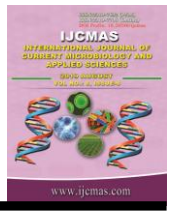
Int.J.Curr.Microbiol.App.Sci (2019) *8*(8): 387-393

International Journal of Current Microbiology and Applied Sciences
***ISSN: 2319-7706* Volume 8 Number 08 (2019)**
Journal homepage: http://www.ijcmas.com



Original Research Article https://doi.org/10.20546/ijcmas.2019.808.044

Study on the Area under Disease Progress Curve (AUDPC) in Natural Field Conditions for *Turcicum* Blight Disease in Maize in the North-East Hill Region

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Keywords

Maize, Turcicum blight, Area under disease progress curve

Article Info

Accepted:
04 July 2019
Available Online:
10 August 2019

A B S T R A C T

Ten maize landraces were evaluated for *Turcicum* blight resistance based on the low area under disease progress curve scores for the selection studies from the North Eastern Hill Region. Inbred lines V-334(C5) and CM-145 (C6) obtained from VPKAS, ICAR, Almora Uttarakhand were used as reference checks for *Turcicum* blight screening. Observational data were recorded based on the successive progression of lesion length and breadth. The area under disease progress curve scores of genotypes N21(3)-9, M23(2)-21, N25(3)-19, M23(9)-14, S2(2)-10, N25(2)-32, N25(3)-6, N25(3)-11, S2(2)-20, N25(5)-23, M23(9)-17, Mi4(3)-17, Mi4(3)-36 and Mi4(3)-3 were lower than that of the resistant check C6 at 28.71 and can be used in breeding programs for introducing resistance to *Turcicum* blight in a population. The maximum lesion area of 22.73 sq. cm, 84 days after sowing was recorded in genotype M23(2)-24. Genotype Mi4(3)-3 was a good performer for disease resistance.

Introduction

Maize (*Zea mays* L.) is a diploid (2n=20), cross-pollinated, monocot plant belongs to the tribe Maydeae of the grass family Poaceae. Maize is considered to be originated in Mexico from its wild relative Teosinte in southern Mexico about 9,000 years back. Several morphologically and genetically diverse maize landraces arose following multiple independent domestications that occurred independently in several regions of Mexico (Matsuoka *et al.*, 2002). Northern leaf blight (NLB) is an endemic disease in maize-

growing regions throughout the world, where it can cause epidemics of moderate to severe yield losses. It is caused by the hemibiotrophic fungal pathogen *Setosphaeria turcica* (anamorph *Exserohilum turcicum*). NLB is of prime concern in the tropical highlands, where conditions favor disease development and subsistence farming and food insecurity are prevalent. *Exserohilum turcicum* possess high genetic variability in terms of virulence, genetic structure and several races in the different geographical localities. It is known to be a threat to corn production in many areas of the world (Muiru *et al.,* 2010). Greater yield losses occur due to the removal of leaves above the ear leaf and position of leaves is considered as critical for yield-loss analysis. To predict disease-yield relationship for most of the pathosystems disease onset and progress at different stages and disease development are known to provide useful information. The area under disease progress curve (AUDPC) is reported to be a better predictor and the best method for describing the relationship between yield and severity of northern leaf blight disease (Abebe *et al.,* 2008). The development of *Turcicum* leaf blight is favored by humidity and susceptibility of maize varieties. The number of lesions varies by location due to the influence of the environment and the increment of the lesion number is consistent in resistant and susceptible varieties. Reports exist for the presence of variability in the reaction of maize genotypes to *Turcicum* leaf blight for resistance to both under greenhouse and field conditions where open-pollinated varieties have been reported to be more resistant (Muiru *et al.,* 2007). Additive gene actions, dominance x dominance type of epistasis with duplicate nature are known to have major importance in controlling resistance to *Turcicum* leaf blight. For developing high yielding and resistant cultivar, pedigree and recurrent selection methods should be practiced (Ishfaq *et al.,* 2014). It is keeping in mind the potential of landraces to increase the frequency of desirable alleles along with sustained disease resistance, a previously screened germplasm that had been identified to exhibit *Turcicum* blight resistance was taken up for selection studies in the present program. The objective of the program was to study AUDPC in natural field conditions for *Turcicum* blight disease.

Materials and Methods

The field experiments were carried out at the Experimental Farm, College of Post Graduate Studies, CAU (Umiam), Meghalaya for two consecutive summer seasons *viz*., April-August, 2014 and March-July, 2015. Ten maize landraces evaluated for *Turcicum* blight resistance based on low AUDPC scores were collected from the four states of North-Eastern Hill Region of India *viz*., Meghalaya (M), Nagaland (N), Sikkim(S) and Mizoram (Mi). Inbred lines V-334 (C5) and CM-145 (C6) obtained from VPKAS, ICAR, Almora Uttarakhand were used as reference checks for *Turcicum* blight screening. The ten landraces were assigned alphanumerical codes according to their respective states, accession number and plant number in parenthesis as listed in Table 1.

In the summer season of 2014, 40 plants per replication for the 10 landraces were planted in randomized block design in 4 rows of 3 m length. Three replications were maintained. The plant to plant spacing was kept at 30 cm and row to row at 50 cm. This constituted the base population. For the selection studies in the second season, 45 plants with highest cob weight were selected from the base population from a mixed harvest. The selected progeny population was sown in 20 plants in 2 rows per replication in the ear to row method replicated thrice. Thinning was carried out two weeks after germination and one seedling/hill was retained. Routine inter-cultural operations

were carried out for uniform growth of the crop.

Plants of the progeny population were given the same alpha-numerical codes as in the base population appended with the plant number. Plants numbered 1-20 constituted replication I, plants numbered 21-40 constituted replication II and plants numbered 41-60 constituted replication III.eg. Mi4(3)-1 would imply the 1st plant in replication I of Mi4(3), Mi4(3)-21 would imply the 21st plant in replication II and Mi4(3)-41 would imply the 41st plant in replication III. The accessions were scored for the percentage of foliage destruction during the growing season. The area under disease progress curve (AUDPC) was computed as per Zadok *et al.,* (1978) using the following formula-

$$AUDPC = \sum_{i=0}^{n-1} [(X_{i+1}+X_i)/2](T_{i+1}-T_i)$$

Where, AUDPC = area under the disease progress curve, X_i = % of foliage destruction at the i^{th} scoring, $(T_{i+1}-T_i)$ =Time elapsed between two scorings, n=Total number of scorings.

Disease progress was recorded in every 3rd - 4th day from the onset of disease at 70 days after sowing up to 84 days post sowing (Fig. 1, 2, 3, and 4). Observations were recorded on a minimum of 24 plants per landrace under study. Observational data were recorded based on the successive progression of lesion length and breadth. A total of five readings up to the flowering stage were recorded.

Results and Discussion

Plants grown in the ear to row method over three replication for a total of forty-five cobs and checks V334 (C5) [susceptible], CM 145 (C6) [resistant] were evaluated in the second generation for studying progress in *Turcicum* blight.

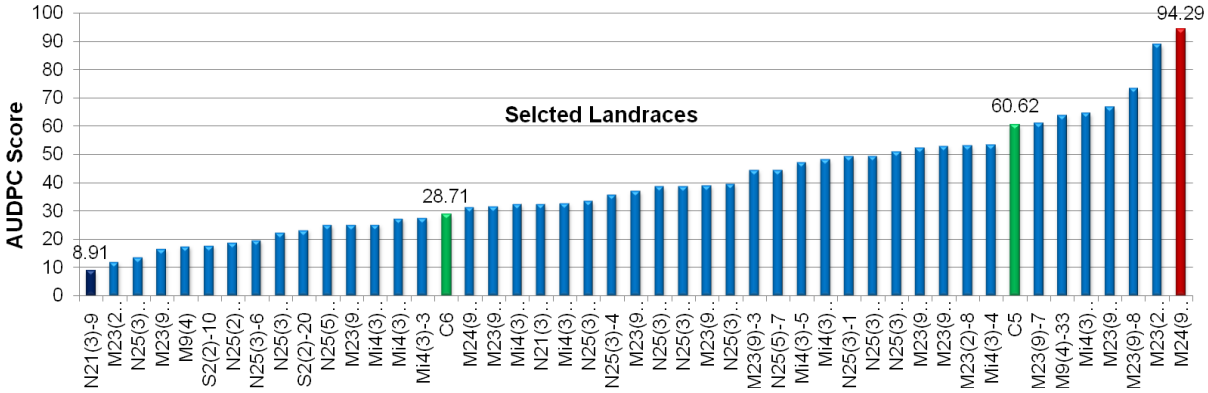
In the initial planting material, AUDPC ranged from 0-18.6 while in the progeny population the AUDPC values ranged from 8.91-94.29.

The maximum AUDPC score of 94.29 was seen in the genotype M24(9)-35 while the minimum AUDPC score of 8.91 was recorded in genotype N21(3)-9 (Figure 1). The susceptible check C5 recorded an AUDPC score of 28.71 while the resistant check C6 recorded an AUDPC score of 60.62 respectively (Figure 2).

The disease Progress in landraces with scores lower than the resistant check C6 at the initiation of leaf senescence was reported. The AUDPC score of landrace N21(3)-9 was reported to be 8.91, while for M23(2)-21 9 it was reported to be 11.91, for N25(3)-19 9 it was reported to be 13.75. The AUDPC score of M23(9)-14 9 was reported to be 16.58, S2(2)-10 9 was reported to be 17.77, for N25(3)-69 it was reported to be 19.54, forN25(3)-11 9 it was reported to be 22.25, for S2(2)-20it was 23.30. The AUDPC score for N25(5)-23 was found to be 25.07, for M23(9)-17 it was found to be 25.14 while for Mi4(3)-17 it was found to be 25.23, for Mi4(3)-36 it was found to be 27.27, for Mi4(3)-3 it was found to be 27.59.

The disease progress in landraces with scores higher than the susceptible check C5 at the initiation of leaf senescence was also reported. The AUDPC score of M24(9)-35 was reported to be 94.29, for M23(2)-24 it was 89.15, for M23(9)-8 it was 73.46, for M23(9)-13 it was 66.93, for Mi4(3)-19 it was 64.76, for M9(4)-33 it was 63.96 while for M23(9)-7 it was reported to be 61.18.

Fig.1 AUDPC (Area under Disease Progress Curve) Score in the progeny population



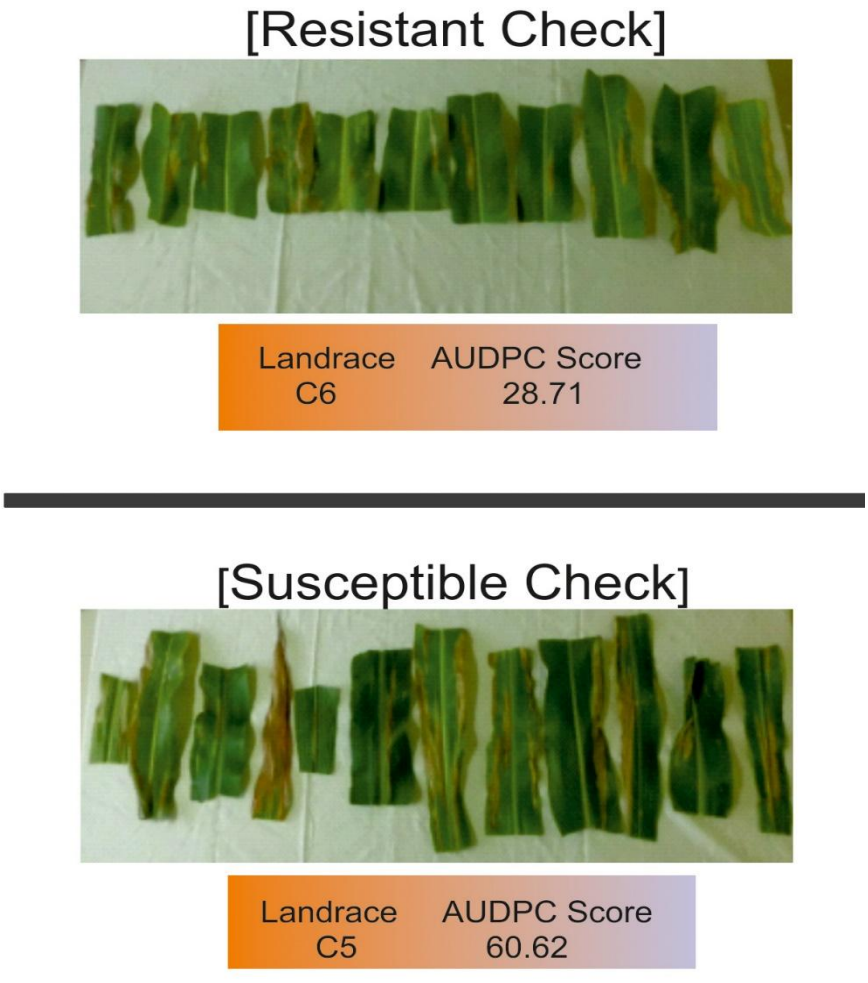


Figure 2. Disease Progress in landraces with scores for C6 and C5 at initiation of leaf senesence

Fig.3 Disease progress for different entries for different genotypes in the progeny population

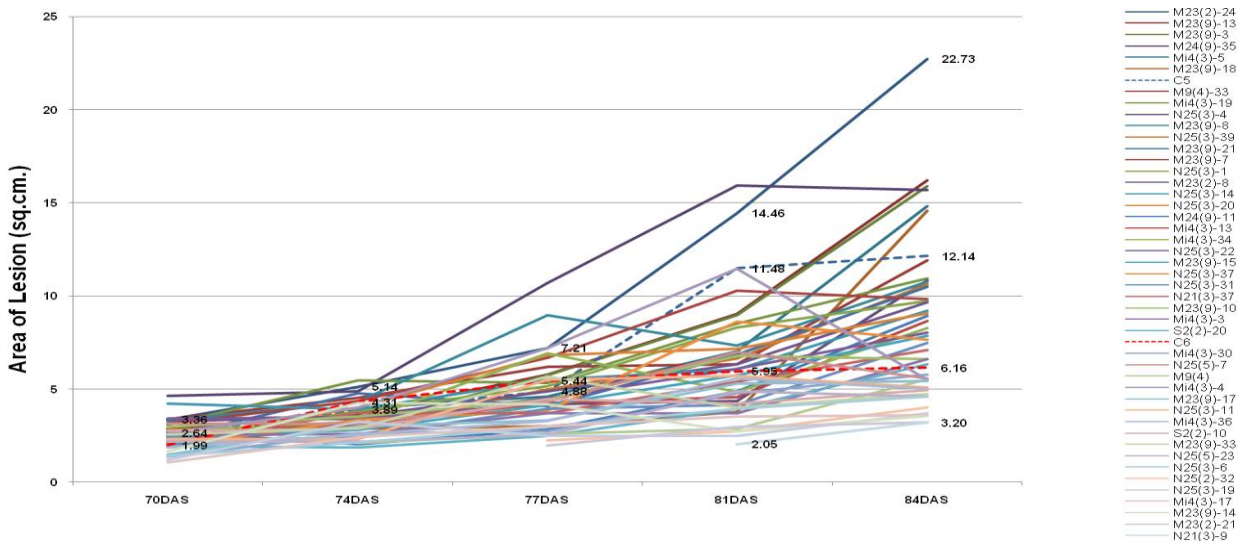


Table.1 List of the ten landraces from different states of North-Eastern Hill Region of India used for selection studies

Sl. No.	Alphanumerical code	State of Origin	AUDPC scores
1	M23(9)	Meghalaya	15.6
2	M23(2)	Meghalaya	12.8
3	M24(8)	Meghalaya	11.2
4	M9(4)	Meghalaya	0
5	N25(5)	Nagaland	18.6
6	N25(3)	Nagaland	12.2
7	N21(5)	Nagaland	15.6
8	S9(3)	Sikkim	18.2
9	S2(2)	Sikkim	15.2
10	Mi4(3)	Mizoram	18.4

AUDPC scores of landraces N21(3)-9, M23(2)-21, N25(3)-19, M23(9)-14, S2(2)-10, N25(2)-32, N25(3)-6, N25(3)-11, S2(2)-20, N25(5)-23, M23(9)-17, Mi4(3)-17, Mi4(3)-36 and Mi4(3)-3 were lower than that of the resistant check C6 at 28.71. They can be therefore be exploited in breeding programs for increasing resistance alleles to *Turcicum* blight in a maize population. Phenotyping disease resistance quantitatively by measures such as AUDPC helps to contribute to the identification of resistant crop cultivars. The area under the disease progress curve (AUDPC), based on multiple disease rating is an important component trait for quantifying *Turcicum* blight resistance and is a highly heritable component (Welz and Greiger, 2000).

The maximum lesion area of 22.73 sq. cm, 84 days after sowing was recorded in genotype M23(2)-24 while the minimum lesion area of 3.20 sq. cm., 84 days after sowing was recorded in landrace N21(3)-9 (Figure 3). The susceptible check C5 recorded a lesion area of 12.14 sq. cm while the resistant check C6

recorded a lesion area of 6.16 sq. cm respectively. Chung *et al.,* (2010) while characterizing the resistance locus in *Turcicum* blight, had phenotyped and rated disease as percent leaf infected leaf area of the entire plant, disregarding decayed bottom leaves for individual plants or on a row basis for fixed lines. A rapid increase in disease area after its onset is an indication of a breakdown in the plant defense mechanism and such genotypes are susceptible to the disease.

Work on *Turcicum* blight by several workers have established that the disease is controlled by several major genes as well as by several reported QTLs (Welz *et al.,* (1999); Xiaoyan *et al.,* (2003); Asea *et al.,* (2009); Chung *et al.,* (2010); Balint-Kurti *et al.,* (2010)). Phenotyping of quantitative disease resistance through the exposure of plants to pathogens and visual observation of disease symptoms is an important stage in many plant breeding programs (Skelsey and Newton, 2014). Therefore, the selection of genotypes based on AUDPC scores would be effective in increasing disease resistance in a population of maize. Based on overall performance, Mi4(3)-3 was found to be a good performer for disease resistance.

Acknowledgement

Authors are thankful to Miranda Sanjenbam for providing experimental material for selection studies. The authors are also thankful to Department School of Crop Improvement, College of Post Graduate Studies, CAU (Umiam), Meghalaya, India for providing all facilities required during experimental work.

References

Abebe, D., Singburaudom, N., Sangchote, S., and Sarobol, E. (2008). Evaluation of maize varieties for resistance to northern leaf blight under field conditions in Ethiopia. *Kasetsart J. (Nat. Sci.),* 42: 1–10.

Asea, G., Vivek, B.S., Bigirwa, G., Lipps, P.E., and Pratt, R.C. (2009). Validation of consensus quantitative trait loci associated with resistance to multiple foliar pathogens of maize. *Phytopathol.,* 99(5): 540-542.

Balint-Kurti, P.J., Yang, J., Esbroeck, G.V., Jung, J., and Smith, M.E. (2010). Use of a maize advanced intercross line for mapping of QTL for northern leaf blight resistance and multiple disease resistance. *Crop Sci.,* 50: 458-466.

Chung, C.L., Jamann, T., Longfellow, J., and Nelson, R. (2010). Characterization and fine-mapping of a resistance locus for northern leaf blight in maize bin 8.06. *Theor. Appl. Genet.*, 121: 205–227.

Chung, C.L., Longfellow, J.M., Walsh, E.K., Kerdieh, Z., Esbroeck, G.V., Balint-Kurti, P., and Nelson, R.J. *(*2010). Resistance loci affecting distinct stages of fungal pathogenesis: use of introgression lines for QTL mapping and characterization in the maize - *Setosphaeria turcica* pathosystem. *BMC Plant Biol.,* 10(103): 1-25.

Ishfaq, A., Dar, Z.A., Lone, A.A., Ali, G., Gazal, A., Hamid, B., and Mohiddin, F.A. (2014). Disease reaction studies of maize (*Zea mays* L.) against *Turcicum* leaf blight involving indigenously identified cytosterile source. *Afr. J. Microbiol. Res.*, 8(27): 2592-2597.

Matsuoka, Y., Vigouroux, Y., Goodman, M.M., Sanchez, G.J., Buckler, E., and Doebley, J. (2002). A single domestication for maize shown by multilocus microsatellite genotyping. *Proc. Natl. Acad. Sci.,* 99(9): 6080-6084.

Muiru, W.M., Koopmann, B., Tiedemann, A.V., Mutitu, E.W., and Kimenju, J.W.

(2010). Race typing and evaluation of aggressiveness of *Exserohilum turcicum* isolates of Kenyan, German and Austrian origin. *World J. Agric. Sci.*, 6(3): 277-284.

Muiru, W.M., Mutitu, E.W., and Kimenju, J.W. (2007). Reaction of some Kenyan maize genotypes to turcicum leaf blight under greenhouse condition. *Asian J. Plant Sci.*, 6(8): 1190-1196.

Skelsey, P., and Newton, A.C. (2014). Scale-dependent assessment of relative disease resistance to plant pathogens.*Agronomy*, 4: 178-190.

Welz, H.G., and Greiger, H.H. (2000). Genes for resistance to northern corn leaf blight in diverse maize populations. *Plant Breed.*, 119: 1-14.

Welz, H.G., Xia, X.C., Bassetti, P., Melchinger, A.E., and Lübberstedt, T. (1999). QTLs for resistance to *Setosphaeria turcica* in an early maturing dent x flint maize population. *Theor. Appl. Genet.*, 99: 649–655.

Xiaoyan, Y., Qinghua, W., Jiliang, Y., Demin, J., Fei, W., Bin, W., and Juren, Z. (2003). Fine mapping of the *Ht2* (*Helminthosporium turcicum* resistance 2) gene in maize. *Chin. Sci. Bull.*, 48(2): 165-169.

Zadoks, J.C., Chang, T., and Konzak, F.C. (1974). A decimal code for the growth stages of cereals. *Weed Res.*, 14: 415-421.

How to cite this article:

Moutushi Sarkar, Devyani Sen, Nitesh Kumar, Subhra Mukherjee and Prabir Kumar Bhattacharyya. 2019. Study on the Area Under Disease Progress Curve (AUDPC) in Natural Field Conditions for *Turcicum* Blight Disease in Maize in the North-East Hill Region. *Int.J.Curr.Microbiol.App.Sci.* 8(08): 387-393. doi: https://doi.org/10.20546/ijcmas.2019.808.044