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Selection of back cross population against sorghum Downey mildew in maize (*Zea mays*)

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Abstract
The present research has been done at Department of Millets, Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu, and India with an objective to select resistant progeny in BC_2F_1 population against Sorghum Downy Mildew (SDM) caused by *Peronoclesropora sorghi*. It is an important disease in maize producing regions worldwide and limiting the maize production in many Asian countries. Hence, it is essential to produce a new variety or hybrid which is resistant to Downey mildew in maize to increase the yield. To achieve this objective, the present research was taken in artificial infection under spreader row technique to pick out the resistant progeny from back cross population. The result of present screening technique revealed that among the ten progenies studied, five progenies derived from UMI 79/936 of BC_2F_1 population such as Progeny number 3 (consists of 80 plants), Progeny number 7 (consists of 122 plants), Progeny number 29 (consists of 110 plants), Progeny number 67 (consists of 118 plants) and Progeny number 101 (consists of 78 plants) were found as resistant.

Keywords: Phenotypic screening, SDM, disease score and maize

Introduction
Maize (*Zea mays* L.) is an important cereal crop in world agriculture since it serves as food, feed and industrial crop. The demand for maize is increasing year after year because of increasing the usage of maize. One of the major pathogen which is affecting the yield of maize crop is Sorghum Downey Mildew disease which is caused by *Peronoclesropora sorghi*. It is one of the peculiar disease infecting maize crops in vegetative stage (leaf) and reproductive stage (tassel). During vegetative stage, the affected leaves are shown yellow striped or yellow leaves. During reproductive stage, it will affect the tassel formation, affected tassels are deformed and stunted with bushy appearance and shortened internodes; and also it will not produce the pollen. By this way it will affect the yield of maize. This disease can be controlled by cultural practices and fungicides. Pathogen infection is not completely controlled by following cultural practices and chemical resistance to the pathogen occurs by using fungicides.
In this situation, the research was aimed to develop new cultivars resistant to SDM pathogen. For this purpose, F_1 was developed by crossing the high yielding inbred UMI 79 which is susceptible to SDM as female parent with UMI 936 as male parent resistant to SDM. The F_1 was back crossed with UMI 79 to produce BC_1F_1 progenies. The BC_1F_1 progenies which were resistant to SDM were back crossed with UMI 936 to develop BC_2F_1 progenies. In this present study, ten BC_2F_1 progenies were used with an objective of to select the resistant progeny against SDM.

Materials and Methods
Selection of BC_2F_1 population under SDM in the Natural Infection
The present assessment was done in the ten BC_2F_1 back cross progenies viz., Progeny number 3 (consists of 80 plants), Progeny number 7 (consists of 122 plants), Progeny number 23 (consists of 65 plants), Progeny number 29 (consists of 110 plants), Progeny number 43 (consists of 120 plants), Progeny number 49 (consists of 83 plants),Progeny number 63 (consists of 95 plants),Progeny number 67 (consists of 118 plants), Progeny number 80 (consists of 82 plants) and Progeny number 101 (consists of 78 plants) derived from BC_1F_1 progenies of UMI 79 and UMI 936. These progenies were screened against SDM in sick plot under natural conditions during *Rabi* 2012 which was conducive environment for the pathogen development in order to select the resistant progeny through field screening. The parents and their BC_2F_1 progenies were screened for SDM in sick plot by spreader row technique.

Spreader row technique for SDM screening

This was done during December to January month of Rabi season due to advantage of monsoon season to create conducive environment for pathogen development. Temperature and relative humidity were recorded during each week which plays a major role to spread disease incidence. The methodology followed by George *et al*., 2003; Nair *et al*., 2004 and Nair *et al*., 2005 [2, 5, 4] was adopted to screen the BC_2F_1progenies *i.e.* artificial conditions for disease incidence was created by planting spreader rows of a susceptible maize inbred, CM 500. To ensure 100% of disease incidence, the CM 500 inbred lines which is susceptible to SDM was raised under sick plot in every 11th rows in between to accommodate test entries 30 days after and CM 500 lines also were raised on all the four sides of sick plot. The 30 days' time gap was given to raise the test entries since to allow pathogen inoculums for infect the test entries.

Conidial inoculums preparation & spraying on spreader row

The conidia of *P. sorghi* are an obligate parasite, and it was collected from the fresh, infected plants for inoculations. In this present study, the procedure followed by Cardwell *et al*. (1994) was adopted for conidial inoculums preparation and by utilizing the natural spore producing cycle of the fungus, which involved spray operation in the middle of the night. Maize leaves infected by SDM pathogen have been collected from infected field showing visible symptom of Downey growth on the infected leaves from the previous day early evening and collected leaves were wiped by using wet absorbent cotton and tissue paper to remove old & matured conidia.

The collected leaves with infected SDM pathogen have been spread in a single layer over a tray lined with moist blotting paper and it was closed with another tray lined with moist blotting paper; and it was incubated at 20 ^oC in the dark for six to seven hours for conidia formation. During this time, conidia was collected by washing the infected leaves in chilled distilled water (5 ^oC) using a camel hairbrush and this suspension has been filtered by using double layered muslin cloth. The concentration was adjusted to 6 x 10^5 per ml using a hemocytometer and it was transferred into backpack sprayer. Then this suspension was taken into field and it was sprayed to 10 days old CM500 plants during early morning 3.30. to 4.30 am to enable natural spore producing cycle of pathogen. The test entries (BC_2F_1 progenies) have been planted after confirming 100 per cent establishment of disease in the spreader rows. In that way test entries were exposed to infection by both oospores from the soil and conidia from spreader rows.

Disease assessment in SDM infected Progenies

Germination count has been taken after one week of sowing. The disease incidence was observed and scored at thirty days after plant emergence of test entries. The disease scoring was done individual progeny wise. In each progeny, total number of plants was counted and number of disease infected plants were also counted and recorded. The percentage of (%) disease score was arrived as per standard procedure (Lal and Singh, 1984) [3].

$$\text{The disease score rated as below Percentage downy mildew incidence} = \frac{\text{Total no .of plants}}{\text{No. of plants infected}} \times 100$$

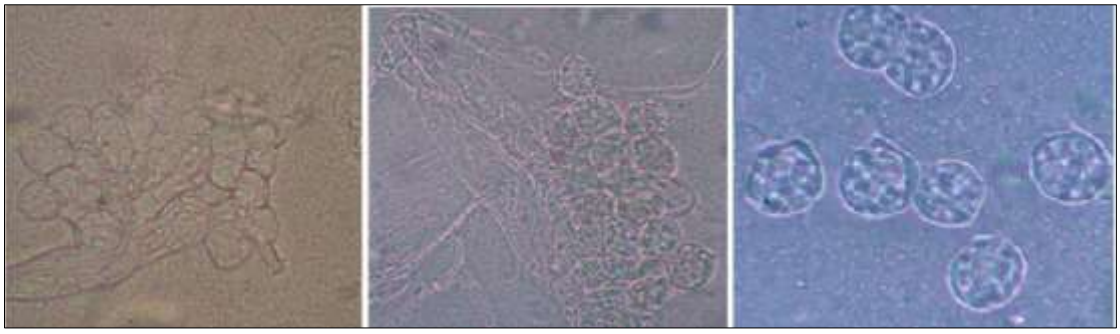
The disease score rated as below

Table 1: Show Percentage of SDM Pathogen infection (%) and Reaction

Percentage of SDM Pathogen infection (%)	Reaction
0-10	Resistance(R)
> 10-30	Moderately Resistance (MR)
> 30-50	Moderately Susceptible (MS)
> 50	Susceptible (S)

Results and Discussion

This research was undertaken to identify the back cross population (BC_2F_1) which was resistant to SDM by adopting the field screening under sick plot. The method followed by Yen *et al.*, 2001 [6] and Nair *et al.*, 2004 and 2005 [4, 5] was adopted to screen the progenies resistant to SDM pathogen. Ten BC_2F_1 back cross progenies viz. Progeny number 3 (consists of 80 plants), Progeny number 7 (consists of 122 plants), Progeny number 23 (consists of 65 plants), Progeny number 29 (consists of 110 plants), Progeny number 43 (consists of 120 plants), Progeny number 49 (consists of 83 plants), Progeny number 63 (consists of 95 plants), Progeny number 67 (consists of 118 plants), Progeny number 80 (consists of 82 plants) and Progeny number 101 (consists of 78 plants) have been used for screening against SDM. (Table.1)



A. Branched Sporangia spores of *Peranosclerosphora sorghi* (SDM) **B.** Sporangia of *Peranosclerosphora sorghi* (SDM) **C.** 100 X Magnification

Fig.1: Electron microscopic observation of sporangia spores in *Perenoscleropora sorghi* fromBC_2F_1plants

Table 1: Phenotypic Screening of Back Cross Population (BC_2F_1) against SDM Pathogen

S.no	Progeny no	Percentage of Disease Incidence (%)	Phenotype (Disease Score –R (Resistant), MS (Moderately Susceptible), S (Susceptible)
1	BC_2F_1 progeny number 3	0	R
2	BC_2F_1 progeny number 7	0	R
3	BC_2F_1 progeny number 23	58	S
4	BC_2F_1 progeny number 29	0	R
5	BC_2F_1 progeny number 43	35	MS
6	BC_2F_1 progeny number 49	42.56	S
7	BC_2F_1 progeny number 63	52.15	S
8	BC_2F_1 progeny number 67	0	R
9	BC_2F_1 progeny number 80	61	S
10	BC_2F_1 progeny number 101	0	R

The progeny number 3 and 7 of BC_2F_1 consists of 80 and 122 plants were observed 0% disease incidence respectively. In the progeny number 23 and 29 consists of 65 and 110 plants have been observed 58% (Moderately susceptible) and 0% (Resistant) disease incidence respectively. The progeny number 43 and 49 with 120 and 83 plants observed 35% (Moderately susceptible) and 42.56% (Moderately susceptible) disease score respectively. Plants from progeny number 63 recorded 52.15% (Moderately susceptible) disease score and the progeny number of 67 observed 0% (Resistant) disease incidence. In the progeny number 80 and 101 consists of 82 and 78 plants were observed 61% (Moderately susceptible) and 0% (Resistant) disease incidence respectively.

The Progenies recorded disease score from 0-10% were selected as resistant progeny. Those progenies recorded > 10% of disease reaction was considered as susceptible progenies and it was excluded from breeding programme. Out of ten progenies studied, five progenies such as Progeny number 3 (consists of 80 plants), Progeny number 7 (consists of 122 plants), Progeny number 29 (consists of 110 plants), Progeny number 67 (consists of 95 plants) and Progeny number 101 (consists of 78 plants) were found as resistant against Sorghum Downey Mildew disease.

Conclusion

It is concluded that the selected five progenies viz., Progeny number 3 (consists of 80 plants), Progeny number 7 (consists of 122 plants), Progeny number 29 (consists of 110 plants), Progeny number 67 (consists of 118 plants) and Progeny number 101 (consists of 78 plants) for resistant SDM will be used for resistance breeding programme.

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