

Research Article

Evaluation of maize genotypes against post flowering stalk rot under terai region of Nepal

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ABSTRACT

The inadequate source of resistance materials in maize against major biotic stresses is one of the main reasons for considerable loss of grain yield in Nepal. Post flowering stalk rot disease caused by *Fusarium moniliforme* is a serious disease that exposes high incidence at grain filling stage of maize in terai region of Nepal during summer season. This study was done to evaluate level of resistance, or tolerance in selected genotypes against the post flowering stalk rot disease of maize. Accordingly, thirty maize genotypes were tested for maize stalk rot resistance during summer season of 2016 and 2017 at National Maize Research Program, Rampur (NMRP), Chitwan. The experiment was done under natural epiphytotic condition at hot spot of the disease by using Randomized Complete Block design with 2 replications for each treatment. The package of practices was followed as per national recommendation. The summer season of 2016 and 2017 were affable for post flowering stalk rot of maize at NMRP, Rampur. Out of 30 genotypes, most of the tested entries showed susceptible reaction during both the years; however, RML-95/RML-96, Across-9942/Across-9944, ZM-401, Rampur 34, RamS03F08 and TLBR07F16 showed resistant reaction against the disease and might be useful for the development of post flowering stalk rot resistant maize varieties for terai region of Nepal.

Keywords: *Fusarium moniliforme*, resistance, post flowering

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INTRODUCTION

Stalk rot complex of maize is recognized as a severe problem in the tropical and sub-tropical maize growing areas of Nepal. This disease slowly becomes a serious threat in most of the terai and mid hill-low lying maize growing areas of Nepal (Subedi *et al.*, 2016). Usually post flowering maize stalk rot is prominent than pre-flowering to reduce maize yield (Batsa & Neupane, 1982). The pre-flowering type of stalk rot includes pythium stalk rot (*Pythium aphanidermatum*) and bacterial stalk rot (*Erwinia chrysanthemi* pv. *Zeeae*) whereas others,

such as *Fusarium* wilt (*Fusarium moniliforme* J. Sheld), late wilt (*Cephalosporium maydis*), black bundle disease and charcoal rot (*Macrophomina phaseolina*), appear in the post-flowering phase (Subedi, 2015). Stalk rot has been distributed throughout the country, but it is most prevalent in the hot and humid areas such as Dang, Chitwan, Nawalparasi, and Surkhet (NMRP, 2015). However, *Pythium* stalk rot is found to be common in the mountains and the valleys in Nepal (Diwakar & Payak, 1975). From global point of view, an estimated yield loss of 9-10% has been reported due to stalk rot complex that varied 4% in northern Europe and 14 % in South Asia and West Africa (Oerke, 2005). It has been estimated that post flowering stalk rot of maize in Nepal can cause up to 80 % yield loss along with other fungal diseases, especially in the terai area (Subedi *et al.*, 2016). Indeed, Fusarium Stalk Rot is associated with stalk rots and causes comparatively more damage in tropical compared to temperate countries (Christensen & Wilcoxson, 1966). The pathogen causes a permanent wilting, where leaves become flabby, basal stalk tissues turns to pinkish to purple tinge colorations (Agrios, 2005). There is no external visible symptom of the fungus. Although several works have been done to cope up with other maize diseases (Manandhar, 1997) but research activities were less in the maize stalk rot complex management in Nepal. In this sense, an instant effort is needed to manage stalk rot aiming to support tropical and subtropical maize growers to help manage this disease. Fungicidal control of Fusarium stalk rot is not successful due to its soil-borne mechanism of infection. Alternatively, the exploration and use of resistance gene(s) to enhance the tolerance of maize to stalk rot is a cost-effective and environmentally sustainable approach to its management. The objective of this research was to evaluate the maize genotypes against post flowering stalk rot disease considering grain yield management and to increase the maize productivity.

MATERIALS AND METHODS

Thirty maize genotypes were screened for maize stalk rot resistance during summer season of 2016 and 2017 at National Maize Research Program (NMRP), Rampur, Chitwan. The latitude, longitude and altitude of the experimental site are 27° 40'N, 84° 19' E, and 228 masl respectively. The experiment was done at natural epiphytotic condition by using Randomized Complete Block design with an arrangement of each treatment with 2 replications. The plot size was 5m long with 75 cm row to row spacing, and each genotype was sown in two rows. All agronomic practices were followed as per standard of National Maize Research Program, Rampur (NMRP, 2015). Farm yard manure (FYM) @15 t/ha in combination with chemical fertilizer @120:60:40 N: P: K kg/ha was applied. Di-ammonium phosphate (DAP) and Murate of potash (MoP) were applied as basal whereas urea was top dressed in three splits. Early plant stand, 50% days to anthesis and silking, plant height (cm), ear height (cm) and final plant stand (number) were recorded (CIMMYT, 1985). The disease severity were recorded from 10 randomly tagged plants/plot on the basis of 1-9 scoring scale (ICAR, 2012), thrice at an interval of 10 days. The area under disease progress curve (AUDPC) was computed using midpoint rule method (Campbell & Madden, 1990). The grain yield (kg/ha) and Thousand kernel weight (g) were recorded. Grain yield (t/ha) at 15% moisture content was calculated using fresh ear weight with the help of the formula adopted by Shrestha *et al.* (2019) and Shrestha *et al.* (2018). All data were analyzed statistically using Microsoft Excel and MSTAT-C computer package program.

RESULTS AND DISCUSSION

The maize growing summer season of 2016 was friendly for post flowering stalk rot development. The early plant stand, disease severity, final plant stand, grain yield, and thousand seed weight were significantly ($p \leq 0.05$) varied among the tested maize genotypes during summer of 2016 at Rampur, Chitwan. Out of 30 genotypes, the lower AUDPC value

Table 1. Screening of maize genotypes against post flowering stalk rot disease at Rampur, Chitwan during summer of 2016

Genotypes	EPS	Disease Severity (1-9)			AUDPC	FPS	GY (kg/ha)	TKW (g)
		60 DAS	70 DAS	80 DAS				
RML-95/RML-96	†35	1.53	2.30	4.53	53.25	30	2127	315
Across-9942/Across-9944	37	1.78	2.40	4.70	56.38	29	1987	348
Poshilo Makai 1	30	3.15	3.60	6.05	82.00	14	1344	283
S99TLYQ-B	37	3.15	3.58	6.05	81.75	22	1329	285
S99TLYQ-HG-AB	40	3.98	4.48	6.88	99.00	18	835	315
BGBYPOP	35	2.80	3.30	5.70	75.50	21	1540	205
R pop-3	31	3.28	3.78	6.30	85.63	17	1232	335
R pop-4	37	2.60	2.98	5.40	69.75	27	1643	268
Rampur Hybrid-4	35	2.63	2.99	5.44	70.20	21	1626	350
Rampur Hybrid-6	34	2.88	3.40	5.80	77.38	19	1509	220
Rampur Composite	40	4.20	4.70	7.08	103.38	18	864	275
RAMS03F08	34	2.20	2.70	4.95	62.75	27	1949	273
ZM-401	33	2.69	3.08	5.60	72.20	20	1670	343
ZM-627	42	5.08	5.30	7.40	115.38	17	505	388
05 SADVI	34	3.80	4.28	6.63	94.88	15	1034	260
07 SADVI	35	3.50	4.00	6.43	89.63	16	1124	335
Rampur 21	38	5.33	5.80	8.08	125.00	11	333	363
Rampur 24	34	3.70	4.20	6.63	93.63	15	1033	305
Rampur 27	36	2.43	2.95	5.20	67.63	25	1731	358
Rampur 32	28	2.80	3.20	5.65	74.25	13	1660	353
Rampur 33	33	3.60	4.08	6.55	91.50	14	1047	268
Rampur 34	33	1.98	2.60	4.90	60.38	25	1935	368
Rampur 36	37	3.08	3.58	6.05	81.38	21	1363	275
TLBRS07F16	38	2.40	2.90	5.08	66.38	26	1762	415
Across 9331 RE	36	3.40	3.90	6.33	87.63	20	1181	365
Arun-2	30	3.73	4.30	6.68	95.00	8	1033	353
BLBSRS07F10	37	2.93	3.43	5.88	78.25	23	1540	318
TLBRS07F14	36	3.63	4.13	6.65	92.63	18	1076	358
Arun-4	40	2.84	3.28	5.73	75.58	26	1545	315
Farmer's Local (SC)	41	5.20	5.55	7.58	119.38	14	422	315
Grand mean	35.43	3.21	3.69	6.06	83.25	19.38	1332.62	317.33
F-test	**	**	**	**	**	**	**	**
CV%	3.98	1.27	1.34	1.11	1.07	4.50	2.39	2.47

† Means of 2 replications. EPS- Early Plant Stand, AUDPC- Area under Disease Progress Curve, FPS- Final Plant Stand, GY- Grain Yield (kilogram/hectare), TKW (g)- Thousand kernel Weight (g), DAS- Days after Sowing, SC- Susceptible Check, **- highly significant ($p < 0.001$)

Table 2. Evaluation of common agronomic traits of maize genotypes in post flowering stalk rot screening nursery at Rampur, Chitwan during summer of 2016

Genotypes	50% days		Plant height (cm)	Ear height (cm)
	anthesis	silking		
RML-95/RML-96	48 [†]	52	180	96
Across-9942/Across-9944	46	50	180	88
Poshilo Makai 1	48	52	178	91
S99TLYQ-B	49	52	156	83
S99TLYQ-HG-AB	52	55	171	87
BGBYPOP	48	52	165	87
R pop-3	50	53	147	88
R pop-4	49	52	176	100
Rampur Hybrid-4	55	58	149	74
Rampur Hybrid-6	55	58	160	81
Rampur Composite	57	60	174	95
RAMS03F08	51	54	185	100
ZM-401	49	53	160	83
ZM-627	53	56	150	75
05 SADVI	54	57	150	70
07 SADVI	54	58	166	82
Rampur 21	52	55	184	75
Rampur 24	55	58	136	60
Rampur 27	57	60	161	79
Rampur 32	55	58	173	85
Rampur 33	54	59	140	73
Rampur 34	55	59	154	66
Rampur 36	55	59	164	73
TLBRS07F16	58	61	173	88
Across 9331 RE	50	53	150	62
Arun-2	54	58	171	73
BLBSRS07F10	51	54	174	87
TLBRS07F14	57	60	157	75
Arun-4	47	50	143	70
Farmer's Local (SC)	58	61	172	84
Grand mean	52.25	55.58	163.15	80.77
F-test	**	**	**	**
CV%	4.66	4.32	2.25	3.28

[†] Means of 2 replication. Cm- centimeter, SC- Susceptible Check, **- highly significant ($p < 0.001$)

(Table 1) were recorded in RML-95/RML-96 (53), Across-9942/Across-9944 (56), RamS03F08 (60), Rampur 34 (63) and TLBRS07F16 (66) respectively. The other remaining genotypes showed moderately susceptible and susceptible reaction to the disease. The high yielding genotypes were RML-95/RML-96 (2127 kg/ha) followed by Across-9942/Across-9944 (1987 kg/ha) and RAMS03F08 (1949 kg/ha) (Table 1). Likewise the genotypes having higher thousand kernel weight were TLBRS07F16 (415 g) followed by ZM 627 (388 g) and Rampur 34 (368 g) (Table 1).

The plant height and ear height were significantly varied among the tested genotypes (Table 2). The 50% anthesis days, 50% silking days, plant height and ear height were also significantly varied among the tested genotypes (Table 2). The results showed that 50%

anthesis days varied from 46 days for Across-9942/Across-9944 to 58 days for TLBRS07F16. Similarly, the 50% silking days varied from 50-61 days. Likewise, the plant height varied from 136 cm for Rampur 24 to 185 cm for RAMS03F08. Similarly, the ear height also varied from 60 cm of Rampur 24 to 100 cm of R pop-4 (Table 2).

Relationship between grain yield (kg/ha) and AUDPC

Findings of this study revealed highly significant negative correlation ($r = -0.99$) with the AUDPC value of post flowering maize stalk rot disease to the grain yield during summer maize season (2016). This relationship was drawn among 6 (3 high yielding- RML-95/RML-96, Across-9942/Across-9944, RAMS03F08, and 3 low yielding- ZM 627, Farmers local, and Rampur 21) genotypes (Figure 1). The predicted linear regression line also displayed downward slope i.e. $y = -0.039x + 136.5$, with regression coefficient $R^2 = 0.99$, where 'y' denoted predicted crop yield of maize genotypes and 'x' stood for AUDPC of post flowering stalk rot of maize (Figure 1). The estimated regression line indicated that with the one unit rise in the AUDPC of stalk rot disease (within 1-9 scale), there existed possibilities of yield reduction by 135.96 kg/ha.

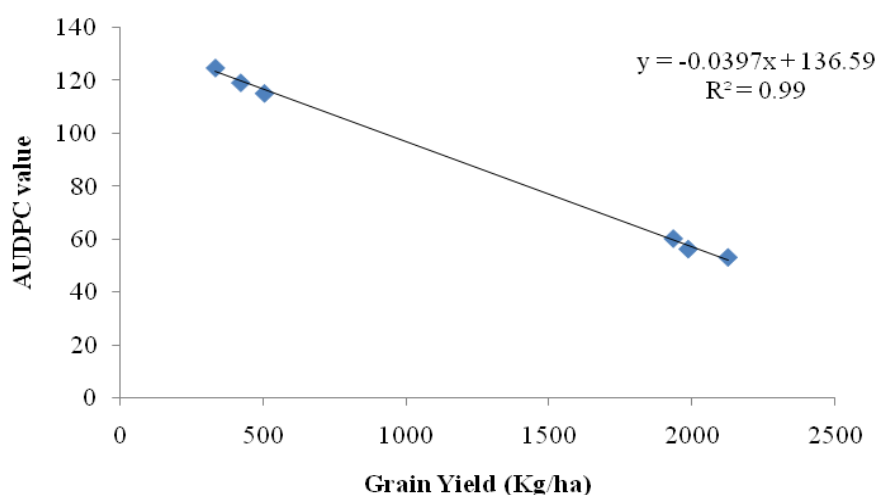


Figure 1. Relationship between crop yield (kg/ha) and AUDPC of maize stalk rot complex in screening experiment at Rampur, Chitwan during 2016

The summer season of 2017 was also favorable for post flowering stalk rot of maize at NMRP, Rampur. Out of 30 genotypes, During 2017 growing year, genotypes having lower AUDPC value were RML-95/RML-96 (73), Across-9942/Across-9944 (78), ZM-401 (81), Rampur-34 (81), RamS03F08 (89) and TLBRS07F16 (89) respectively (Table 3). The high yielding genotypes were RML-95/RML-96 (3883 kg/ha) followed by Across-9942/Across-9944 (3395 kg/ha), and Rampur 34 (3275 kg/ha) respectively (Table 3).

Table 3. Screening of maize genotypes against post flowering stalk rot disease at Rampur, Chitwan during summer of 2017

Genotypes	AUDPC	Grain yield (kg/ha)	TKW (g)
RML-95/RML-96	†72.50	3883	300
Across-9942/Across-9944	77.75	3395	270
Poshilo Makai 1	104.00	1873	280
S99TLYQ-B	120.00	2298	310
S99TLYQ-HG-AB	122.50	1408	290
BGBYPOP	104.00	1983	275
R pop-3	131.50	2053	355
R pop-4	131.50	1444	275
Rampur Hybrid-4	117.50	1761	300
Rampur Hybrid-6	122.50	1199	210
Rampur Composite	110.00	1441	290
RAMS03F08	88.50	3248	270
ZM-401	81.25	2733	300
ZM-627	136.25	341	350
05 SADVI	135.00	1691	250
07 SADVI	134.00	1939	315
Rampur 21	155.00	588	100
Rampur 24	151.25	1772	290
Rampur 27	118.75	2952	285
Rampur 32	117.50	2717	295
Rampur 33	94.00	1779	235
Rampur 34	81.25	3275	350
Rampur 36	119.25	1976	290
TLBRS07F16	89.00	2954	335
Across 9331 RE	141.25	2005	260
Arun-2	97.50	1721	340
BLSBRS07F10	107.50	2634	290
TLBRS07F14	94.00	1793	355
Arun-4	104.00	2535	300
Farmer's Local (SC)	107.00	1786	335
Grand mean	112.20	2106	290
F-test	**	**	NS
CV%	2.3	1.76	19.59

† Means of 2 replications. AUDPC-Area under Disease Progress Curve, kg/ha-kilogram/hectare, TKW (g) - Thousand Kernel Weight (gram), SC- Susceptible Check, **- highly significant ($p < 0.001$)

Maize stalk rot is more prominent in Nepal, India, Indonesia, Pakistan, Philippines, Thailand and Vietnam. This could be observed more commonly if there is a period of drought during, or shortly after pollination (Subedi, 2015). Stalk rot complex include both bacterial (Burlakoti & KC, 2004) and fungal association to cause the significant yield loss in Nepal. Agronomically desirable stalk rot-resistant materials are available in Pakistan, India, Mexico and Zimbabwe, where selections against these diseases have been made (Kulkarni & Anahosur, 2011). The stay green character, in which plants remain green after attaining physiological maturity, has been associated with resistance to certain post-flowering stalk rots (Singh *et al.*, 2012). There is evidence of mammalian toxicity where stalks infected with these pathogens (Agris, 2005). The maximum disease development occurs within a temperature range of 30-35°C, with a relative humidity of 80-100% (Subedi *et al.*, 2016). Waterlogged, low-lying, or poorly drained field conditions favor a high degree of disease development. Plant age (pre-flowering growth stage) and a large plant population (≥ 60000)

per ha) favor a high incidence of disease (Diwakar & Payak, 1980). Resistance to stalk rot disease involves several traits including physiological, morphological and functional characters. Maize stalk strength is determined by both stalk morphology and abiotic stress factor (Singh *et al.*, 2012). The finding of this experiment is in agreement with the finding of Shekhar *et al.*, (2010) as the authors reported that after extensive screening, three resistant lines- PFSR-13-5, JCY2-2-4-1-1-1-1, and JCY3-7-1-2-1-b-1 were identified and also the resistance level of five pools/populations; (PFSR (Y)-C1, PFSR (white), Extra-early (White), P-100, P-300 and P-345) was upgraded to an acceptable level (Shekhar *et al.*, 2010). Stalk rot infectivity depends on environmental factors, the genotype and environment interaction (G×E) and host resistance of maize genotypes to the pathogens (Szoke *et al.*, 2007). Ledencan *et al.*, (2003) marked low disease scoring of hybrids than inbreds and differed significantly in resistance and infection types. Hybrids Ganga Safed-2, Hi-starch, and composites Suwan 1 and Suwan 2, have shown resistance in India (Khokhar *et al.*, 2014). Globally, large numbers of maize germplasm have been tested for stalk rot resistance and some have shown high resistance levels (Ali & Yan, 2012). Studies have shown that resistance to stalk rot is quantitatively inherited and controlled by multiple genes with additive effects (Hooda *et al.*, 2012). From this experiment, it is clear that maize genotypes varied significantly in resistance and infection forms, and the hybrid disease score was typically lower than that of others. This would allow the identification of potential resistance genes for resistance to stalk rot in maize.

CONCLUSION

Throughout the years, maize genotypes RML-95/RML-96, Across-9942/Across-9944, ZM-401, Rampur 34, RamS03F08 and TLBRS07F16 showed resistant reaction against the post flowering stalk rot disease with higher yield at Rampur Chitwan. The genotypes having resistance against post flowering stalk rot would be further evaluated in maize breeding program for the development of stalk rot resistant high yielding maize varieties, thus are critically considered as selected and promising ones.

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Authors' contributions

Dr. S. Subedi was the principle investigator of this research who prepared and finalized the manuscript. Dr. S. Neupane helped during field research and DR. KB Koirala reviewed the manuscript and helped during draft preparation. Mr. L. Oli helped during data recording and field work.

Conflict of interest

The authors declare that there is no conflict of interest.

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