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Identification of Stable Source of Resistance to Sorghum Downy Mildew in Maize (Zea mays L.)

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Abstract: *Breeding for sorghum downy mildew (SDM) is a major focus for corn, which is continuously subjected to yield losses due to this disease in India. Several methods have been used to control the disease, including the use of fungicides like Metalaxlyl but development of resistant hybrids is most effective and eco-friendly approach. Present study investigated the reactions of 50 corn inbred lines to sorghum downy mildew infection at the national sorghum downy mildew screening nursery, Zonal Agricultural Research Station during the Kharif and Rabi season of 2010. Of the 50 maize inbred lines, three inbred lines viz., CML226, SKV50 and EC598475, were found to be resistant with less than 10 per cent sorghum downy mildew infection. Two inbreds were moderately susceptible and remaining inbreds were either susceptible or highly susceptible. The overall results indicate that the three lines are resistant to downy mildew.*

1. INTRODUCTION

Maize (Zea mays L.) occupies a unique position in world agriculture as a food, feed and industrial crop. In India, maize has emerged as third most important grain crop next to rice and wheat. Cultivation of high yielding hybrids is majorly threatened by a fungal disease called “downy mildew”, particularly in South India. Downy mildew causes considerable damage to maize, sometimes up to 100 per cent, so there exists enough scope to identify stable source of resistance to downy mildew which improve the production and productivity of maize by development of high yielding single cross maize hybrids with resistance to downy mildew.

Downy mildews in maize, belonging to the genera *Peronosclerospora* and *Sclerophthora*, are the most destructive diseases of this crop in tropical Asian countries. The major downy mildew diseases occurring in Asia include sorghum downy mildew [*Peronosclerospora sorghi* (Weston & Uppal)], Philippine downy mildew [*P. philippinensis* (Weston) Shaw], Java downy mildew [*P. maydis* (Raciborski)], sugarcane downy mildew [*P. sacchari* (Miyabe) Shirai and Hara] and brown stripe downy mildew [*Sclerophthora rayssiae* var. *zeae* Payak. The downy mildews are the “old world” diseases causing enormous losses in various crop plants, including maize. Twenty one species of downy mildew fungal pathogens have been reported to attack members of the family Poaceae, of which 10 species in three genera of fungi have been reported to cause different types of downy mildews in maize [3. 11, 12].

Downy mildew caused by *Peronosclerospora sorghi* ((Weston & Uppal) C.G. Shaw) is a major disease of corn in southern India. It was first observed and reported by Butler [2] in Maharashtra and Tamil Nadu states of India as *Sclerospora graminicola*. Later, Melechers [7] reported the downy mildew of maize and sorghum in Egypt. He gave the evidence that it might have entered Egypt through the packing material from India. The disease seriously damages corn in major corn producing area, especially where corn is grown continuously throughout the year. Sorghum downy mildew (SDM) is particularly prevalent in the peninsular India (Tamil Nadu, Karnataka, Andhra Pradesh) causing losses of 30 per cent and higher [6]. *P. sorghi* can damage corn from the seedling until the flowering stage and grows well at temperatures of 12ºC to 32ºC [5]. The disease cultured from single conidia on corn can produce spores in many shapes and sizes of around 24-26 x 12-20 microns {9]. The spread of the disease is serious in the rainy season (May-Sep) when relative humidity is high. It has been reported that Metalaxlyl can control the disease effectively, but only in some areas. Therefore, the most efficient, effective and economically long term control of downy mildews of maize is identification and exploitation of host resistance. Present study is to identify stable source of resistance to sorghum downy mildew using corn inbred lines is an effort in that direction.

2. MATERIAL AND METHOD

A set of 50 maize inbred accessions formed the basic material for screening downy mildew resistance. The selfed seeds of 50 inbred lines were obtained from the All India Co-ordinated Maize Improvement Project, Zonal Agricultural Research Station, V. C. farm, Mandya.

Screening for downy mildew resistance: Screening of inbred lines for downy mildew resistance in order to identify and select parents for further study I e, development of $F_{2:3}$ mapping population to identify QTLs conferring resistance to SDM. During *Kharif* and Rabi season of 2010, inbred accessions were raised in national sorghum downy mildew sick plot nursery, maintained at VC Farm, Mandya adopting randomized block design with two replications. The 'sandwich method and spreader row technique' was used for screening the genotypes against SDM [2]. The spreader rows were planted on all sides of the experimental block 30 days prior to the planting of the test entries. One bed of spreader row was planted for every two beds of test entries. As a susceptible check, uninfected CM 500 seeds were planted after every tenth row of test entries. Spraying of spores of the pathogen was done seven days after sowing, using Knapsack sprayer in the early morning at 3AM for about seven to ten days i e., till the disease symptoms appeared on the seedlings of susceptible check (CM500). Severe infection (98–100% DM incidence) in the check rows across the experimental block indicated uniform and strong pathogen pressure, leaving no possibility for 'disease escapes'. The disease reaction was assessed at 35 days after planting by scoring for systemic DM infection in the individual plants. Disease incidence was calculated as per a modified method reported by [2] and reactions of the genotypes were classified into six different classes as given by [9]: 0%infection (no symptom)=Highly Resistant (HR), 1-10% infection=Resistant (R), 11-25% infection=Moderately resistant (MR), 26-50% infection=Moderately susceptible (MS), 51-75% infection=Susceptible (S) and 76-100% infection=Highly susceptible (HS)..

3. RESULTS AND DISCUSSION

The evaluation of inbred lines for the identification of sources of *P. sorghi* resistance in replicated trials over various seasons to verify the disease reaction. Out of fifty inbred accessions screened for downy mildew under sick plot, three inbreds viz., CML226, SKV50 and EC598475, were found to be resistant with less than 10 per cent sorghum downy mildew infection and exhibiting mean disease incidence of 5.34, 8.17 and 9.13 per cent, respectively. Two inbreds, LM13 and CML224were moderately susceptible with mean disease incidence of 26.26 and 45.04 per cent. CM144, CM502, CML166, CML172, CML358, CML411, CML470 and CML483 had disease incidence between 30.53% and 73.26% and were considered susceptible. Remaining all inbreds were highly susceptible showing more than 75% disease incidence (Table 1). The analysis of variance revealed that the differences among the genotypes were highly significant for this trait.

The overall results indicated that CML226, SKV50 and EC598475 inbreds were identified as stable resistant sources to *P. sorghi* which are similar to the studies of [4], [8] and [11], they also screened maize inbreds to isolate contrasting parents for development of $F_{2:3}$ mapping populations against sorghum downy mildew for further mapping studies. Identified resistance sources can be utilized to develop high yielding single cross hybrids with resistance to SDM which are suitable for both the subsistence and commercial farmer.

Table 1: Per cent incidence of sorghum downy mildew in 50 maize inbred lines screened at Mandya over two seasons

Sl. No.	Pedigree	*Kharif* 2010	Rabi 2010	Mean	Reaction
1	CM 132	77.05	89.96	83.51	HS
2	CM 137	64.16	52.89	58.53	HS
3	CM139	64.38	71.11	67.75	HS
4	CM144	32.67	39.58	36.13	S
5	CM149	66.82	69.52	68.17	HS
6	CM212	89.89	82.86	86.37	HS
7	CM502	38.73	40.19	39.46	S
8	CML137	81.75	78.31	80.03	HS
9	CML-153	92.96	89.96	91.46	HS
10	CML-161	73.54	78.43	75.99	HS
11	CML-163	89.96	80.96	85.46	HS
12	CML-166	34.77	50.14	42.46	S
13	CML-169	79.79	82.79	81.29	HS
14	CML-172	76.21	70.31	73.26	S
15	CML224	41.51	48.57	45.04	MS
16	CML226	2.61	8.07	5.34	R
17	CML238	57.45	60.83	59.14	HS
18	CML304	71.68	61.25	66.46	HS
19	CML326	76.95	77.43	77.19	HS
20	CML335	71.44	69.27	70.36	HS
21	CML337	80.19	83.07	81.63	HS
22	CML338	68.74	62.48	65.61	HS
23	CML358	38.89	45.65	42.27	S
24	CML359	72.95	67.19	70.07	HS
25	CML41	47.53	54.04	50.79	HS
26	CML411	47.37	31.35	39.36	S
27	CML439	78.31	76.91	77.61	HS
28	CML470	25.65	35.41	30.53	S
29	CML483	32.26	36.57	34.42	S
30	CML490	71.54	52.75	62.14	HS
31	DMR-N11	76.34	80.37	78.35	HS
32	DMR-N21	80.96	79.96	80.46	HS
33	DMR-QPM-58	89.66	78.86	79.76	HS
34	DMSC 4-1 DR10	83.85	81.3	82.57	HS
35	DMSC-16	79.96	90.6	85.28	HS

36	EC-598475	8.43	9.82	9.13	R
37	EC-619112	69.77	52.79	61.28	HS
38	HKI-162	86.16	83.45	84.8	HS
39	HKI-164-3	61.37	47.37	54.37	HS
40	HKI-164-4	76.88	80.75	78.82	HS
41	HKI191-1-2-5	71.84	71.69	71.77	HS
42	HKI-26-2-4	59.98	46.77	53.37	HS
43	HKI-34	61.34	49.65	55.49	HS
44	LM 13	25.09	27.42	26.26	MS
45	S91S1WQ-B-B-B-11	80.29	85.83	83.06	HS
46	SARHAD HSRB	91.6	79.96	85.78	HS
47	SKV-50	6.99	9.36	8.17	R
48	MAI105	54.78	62.82	58.8	HS
49	CM202	77.05	89.96	83.51	HS
50	CM500	89.96	89.96	89.96	HS
SEm±		**7.02**	**3.13**	**6.95**	-
CD @ 0.05		**14.18**	**6.29**	**11.65**	-

HS= highly susceptible; MS= moderately susceptible; S= susceptible; HR= highly resistant; MS=moderately resistant; R=Resistant

Table 2: Analysis of variance in maize inbreds evaluated for SDM incidence during Kharif 2010 at Mandya

Source		**Replication**	**Genotypes**	**Error**
df		**1**	**49**	**49**
Kharif 2010	Mean Square	3197.27	1060.5	98.7
	F Val	32.4	10.7	-
	Pr > F	<.0001	<.0001	-
	C (%)	5.33	86.61	8.06
Rabi 2010	Mean Square	673.25	1021.7	19.59
	F Val	34.37	52.15	-
	Pr > F	<.0001	<.0001	-
	C (%)	1.3	96.84	1.86

C=Contribution of different sources of variation towards total variation

4. CONCLUSION

Identified resistance sources can be utilized to develop mapping populations for identification of QTLs and high yielding single cross hybrids with resistance to SDM which are suitable for both the subsistence and commercial farmer.

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