing and pollination with pollen the following day between 8-10 AM. Subsequently, F1 progeny were harvested. The F1 generation was grown during the early rainy

season and self-pollinated within the same season, with subsequent harvest. In late rainy season, the F2 population (consisting of 150 plants) was cultivated in three plots, each measuring 5 meters in length and arranged in four rows with a spacing of 70cm × 20cm. Polysora rust-susceptible genotype 219 J was planted as a border row, and artificial inoculation was conducted as previously described.

2.3 Assessment of Disease Severity

Disease severity/incidence data were recorded on individual plants at two intervals: first at anthesis and then at the dough stage, using a standard scale ranging from 1 to 5 (Cramer, 1967). Subsequently, these scores were converted to percentages of disease severity (0-100%) following the method outlined by James (1971).

2.4 Statistical Analysis

The segregation pattern in the cross was statistically analyzed using the Chi-square test to assess the inheritance pattern of the resistance trait.

By adhering to standardized protocols for plant material selection, crossing procedures, disease assessment, and statistical analysis, this study aimed to elucidate the inheritance pattern of polysora rust resistance in maize and contribute to the genetic improvement of maize cultivars for enhanced disease resistance.

3. Results and Discussion

The F2 population, comprising 150 plants resulting from the cross between the susceptible inbred line CM 202 and the resistant inbred line MAI 105, was meticulously cultivated and assessed for polysora rust disease severity on an

individual plant basis. Disease severity was quantified using the PLAC (Percent Leaf Area Covered) method, which assigns a severity score ranging from 0 to 100% to each plant based on the proportion of leaf area affected by the disease.

To elucidate the inheritance pattern of polysora rust resistance, a genetic ratio analysis was conducted. The observed segregation ratio of 3 (resistant):1 (susceptible) was evaluated using the Chi-square test. The calculated Chi-square value was found to be lower than the tabulated Chi-square value, leading to the acceptance of the null hypothesis (Table 1). This statistical analysis supports the conclusion that the trait of polysora rust resistance in this population is governed by the control of a single dominant gene.

Table 1: Analysis of Polysora rust severity on F2 population

Description	No. of Plants in F2 Population		Total
	Resistant	Susceptible	
Observed frequency (O)	118	32	150
Expected frequency (E)	113	37	150
$\chi^2 = \sum(O-E)^2/E$	0.22	0.68	0.90 (NS)

NS – Non Significant

Table 2a and 2b presents the comprehensive data on disease severity within the F2 population. Among the 150 plants assessed, 53 demonstrated resistance to polysora rust, while 66 exhibited moderate resistance. Additionally, 27 plants displayed moderate susceptibility to the disease, while the remaining 5 plants were categorized as susceptible. This result underscores the genetic basis of polysora rust resistance in maize, providing valuable insights into the inheritance pattern of this trait.

Table 2a: Reaction of F₂ population of maize line (CM-202×MAI-105) to Polysora rust

Sl. No.	Disease severity (%)	Disease reaction	Sl. No.	Disease severity (%)	Disease reaction	Sl. No.	Disease severity (%)	Disease reaction	Sl. No.	Disease severity (%)	Disease reaction
1	25	MR	26	45	MS	51	1	R	76	25	MR
2	1	R	27	45	MS	52	5	R	77	45	MS
3	5	R	28	25	MR	53	25	MR	78	5	R
4	1	R	29	15	MR	54	25	MR	79	45	MS
5	15	MR	30	15	MR	55	15	MR	80	5	R
6	5	R	31	15	MR	56	15	MR	81	1	R
7	15	MR	32	5	R	57	25	MR	82	5	R
8	25	MR	33	1	R	58	15	MR	83	15	MR
9	45	MS	34	1	R	59	1	R	84	15	MR
10	25	MR	35	1	R	60	45	MS	85	15	MR
11	5	R	36	1	R	61	1	R	86	45	MS
12	1	R	37	1	R	62	5	R	87	45	MS
13	1	R	38	15	MR	63	25	MR	88	25	MR
14	5	R	39	45	MS	64	15	MR	89	45	MS
15	25	MR	40	5	R	65	5	R	90	45	MS
16	25	MR	41	1	R	66	1	R	91	1	R
17	25	MR	42	1	R	67	1	R	92	5	R
18	15	MR	43	25	MR	68	45	MS	93	15	MR
19	5	R	44	5	R	69	15	MR	94	5	R
20	15	MR	45	15	MR	70	45	MS	95	25	MR
21	45	MS	46	5	R	71	45	MS	96	15	MR
22	5	R	47	25	MR	72	45	MS	97	25	MR
23	5	R	48	15	MR	73	45	MS	98	5	R
24	1	R	49	25	MR	74	25	MR	99	15	MR
25	1	R	50	1	R	75	45	MS	100	1	R

Note: R=Resistant MR=Moderately Resistant S=Susceptible HS=Highly Susceptible

Table 2b: Reaction of F2 population of maize line (CM-202×MAI-105) to Polysora rust (Contd..)

Sl. No.	Disease severity(%)	Disease reaction	Sl. No.	Disease severity(%)	Disease reaction	Sl. No.	Disease severity (%)	Disease reaction
101	15	MR	121	15.00	MR	141	5	R
102	15	MR	122	5	R	142	15	MR
103	5	R	123	5	R	143	15	MR
104	15	MR	124	1	R	144	45	MS
105	25	MR	125	25	MR	145	65	S
106	25	MR	126	45	MS	146	65	S
107	15	MR	127	45	MS	147	25	MR
108	25	MR	128	25	MR	148	15	MR
109	15	MR	129	45	MS	149	25	MR
110	5	R	130	65	S	150	65	S
111	15	MR	131	45	MS	CM202 MAI105		
112	1	R	132	45	MS	65	1	
113	1	R	133	15	MR	45	1	
114	25	MR	134	45	MS	65	1	
115	5	R	135	25	MR	85	5	
116	5	R	136	45	MS	4	10	
117	25	MR	137	25	MR	45	1	
118	15	MR	138	65	MS	45	1	
119	25	MR	139	45	MR	45	5	
120	15	MR	140	25	MR	25	1	

Note: R = Resistant MR = Moderately Resistant S = Susceptible HS = Highly Susceptible

Such findings hold significant implications for maize breeding programs aimed at developing cultivars with enhanced resistance to polysora rust, thereby contributing to sustainable maize production and food security.

4. Conclusion

The findings of this study shed light on the inheritance pattern of polysora rust resistance in maize, providing valuable insights into the genetic mechanisms underlying this important trait. The observed segregation ratio of 3 (resistant):1 (susceptible) in the F₂ population suggests that the resistance to polysora rust is governed by the control of a single dominant gene. This finding aligns with previous research demonstrating the monogenic inheritance of rust resistance in maize (Takan *et al.*, 1998; Chungu *et al.*, 2007). Furthermore, understanding the genetic basis of rust resistance enables breeders to employ advanced breeding strategies such as gene pyramiding, which involves stacking multiple resistance genes to enhance durability and broaden the spectrum of resistance (Singh *et al.*, 2017).

The moderate resistance observed in a substantial proportion of the F₂ population suggests the presence of modifiers or quantitative trait loci (QTLs) influencing the expression of rust resistance. These modifiers may interact with the major resistance gene, influencing the degree of resistance conferred by the gene and contributing to the observed phenotypic variation (Kuchel *et al.*, 2007). Further research is warranted to elucidate the genetic basis of moderate resistance and identify potential QTLs associated with this trait.

It is noteworthy that a small percentage of plants in the F₂ population exhibited susceptibility to

polysora rust despite originating from a resistant × susceptible cross. This phenomenon could be attributed to factors such as incomplete penetrance, environmental influences, or genetic background effects (Michelmore *et al.*, 1991). Understanding the mechanisms underlying susceptibility in these individuals is essential for comprehensive elucidation of rust resistance in maize and may uncover novel genetic factors contributing to disease susceptibility.

The utilization of the PLAC method for disease severity assessment enabled precise quantification of rust symptoms, providing valuable data for genetic analysis. However, it is essential to acknowledge potential limitations associated with this method, such as subjectivity in symptom evaluation and variability in disease expression under different environmental conditions (Jeger *et al.*, 2018). Integrating additional phenotypic and molecular approaches, such as histological analysis and gene expression profiling, could provide deeper insights into the mechanisms of rust resistance and complement the findings of this study.

In conclusion, the identification of a single dominant gene controlling polysora rust resistance in maize represents a significant advancement in our understanding of rust resistance genetics. This knowledge lays the foundation for targeted breeding efforts aimed at developing rust-resistant maize varieties with enhanced productivity and resilience. Continued research into the genetic basis of rust resistance, coupled with advancements in breeding technologies, holds promise for addressing the challenge of rust disease in maize and ensuring global food security.

6. Reference

- Chungu C, Magorokosho E, Brown J A and Labuschagne M T. 2007. Genetic diversity in tropical maize inbred lines for resistance to Polysora rust (*Puccinia polysora* Underw.). *Euphytica* **158**(1-2): 181-191.
- Cramer H H. 1967. Plant protection and world crop production. Bayer, Leverkusen, West Germany. pp. 54.
- James W C. 1971. An illustrated series of assessment keys for plant diseases, their preparation and usage. *Canadian Plant Disease Survey* **51**: 39-65.
- Jeger M J, Pautasso M, Holdenrieder O and Shaw M W. 2018. Modelling disease spread and control in networks: implications for plant sciences. *New Phytologist* **218**(1): 41-53.
- Kuchel H, Williams K J, Langridge P and Eagles H A. 2007. Genetic dissection of grain yield in bread wheat. II. QTL-by-environment interaction. *Theoretical and Applied Genetics* **115**(7): 1015-1027.
- Michelmore R W, Paran I and Kesseli R V. 1991. Identification of markers linked to disease-resistance genes by bulked segregant analysis: a rapid method to detect markers in specific genomic regions by using segregating populations. *Proceedings of the National Academy of Sciences* **88**(21): 9828-9832.
- Munkvold G P and Mengistu A. 1998. Resistance of maize hybrids and inbred lines to northern leaf blight and Polysora rust. *Plant Disease* **82**(2): 179-184.
- Singh V K, Khan A W, Jaganathan D, Thudi M, Roorkiwal M, Takagi H, Kumar V, Chitikineni A, Gaur P M, Sutton T, Terauchi R, Varshney R K. 2017. QTL-seq for rapid identification of candidate genes for 100-seed weight and root/total plant dry weight ratio under rainfed conditions in chickpea. *Plant Biotechnology Journal* **15**(7): 907-919.
- Takan J P, Lyon A K, Williams P H and Labuschagne M T. 1998. Characterization of resistance to Polysora rust in maize. *Euphytica* **99**(3): 187-192.