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Source of Stable Resistance against Post Flowering Stalk Rot of Maize (Zea mays L.) in Various Maturity Groups and Specialty Corn in Subtropical Regions of India

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ABSTRACT: Post flowering stalk rot is a serious biotic compulsion to corn production in subtropical or tropical areas. It is a disease which is incited by multiple infectives, among them Fusarium verticillioides and *M. phaseolina* are the utmost that involved in pith decaying, wilting and drying in early age of plants in India's subtropical regions. Almost all the maize cultivars have exhibit a crucial level of disease incidence at tessling and silking stage. A systematic breeding programme for screening on PFSR initiated in India, collaboration with Indian Institute of Maize Research (IIMR), Ludhiana and Asian Regional Maize Program of CIMMYT. In the process of these programme, genotypes screening was carried out at 'hotspot' location in Udaipur, Rajasthan for PFSR, inoculated through toothpick method were using artificially the promising maize genotypes, repeatedly, resistant plants were selfed to acquire resistant cultivars. After considerable regular screening, Fusarium stalk rot, 150 maize germplasm were screened in field. Eight genotypes namely AH1625, BAU-MH-18-2, GGMH-114, GK 3207, CMH-12-686, CAH 1511, ADH 1619, and FQH-148 reveal highly resistant genotypes with disease score of 1.0-2.0. previously mentioned genotypes may be convenient for resource use in breeding for resistant to PFSR disease.

Keywords: Fusarium verticilloides, Genotypes, Resistant source, Artificial inoculations, Pre mature wilting etc.

INTRODUCTION

Maize (Zea mays) is prominent crop across the world after 1211.64 m ton production and 5573 kg ha⁻¹ roductivity from 191.89 m ha area (Anno., 2021). India stand 4th in terms of area and 7th in production among maize growing countries, which mean India has 4% of area and contributes 2% in production of maize, globally (India stat, 2018-19). According to AICRP Report, 2017, Maize production is bounded by different living and non living causes including the fungal, bacterial, viral, nematodes and others. In India, Total 65 diseases were reported, among them 13 were point out as vital diseases that affect very badly the crop yield. Apart from all the diseases, fungal disease post flowering stalk rot caused by Fusarium verticillioides is most crucial disease of maize worldwide Khokhar et al., 2014). PFSR is reported from all major maize growing countries, including India, China, Indonesia, Laos, Philippines, Thailand, Cambodia, Pakistan and Vietnam (Yang et al., 2010; Lal and Singh, 1984). Some of the major restraint that obstruct maize production worldwide are disease PFSR, and in Asia,

losses due to PFSR range from 10% to 80 per cent (Swamy et al., 2019; Yu, et al., 2017; AICRP, 2014; Li et al., 2010; Mahuku, 2010; Logrieco et al., 2002). Stalk rot symptoms are observed at post flowering stage and pre harvest stage at partial maturity. PFSR become crucial at moisture stress condition after silking and tasseling (Kumar and Shekhar, 2005, Williams et al., 2008; Chowdary et al., 2018). Affected plants leaves dry one after the other, wilted and die within few days. thereby, producing light weight ears, undergo partially or poorly filled kernels and stalk rot infected plants may easily lodge and ears tilted at harvest, which makes harvesting difficult (Singh et al., 2012). The entity Fusarium enters maize plants through root system or through above ground wounds caused by mechanical injury, Nematodes, insects, or hail. After entrance of macro and micro conidia, they either remain dormant up to the crop fully grown or instant start to colonizing and disrupt the metabolic and physiological functions of the plant. As we know, stalk rot of maize is a multipathogenic disease involving more than one pathogen, so is very strenous to manage with solitary

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control techiques. The unavailability of potent resistant sources to the *Fusarium* has been a limitation to control the disease. The Major motive of this field work was to identify new potent sources of resistance to PFSR and persuasion their steadiness across multi locations by multiyear trails in different seasons. Thus, the identified 08 potent disease resistance sources could be used for developing promising maize hybrids.

MATERIALS AND METHODS

Sample Collection, Isolation, Purification, Identification and Maintenance of Fusarium Culture: A random survey was conducted in southern Rajasthan for collection of diseased Samples of PFSR from severely infected fields for experiment and were brought to the laboratory for isolation, proving pathogenecity and purification of the Fusarium spp. Culture of *Fusarium spp.* was isolated from moisture stressed conditions infected stem of maize through splitting under aseptic surroundings in laboratory. The sporulating cultures were identified on the basis of general morphological, cultural pattern and characters of somatic and reproductive structures with the help of "Laboratory Manual for Identification of Fusarium Species" (Booth, 1971) and on the basis of identification reports, which received from ITCC, New Delhi. The pathogen isolates were again sub cultured on PDA medium and slants and allowed to colony growth at $28 \pm 2^{\circ}$ C temperature for seven days and maintain in refrigerator for further use at 5°C temperature.

Location of Experiment conducted & Sources of Genotypes: Different specialty corn genotypes and different maturity gropus maize genotypes around 150 genotypes were sowed for potent source of resistance in field against *F*. verticillioides received from IIMR, Ludhiana. This experiment was conducted in *Kharif*-2019 and *Kharif*-2020 to screen the test genotypes in every group of maturity and specialty corn. Various maturity groups including NIVT-Late (15 entries), NIVT-Medium (15 entries), NIVT-Medium A (15 entries), NIVT-Early (15 entries), AVT-Late (10 entries), AVT-Medium (10 entries), AVT-Early (10 entries), Rainfed maize –Late (10 entries), Rainfed maize-Medium (10 entries), Rainfed maize-Early (10 entries) and different specialty corn groups *viz*. Sweet

corn (10 entries), Baby corn (10 entries) and QPM (10 entries) were picked over through artificially using tooth pick inoculations. These various germplasm lines were received from different sources like Indian Institute of Maize Research, Ludhiana and station breeder AICRP-Maize (All India Coordinated Research Project), plant pathology maize departmental field B3a, MPUAT, Udaipur. Seeds were sown in rows each of 3 m length and row to row and plant to plant distance were maintained as 60×20 cm respectively. For artificial inoculations, toothpick method was used after tassling as per methods. All the endorsed agronomic operations were followed to maintain a good crop field. Tooth Pick Inoculation technique: Toothpick inoculation was done with different isolates of Fusarium verticillioides at flowering stage around 55-60 days old maize plant using one toothpick per plant given by Leslie and Summerell (2006). For inoculation, a slanted hole (2 mm) was made in the second or third inter node of maize stalk from the ground level with the help of a Zebber and the tooth pick with culture of Fusarium verticillioides was inserted in the hole. This procedure has been used for pot as well as field trials and all screening experiments during the course of analysis. Inoculums multiplied on sawdust based substrate was also added in furrows for additive effect of PFSR.

Disease scoring : Observations were taking on the appearance of weaker plants which is showing disease symptoms and disease severity at the harvesting stage. Just before harvesting or at the time of harvesting, inoculated internodes of maize plants were split open longitudinally to see the expanse of stalk pith damage in the form of brownish, blackish or pinkish discolored stalk according to species inoculated. The percent disease index was recorded on 1 to 9 standard disease rating scale which is given by Young (1943);Sobowale (2011). The disease percent reaction was quantifiable described as 1.0-2.0 as Highly Resistant, 2.1-4.0 as Resistant, 4.1-5.0 as Moderately Resistant, 5.1-6.0 as Moderately Susceptible, 6.1-7.0 as Susceptible and 7.1-9.0 as Highly Susceptible (Anita, 2016).

Per cent disease index (PDI) was calculated using following the standard formula

 $PDI = \frac{Grand \ total \ of \ individual \ disease \ rating}{Total \ number \ of \ plants \ assessed \ \times Maximum \ rating \ scale} \times 100$

RESULTS AND DISCUSSION

Screened out of the maize genotypes against stalk rot pathogen (*F. verticillioides*): Host plant resistance (HPR) is most effective, environmentally safe or cost effective component in management module of PFSR. Therefore, a screening programme was conducted to identifing the source of resistance as well as resistant genotypes to PFSR which can be used for development of resistant varieties or can directly be used as such to diminish loss to Farmer. Identification of potent novel source of resistance to *Fusarium* stalk rot principal developing disease free hybrids from genotypes which reduce the inoculum potential and load, lengthen the life of hybrids and reduce the cultivation cost. A collaborative screening programme with IIMR (Ludhiana), winter nursery, Hyderabad and CIMMYT, India was carried out at Udaipur, Plant Pathology maize Departmental field B3a and germplasm were screened under artificial inoculation combined with sick plot condition. A total of 150 inbreds received from IIMR and screening of the lines was carried out during *Kharif* season 2019 and *Kharif* season 2020 with distinct diversified disease response in received genotypes to *F. verticilloides*.

The present study revealed that out of 150 genotypes, most of the genotypes showed resistance against PFSR that was investigated on 1-9 scale based. Less than 2 rating showed high level of resistance, while resistant genotypes exhibit rating between 2 to 4, rating above 5 exhibit susceptibility and rating 9 showed highly susceptible. In this investigation HR, R, MR, S, MS, and HS genotypes were identified. Trial NIVT had 60 genotypes, out of them 4 genotypes were identified as HR, 24 genotypes were identified as resistant, 13 genotypes were identified as MR, 10 genotypes were identified as MS, 6 genotypes were identified as S (susceptible) and 3 genotypes were identified as HS. AVT trial had 30 genotypes, out of them 8 genotypes were identified as R, 12 genotypes were identified as MR, 6 genotypes were identified as MS, 3 genotypes were identified as S and 1 genotype was HS. In this same way, Raifed trials had 30 genotypes in which 3 genotypes were identified as HR, 9 genotypes were identified as MR, 9 genotypes were identified as MS, 4 genotypes were identified as S and 5 genotypes were identified as HS. In case of QPM trail had 10 genotypes in which, 1 genotype was HR, 7 genotypes were identified as R and 2 genotypes were identified as MR. In this same manner, Baby corn trial had 10 genotypes in which 4 genotypes were identified as R, 2 genotypes were identified as MR, 3 genotypes were identified as MS and 1 genotype was HS. In case of Sweet corn

trail, total genotypes were 10 in which 9 genotypes were identified as R and 1 genotype was MR. Thus, it conceivable accentuated from the observations that these identified highly resistant genotypes and resistant genotypes had principal resistant genes against F. *verticilloides* can be used for future programme and seed multiplication purpose.

Similar screening to search the source of resistance were done by Subedi, et al. (2021), screened thirty genotypes of maize for maize stalk rot resistance during kharif season for terai region of Nepal and found that -95/RML-96, ZM-401, Rampur 34, Ram S 03 F 08 and TLBR S 07 F 16 showed resistant reaction against the disease. Lingaraj et al. (2019), exhaustively screened through artificial inoculations in 50 inbreeds and 50 hybrids against F. verticillioides. Among these 50 inbred lines of maize, only 5 lines were recorded as resistant inbred and 19 inbred were recorded as moderately resistant lines. Jat, et al. (2017) supported this result with notable reactions in disease development index (1-9 scale) for PFSR in different lines. They evaluated 80 genotypes of maize and found that there are 2 lines, i.e., QPM PMSQ 5 and L QPMH 115 showing highly resistant reaction, 50 genotypes were identified resistant, 13 genotypes were moderately resistant, and 10 genotypes were moderately susceptible, 3 genotypes were susceptible and 2 genotypes were highly susceptible against PFSR. Likewise, Khokhar and Sharma (2014) identified resistant germplasms of maize against PFSR. They screened 189 lines of maize germplasm out of them 12 lines are pick out as highly resistant, 73 lines as resistant and 29 lines were pick out as moderate resistant genotype.





The resistant inbred lines to PFSR are CA14514-4-3-1-B, CA14514-8-1-2-B AND CA14514-7B-2-B. Small *et al.* (2012) also reported 5 maize inbred lines showed resistance to *Fusarium* stalk rot *viz.*, CML 390, CML 444, CML 182, VO617Y-2 and RO549W and 19 expressed moderately resistant reaction. Two lines *viz.*, CM 202 and MAI 766 were moderately resistant to *Fusarium* stalk rot (Archana, 2017). Singh *et al.* (2000), also identified composite and hybrid varieties of Rabi season maize cultivars, showed resistant reaction against PFSR (*F. moniliforme*). He found hybrids BH 6078, ICI 736, KH 4201, KH 9204 and SSF 3128 were highly resistant. In Addition 61 and 30 germplasm were moderately resistant to PFSR. The promising resistance sources were also reported by Bohra *et al.* (2001), pick out Deccan-103 and 9 other genotype showing resistant reaction to PFSR of Maize.

 Table 1: Category wise disease reaction of different maize genotypes against PFSR under artificial inoculation in field

Sr. No.	Rating	Disease Reaction of Genotype	Maize Genotype			
1.	1.0-2.0	Highly Resistant	AH1625, BAU-MH-18-2, GGMH-114, GK 3207, CMH-12-686, CAH			
	2.1- 4.0	Resistant	CMH 15 006 CMH 15 008 CD 555 CD 802 DKC 0207 CHI 6352 AH			
2.			8245, AH 8452, AH 4142, AH 4167, ADV 7745, DKC 8209, HKH-371,			
			HKH-372, IIMWH-1901, AH 8622, AH 3254, BAU-MH-18-1, DH 321,			
			DH 329, DKC 7204, EH 3524, FH 3912, HKH 370, BLH 137, BH 416215,			
			BLH 118, CAH 1511, DKC 9190, DKC 9198, JH 32094, APH-1, APH-2,			
			APH-3, APQH-1, APQH-8, IIMRQPMH-1705, IQPMH-18-4, ABHS4-2,			
			AH 7204, DBCH-326, IMHSB-19KB-1, BSCH 417006, BSCH 417139,			
			CPSC-301, ISCH-0913, ISCH-1901, NUZI 205, NUZI 260, Super sweet,			
			Sweet purple			
	4.1- 5.0	Moderately Resistant	ADV 7/13, AH 80/2, AH 5158, BRMH-1/068, AH 1634, BAU-MH-18-3,			
			CMH-12-080, DKC 8205, HM-19203, H1 519015, AH 8323, AH 1608,			
			BYMH-13-5, ADV 1390064, ADV /132, BIO 534, JH 16041, BH 416032,			
3.			DKC 8181, DKC-9194, AH 8181, FH 38/9, JH 31947, JH 32014, JH			
			52050, CMH-15-005, SUFYA, CMH-08-287, OMH14-27, KCKM 177, BIO 0544 ADH 2106 DKC 7074 JIMDODMH 1702 JODMH 12.2 ADHS4 1			
			9544, ADH 8100, DKC 7074, IIMKQFMH-1708, IQFMH-18-2, ADH54-1, AHD 7085, CDeveat 2			
			AIL 4120 DIL 417002 DIL 417152 CMIL 15 012 DIL 207 DIL 208 LIM			
4.	5.1-6.0	Moderately Susceptible	An 4159, Dn 41/202, Dn 41/152, CMn-15-012, Dn 527, Dn 528, nm 10305 IMHSB 10K 10 IMHSB 10K 11 AH 8178 EH 3571 ADV			
			1300164 CD 858 AH 4271 EH 3861 IH 31050 IH 32057 ADV 7022			
			BIO 9682 CMH-08-282 VAMH 15036 ADV 7022 AH 8127 BIO 605			
			AH 5021, AH 7043, BAUBCH-18-1			
_	< 4 = 0		AH 4272, BH 417182, IAHM 2016-38, IAMH 2016-2, DH-330, B 57, HT			
5.	6.1-7.0	Susceptible	17169, ADV 7022, Early composite, CMH-08-292, DMH 121			
6.	7.1-9.0	Highly Susceptible	AH 8753, AH 1645,BH 417193, AH 7067R, NK 6240, RCRMH-4-1,			
		inginy susceptible	RCRMH-4-1, Vivek Hybrid 45			

 Table 2: Summary of the tested maize entries in highly resistant reaction, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible.

	Maize germplasm maturity group	Total Entries	PFSR Disease Rating (1-9)						Maximum
Sr. No.			HR 1.00-2.00	R 2.10-4.00	MR 4.10-5.00	MS 5.10- 6.00	S 6.10-7.00	HS 7.10- 9.00	disease Rating of Genotypes in different groups
1.	NIVT - Late	15	-	6	4	2	1	2	7.4
2.	NIVT -Medium	15	2	4	3	4	1	1	7.15
3.	NIVT- Medium A	15	2	5	3	2	3	-	6.2
4.	NIVT- Early	15	-	9	3	2	1	-	6.3
5.	AVT Late	10	-	2	4	2	2	-	6.1
6.	AVT Medium	10	-	5	3	1	-	1	7.5
7.	AVT Early	10	-	1	5	3	1	-	6.1
8.	Rainfed Maize-Late	10	1	-	3	3	1	2	7.7
9.	Rainfed Maize- Medium	10	1	-	3	3	2	1	7.2
10.	Rainfed Maize- Early	10	1	-	3	3	1	2	7.4
11.	QPM	10	1	7	2	-	-	-	4.5
12.	Sweet Corn	10	-	9	1	-	-	-	4.6
13.	Baby Corn	10	-	4	2	3	-	1	5.9
	Total	150	8	52	39	28	13	10	

CONCLUSION

Throughout the years, maize genotypes AH1625, BAU-MH-18-2, GGMH-114, GK 3207, CMH-12-686, CAH 1511, ADH 1619, and FQH-148 pick up as highly resistant response with disease score of 1.00-2.00. These genotypes show beyond doubt useful for utilization for breeding programmers to resistant response against the post flowering stalk rot disease with maximum yield in subtropical India and specially in southern Rajasthan for higher grain yield in maize.

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Conflicts of Interest. None.

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