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Pathogenic variability in *Exserohilum turcicum* and identification of resistant sources to turcicum leaf blight of maize (*Zea mays* L.)

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Abstract: Turcicum leaf blight of maize incited by *Exserohilum turcicum* (Pass.) Leonard and Suggs is the major limiting factor of maize production in temperate agro-ecologies. Disease management through host plant resistance is the most effective strategy. In the present study among 26 maize genotypes which were initially screened for resistance against *E. turcicum* under field conditions, 8 genotypes *viz.*, PS 39, CML 451, CML 470, CML 472, VL 1030, VL 1018140, VL1018527 and SMI178-1 were found resistant when screened against twelve isolates of *E. turcicum* under artificial epiphytotic conditions. Eight genotypes *viz.*, PS45, CML165, CML459, VL1249, VL0536, SMC-5, SMC-3 and KDL 211 were found moderately resistant with disease grade ranged from 2.1-2.5. These maize genotypes possess resistance to turcicum leaf blight can be used successfully in developing high yielding early maturing varieties for high altitude temperate agro-ecologies. The fungus *E. turcicum* is highly variable in nature. Variability studies on pathogenicity were conducted on twelve isolates of *E. turcicum* on eleven putative differential maize lines. During the present study a wide pathogenic variation was observed among the twelve isolates of *E. turcicum.* Cluster analysis on the basis of similarity or dissimilarity in reaction types exhibited by the differential hosts, clustered the isolates into 6 pathogenic groups. The isolates belonged to higher altitudes (Kti 10, Kti11, Kti5) were found to be more aggressive as compared to the isolates of low altitude areas.

Keywords: *Exserohilum turcicum*, Maize, TLB resistance, Variability

INTRODUCTION

Turcicum leaf blight also called as Northern leaf blight of maize incited by the fungus *Exserohilum turcicum* (Pass.) Leonard and Suggs is widely spread and economically most important disease of maize globally and occur frequently under mountain agro ecologies of Jammu and Kashmir. Valley of Kashmir (longitude 73.0-74.2^0 E and latitude 33-34^0 N) is agro-climatically a typical temperate region where maize is grown as sole crop or intercropped with pole type common beans at an altitude of 1850-2800 m above mean sea level. Major challenge to increase maize production primarily involves the predominance of cultivated land races which are more susceptible to various biotic stresses particularly Turcicum leaf blight. The disease causes enormous damage to crop in terms of grain yield particularly if the disease establishes before silking (Nwanosike *et al*., 2015). Moreover the disease causes immense damage to crop straw which is of great value under temperate agro climatic conditions of Kashmir as the same is being fed to the cattle during lean season. The disease epidemics at an early stage causes premature death of blighted leaves which lose their value as fodder (Li and Wilson, 2013).

Genetic resistance of crop plants to infection by the pathogen is a safe alternative and most economical and eco friendly disease management venture. The genetic variability and pathogenicity are the key factors for host-plant resistance and for the formulation of viable strategies for disease management. The fungus *E. turcicum* is known to be highly variable in cultural characteristics, pathogenicity and genetic traits and the frequency of variation differs with each species. Most of the commercial cultivars of maize are more or less susceptible to Turcicum leaf blight. The reasons for lack of substantial durable resistance in the material may be attributed to the presence of variability in the population as the fungus *E. turcicum* is known to be highly variable in nature (Reddy *et al*. 2013; De-Rossi *et al*., 2015). In order to develop the high yielding disease resistant cultivars, it is imperative to analyse and understand the variability in the pathogen. Host plant resistance depends on the effectiveness of resistance against all the virulent isolates of the pathogen present in the region. Identification of variability among the isolates of a pathogen is an important step to devise a disease management programme for a particular region and for the development of disease resistant cultivars in many host pathogen systems where major genes

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control resistance. The present investigation was conducted to study the pathogenic variability in *E. turcicum* and to identify new sources of resistance against Turcicum leaf blight of maize under high altitude temperate ecologies.

MATERIALS AND METHODS

Pathogen isolation: Diseased maize leaf samples collected during survey from 12 different locations representing nine districts of Kashmir Province during *kharif* 2013-14 were attempted for the isolation of *E. Turcicum* isolates. The cultures of *E. turcicum* isolates were obtained by single spore isolation technique (Tuite, 1969). Twelve single spore cultures of *E. turcicum* isolated from diseased samples of 12 diverse locations representing 4 maize cultivars and 8 local land races were maintained on potato dextrose agar slants for screening of maize genotypes and studying the pathogenic variability of the pathogen.

Field screening of maize germplasm against turcicum leaf blight: For the identification of sources of resistance to *E. turcicum*, a set of 60 accessions of maize consisting of indigenous and exotic lines in advanced stages of maintenance along with popular commercial cultivars available with the Mountain Crop Research Station, Sagam, SKUAST-K, were initially screened under artificially inoculated field conditions. The experiment was carried out at Mountain Crop Research Station, Larnoo located at latitude 33° 37' N, longitude 75° 22' E and an altitude of 2286 metres above mean sea level. The experiment was established during *Kharif* 2014, following a randomised complete block design with two replications. Test lines were planted in 2 row plots of 3m length with plant spacing of 60 × 20 cm. The plot was bordered by susceptible disease spreader rows on each side of the inbred CM 202.

Preparation of inoculum and inoculation: Spore suspension of each isolate was prepared by washing the conidia with distilled water from 20 days old cultures of *E. turcicum*. The spore concentration was measured by haemocytometer and maintained at 3×10^5 spore ml^{-1}. Two to three drops of Tween 20 were added per litre of suspension. Equal volume of spore suspension of twelve isolates was mixed and spraying of spore suspension was done in evening by using a glass atomizer at three to four leaf stages of plants. Control plants were treated similarly with distilled water. Disease reaction was recorded by using 1 to 5 evaluating scale (Shekhar and Kumar, 2012) with slight modification, commenced from 60 days after planting and assessment of disease severity was continued on weekly basis for 6 weeks. Plants showing reaction 1 and 2 were graded as resistant while as plants with disease grade of 3, 4 and 5 were considered as susceptible. From this screening relatively resistant lines from various genetic backgrounds, were selected and were further evaluated against all the twelve isolates of *E. turcicum* under controlled conditions.

Evaluation of selected maize genotypes against *E. turcicum* isolates under controlled conditions: In order to validate the resistance, a selected set of 26 genotypes which showed moderately resistant to resistant reaction against Turcicum leaf blight under field conditions, was further screened under controlled conditions against all the collected isolates separately, to investigate genotype–isolate interactions.

Five seeds of each genotype were sown in pots, filled with sterilized potting medium prepared by mixing soil, FYM and sand at the ratio of 6:2:1, respectively. Fertilizers were applied as per recommendation and watering was done as per the moisture status of the potting medium. After germination one plant was maintained in each pot. The treatments were arranged in a completely randomized block design with three replications per treatment.

Spore suspension of each isolate was prepared separately as discussed above and spraying of spore suspension of each isolate was done separately in evening by using a glass atomizer at three to four leaf stages of plants, grown in glass house.

Disease assessment: Development of disease was assessed by using 0-5 scale. The genotypes showing disease score between 0.1-2.0 were considered as resistant (R), 2.1-2.5 as moderately resistant (MR), 2.6-3.0 as moderately susceptible (MS), 3.1-4.0 as susceptible (S) and 4.1-5.0 as highly susceptible (HS). The observations were recorded on weekly basis for 6 weeks**,** commenced from 45 days after sowing. The data were subjected to cluster analysis on the basis of accession performances and the relatively resistant accessions were used as differential set to discern the different isolates of *E. turcicum.*

Assessment of pathogenic variability of *E. turcicum* isolates: Twelve isolates of *E. turcicum* were tested for their reaction on a set of eleven putative differential maize lines which showed varied level of resistance after screening in field and controlled conditions. On the basis of similarity in reaction pattern of the test isolates on these putative maize differential lines, the isolates were discerned into different pathogenic groups. The average data categorized into 0-5 scales was subjected to cluster analysis to identify the similarity of virulent pattern among isolates. For this analysis, a similarity matrix was derived with the Simqual Programme (NTSYS 1993 pc, version 1.7) using simple matching coefficient of similarity. A dendrogram was produced by the unweighted pair group method for arithmetic average (UPGMA) in the SAHN program.

Virulence of isolates: The virulence of isolates in terms of incubation period, virulence index and lesion size was tested on maize cultivar SMI154. Incubation period was taken as time in number of days from inoculation to appearance of first disease symptoms. Disease severity and virulence index was observed as

Table 1. *E. turcicum* isolates collected from different locations of Kashmir valley.

S. N.	Isolate	Maize cultivar	Place of origin
1	Kti-1	Local	Pahalgam Anantnag
2	Kti-2	Local	Gandarbal
3	Kti-3	SMC-3	Khudwani Kulgam
4	Kti-4	Local	Tahab Pulwama
5	Kti-5	SMC-5	Pombay Kulgam
6	Kti-6	Local	Kupwara
7	Kti-7	C6	Shalimar Srinagar
8	Kti-8	Local	Shopian
9	Kti-9	Local	Bandipora
10	Kti-10	Local	Larnoo Anantnag
11	Kti-11	Local	Verinag Anantnag
12	Kti-12	C15	Budgam

given by Reddy *et al*. (2013).

RESULTS AND DISCUSSION

The turcicum leaf blight disease of maize was prevalent in all the surveyed areas of Kashmir valley. Twelve single spore cultures of *E. turcicum* isolates of diverse locations were maintained on potato dextrose agar medium. The isolates were designated as Kti-1 to Kti-12 (Table 1).

Germplasm screening under field conditions: Sixty maize genotypes were initially screened for resistance against *E. turcicum* under artificially inoculated field conditions (Table 2). The genotypes *viz*., PS 39, CML 165, CML470, CML 474, CML 472, CML451, V370, V341, VL1030, VL1034, VL1018527, VL1018140, VL109452, VL0512421, VL0536, SMI178-1 and KDL 211 showed resistant reaction with disease grade < 2 against *E. turcicum*, while as PS 45, PS 77, PS83, CML239, CML244, CML245, CML459, CML460, CML152, CML350, CML242, VL1249, ZVL127, VL 109138, SMI114-2, SMI 105, SMC-5, SMC-3, SMH-1, C6, KDL227, KDL170, KDL310, KDL288 and DML1126 were found moderately resistant with disease score of 2.0-3.0. The remaining genotypes showed moderately susceptible to highly susceptible reaction. The genotypes Pahalgam local and SMI154 showed maximum disease intensity of 56.3 and 54.6 per cent respectively. From the sixty test genotypes, 26 genotypes which showed resistant to moderately resistant reaction against *E. turcicum* were selected along with highly susceptible genotype for further evaluation under controlled conditions. Singh *et al.* (2014) evaluated 118 maize genotypes out of which 26 were found resistant, 56 moderately resistant, 26 susceptible and 10 highly susceptible against turcicum leaf blight.

The resistant sources with varied levels of resistance do exist against the Turcicum leaf blight disease of maize. The determination of genetic basis of these sources and incorporation of their resistant genes into susceptible commercial cultivars is prerequisite in the development of high yielding TLB resistant maize cultivars**.**

Babita and Mani (2011) screened the temperate maize lines against northern corn leaf blight and found five inbreds, *viz*., V 335, V 13, V 336, V 53 and V 27 resistant to disease. Inherent resistance or tolerance of crop plants to infection by the pathogen is a safe alternative and most economical and eco friendly disease management venture. Varied response of maize germplasm against TLB was observed by Muiru *et al*. (2015) and suggested that there is a need to pyramid genes for resistance in the elite varieties to enable farmers increase their productivity. The fungus *E. turcicum* is known to be highly variable and the specialization in the fungus population, results the breakdown of substantial durable resistance in the commercial cultivars of maize. The ideal maize breeding programme with high level of TLB resistance requires to be supported by additional new sources of resistance at regular intervals which are obtained by continuous screening of germplasm across the years and environment.

Screening of maize genotypes against the isolates of *E. turcicum* under controlled conditions: In order to validate the resistance, 26 genotypes, found moderate to highly resistant against Turcicum leaf blight under field screening were further evaluated against all the collected isolates of *E. turcicum* under controlled epiphytotic conditions. The genotypes viz., PS 39, CML 451, CML 470, CML 472, VL 1030, VL 1018140, VL1018527 and SMI178-1 were found resistant to TLB with average disease grade of 1.6 to 1.9. These genotypes exhibited resistant response against 7 to 11 test isolates (Table 3). 8 genotypes *viz* PS45, CML165, CML459, VL1249, VL0536, SMC-5, SMC-3 and KDL 211 with average disease grade ranging from 2.1-2.5 were found moderately resistant and remaining 10 genotypes showed moderately susceptible to susceptible reaction with average disease grade ranging from 2.6 to 4.0. The genotypes SMI154 and Pahalgam local showed maximum disease grade of 4.0 and 3.7 respectively and showed resistant response to none of the 12 test isolates.

Table 2. Reaction of maize genotypes to *E. Turcicum* under artificially inoculated field conditions.

S. N.	Genotypes	Source	Disease intensity (%)	Grade	Response
1	PS 45	MCRS Sagam	13.4	2	MR
2	PS 66	MCRS Sagam	29.5	3	MS
3	PS-39	MCRS Sagam	5.0	1	R
4	PS 76	MCRS Sagam	35.1	3	MS
5	PS 77	MCRS Sagam	10.4	2	MR
6	PS 80	MCRS Sagam	26.8	3	MS
7	PS 83	MCRS Sagam	23.4	2	MR
8	PS I03	MCRS Sagam	28.9	3	MS
9	PS 104	MCRS Sagam	30.2	3	MS
10	CML 239	CIMMYT	16.3	2	MR
11	CML 240	CIMMYT	27.9	3	MS
12	CML165	CIMMYT	4.4	1	R
13	CML 244	CIMMYT	19.5	2	MR
14	CML 245	CIMMYT	17.2	2	MR
15	CML 446	CIMMYT	35.3	3	MS
16	CML 459	CIMMYT	8.5	2	MR
17	CML 460	CIMMYT	9.9	2	MR
18	CML 470	CIMMYT	3.5	1	R
19	CML 152	CIMMYT	12.7	2	MR
20	CML 474	CIMMYT	3.9	1	R
21	CML 472	CIMMYT	3.5	1	R
22	CML-350	CIMMYT	15.8	2	MR
23	CML-242	CIMMYT	19.5	2	MR
24	CML451	CIMMYT	4.2	1	R
25	V370	VPKAS Almora	4.8	1	R
26	V-341	VPKAS Almora	8.2	1	MR
27	V-345	VPKAS Almora	9.7	2	MR
28	VL1018140	CIMMYT	4.9	1	R
29	VL 1249	CIMMYT	6.9	2	MR
30	VL 1034	CIMMYT	4.2	1	R
31	VL109452	CIMMYT	4.3	1	R
32	VL1030	CIMMYT	4.6	1	MS
33	VL127	CIMMYT	10.0	2	MR
34	VL1018527	CIMMYT	13.9	1	MR
35	VL0536	CIMMYT	5.0	1	R
36	VL109138	CIMMYT	6.3	2	MR
37	VL0512421	CIMMYT	4.5	1	MS
38	SMI 114-2	MCRS Sagam	21.3	2	MR
39	SMI-105	MCRS Sagam	20.8	2	MR
40	SMI 154	MCRS Sagam	54.6	4	S
41	SMI 187-1	MCRS Sagam	5.0	1	MR
42	W3	MCRS Sagam	29.0	3	MS
43	W5	MCRS Sagam	34.6	3	MS
44	MS 401	MCRS Sagam	21.4	2	MR
45	MS15C	MCRS Sagam	28.0	3	MS
46	SMC-5	Commercial Cultivar	18.5	2	MR
47	SMC-3	Commercial Cultivar	14.7	2	MR
48	SMH1	Commercial Cultivar	14.4	2	MR
49	C 15	Commercial Cultivar	26.2	3	MS
50	C6	Commercial Cultivar	19.4	2	MR
51	Anantnag local	Local	41.2	3	MS
52	Wailoo local	Local	52.8	4	S
53	Pahalgam local	Local	56.3	4	S
54	KDL211	IIMR	5.0	1	R
55	KDL222	IIMR	15.0	2	MR
56	KDL170	IIMR	8.6	2	MR
57	KDL310	IIMR	26.4	2	MS
58	KDL288	IIMR	9.8	2	MR
59	DML1126	IIMR	23.6	2	MR
60	DML1295	IIMR	27.5	3	MS

1=Resistant (R); 2=Moderately resistant (MR); 3=moderately susceptible (MS); 4= Susceptible (S); 5= Highly susceptible (HS).

Significant difference was observed in disease ratings among the genotypes under field and controlled conditions. The effect of the disease was more severe in the greenhouse plants. The differences are attributed to several factors including controlled environmental conditions, host genotype, inoculation methods and resistance variation among the genotypes. Similar observations were recorded by Muriithi and Mutinda

Table 3. Disease response of maize genotypes to different isolates of *E. Turcicum* under artificially inoculated controlled conditions.

Genotypes	Disease reaction												Aver-age
	Kti-1	Kti-2	Kti-3	Kti-4	Kti-5	Kti-6	Kti-7	Kti-8	Kti-9	Kti-10	Kti-11	Kti-12	
PS45	3.0	2.1	1.7	2.0	3.0	2.2	2.0	2.3	2.6	4.0	3.0	2.0	**2.4**
PS39	2.0	2.2	1.0	2.5	2.2	2.0	1.5	2.5	1.7	2.0	2.2	1.2	**1.9**
PS77	4.0	2.5	3.0	2.2	4.2	3.2	2.2	2.4	2.0	4.2	3.0	2.3	**2.9**
PS83	4.2	3.2	2.0	3.4	4.0	3.4	2.0	3.5	2.4	4.4	4.5	2.0	**3.3**
CML239	3.2	2.0	3.5	2.0	4.4	2.2	2.3	3.3	2.2	4.5	4.0	2.1	**3.0**
CML459	3.1	2.3	2.2	2.1	3.2	2.1	2.2	3.1	2.0	3.1	3.0	2.0	**2.5**
CML165	2.0	2.0	2.2	2.3	2.2	2.4	2.0	2.0	2.4	3.5	2.2	2.0	**2.3**
CML470	2.2	1.8	2.2	1.2	2.2	1.4	1.4	2.2	1.0	2.2	2.0	1.5	**1.8**
CML472	2.0	1.0	2.2	1.5	2.2	1.0	1.0	1.8	1.5	2.2	1.5	2.2	**1.7**
CML451	1.0	2.2	1.2	2.3	1.4	2.0	2.0	1.3	2.3	2.4	2.2	2.0	**1.9**
CML244	3.0	3.0	3.4	3.3	3.3	3.0	2.2	3.5	2.2	3.5	3.8	2.0	**3.0**
VL1249	2.1	1.8	2.0	2.2	3.8	2.2	1.8	2.0	1.8	2.4	3.5	2.2	**2.3**
VL1030	2.3	1.3	2.2	1.5	2.6	1.0	1.0	2.2	1.4	2.0	2.0	1.0	**1.7**
VL1018140	1.0	1.2	2.0	1.5	2.2	1.3	1.5	2.0	1.0	2.0	2.2	1.2	**1.6**
VL1018527	2.2	1.5	2.0	2.4	2.0	1.3	1.2	2.0	1.5	2.5	2.0	1.4	**1.8**
VL127	3.5	2.2	3.8	2.5	3.4	3.3	2.0	3.8	2.0	3.5	3.6	2.3	**3.0**
VL0536	2.0	2.3	2.6	2.5	3.7	2.8	2.3	3.3	1.3	3.0	2.0	1.0	**2.4**
SMI178-1	2.2	1.2	2.0	2.0	2.5	2.1	1.3	2.0	1.4	2.3	2.3	1.0	**1.9**
SMI105	4.0	2.0	3.3	3.3	4.0	3.0	2.0	3.2	2.2	4.3	3.4	2.0	**3.1**
SMI154	4.4	4.5	4.0	4.0	4.5	4.8	4.0	4.7	4.2	3.8	3.6	4.8	**4.3**
SMC5	3.0	2.3	3.2	2.2	3.0	2.0	2.1	2.3	2.0	4.0	3.1	2.1	**2.5**
SMC3	4.2	2.0	3.2	2.1	3.3	2.1	2.2	2.0	2.0	3.0	2.2	2.2	**2.5**
C15	4.0	2.1	3.2	2.1	4.2	3.3	2.0	3.0	2.3	4.4	3.5	2.5	**3.1**
KDL211	2.2	1.0	2.4	2.5	3.0	2.0	2.2	3.3	2.4	3.1	3.2	1.0	**2.4**
KDL170	4.2	2.0	3.3	2.2	4.3	4.3	2.0	4.0	2.2	3.5	4.5	2.0	**3.2**
Pahalgam local	4.2	4.4	4.5	3.8	3.0	4.0	3.2	4.4	4.5	3.8	4.0	3.3	**3.9**
Average	**2.9**	**2.2**	**2.6**	**2.4**	**3.2**	**2.5**	**2.0**	**2.8**	**2.1**	**3.2**	**3.0**	**2.0**	

The genotypes showing disease score between 0.1-2.0 were considered as resistant , 2.1-2.5 as moderately resistant (MR), 2.6-3.0 moderately susceptible (MS), 3.1-4.0 susceptible (S) and 4.1-5.0 as highly susceptible (HS)

Table 4. Pathogenic variability of *E. turcicum* isolates on putative differential maize lines .

S. N.	Genotype	Kti-1	Kti 2	Kti 3	Kti 4	Kti 5	Kti 6	Kti 7	Kti 8	Kti 9	Kti 10	Kti 11	Kti 12
1	SMC 3	S	R	S	R	S	R	R	R	R	S	S	R
2	CML 239	R	R	S	R	S	R	R	S	R	S	S	R
3	PS 77	S	R	S	R	S	S	R	R	R	S	S	R
4	SMI 105	R	R	S	S	S	S	R	S	R	S	R	R
5	CML 165	S	R	S	R	S	S	R	S	R	S	S	R
6	VL1018527	R	R	R	R	S	R	R	R	R	S	S	R
7	VL1018140	S	R	R	R	R	R	R	R	R	S	R	R
8	VL1030	R	R	R	R	R	R	S	R	R	R	R	R
9	CML472	R	R	R	S	R	R	R	R	R	S	R	R
10	KDL 211	R	R	R	R	S	R	R	S	R	R	S	R
11	SMI 154	S	S	S	S	S	S	S	S	S	S	S	S

(2001). Chandrashekara *et al.* (2014) evaluated 35 short-duration maize inbred lines against TLB and maydis leaf blight (MLB) under natural conditions and identified 12 inbred lines resistant against TLB and 19 inbred lines exhibited resistance against MLB. The inbred lines identified to possess resistance to Turcicum leaf blight in the present study, can be used successfully in developing high yielding early maturing hybrids/composites for the temperate mountain ecology, having resilience to Turcicum leaf blight.

Pathogenic variability: Reaction pattern of twelve isolates of *E. turcicum* obtained from diseased samples collected from different locations of Kashmir valley was recorded on a set of eleven putative differential maize lines (Table 4). The results revealed considerable pathogenic variability among the different isolates of *E. turcicum. Bunker and Mathur (2010*) reported that *E. Turcicum* isolates of maize exhibited considerable variations in cultural, morphological and pathogenic characteristics, studied on a set of 14 differential lines. Cluster analysis (Fig. 1) on the basis of similarity or dissimilarity in reaction types exhibited by these differential hosts, grouped the isolates into 6 pathogenic groups. Kti-2, Kti-9 and Kti-12 got resistant re-

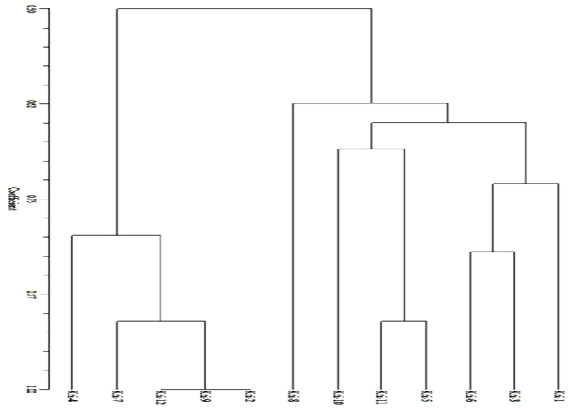

Fig. 1. *Dendrogram showing virulence similarity and successive clustering of 12 isolates of E. turcicum on selected maize lines.*

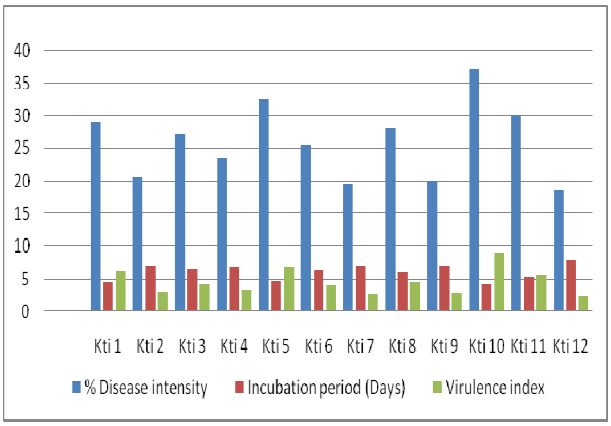

Fig. 2. *Virulence of E. turcicum isolates on maize cultivar SMI-154* **.**

sponse from all the differential lines except SMI154. On the basis of disease reaction of 11 different genotypes with 12 different isolates of *E. turcicum* it was found that Kti 10 showed highest average disease intensity followed by Kti5, Kti 11 and Kti1. The isolate Kti 12 was least aggressive with average disease intensity and exhibited resistant response from all the genotypes except SMI154. The isolate Kti-4 exhibited susceptible reaction with three genotypes while as Kti-7 exhibited susceptible reaction with two genotypes. Abebe and Singburaudom (2006) evaluated twenty representative isolates of *E. turcicum* for pathognicity on 11 maize varieties. The isolates were grouped into five clusters of virulent patterns by applying the UPGMA in the SAHN program for cluster analysis.

During the present study a wide variation among the isolates of *E. turcicum* was observed in terms of cultural characteristics, morphology and pathogenicity. The variability among isolates might be due to variation in the resistance of host plants, variation in environment, or from interaction among these variables. The significant interaction of genotypes and isolates may suggest some kind of specialization in the fungus population, because there are variations both in the resistance level of maize varieties and in the aggressiveness of the pathogen isolates. Reddy *et al*. (2013) in his variability studies on seven *E. turcicum* isolates demonstrated that isolates exhibited considerable variations in per cent disease index, latent period and lesion length. The fungus *E. turcicum* is known to be highly variable in cultural characteristics and pathogenicity. Considerable variation in morphology (Bunker *et al*., 2011) pathogenicity (Zhang *et al*., 2013) and genetic diversity (Aci *et al*., 2013) has been observed among isolates of *E. turcicum.* Heterokaryosis might be the reason for high variability of the pathogen population. Bunkoed *et al*. (2014) first time investigated the sexual stage *Setosphaeria turcica*, of *E. turcicum* in Thailand and suggested that sexual reproduction of *S. turcica* has caused genetic variation in the fungal pathogen, supported by previous analysis with inter-simple sequence repeat markers. Furthermore, the virulence may be enhanced or new physiological races may be generated through sexual hybridization.

Virulence variability: The isolates of *E. turcicum* tested in the present study exhibited considerable variation in the per cent disease intensity, virulence index, incubation period and lesion size (Fig. 2). The isolates showed shorter incubation period were more virulent. Shorter latent period benefit the pathogen development (Agrios, 2005) while as longer latent period indicates the implication of dilatory resistance by the host as reported by Thakur *et al*. (2007). Most of the isolates, which were more aggressive, belonged to the higher altitudes of Kashmir valley. Kti 10 showed highest average disease intensity (37.03 per cent) which belonged to Larnoo area with an altitude of 2286 m mean above sea level. The isolate Kti 12 belonged to Budgam with an altitude of 1610 m mean above sea level was least aggressive with an average disease intensity of 18.5 per cent and all the differentials showed resistant response with it except SMI154. Once the pathogens adopted in harsh conditions, gets favourable environmental conditions it becomes more aggressive. Variability among the isolates may be attributed to long term influence of weather conditions of particular location and ability of the pathogen to adapt to the varieties developed in a specific situation (Reddy *et al*., 2013).

Conclusion

The inbred lines identified to possess resistance to Turcicum leaf blight in the present study, can be used successfully in developing high yielding early maturing varieties having high level of resistance to Turcicum leaf blight suitable for temperate mountain ecologies. There exists a wide variation among the different test isolates of *E. turcicum* in terms of cultural, morphology and pathogenicity characteristics. The occurrence and distribution of different isolates of *E. turcicum* with wide pathogenic variability in the field provides important information to devise a suit-

able disease management programme of TLB.

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