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Studies on Seed-Borne Fungal Pathogens of Maize Prevailing in Northern Karnataka, India

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A B S T R A C T

Maize is the world's one of the most significant cereal crop along with rice and wheat with several production constraints. Among the biotic stresses, diseases are one of the most important limiting factors in maize production which also include seed-borne fungal diseases. The study including the twelve genotypes from seven locations of Northern Karnataka revealed that, the pathogens like *Fusarium* spp., *Pencillium* spp., *Aspergillus* spp., *Exserohilum turcicum*, *Curvularia lunata*, *Rhizoctonia bataticola* and *Rhizopus* spp. found associated with maize seeds collected in seven multi-location trials. Among the pathogens, *Fusarium* spp. was found dominant in seeds from all the locations followed by few saprophytes and *Exserohilum turcicum.* The seed samples from the Bailhongal location were recorded the highest mean location infection followed by the Konnur and among the genotypes DKC 9133 recorded high per cent seed infection.

Introduction

Maize (*Zea mays* L.) belongs to the cereal family Graminaceae and is one of the leading cereals in the world and ranks third next to rice and wheat (Aldrich *et al.,* 1975). It is grown in wide agro-climatic regions across the world from tropic to temperate countries. It is called as "Queen of cereals" because of its high genetic yield potential with production of 1147.7 million tonnes and productivity of 5.75 tonnes per hectare (Anon., 2021).

Maize is grown in over 170 countries in the world with several production constraints including both biotic and abiotic stress. Biotic stress majorly

includes pests and pathogens. 112 pathogens are known to occur in maize (USDA, 1960), and more than 70 pathogens are seed transmitted. Seed-transmitted pathogens in maize include all three major groups of pathogens *viz*., fungus, bacteria, and virus (Richardson, 1979).

Among the seed-borne fungal pathogens of maize, the major ones are *Alternaria alternata, Aspergillus candidus, Aspergillus flavus, Aspergillus niger, Aspergillus terreus, Fusarium moniliforme, Penicillium* spp., *Cephalosporium acremonium*, *Cladosporium cladosporiodes*, *Curvularia lunata*, *Drechslera maydis,* and *Verticillium alboatrum*.

Besides these, *Mucor* spp., *Rhizopus stolonifer*, *Syncephalastrum racemosum*, *Pencillium* spp., *Trichoderma viride*, *Trichothecium* sp., *Monodicty* spp., *Nigrospora* spp. and *Helminthosporium turcicum*.

The pathogens besides transmitting through seeds, also cause deformities, reduced seed size, necrotic lesions on seeds, seed rot, and other physiological alterations in seeds. It has been noted that seed-borne fungal pathogens are responsible for reducing seed quality, protein, and carbohydrate content.

Reduction or elimination of germination capacity as well as seedling damage, which results in the reduction of crop yield (Dawood and Elshamry, 2015). The fungal invasion may occur during both pre-harvest and post-harvest conditions.

In post-harvest storage, seeds may develop discoloration, seed rotting and caking, mycotoxin contamination, and loss of viability (Kulkarni and Chavan, 2010). These seeds serve as a medium for the survival of these fungi and also facilitate their dispersal to disease-free areas (Somada *et al.,* 2008).

So, the current study was undertaken to learn about the seed-borne fungal pathogens of maize from various locations in northern Karnataka, keeping all the aforementioned issues in mind.

Materials and Methods

The seed samples of twelve genotypes mentioned in Table 1b were collected from seven different multi-location trials of maize *viz.* Arabhavi, Bagalkot, Bailhongal, Dharwad, Konnur, Mudhol and Nippani. These seed samples were screened for seed-borne fungi pathogens by the standard blotter method. Further, one sample was used for the evaluation of seed health testing methods in the detection of seed-borne fungal pathogens.

Standard blotter method

The standard blotter method was developed in 1938 and was later included in the International Seed Testing Association Rules of 1966. Four hundred seeds of each sample were tested by employing the standard blotter method in replications. Three pieces of blotting paper of 90 mm size were moistened with distilled water and placed in 90 mm sterilized Petri plates after draining excess water. Ten untreated seeds were distributed evenly over each Petri plate while placing the untreated seeds. The plates were incubated at 25°C under alternate cycles of 12 hours of NUV illumination and complete darkness. The related fungi were looked for in the seeds after eight days of incubation using a stereoscopy-binocular microscope, and their habits and colony characteristics were used to identify them (Anon., 1999).

Identification of fungi

The identification of fungi was done based on the signs and symptoms observed on seeds. Further confirmation was done after isolation based on spore morphology and colony character according to the description given in Ellis (1971) and Barnett and Hunter (1972).

Results and Discussion

The examining the seed samples of twelve genotypes from seven multi location trials reveled that, the highest seed infection was observed on seed

samples from Bailhongal with location mean per cent seed infection of 56.66 and lowest in Dharwad with 35.00 per cent. The pathogens *viz*., *Fusarium* spp. (34.45%), *Penicillium* spp. (26.42%), *Aspergillus* spp. (21.24%), *Exserohilum turcicum* (7.77%), *Curvularia lunata* (2.59%), *Rhizoctonia bataticola* (1.55%) and *Rhizopus* spp. (5.95%) were among the pathogens discovered associated with maize seeds, which includes both pathogens and saprophytes.

With a relative seed infection rate of 34.45, *Fusarium* spp. dominated the pathogen population in seed samples from every location, followed by *Penicillium* spp. and *Aspergillus* spp. Among the genotypes, DKC 9133 had the highest mean seed infection rate, 54.28, and BRMH 10 had the lowest, 34.28.

The seed samples of twelve maize genotypes collected from seven Multi Location Trials (MLT) were screened initially for seed-borne mycoflora by employing standard blotter method. The results of this study indicated the dominance of *Fusarium* spp. along with the other six pathogens *viz*. *Penicillium* spp., *Aspergillus* spp., *Exserohilum turcicum, Curvularia lunata*, *Rhizoctonia bataticola* and *Rhizopus* spp. which was similar to the organisms reported by Rahmatzai and Saifulla (2011) during screening of seed samples from twenty-three maize genotypes collected from eleven districts of Karnataka by standard blotter method.

The fungal pathogens found associated with those seed samples includes *Aspergillus flavus, Aspergillus niger*, *Penicillium* sp., *Fusarium* sp., *Nigrospora oryzae, Acremonium strictum, Alternaria* sp., *Bipoloris* sp. and *Curvularia* sp. Debnath *et al.,* (2012) subjected the maize seed samples to standard blotter method and they found that *Aspergillus niger, Aspergillus flavus, Fusarium* spp., *Pencilium oxalicum, Curvularia lunata,* and *Rhizopus stolonifera* were associated with maize seeds and Akonda *et al.,* (2016) also examined a seed sample of maize collected from four maize growing districts and examined for seed-borne microflora by standard blotter method. The fungi namely *Aspergillus flavus, Aspergillus niger*, *Alternaria alternata*, *Bipolaris maydis*, *Curvularia lunata, Fusarium oxysporum, Fusarium moniliforme*, *Penicillium oxalicum, Rhizoctonia bataticola,* and *Rhizopus stolonifer* were found on seeds. As a results of Dawood and Elshamry (2015), they compared the relative density and frequency of external and internal microflora associated with maize grains. Based on the relative density and percentage frequency. The organisms of the genus *Fusarium* were predominantly isolated from maize grains. *Fusarium* spp. was found widespread as it was observed in seed samples from all the locations.

Fusarium is both an internally and externally seed-borne pathogen, it is transmitted by various parts of seeds showing various mechanisms such as internally or externally seed-borne disease leading to localized or systemic infection in some cases. Gonzalez *et al.,* (1995) in corn samples from five locations in Argentina.

The frequency and relative density of the predominant genera of fungi comprising both the internal and external mycoflora associated with corn produced at five locations indicates *Fusarium* was the most prevalent component of the internal and external seedborne mycoflora with respect to both frequency and relative density at all locations and Singh *et al.,* (2018), when they examined the maize seed samples collected forty-five locations in nine districts from Delhi, Haryana and Uttar Pradesh to evaluate the post-harvest seed mycoflora. 270 seeds were analyzed from each location to identify the seed-colonizing fungi. *Fusarium* spp. showed a widespread occurrence in all the samples tested.

In the current analysis, the highest percent seed infection location mean was found in Bailhongal (56.66%) and the lowest in Dharwad (35.00%) among the seed samples of twelve genotypes evaluated from seven MLTs. This could be a result of the provenance impact and local microclimates to which the seeds were exposed both during and after harvest.

Table.1a Location pooled per cent seed infection on seed samples collected from different multi location trials

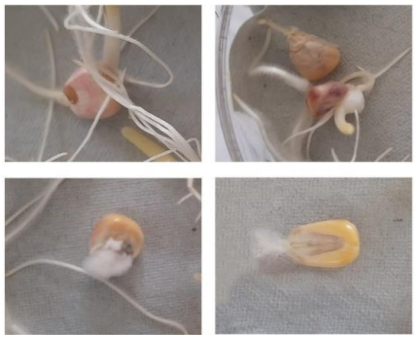
Sl. No.	Location	*Fusarium* spp.	*Exserohilum turcicum*	*Rhizoctonia bataticola*	*Curvularia lunata*	*Aspergillus* spp.	*Penicillium* spp.	*Rhizopus* spp.	Location mean
1	Arabhavi	19.16	3.33	0.00	1.66	4.16	18.30	1.66	48.33
2	Bagalkot	19.16	2.50	1.66	1.66	3.33	13.33	5.00	45.00
3	Bailhongal	12.50	4.16	0.83	0.83	22.50	10.83	5.00	56.66
4	Dharwad	14.16	4.16	1.66	2.50	10.00	6.66	0.00	35.00
5	Konnur	17.50	3.33	0.00	0.83	11.66	16.66	3.33	53.33
6	Mudhol	13.33	4.16	0.00	0.00	12.50	10.00	3.33	42.50
7	Nippani	15.00	4.16	0.83	0.83	10.00	10.00	1.66	41.66
	Relative per cent seed infection	34.45	7.77	1.55	2.59	21.24	26.42	5.95	

Table.1b Genotype pooled per cent seed infection on seed samples collected from different locations

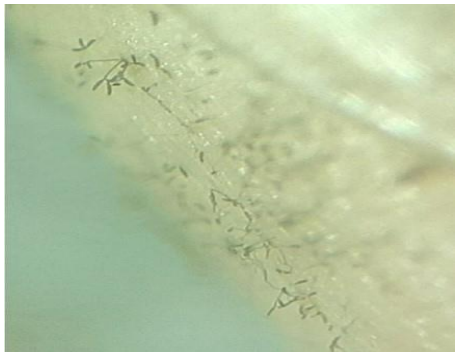
Sl. No.	Genotype	Per cent seed infection in different locations							Mean per cent seed infection
		Arabhavi	Bagalkot	Bailhongal	Dharwad	Konnur	Mudhol	Nippani	
1	RCRMH 3	40	60	40	50	80	40	30	48.57
2	BRMH 17082	30	70	80	50	30	30	40	47.14
3	GH 1851	70	50	40	30	40	80	40	50.28
4	GH 150125	60	20	80	30	60	20	10	40.00
5	GH 0727	60	10	50	60	60	10	40	41.71
6	RCRMH 18	60	40	40	40	70	50	30	47.71
7	NK 6240	30	50	60	20	80	50	30	45.71
8	AH 8067	50	40	50	50	60	60	50	51.42
9	DKC 9133	50	70	70	20	60	40	70	54.28
10	RCRMH 16	70	30	90	10	40	70	60	52.85
11	BRMH 10	40	30	30	50	40	30	20	34.28
12	AH 8089	20	70	50	10	20	30	80	40.00

Fig.1 Microphotograph of different seed-borne fungi propagules on maize seeds

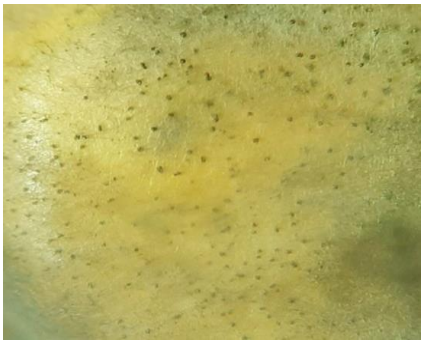
Fusarium spp.



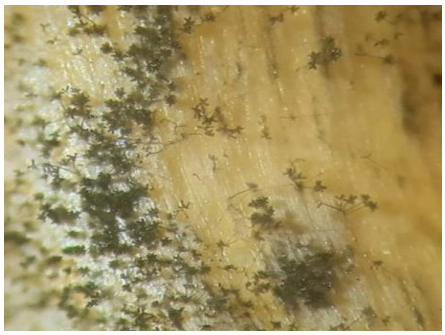
Exserohilum turcicum



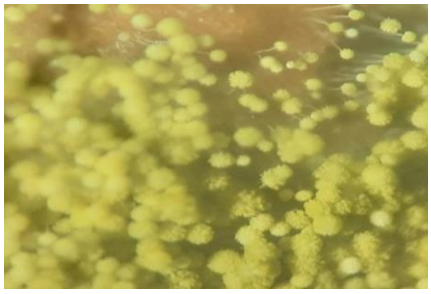
Rhizoctonia bataticola



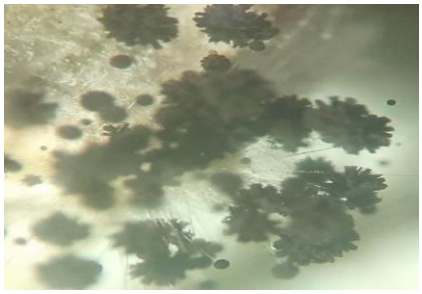
Curvularia lunata



Aspergillus flavus



Aspergillus niger



Penicillium spp

Rhizopus spp.

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Conflict of interest

On behalf of all authors, the corresponding author states that there is no conflict of interest.

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