



Effect of fungicides and evaluation of maize genotypes for identifying resistance source against *Rhizoctonia solani* f. sp. *sasakii*

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Abstract

Maize is the most important cereal crop which has dual purpose for the feed and fodder and also one of the important crop for industrial purpose crops, among the many biotic challenges soil borne fungus known as *Rhizoctonia solani* causes banded sheath blight which mainly affect the photo synthetic ability of the plants and also lead to premature death of the plant, chemical as one of the prerequisite of the disease management but encouraging the natural antagonistic population against the soil borne pathogen considered as the best eco- friendly management practices and screening for the host resistance also helps in determine the genotypes to know the resistance pattern among the chemical management Tebuconazole + Trifloxystrobin (0.10%) recorded lowest disease severity (25.71 %) over untreated control (51.43 and 53.09%) followed by Fluxopyraxod + difeconazole (28.29 and 29.39%) as the best compare to biological control.

Keywords: *Rhizoctonia solani*, *sasakii*, tebuconazole, trifloxystrobin

Introduction

Maize (*Zea mays*) is the third most important cereal crop in the world known as “Queen of cereals”, the socio-economic importance of the maize plays a different role in the mode of utilization of the maize crop in different ways such as maize flour for human as food, kernels for the cattle, fodder in the dairy industry, sweet corn in food and beverages industry (Anonymous FAO STAT, 2013).

The grain consumption accounts for 5 per cent of total human dietary calories and proteins consumed globally (direct food pathway, processed or unprocessed). The average daily dietary energy intake per capita from maize food was 156 kcal, compared to a total intake of 2,919 kcal (Sharma *et al.*, 1993) ^[8] (of which 1,311 kcal come from cereals). On average, the daily protein intake per capita from maize as food was 3.8 g (82.5 g, and 12% of the proteins provided by cereals, 32.4 g). food also provides a small amount of fat (1.4 g, or 1.6% of daily intake) (Ullah *et al.*, 2010) ^[9].

The state of Jammu and Kashmir was divided into three climatic zones in which the cold desert region of Ladakh, temperate Kashmir valley and the sub- tropical Jammu region with their own region-specific climatic conditions, the maize crop particularly confined to the Sub tropical regions of the Jammu mostly cultivating in the hilly terrains and some portions of the plains adjoining to the Punjab areas, it have been growing as the rainfed crop in the areas of the well- drained soils of the hilly areas of the Jammu province. Banded leaf and sheath blight of maize caused by the *Rhizoctonia solani* causes the premature death and reducing the yield of the maize crop, the wide host nature of the pathogen can affect over 32 families of the plant species, among the Gramineae family of the Rice and maizemost important,(Sharma and Saxena, 2002) ^[7]. The yield losses

recorded nearly 40.5% in maize with 70.1% of the disease severity and the grain yield loss was estimated 23.9 to 31.9% at disease grading scale of (Malik *et al.*, 2018) ^[3]

.However the serious epidemics the break out estimated as far as 90 per cent in the maize grain yield (Chaudhary *et al.*, 2016) ^[2]. Management of the BLSB is very difficult as the complete soil inoculum must be destroyed in order to control the disease, however the present disease management strategies like the cultural, biological and chemical practices fallowed for the management of the disease, the development of the host resistance that acts the most important source of the management among different control measures (Rani *et al.*, 2013) ^[6].

Evaluation of maize genotypes against BLSB of maize

Maize genotypes of 25 genotypes procured from different sources i.e. MRS Udhampur, IIMR, Ludhiana, MBRSS, Poonch and other local markets. The germplasm was screened under field conditions during *Kharif* seasons of 2021 and 2022 at Maize Research Station SKUAST-J Udhampur. Sowing was done in Augmented Block Design (RBD) with the plot size of 4m×3m with spacing of 60 cm between rows and 40 cm between plants. Recommended agronomic practices and insect pest control measures were followed (Anonymous, 2007). The disease severity was calculated by using the disease rating recorded on the basis of 1-5 scale ((Payak and Sharma, 1981) ^[4].

Results and Discussion

Field evaluation studies reveal that all the treatments were significantly effective and recorded lower disease severity of BLSB in both the crop seasons. The combined treatments of fungal bioagents andfungicides were significantly effective of 1-5 scale (Akhtar *et al.*, 2009) ^[1] at physiological maturity of the crop for screening.

Table 1

| Scale | Disease severity (%) | Disease reaction |
|-------|----------------------|----------------------------|
| 1.0 | 1-10% | Highly resistance (HR) |
| 2.0 | 10%-25% | Resistance (R) |
| 3.0 | 25%-50% | Moderately resistance (MR) |
| 4.0 | 50%-75% | Susceptible (S) |
| 5.0 | >75% | Highly Susceptible (HS) |

Per cent disease intensity (PDI) on foliage due to Banded leaf and Sheath blight was calculated using 1-5 disease rating scale ((Payak and Sharma, 1981)^[4].

$$PDI = \frac{\text{sum of all disease ratings}}{\text{Total no. of leaves} \times \text{maximum grad}} \times 100$$

singly or in combinations in either of the crop seasons. However, foliar spray of Tebuconazole + Trifloxystrobin (0.10%) recorded lowest disease severity (25.71 %) over untreated control (51.43%) (Raman, 2021)^[5] followed by

Fluxapyroxad + difenoconazole 28.29 was correlated by (Zhao *et al.*, 2022)^[10] and azoxystrobin (34.2%) all of which were statistically superior to one another, followed further by foliar spray of Flusilazole (36.62 and 37.29% and propiconazole (36.62 %), respectively during *Kharif* 2021 and *Kharif* 2022 (Table.1). The next treatments lower in superiority recording higher disease severity were Validamycin (40.75%) and propineb (47.32 %) respectively during *Kharif* 2021.

Yield

Table 2: Disease severity and AUDPC values of selected genotypes

| S.no | Genotypes | Disease severity | AUDPC |
|------|---------------|------------------|---------|
| 1 | WN 5988 | 20.8 | 431.96 |
| 2 | WN 32296 | 19.16 | 402.09 |
| 3 | WN1439 | 17.49 | 375.08 |
| 4 | HKI -536 | 28.55 | 617.55 |
| 5 | WN 33153 | 30.47 | 685.28 |
| 6 | HKI 1105-2-1 | 31.12 | 677.79 |
| 7 | WN 2489 | 34.33 | 740.02 |
| 8 | WN 5236-2 | 33.71 | 728.2 |
| 9 | EV 1463 | 34.3 | 740.01 |
| 10 | CM 152 | 34.97 | 753.22 |
| 11 | WN 2424-9-1 | 35.45 | 764.21 |
| 12 | CLM 4482 | 64.08 | 1349.85 |
| 13 | B63 | 28.57 | 596.83 |
| 14 | Double Dekalb | 30 | 657.52 |
| 15 | KH 517 | 27.93 | 608.81 |
| 16 | CP 333 | 31.06 | 668.93 |
| 17 | CP 555 | 29.42 | 636.45 |
| 18 | AJANTA | 56.3 | 1186.13 |
| 19 | C8 | 33.24 | 722.72 |
| 20 | CLM 299 | 35.04 | 757.37 |
| 21 | CLRY030 | 62.39 | 1311.73 |
| 22 | HKI 040-7 | 63.13 | 1329.66 |
| 23 | KDM-500 | 69.94 | 1466.07 |
| 24 | M-4-3 | 65.38 | 1374.4 |
| 25 | MYS-4493 | 65.27 | 1372.22 |

Highest yield was recorded in Tebuconazole + Trifloxystrobin (0.10%) recorded (55.12 q/ha) and lower was recorded in (38.32q/ha) followed by Fluxapyroxad + difenoconazole (49.83 %) and azoxystrobin (30.2 q/ha) all of which were statistically superior to one another, followed further by foliar spray of Flusilazole (36.62 and propiconazole (22.79 q/ha) respectively during *Kharif* 2021.

Screening of maize genotypes for Host Resistance

20-Fig -2 Graphical representation of the AUDPC values

Fig 2: Cluster dendrogram analysis of genotype based on disease severity

Dendrogram analysis of disease severity

The cluster analysis of the dendrogram of the disease severity of the genotypes divided in to two clusters one of the clusters which contain 7 genotypes comes under highly susceptible cluster and another cluster is divided into which 18 genotypes grouped in to one cluster where it contains resistant and moderately resistant with disease severity values of 19-30% disease severity

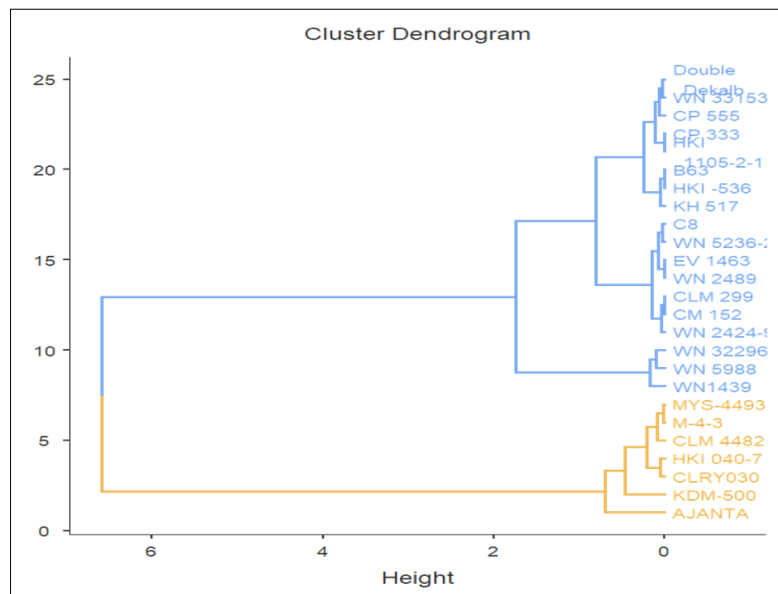


Fig 2: Dendrogram analysis clustering of genotypes of based on the disease severity

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