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Inheritance of Tolerance of Maize Inbreds to *Exserohilum turcicum* in North Korea

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ABSTRACT *Exserohilum turcicum* is considered serious destructive disease of maize (*Zea mays* L.) in North Korea. This study aimed to understand genetic inheritance and combining ability of newly bred lines of maize tolerant to *E. turcicum* by diallel crosses. Three diallel sets for two different ecological regions and one agronomic trait; eastern (E), northern (N) and stay green (SG) involving 29 inbred lines were tested in eight locations of 2000 and 2001. *E. turcicum* infections were under natural conditions, respectively. Lines used were selected for high yield potential in test crosses with good agronomic traits and tolerance to biotic and abiotic stresses. Selection for race specific high resistance to biotic stresses was avoided to select quantitatively inherited genes. Host plant responses to *E. turcicum* were rated on a scale of 1 (highly tolerant) to 9 (highly susceptible). Highly significant variations were recorded in all trials. General combining ability (GCA) mean square was roughly twice that of specific combining ability (SCA). The genotype (G) by environment (E) interaction was highly significant. The overall results of genetic studies in three diallel sets show that genetic control for inbred tolerance to *E. turcicum* is polygenic and quantitatively inherited. New inbreds; E-3, N-1 and SG-4 confer better tolerance to *E. turcicum* than the widely used inbreds; Mo17, and B73. Proper use of genetic information from this study shall increase of corn production under high *E. turcicum* infection in the Far Eastern Regions of Korea and China.

Keywords : northern corn leaf blight, diallel crosses, quantitative inheritance, durable resistance

The 1/4 of maize in the world is grown in USA that produces half of the total production. While another 1/4 of maize is cultivated in China, the main Corn Belt of the Far Eastern region. Northern corn leaf blight (NCLB) caused by *Exserohilum turcicum* is a constraint to global maize production. It is a ubiquitous foliar wilt disease of maize in many temperate and tropical environments which can cause yield losses up of to 70% (Yeshitila, 2003). Apart from yield loss, the disease causes qualitative changes in the seed resulting in decreased sugar content, germination capacity and severely infected plants are predisposed to stalk rot (Cardwell *et al*., 1997; Gowda *et al*., 1992). Although the disease has a worldwide distribution, it is more severe in cool humid regions characterized by heavy dew (Dorothea *et al*., 1998; Juliana *et al*., 2005).

Maize or corn is the staple food and most widely cultivated crop (730,000 ha) in North Korea. A food shortage in North Korea can be caused by a shortfall in the production of maize as it is the staple food for 70% of the people (Kim *et al*., 2008; Kim *et al*., 2012). Ecological conditions for maize cultivation in North Korea and the North Eastern region of China are very favorable to NCLB with similar latitude to that of the US Corn Belt (38°N-42°N). Among diseases of maize occurring in North Korea (corn smut caused by *Ustilago maydis* and stalk and ear rot complex), *E. turcicum* has affected the yield of the crops more than any other biotic stresses (Kim *et al*., 2001; Kim *et al*., 2012). Severe epiphytotics of the disease occurred in North Korea in 1999 and 2001. An average reduction of grain yield by *E. turcicum* was estimated to be 40% under a severe infection.

Historical data showed that the highest damage of maize by the blight in the North Korea was around 1975 when

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an introduced hybrid, "SAR4" from Yugoslavia was cultivated on about 50,000 ha. The major cause of incidence was due to the break down of a single gene, *Ht*1A. A similar *E. turcicum* epidemic was experienced in South Korea when a double cross hybrid, "Bokkyo #2" (Park *et al*., 1975) having the same resistant gene *Ht*1A was broken down after two years of promotion to the Corn Belt of Gangwon Province, on the eastern border of North Korea.

NCLB is mainly controlled by resistant cultivars. The resistance is either qualitative or quantitative. Qualitative resistance is typically race-specific and inherited by single genes whereas quantitative resistance is race-non-specific and oligogenic or polygenic (Singh *et al*., 2004; Welz and Geiger 2000). Depending on the environment, the qualitative resistance of maize to *E. turcicum* may have a partial effect while quantitative resistance may have a substantial effect. For example, the race-specific gene *Ht*1 was unable to control *E. turcicum* in US Corn Belt inbred lines planted in Africa (Adipala *et al*., 1993; Kim *et al*., 1990; Kim *et al*., 2012; Welz 1998) and in Hawaii (*Personal Communication*, J. L. Brewbaker). CIMMYT inbred line CML191 providing partial resistance with oligogenic or polygenic inheritance in Africa (Schechert *et al*., 1999; Schechert *et al*., 1997) remained completely uninfected in an inoculated field trial in Europe (Welz *et al*., 1999).

Current breeding programs rely predominantly on qualitative resistance conferred by *Ht* genes but the emergence of new races of pathogen is a constant threat (Freymark *et al*., 1994; Juliana *et al*., 2005). *E. turcicum* exhibits a wide pathogenic variability (Yeshitila, 2003) and reports of new races overcoming previously resistant cultivars have been documented. Although many corn genotypes have been released from breeding programs, their reactions to NCLB pathogen in North Korea remain largely unknown. Several authors have suggested that the combination of resistance conferred by *Ht* genes and general resistance would enhance the level of resistance and result in greater stability and longer protection against *E. turcicum* (Hooker 1977; Hooker and Kim 1973; Kim *et al*., 2012; Pratt *et al*., 1993; Raymundo and Hooker 1982). However, this accumulation needs extra efforts in breeding. Uses of stable tolerance genes across races can be simpler and more durable (Kim 1996; Kim 2000).

Since *E. turcicum* is the most destructive disease of staple food corn in North Korea, breeding corn cultivars for durable resistance (we call it as tolerance because selection has been carried out based on yield potential and combining ability as well as host withstand to pest) is important to prevent of yield losses of maize in the Far Eastern region where 1/4 of the world corn cultivation. This can be another way of increasing food security. Thus, this study aimed to understand genetic inheritance and combining ability of newly developed but randomly chosen maize inbred lines tolerant to *E. turcicum*.

MATERIALS & METHODS

Plant Materials

The extraction of inbred lines was done by using germplasm from the USA, South Korea (SK), North Korea (NK), China, Europe and IITA and test crossed with high combining lines Mo17, B14 and B73 and two single crosses "Suwon 19" (Kim *et al*., 1978) from SK and "Hwaseong #1" from NK started from 1998. Within two years (1998-1999), over 10,000 inbreeding lines were developed using 2 to 3 generations per year and testcross of these lines were tested in multiple locations. Selection for lines was carried out for high yield potential and tolerance to major biotic (*E. turcicum*, corn smut caused by *Ustilago maydis*, Oriental corn borers caused by *Ostrinia furnacalis*)) and abiotic stresses (drought, lodging) in test crosses. In the breeding program, we have avoided to select race-specific resistance lines against *E. turcicum*. Tolerant plants had similar level of disease infection at the seedling stage but its tolerability was increased upon plant growth. Genetics of NCLB tolerance was studied by testing of three different sets (NKE-eastern region selection, NKN-northern region selection and SG- stay green trait) of diallel crosses formed for various target objectives (yield potential, tolerance to biotic and abiotic stresses) at eight locations in North Korea during 2000 and 2001. Lines used in this study were generated during the hybrid breeding process of maize for different ecological zones in North Korea since 1998. Selected inbreeding lines were grouped into two ecologies and one agronomic trait: eastern (E) and northern (N) region, and stay green (SG). The diallel F_1 seed

Table 1. Summary Information of Parental Lines.

Trial Name	No.	Pedigree No.	Grain color	Grain texture	Origin
NKE	E-1	99A-309-1802-S5	Yellow	Dent	Korea
	E-2	99A-309-1503-S3	Yellow	Flint/Dent	Korea
	E-3	99A-309-119-S4	Yellow	Dent/Flint	Korea
	E-4	99A-309-316-S5	Yellow	Flint/Dent	Korea
	E-5	99A-309-645-S3	Yellow	Dent/Flint	Korea
	E-6	99A-309-1177-S5	Yellow/Brown	Dent	Korea
	Mo17		Yellow	Dent	US
	B14		Yellow	Dent	US
	B73		Yellow	Dent	US
	B68		Yellow	Dent	US
NKN	N-1	99A-309-782-S5	Yellow	Dent	Korea
	N-2	99A-309-1069-S4	Yellow	Dent/Flint	Korea
	N-3	99A-309-1587-S5	Yellow	Dent	Korea
	N-4	99A-309-1375-S4	Yellow	Dent	Korea
	N-5	99A-309-607-S5	Yellow/White	Dent	Korea
	N-6	99A-309-791-S5	Yellow	Dent	Korea
	N-7	99A-309-1636-S5	Cream Yellow	Flint/Dent	Korea
	Mo17		Yellow	Dent	Korea
	H95		Yellow	Dent	US
	B68		Yellow	Dent	US
SG	SG-1	99A-309-41-S5	Yellow	Dent/Flint	Korea
	SG-2	99A-309-600-S5	Yellow/Brown	Flint	Korea
	SG-3	99A-309-745-S5	Yellow/Brown	Flint	Korea
	SG-4	99A-309-816-S5	White	Dent/Flint	Korea
	SG-5	99A-309-1006-S6	Yellow/Brown	Flint/Dent	Korea
	SG-6	99A-309-1563-S5	Yellow	Flint/Dent	Korea
	SG-7	99A-309-1680-S5	Yellow	Dent	Korea
	Mo17		Yellow	Dent	US
	B73		Yellow	Dent	US

Table 2. Name of diallel sets, no. of inbred lines included and site of trials studied for *E. turcicum* in North Korea in 2000 and 2001.

Year	Name	No. of Inbred	Site	
			No.	Name
2000	NKE	10	3	Gaecheon, Ongjin, and Cheongdan
	NKN	10	4	Gaecheon, Ongjin, Cheongdan, and Mirim
	SG	9	3	Gaecheon, Ongjin, and Cheongdan
2001	NKE	10	4	Gaecheon, Eunsan, Jeongju, and Mirim
	NKN	10	5	Gaecheon, Eunsan, Mirim, Jeongju and Hwangju
	SG	9	5	Gaecheon, Eunsan, Jeongju, Haeju and Hwangju

FIG. 1. The sites of experimental station in North Korea.

production was done in Milyang, South Korea during winter season. Popular US inbred lines; Mo17 and B73 were included in respective diallel crosses as parents. Details information of the diallel sets and testing locations are listed in Table 1 and 2.

Field Experiments

Three sets of diallel crosses were tested in eight different locations (Fig. 1) of NK; Mirim (39°21' N, 125°57' E) in Pyongyang, Gaecheon (39°42' N, 125°47' E), Eunsan (39°24' N, 125°59' E) in South Pyongan, Jeongju (39°41' N, 125°12' E) in North Pyongan, Cheongdan (39°58' N, 125°56' E), Ongjin (37°55' N, 125°21' E) and Haeju (38°02' N, 125°42' E) in South Hwanghae and Hwangju (38°40' N, 125°56' E) in North Hwanghae Province. The experiments were planted in a randomized complete block design with three replicates during May 2000 and 2001. A block consisted of 36 to 45 entries with double row plots of 12 plants, 2 m row, gave a recommended density of 56,000 ha^{-1}. Fertilizers were applied 300 kg ha^{-1} of N with 150 kg ha^{-1} P and 250 kg ha^{-1} K before planting. An additional half of N was given at 4 weeks after the planting. There was no irrigation, and no application of fungicide during the experiment.

Data Collection

Blight infections occurred naturally. Visible blight ratings on F1 host plants per plot were taken at two weeks after mid-silking on a scale of 1 to 9. Details of the rating are as: 1=highly tolerance, no blight symptoms or hypersensitive response; 2=a mild blight symptom, a few lesions in the lower leaves, almost normal plant growth; 3=several lesions in the lower leaves with apparent tolerance symptoms, mild blotches; 4=some blotching with mild tolerance symptoms; 5=intermediate response between tolerance and susceptibility; 6=mild damage of host plant and have a little chance to recover; 7=some damage with little chance to recover; 8=apparent damage of plant and caused significant yield reduction; 9=highly susceptible, severe damage of host plant and over 80% blighted. Data was taken from five individual plants and average data was used for statistical analysis.

Statistical analysis

A separate analysis for each location was run and after testing for the homogeneity of error variance, combined analysis was performed with the GLM procedure of the SAS program (SAS Institute 2001). The effects of genotypes, environments and all possible interactions were tested with the appropriate mean squares, as determined from the expected mean squares. The interactions of genotypes and years for three diallel sets were estimated only from Gaecheon, South Pyongan Province where yield potential of maize is the highest. Mean squares from Type III sums of squares, mean separation by Duncan test and orthogonal group comparison were calculated by the statement MEANS and CONTRAST of GLM procedure of SAS program. This was followed by diallel analysis to obtain general (GCA) and specific (SCA) combining ability effects using Griffing's (Gowda *et al.*, 1992) method 4, Model II for random effects and GCA and SCA effects were analyzed. To estimate the value of new inbred lines developed, lines were grouped into three; new lines, new plus widely used, and widely used lines, respectively.

RESULTS & DISCUSSION

A 10×10 diallel cross for NKE (NK-Eastern), NKN (NK-Northern) and 9×9 diallel cross for SG (Stay Green) were made and these single-cross hybrids were evaluated at different locations in 2000 and 2001 (Table 2).

The combined analysis of variance for each year over a different environment is presented in Table 3 and 4. Results showed that highly significant differences were found among the environments (E) and among the hybrids in

Table 3. Combined analysis of variance (Mean Square) for *E. turcicum* tolerance rating in three respective diallel sets NKE, NKN, SG grown under different environments in 2000, North Korea.

Source of variation	NKE		NKN		SG	
	df	MS	df	MS	Df	MS
Env (E)	2	172.14***	3	243.69***	2	25.06***
Rep (R)	6	1.14^{ns}	8	5.83***	6	6.33***
Hybrid	44	3.20***	44	1.65***	35	1.58***
Contrast:						
Group I vs Group II	1	0.002^{ns}	1	1.049 ^{ns}	1	14.058***
Group I vs Group III	1	2.593^{ns}	1	0.040 ^{ns}	1	0.001 ^{ns}
Group II vs Group III	1	2.801^{ns}	1	0.097 ^{ns}	1	1.486 ^{ns}
Group(I+II) vs Group III	1	3.077^{ns}	1	0.003 ^{ns}	1	0.229 ^{ns}
Group(II+III) vs Group I	1	0.278^{ns}	1	0.956 ^{ns}	1	12.801***
Group (I+III) vs Group II	1	0.486^{ns}	1	1.013 ^{ns}	1	14.286***
GCA	9	7.788***	9	3.610***	8	3.468***
SCA	35	2.010**	35	1.150^{ns}	27	1.024^{ns}
Hybrid×E	88	2.978***	132	1.340***	70	1.563***
GCA×E	18	9.860***	27	2.200***	16	3.639***
SCA×E	70	1.320^{ns}	105	1.310*	54	1.088*
Pooled error	263	1.017	352	0.799	210	0.701
CV%		28.34		22.77		27.49

^{ns} non significant, *, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

all trials tested. These results indicated that environmental conditions influenced the expression of *E. turcicum* infection and disease severity. Interaction of hybrids with the environment (hybrid×E) was found to be highly significant in almost all trial sets indicating that the hybrids reacted differently to environmental conditions.

Significant differences between hybrids means and inbred GCAs were detected in all trial sets in both years. The interaction of GCA effects and environment (GCA×E) was also significantly evident for all trials which revealed that additive genetic effects were more important in the inheritance of *E. turcicum*. These are quantitatively inherited additive genes which influenced by the environmental factors including disease severity and time of natural infection.

For specific combining ability (SCA) analysis, significant effects were found for three trials (NKE trial in both years, SG trial in 2001) prevailing that the significant role of non-additive effects was also involved in the inheritance of *E. turcicum* tolerance. The interaction of SCA effects with environment (SCA×E) was not observed in most of the trial sets.

The mean square of GCA was 3.14 (NKN, 2000) to 6.13 (NKN, 2001) times larger than those of SCA effects, respectively. The larger GCA than SCA mean squares implies that additive gene action is by far more important in the inheritance of *E. turcicum* in this study. However, estimates of additive effects would be greatly influenced by the environmental conditions such as disease severity.

The combined analysis of variance for *E. turcicum* tolerance rating among hybrids for two years in Gaecheon (highest yield potential area for corn) differed significantly in two trials, NKE and NKN (Table 5). The estimates of GCA and SCA were highly significant in all trials except SCA for NKN. GCA mean squares were nearly six times larger in NKE and SG, while three times larger in NKN. These could confirm that additive gene action has a higher preponderance in *E. turcicum* tolerance. The interactions between GCA and year (GCA×Y) were also highly significant

Table 4. Combined analysis of variance (Mean Square) for *E. turcicum* tolerance rating in three respective diallel sets NKE, NKN, SG grown under different environments in 2001, North Korea.

Source of variation	NKE		NKN		SG	
	df	MS	df	MS	df	MS
Env (E)	3	146.87***	4	58.22***	4	70.923***
Rep (R)	8	1.35*	10	1.71**	10	6.20***
Hybrid	44	2.35***	44	1.47***	35	1.526***
Contrast:						
Group I vs Group II	1	13.328***	1	16.839***	1	1.691^{ns}
Group I vs Group III	1	2.901*	1	6.300**	1	0.0174^{ns}
Group II vs Group III	1	0.689^{ns}	1	0.209^{ns}	1	0.092^{ns}
Group(I+II) vs Group III	1	0.036^{ns}	1	2.349^{ns}	1	0.002^{ns}
Group(II+III) vs Group I	1	12.675***	1	18.979***	1	1.602^{ns}
Group (I+III) vs Group II	1	10.463***	1	12.889***	1	1.676^{ns}
GCA	9	5.730***	9	4.350***	8	3.490***
SCA	35	1.470***	35	0.710^{ns}	27	0.943*
Hybrid× E	132	0.671^{ns}	176	0.712^{ns}	140	0.987***
GCA × E	27	1.112**	36	1.034*	32	2.044***
SCA × E	105	0.525^{ns}	140	0.651^{ns}	108	0.546^{ns}
Pooled error	352	0.579	440	0.643	350	0.607
CV%		17.18		20.39		18.50

^{ns} non significant, *, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

Table 5. Combined analysis of variance (Mean Square) for *E. turcicum* tolerance rating in three diallel sets NKE, NKN, SG grown under two year (2000 and 2001) in Gaecheon, North Korea.

Source of variation	NKE		NKN		SG	
	df	MS	df	MS	df	MS
Year (Y)	1	85.573***	1	92.459***	1	0.907^{ns}
Rep(R)	4	1.537^{ns}	4	3.004*	4	5.269***
Hybrid	44	5.004***	44	1.791***	35	3.082***
Contrast:						
Group I vs Group II	1	9.047**	1	0.397^{ns}	1	20.572***
Group I vs Group III	1	6.287*	1	0.438^{ns}	1	0.009^{ns}
Group II vs Group III	1	0.235^{ns}	1	0.120^{ns}	1	2.579^{ns}
Group(I+II) vs Group III	1	1.884 ^{ns}	1	0.271^{ns}	1	0.508^{ns}
Group(II+III) vs Group I	1	10.696**	1	0.548^{ns}	1	18.502***
Group (I+III) vs Group II	1	4.645*	1	0.230^{ns}	1	21.072***
GCA	9	14.805***	9	4.219***	8	8.427***
SCA	35	2.483***	35	1.421^{ns}	27	1.498**
Hybrid × Y	44	3.032***	44	2.118***	35	2.231***
GCA × Y	9	11.611***	9	4.900***	8	9.246***
SCA × Y	35	1.033^{ns}	35	1.778**	27	1.059^{ns}
Pooled error	176	1.094	176	0.818	140	0.769
CV%		24.56		25.39		25.38

^{ns} non significant, *, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

and the magnitude of mean squares for GCA×Y were roughly eleven times higher in NKE, nine times higher in SG and three times higher in NKN. This result confirmed that there is a high variation in *E. turcicum* infection levels

Table 6. Mean *E. turcicum* tolerance rating (1-9), specific combining ability effects (sij) for three groups, 45 crosses of NKE trial evaluated over three environments in 2000, four environments in 2001 and two years in Gaecheon, North Korea.

Crosses	NKE(2000)		NKE(2001)		NKE(Gaecheon)	
	Mean Rating[†]	SCA	Mean Rating[†]	SCA	Mean Rating[†]	SCA
Group I(New Inbred × New Inbred)						
E-1 × E-2	3.89^{b-g}	0.17	3.92^{i-l}	-0.21	4.17^{e-j}	-0.09
E-1 × E-3	3^{e-i}	-0.22	3.63^{kl}	-0.22	2.83^{j}	-0.49
E-1 × E-4	2.89^{f-i}	-0.61^{*}	4.42^{c-j}	0.32	3.67^{f-j}	-0.11
E-1 × E-5	4^{b-f}	0.51	3.58^{l}	-0.45^{*}	3.33^{h-j}	-0.13
E-1 × E-6	4.44^{a-c}	0.05	5^{a-d}	0.49^{*}	5.83^{a-c}	0.64
E-2 × E-3	3.33^{c-i}	0.33	3.96^{h-l}	-0.14	3.5^{g-j}	-0.11
E-2 × E-4	2.78^{g-i}	-0.5	4.21^{e-l}	-0.14	3.5^{g-j}	-0.57
E-2 × E-5	3.22^{d-i}	-0.04	4.21^{e-l}	-0.08	3.67^{f-j}	-0.09
E-2 × E-6	4.67^{ab}	0.5	5.29^{ab}	0.53^{**}	6.67^{a}	1.18^{**}
E-3 × E-4	3.56^{b-i}	0.78^{**}	3.71^{j-l}	-0.36	3.33^{h-j}	0.2
E-3 × E-5	3.67^{b-h}	0.90^{**}	3.75^{j-l}	-0.26	3.17^{ij}	0.34
E-3 × E-6	3.22^{d-i}	-0.45	4.38^{c-j}	-0.11	4.17^{e-j}	-0.38
E-4 × E-5	2.56^{hi}	-0.49	4.25^{d-l}	-0.01	3.17^{ij}	-0.11
E-4 × E-6	4.33^{a-d}	0.39	4.46^{c-j}	-0.27	5.33^{a-e}	0.32
E-5 × E-6	3.22^{d-i}	-0.71^{*}	4.46^{c-j}	-0.22	3.33^{h-j}	-1.36^{***}
Group I Mean	3.52		4.22		3.98	
Group II(New Inbred × Popular Inbred)						
E-1 × Mo17	3.22^{d-i}	-0.75^{*}	4.04^{h-l}	0.01	3.67^{f-j}	-0.74
E-1 × B14	4.11^{b-e}	0.46	4.63^{b-i}	0.15	4.67^{c-i}	0.39
E-1 × B73	4.01^{b-f}	0.03	4.08^{g-l}	-0.37	4.83^{c-h}	0.24
E-1 ×B68	4.00^{b-f}	0.36	4.33^{c-j}	0.28	4.17^{e-j}	0.31
E-2 × Mo17	3.67^{b-h}	-0.08	4.13^{f-l}	-0.16	4.00^{e-j}	-0.70
E-2 × B14	3.10^{1e-i}	-0.32	4.67^{b-i}	-0.07	4.67^{c-i}	0.09
E-2 × B73	3.78^{b-g}	0.03	5.04^{a-c}	0.34	5.67^{a-d}	0.78^{*}
E-2 × B68	3.33^{c-i}	-0.08	4.25^{d-l}	-0.06	3.67^{f-j}	-0.49
E-3 × Mo17	2.44^{i}	-0.81^{**}	4.08^{g-l}	0.07	2.83^{j}	-0.93^{*}
E-3 × B14	2.78^{g-i}	-0.15	4.92^{a-e}	0.46^{*}	4.17^{e-j}	0.53
E-3 × B73	3.00^{e-i}	-0.25	4.92^{a-e}	0.49^{*}	4.33^{d-i}	0.39
E-3 × B68	2.78^{g-i}	-0.14	4.13^{f-l}	0.09	3.67^{f-j}	0.45
E-4 × Mo17	4.11^{b-e}	0.58	4.21^{e-l}	-0.05	5.00^{c-g}	0.78^{*}
E-4 × B14	3.44^{c-i}	0.24	5.04^{a-c}	0.34	4.17^{e-j}	0.07
E-4 × B73	3.44^{c-i}	-0.08	4.83^{a-f}	0.16	4.17^{e-j}	-0.24
E-4 × B68	2.89^{f-i}	-0.31	4.29^{c-l}	0.01	3.33^{h-j}	-0.34
E-5 × Mo17	4.11^{b-e}	0.60^{*}	4.88^{a-f}	0.67^{***}	5.01^{c-g}	1.09^{**}
E-5 × B14	2.89^{f-i}	-0.31	5.21^{ab}	0.56^{**}	4.50^{c-i}	0.72
E-5 ×B73	3.00^{e-i}	-0.51	4.38^{c-j}	-0.24	3.67^{f-j}	-0.43
E-5 × B68	3.22^{d-i}	0.04	4.25^{d-l}	0.03	3.33^{h-j}	-0.03
E-6 × Mo17	4.44^{a-c}	0.03	4.33^{c-j}	-0.34	5.33^{a-e}	-0.30
E-6 × B14	3.78^{b-g}	-0.31	4.42^{c-j}	-0.70^{***}	4.50^{c-i}	-1.01^{**}
E-6 × B73	5.22^{a}	0.80^{**}	5.50^{a}	0.41^{*}	6.50^{ab}	0.68
E-6 ×B68	3.78^{b-g}	-0.31	4.92^{a-e}	0.22	5.33^{a-e}	0.24
Group II Mean	3.52		4.56		4.38	
Group III(Popular Inbred × Popular Inbred)						
Mo17×B14	3.89^{b-g}	0.21	4.63^{b-i}	-0.02	4.67^{c-i}	-0.05
Mo17×B73	4.00^{b-f}	0.00	4.42^{c-j}	-0.2	5^{c-g}	-0.03
Mo17×B68	3.89^{b-g}	0.22	4.25^{d-l}	0.03	5.17^{b-f}	0.87^{*}
B14×B73	3.67^{b-h}	-0.01	4.71^{b-h}	-0.35	4.33^{d-i}	-0.57
B14×B68	3.56^{b-i}	0.21	4.29^{c-l}	-0.37	4.00^{e-j}	-0.18
B73×B68	3.67^{b-h}	0.00	4.42^{c-j}	-0.22	3.67^{f-j}	-0.82^{*}
Group III Mean	3.78		4.45		4.47	

[†] Means with different letters in column are significantly different at P=0.05, ^{ns} non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

Table 7. Mean *E. turcicum* tolerance rating (1-9), specific combining ability effects (sij) for three groups, 45 crosses of NKN trial evaluated over four environments in 2000, five environments in 2001 and two years in Gaecheon, North Korea.

Crosses	NKN(2000)		NKN(2001)		NKN(Gaecheon)	
	Mean Rating[†]	SCA	Mean Rating[†]	SCA	Mean Rating[†]	SCA
Group I(New Inbred × New Inbred)						
N-1 × N-2	3.58^{c-f}	-0.02	4.07^{b-h}	-0.13	3.00^{d-f}	-0.32
N-1 × N-3	3.75^{b-f}	-0.25	3.73^{d-h}	-0.2	3.00^{d-f}	-0.53
N-1 × N-4	4.00^{a-f}	0.04	3.93^{b-h}	-0.24	3.50^{c-f}	0.06
N-1 × N-5	3.67^{b-f}	-0.03	4.00^{b-h}	0.04	3.33^{d-f}	0.27
N-1 × N-6	3.50^{d-f}	-0.39	3.73^{d-h}	-0.05	3.50^{c-f}	0.20
N-1 × N-7	4.00^{a-f}	0.28	3.67^{d-h}	-0.10	3.17^{d-f}	0.18
N-2 × N-3	3.92^{b-f}	0.01	4.47^{a-c}	0.17	4.67^{a-c}	0.62
N-2 × N-4	3.83^{b-f}	-0.03	4.80^{a}	0.26	4.17^{a-d}	0.20
N-2 × N-5	3.42^{ef}	-0.19	4.13^{a-g}	-0.20	3.33^{d-f}	-0.25
N-2 × N-6	4.00^{a-f}	0.20	4.00^{b-h}	-0.15	3.83^{a-f}	0.02
N-2 × N-7	3.83^{b-f}	0.21	4.60^{ab}	0.47^{**}	3.67^{b-f}	0.16
N-3 × N-4	4.58^{ab}	0.32	4.13^{a-g}	-0.14	4.83^{ab}	0.66^{*}
N-3 × N-5	3.92^{b-f}	-0.08	4.07^{b-h}	0	3.50^{c-f}	-0.30
N-3 × N-6	4.42^{a-d}	0.22	3.87^{c-h}	-0.02	3.83^{a-f}	-0.19
N-3 × N-7	3.75^{b-f}	-0.27	3.93^{b-h}	0.07	3.67^{b-f}	-0.05
N-4 × N-5	3.33^{ef}	-0.62^{**}	4.40^{a-d}	0.10	3.33^{d-f}	-0.38
N-4 × N-6	4.50^{a-c}	0.34	4.27^{a-f}	0.14	4.17^{a-d}	0.22
N-4 × N-7	3.92^{b-f}	-0.06	4.33^{a-e}	0.23	3.17^{d-f}	-0.46
N-5 × N-6	3.92^{b-f}	0.02	4.07^{b-h}	0.15	3.17^{d-f}	-0.40
N-5 × N-7	3.83^{b-f}	0.12	4.00^{b-h}	0.10	3.50^{c-f}	0.25
N-6 × N-7	3.83^{b-f}	-0.08	3.67^{d-h}	-0.05	3.50^{c-f}	0.02
Group I Mean	3.88		4.09		3.61	
Group II(New Inbred × Popular Inbred)						
N-1× Mo17	4.17^{a-e}	-0.04	4.07^{b-h}	0.40^{*}	3.5^{c-f}	-0.11
N-1 × H95	3.75^{b-f}	0.07	3.93^{b-h}	0.22	3.33^{d-f}	0.39
N-1 × B68	4.00^{a-f}	0.33	3.73^{d-h}	0.06	2.67^{f}	-0.15
N-2× Mo17	4.50^{a-c}	0.39	3.60^{e-h}	-0.44^{*}	4.17^{a-d}	0.04
N-2 × H95	3.17^{f}	-0.42	4.13^{a-g}	0.05	3.33^{d-f}	-0.13
N-2 × B68	3.42^{ef}	-0.16	4.00^{b-h}	-0.04	3.00^{d-f}	-0.34
N-3× Mo17	4.83^{a}	0.32	3.60^{e-h}	-0.17	5.00^{a}	0.66^{*}
N-3 × H95	3.92^{b-f}	-0.06	3.87^{c-h}	0.05	3.17^{d-f}	-0.50
N-3 × B68	3.75^{b-f}	-0.22	4.00^{b-h}	0.23	3.17^{d-f}	-0.38
N-4× Mo17	4.83^{a}	0.37	4.00^{b-h}	-0.01	5.00^{a}	0.75^{*}
N-4 × H95	3.75^{b-f}	-0.19	3.87^{c-h}	-0.19	2.83^{ef}	-0.75^{*}
N-4 × B68	3.75^{b-f}	-0.18	3.87^{c-h}	-0.15	3.17^{d-f}	-0.30
N-5× Mo17	4.42^{a-d}	0.21	4.00^{b-h}	0.20	4.17^{a-d}	0.29
N-5 × H95	4.00^{a-f}	0.32	3.80^{c-h}	-0.05	3.50^{c-f}	0.29
N-5 × B68	3.92^{b-f}	0.25	3.47^{gh}	-0.34	3.33^{d-f}	0.25
N-6× Mo17	3.67^{b-f}	-0.74^{**}	3.53^{f-h}	-0.10	3.17^{d-f}	-0.94^{**}
N-6× H95	4.50^{a-c}	0.63^{**}	3.60^{e-h}	-0.07	4.00^{a-e}	0.56
N-6× B68	3.67^{b-f}	-0.20	3.80^{c-h}	0.17	3.83^{a-f}	0.52
N-7× Mo17	4.08^{a-f}	-0.14	3.47^{gh}	-0.14	3.67^{b-f}	-0.13
N-7× H95	3.58^{c-f}	-0.11	3.33^{h}	-0.31	3.17^{d-f}	0.04
N-7× B68	3.75^{b-f}	0.06	3.33^{h}	-0.27	3.00^{d-f}	0
Group II Mean	3.97		3.76		3.53	
Group III(Popular Inbred × Popular Inbred)						
Mo17×H95	3.83^{b-f}	-0.35	3.67^{d-h}	0.11	3.33^{d-f}	-0.42
Mo17×B68	4.17^{a-e}	-0.01	3.67^{d-h}	0.15	3.50^{c-f}	-0.13
H 95× B68	3.75^{b-f}	0.11	3.73^{d-h}	0.18	3.50^{c-f}	0.54
Group III Mean	3.92		3.69		3.44	

[†] Means with different letters in column are significantly different at P=0.05, ^{ns} non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

Table 8. Mean *E. turcicum* tolerance rating (1-9), specific combining ability effects (sij) for three groups, 36 diallel crosses of SG trial evaluated over three environments in 2000, five environments in 2001 and two years in Gaecheon, North Korea.

Crosses	SG(2000)		SG(2001)		SG(Gaecheon)	
	Mean Rating[†]	SCA	Mean Rating[†]	SCA	Mean Rating[†]	SCA
Group I(New Inbred × New Inbred)						
SG-1×SG-2	3.67^{a-c}	0.44	4.00^{c-g}	-0.28	4.17^{a-d}	0.04
SG-1×SG-3	3.00^{b-f}	-0.12	4.13^{b-g}	-0.39^{*}	3.50^{b-g}	-0.37
SG-1×SG-4	3.00^{b-f}	-0.24	4.13^{b-g}	0.12	3.33^{b-g}	0.11
SG-1×SG-5	3.11^{b-f}	-0.21	4.40^{a-f}	-0.05	3.67^{b-f}	-0.39
SG-1×SG-6	3.44^{a-e}	0	4.40^{a-f}	0.18	3.67^{b-f}	-0.15
SG-1×SG-7	2.56^{ef}	-0.69^{**}	4.27^{a-f}	-0.02	3.67^{b-f}	-0.49
SG-2×SG-3	2.56^{ef}	0.02	4.47^{a-e}	0.14	3.50^{b-g}	0.25
SG-2×SG-4	2.78^{c-f}	0.08	4.27^{a-f}	0.44^{*}	2.83^{e-g}	0.23
SG-2×SG-5	2.56^{ef}	-0.23	4.13^{b-g}	-0.13	3.17^{c-g}	-0.27
SG-2×SG-6	2.44^{f}	-0.46	3.87^{d-g}	-0.17	2.67^{fg}	-0.54
SG-2×SG-7	2.67^{d-f}	-0.04	4.13^{b-g}	0.03	3.00^{d-g}	-0.54
SG-3×SG-4	2.78^{c-f}	0.19	3.80^{e-g}	-0.26	2.33^{g}	-0.01
SG-3×SG-5	2.67^{d-f}	0	4.73^{ab}	0.23	4.00^{a-e}	0.82^{**}
SG-3×SG-6	3.00^{b-f}	0.20	4.53^{a-d}	0.26	3.00^{d-g}	0.06
SG-3×SG-7	2.78^{c-f}	0.19	4.53^{a-d}	0.20	3.67^{b-f}	0.39
SG-4×SG-5	2.67^{d-f}	-0.13	3.80^{e-g}	-0.20	2.33^{g}	-0.20
SG-4×SG-6	2.56^{ef}	-0.37	3.53^{g}	-0.23	2.33^{g}	0.04
SG-4×SG-7	3.00^{b-f}	0.28	3.80^{e-g}	-0.03	2.33^{g}	-0.30
SG-5×SG-6	3.22^{b-f}	0.22	4.20^{a-g}	0	3.00^{d-g}	-0.13
SG-5×SG-7	3.00^{b-f}	0.20	4.60^{a-c}	0.33	3.67^{b-f}	0.20
SG-6×SG-7	3.00^{b-f}	0.08	3.73^{fg}	-0.31	3.50^{b-g}	0.27
Group I Mean	2.88		4.20		3.21	
Group II(New Inbred × Popular Inbred)						
SG-1×Mo17	3.89^{ab}	0.15	4.40^{a-f}	0.18	5.17^{a}	0.85^{**}
SG-1×B73	4.22^{a}	0.66^{**}	4.87^{a}	0.27	5.00^{a}	0.42
SG-2×Mo17	3.44^{a-e}	0.25	4.20^{a-g}	0.17	4.33^{a-c}	0.63^{*}
SG-2×B73	3^{b-f}	-0.02	4.20^{a-g}	-0.20	4.17^{a-d}	0.20
SG-3×Mo17	2.89^{c-f}	-0.19	4.40^{a-f}	0.13	3.00^{d-g}	-0.44
SG-3×B73	2.67^{d-f}	-0.24	4.33^{a-f}	-0.31	3.00^{d-g}	-0.70^{*}
SG-4×Mo17	3.44^{a-e}	0.23	4.00^{c-g}	0.23	3.17^{c-g}	0.37
SG-4×B73	3.00^{b-f}	-0.04	4.07^{b-g}	-0.07	2.83^{e-g}	-0.23
SG-5×Mo17	3.11^{b-f}	-0.18	3.87^{d-g}	-0.34	3.33^{b-g}	-0.30
SG-5×B73	3.44^{a-e}	0.33	4.73^{ab}	0.16	4.17^{a-d}	0.27
SG-6×Mo17	3.44^{a-e}	0.03	4.00^{c-g}	0.02	3.00^{d-g}	-0.39
SG-6×B73	3.56^{a-d}	0.31	4.60^{a-c}	0.25	4.50^{ab}	0.85^{**}
SG-7×Mo17	3.56^{a-d}	0.35	3.80^{e-g}	-0.24	4.00^{a-e}	0.27
SG-7×B73	2.67^{d-f}	-0.37	4.47^{a-e}	0.05	4.17^{a-d}	0.18
GroupII Mean	3.31		4.24		3.85	
Group III(Popular Inbred × Popular Inbred)						
Mo17×B73	2.89^{c-f}	-0.64^{**}	4.20^{a-g}	-0.15	3.17^{c-g}	-0.99^{***}
GroupIII Mean	2.89		4.20		3.17	

[†] Means with different letters in column are significantly different at P=0.05, ^{ns} non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

and host plant tolerance across years. Therefore, recurrent selection could be used to improve the performance of the population developed from the high GCA lines while the lines *per se* or their derivatives could be used to develop *E. turcicum* tolerance hybrids.

The results from this field research are similar with the finding in QTL mapped NCLB. Wisser *et al.* (Welz *et al*., 1993; Welz *et al*., 1999) reported that the numerous QTL mapped for NCLB were scattered over the genome and available evidence on the genetic architecture of NCLB resistance is ambiguous. This is the exactly the reason why we avoided to select race specific high resistance in our breeding against *E. turcicum*. Under the quantitatively resistance model, recurrent selection would be the most appropriate breeding method for improving tolerance. Indeed, several studies have documented significant gains from recurrent selection for NCLB resistance (Brewbaker *et al*., 2011; Campaña and Pataky 2005; Carson 2006; Ceballos *et al*., 1991; Jenkins *et al*., 1954; Pataky 1994) with 15 to 20% reduction in susceptibility per generation (Campaña and Pataky 2005; Carson 2006; Ceballos et al., 1991).

To compare the value of new inbreds compared to popular inbreds, the diallel crosses under study were divided into three groups based on the combination of inbred parents. Group I consisted of the combinations between new inbred lines, group II consisted of the combinations from new inbred lines and popular inbred lines and group III consisted of the combinations among popular inbred lines (Table 6, 7, 8).

In NKE trial, no differences between group comparisons of *E. turcicum* rating were examined in 2000 but the contrast of group I versus group II, group I versus group III and group (II+III) versus group I were significantly different in 2001 and combined years analysis in Gaecheon (Table 3, 4, 5). The mean value of group I showed better *E. turcicum* tolerant score than group II and group III (Table 6), indicating new information of our bred inbred lines.

Out of 45 crosses of NKE, 22 crosses (48.89%) from the 2000 trial and 25 crosses (55.56%) from 2001 showed negative SCA effect (for more tolerance). The lowest mean

Table 9. Array means for *E. turcicum* tolerance rating (1-9), general combining ability effects (gi) of 10 lines of NKE trial and mean square comparisons of elite lines evaluated over three environments in 2000, four environments in 2001 and two years in Gaecheon, North Korea.

Parent	2000		2001		Gaecheon	
	Array Mean[†]	GCA	Array Mean[†]	GCA	Array Mean[†]	GCA
E-1	3.73^{ab}	0.19	4.18^{d}	-0.28***	4.13^{b-d}	-0.15
E-2	3.53^{bc}	-0.03	4.41^{a-d}	-0.03	4.39^{bc}	0.15
E-3	3.09^{c}	-0.53***	4.16^{d}	-0.30***	3.56^{d}	-0.79***
E-4	3.33^{bc}	-0.25*	4.38^{b-d}	-0.06	3.96^{cd}	-0.33*
E-5	3.32^{bc}	-0.26*	4.33^{cd}	-0.11	3.69^{d}	-0.65***
E-6	4.12^{a}	0.64***	4.75^{a}	0.36***	5.22^{a}	1.08***
Mo17	3.75^{ab}	0.22	4.33^{cd}	-0.11	4.52^{bc}	0.29*
B14	3.47^{bc}	-0.10	4.72^{ab}	0.33***	4.41^{bc}	0.17
B73	3.75^{ab}	0.22	4.7^{a-c}	0.30***	4.69^{ab}	0.48***
B68	3.46^{bc}	-0.11	4.35^{cd}	-0.09	4.04^{b-d}	-0.25
Contrast:	Mean Square					
E-3 vs Mo17	2.490***		0.154 ^{ns}		5.220***	
E-3 vs B14	0.830^{ns}		1.764***		4.096**	
E-3 vs B73	2.500***		1.613***		7.183***	
E-3 vs B68	0.770 ^{ns}		0.189 ^{ns}		1.308 ^{ns}	

[†] Means with different letters in column are significantly different at P=0.05, ns non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

value (2.44) and best negative SCA value (-0.81) was observed in E-3×Mo17. The moderate resistant parent Mo17 produced the highest significant positive SCA (0.67) when cross with E-5 in 2001. Mo17 and its relatives are the widely used inbred in the Far Eastern region. The most susceptible cross was detected in E-6 cross with B73 (susceptible parent) having F_1 mean value of 5.2 in 2000. Limited uses of B73 inbred have not been popular in the region. High susceptibility of *E. turcicum* and *Ostrinia furnacalis* might be the cause.

Four crosses form the 2000 trial, E-3×Mo17 (-0.81), E-1×Mo17 (-0.75), E-5×E-6 (-0.71), E-1×E-4 (-0.61) and two crosses from 2001 trial, E-1×E-5 (-0.45) and E-6×B14 (-0.70) had significant negative SCA values. The combined analysis over years in Gaecheon resulted that E-3×Mo17 performed best with minimum array mean (2.83) and highest negative SCA (-0.93). The most susceptible performance was found in E-2×E-6 with maximum mean (6.67) and largest positive SCA (1.18) (Table 6).

E. turcicum rating of E-3 showed the most tolerant reaction with lowest arrays mean, an average value of all possible crosses (3.09, 4.16) and highest significant negative GCA value (-0.53, -0.3) in 2000 and 2001 (Table 9). Negative values for general combining abilities indicate a contribution toward tolerance to *E. turcicum*. The most susceptible parent was found in E-6 having the highest array mean (4.12, 4.75) and significant positive GCA value (0.64, 0.36) in 2000 and 2001, prevailed that array mean reflected GCA value in NKE trial.

The result from the analysis across the years in Gaecheon (Table 9) also showed that E-3 was the most tolerant parent with a minimum array mean (3.56) and highest negative GCA (-0.79) and E-6 had a maximum array mean (5.22) and highest GCA (1.08).

The result from both combined analysis (environments, years) indicated that E-3 seemed to be good source of tolerance parent with lowest array mean and the significant negative GCA. The *E. turcicum* tolerant potency of E-3 was significantly higher from the well known moderately resistant check Mo17 and susceptible check B73 (Table 9). Our experiences on inbred B14 showed that it confers high GCA effects for yield potential in crosses in the northern region of North Korea and China where *E. turcicum* is prevalent. E-6 can be considered as a most susceptible parent with the highest array mean and highest positive GCA values.

The results of our studies show that the new tolerant inbred sources are more important to control *E. turcicum* in the region. A commercial hybrid using E-3 has been bred.

In NKN trial, group I mean value (3.88) was smaller than group II (3.97) and group III (3.92) in 2000 but mean value of group I (4.09, 3.61) was higher than group II (3.76, 3.53) and III (3.69, 3.44) in 2001 and combined analysis of years in Gaecheon, respectively (Table 3, 4, 5, 7). Although group III showed the lowest mean value, this group could not produce the desirable combination with negative SCA in 2001, indicating results of various studies of *E. turcicum* resistance in USA and Europe may not be adequate in the Far East region.

Among 45 diallel crosses, 24 crosses (53.33%) from 2000 and 23 crosses (51.11%) from 2001 gave the negative SCA value. Among these, two crosses (N-6×Mo17, N-4×N-5) from the 2000 trial and only one cross (N-2×Mo17) from 2001 showed significant effect. Interestingly, (N-6×Mo17) which showed the highest negative performance in SCA came from the parents of both positive GCA in 2000 (Table 6, 9).

In the combined analysis over two years in Gaecheon, 22 out of 45 crosses performed negative SCA effect, among them N-4×H95 (-0.75) and N-6×Mo17 (-0.94) revealed desirable significant effect. The most susceptible cross N-4 ×Mo17 having the largest SCA (0.75) value and F_1 mean (5.00).

The array mean of parents ranged from 3.74 (N-2) to 4.28 (Mo17) in 2000 and 3.36 (Mo17) to 3.78 (N-2) in 2001 (Table 10). The highest positive GCA effect was found in Mo17 (0.40) in 2000 and N-2 (0.33) in 2001. The highest negative GCA effect was found in N-2 (-0.21), Mo17 and B68 (-0.20) in 2000 and 2001, respectively. The two parents N-2 and Mo17 performed differently in 2000 and 2001. Again, the tolerance level of Mo17 may not be high enough to control of *E. turcicum* in North Korea. In combined analysis over two years, the maximum array mean (3.95) and highest positive significant GCA (0.43) was found in Mo17. The minimum array mean (3.22) and lowest significant value (-0.38) was observed in N-1

Table 10. Array means for *E. turcicum* tolerance rating (1-9), general combining ability effects (gi) of 10 lines of NKN trial and mean square comparisons of elite lines evaluated over four environments in 2000, five environments in 2001 and two years in Gaecheon, North Korea.

Parent	2000		2001		Gaecheon	
	Array Mean[†]	GCA	Array Mean[†]	GCA	Array Mean[†]	GCA
N-1	3.82^{bc}	-0.11	3.87^{bc}	-0.04	3.22^{d}	-0.38^{**}
N-2	3.74^{c}	-0.21^{*}	4.20^{a}	0.33^{***}	3.69^{a-d}	0.14
N-3	4.09^{ab}	0.19^{*}	3.96^{bc}	0.06	3.87^{ab}	0.35^{**}
N-4	4.06^{a-c}	0.15	4.17^{a}	0.30^{***}	3.79^{a-c}	0.26^{*}
N-5	3.82^{bc}	-0.11	3.99^{ab}	0.09	3.46^{b-d}	-0.11
N-6	4.00^{a-c}	0.08	3.83^{bc}	-0.08	3.67^{a-d}	0.12
N-7	3.84^{bc}	-0.09	3.81^{bc}	-0.11	3.39^{cd}	-0.20
Mo17	4.28^{a}	0.40^{***}	3.73^{bc}	-0.20^{**}	3.95^{a}	0.43^{***}
H95	3.81^{bc}	-0.14	3.77^{bc}	-0.16^{*}	3.35^{cd}	-0.24
B68	3.80^{bc}	-0.15	3.73^{c}	-0.20^{**}	3.24^{d}	-0.36^{**}
Contrast:	Mean Square					
N-1 vs Mo17	1.156^{***}		0.109^{ns}		2.943^{***}	
N-1 vs H95	0.002^{ns}		0.060^{ns}		0.093^{ns}	
N-1 vs B68	0.004^{ns}		0.110^{ns}		0.002^{ns}	
N-2 vs Mo17	1.620^{***}		1.220^{***}		0.380^{ns}	
N-2 vs H95	0.020^{ns}		1.04^{***}		0.630^{ns}	
N-2 vs B68	0.010^{ns}		1.230^{***}		1.110^{*}	
N-7 vs Mo17	1.254^{***}		0.007^{ns}		1.988^{***}	
N-7 vs H95	0.007^{ns}		0.011^{ns}		0.009^{ns}	
N-7 vs B68	0.010^{ns}		0.037^{ns}		0.127^{ns}	

[†] Means with different letters in column are significantly different at P=0.05, ^{ns} non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

(Table 10).

The overall results from the NKN trial demonstrated that B68, H95, N-1 and N-7 were good combiners for *E. turcicum* tolerant with negative GCA values and suitable array means. The moderately tolerant check, Mo17, failed to show its efficiency in this diallel set. The new inbred lines such as N-1, N-7 seemed to have more *E. turcicum* tolerant power and statically highly tolerant than Mo17 (Table 10). But the combination of Mo17 and other susceptible parent (N-6) formed an outstanding cross in Gaecheon, indicating plant health and combining ability for yield potential and stability might affect NCLB infection. It could be a challenge to the plant breeders in further breeding programs.

In SG trial, the different group comparisons were noticed in group I versus group II, group II+III versus group I and group I+III versus group I in 2000 and combined analysis of years in Gaecheon (Table 3, 5). The lowest group mean value was found in group I (2.88), 2000 and group III (3.17) in Gaecheon (Table 8).

Among the 36 crosses, 17 crosses (47.2%) each from 2000 and 2001 exhibited persistent tolerance reaction to *E. turcicum*. The highest susceptible cross was observed in SG-1×B73 having the highest cross mean (4.22) and SCA effect (0.66) in 2000. The most susceptible rating (4.87) for 2001 was also found in this cross. The most desirable SCA was found in SG-1×SG-7(-0.69) in 2000.

The best tolerant rating 2.33 was observed in four cross (SG-4×SG-5, SG-4×SG-6, SG-4×SG-7 and SG-3×SG-4). The common parent with SG-4 showed importance of

Table 11. Array means for *E. turcicum* tolerance rating (1-9), general combining ability effects (gi) of 9 lines of SG trial and mean square comparisons of elite lines evaluated over three environments in 2000, five environments in 2001 and two years in Gaecheon, North Korea.

Parent	2000		2001		Gaecheon	
	Array Mean[†]	GCA	Array Mean[†]	GCA	Array Mean[†]	GCA
SG-1	3.36^{a}	0.36^{***}	4.33^{ab}	0.13	4.02^{a}	0.65^{***}
SG-2	2.89^{cd}	-0.18	4.16^{a-c}	-0.06	3.48^{a-c}	0.03
SG-3	2.79^{d}	-0.29^{**}	4.37^{ab}	0.18^{*}	3.25^{c}	-0.23
SG-4	2.90^{cd}	-0.16	3.91^{c}	-0.33^{***}	2.69^{d}	-0.88^{***}
SG-5	2.97^{b-d}	-0.08	4.31^{ab}	0.11	3.42^{bc}	-0.04
SG-6	3.08^{a-d}	0.04	4.11^{bc}	-0.12	3.21^{c}	-0.28^{*}
SG-7	2.9^{cd}	-0.16	4.17^{a-c}	-0.05	3.50^{abc}	0.05
Mo17	3.33^{ab}	0.33^{**}	4.11^{bc}	-0.12	3.65^{a-c}	0.22
B73	3.18^{a-c}	0.15	4.43^{a}	0.25^{***}	3.88^{ab}	0.48^{***}
Contrast:	Mean Square					
SG-4 vs Mo17	0.95^{**}		0.17^{ns}		4.75^{***}	
SG-4 vs B73	0.39^{ns}		1.33^{***}		7.29^{***}	

[†] Means with different letters in column are significantly different at P=0.05, ^{ns} non significant,
*, **, *** significant at the 0.05, 0.01 and 0.001 probability level, respectively.

locally adapted line development in tolerant breeding program.

The minimum array mean (2.79) and largest negative GC value (-0.29) was found in SG-3. While the maximum array mean (3.36) and highest positive GCA effect (0.36) was found in SG-1 in 2000. The largest array mean (4.43) and GCA value (0.25) was found in B73. The best rating (3.91, 2.69) and GCA value (-0.33, -0.88) were detected in SG-4, 2001 and combined two years analysis in Gaecheon, respectively. The performance of tolerance to *E. turcicum* in SG-4 was significantly higher than Mo17 and B73 (Table 11).

Accordingly SG-4 can be supposed to a good contributor of tolerance gene showing minimum array mean and negative GCA effect in most of the trials. Among the seven parents of SG group, at least four new inbred parents showed tolerant to *E. turcicum* in every trial set. It could be conferred that stay green (SG) character for parent selection is beneficial to disease resistance.

One of the most widely used inbred Mo17 in the region performed erratically in this study. It contributed as a tolerant donor in NKE, NKN and SG in 2000 but showed a susceptible source in NKE, NKN and SG, in the high infectious 2001 trials. The over year combined analysis in Gaecheon described that Mo17 consisted of a susceptible parent in all NKE, NKN and SG trials. This result shows that NCLB tolerance sources of newly bred inbred lines in North Korea are better than the popular inbred such as Mo17, B14 and B73. We have similar experiences of these lines in the north Eastern region of China (Shenyang, Dandong, Gongjuliang and Harbin). To improve NCLB tolerance, it might be appropriate to use inbred lines reported in this field study. Recurrent selection might be the most effective way to improve the level of *E. turcicum* tolerance.

The results of this study reveal that the genotype (G)×environment (E) interaction, genotype (G)×year (Y) interaction for *E. turcicum* tolerant in North Korea were highly significant, indicating the presence of different levels of disease infection in different environments. In addition, racial variation may not be totally ignored in North Korea. The nearest neighbor, China, Jingao *et al.* (Jingao *et al.*, 2008) reported that the distribution of 13 physiological races(0, 1, 12, 3, 13, 23, N, 1N, 2N, 12N, 3N, 23N and 123N) of *E. turcicum* varied among the six provinces of Northern China. The race 123N that was virulence to corn lines worth all four existing major resistant genes implies the possibility of present hybrids to loss their resistance in some regions of China. A single hybrid with stable level of tolerance to *E. turcicum* might be more durable than ten hybrids with different race specific gene resistance (Kim *et al*., 2008). Under rapid climate change as all have experiences in recent, new races may occur more so in future. Host tolerance can be a novel option to breed crops against climate change. It can be a real principle for co-survive and host crop as well as pathogen evolution in nature.

During the past two decades, an increasing number of novel races had been identified in China (0 and 1), in Mexico (23N, 23 and 2N), in Zambia (23, 23N and 0) and Uganda (0, 2, N, 23N) that led to rapid resistance loss in many hybrids containing *Ht*1, *Ht*2, *Ht*3, or *HtN* gene (Welz *et al*., 1993). Therefore, the occurrence of novel pathogenic races was continuously a threat to maize with single-locus resistant genes.

Breeding for a single gene controlled hypersensitive type of high resistance is a dangerous approach that we experienced in both South and North Korea (1970s) and others e.g. in Africa (Nigeria and Zimbabwe) and Asia (Thaialand) (S. K. Kim, unpublished) cannot sustain the durability of resistance. Tolerance, general or partial resistance must be pursued (Kim, 1993a, 1993b, 1994a, 1994b, 1996). However, scientists of many developing countries still look for un-durable race-specific single gene controlled of high resistance (Kim, 2000).

In nature, pests and hosts must co-survive and co-exist. If any one side is over-dominates the other, mutation of a new biotype occurs naturally for their survival. The senior author called the tolerance and durable resistance approach of crop breeding the Genetic IPM (Integrated Pest Management) (Kim, 1996, 2000). A crop cultivar that co-survives with pests in nature confers very powerful effects comparing to the high resistance, chemical spray, and other method of control. For environmentally friendly green food production, the host tolerance is the key for the crop stability and durability. Others presented this principle as horizontal resistance or race non-specific (Singh *et al*., 2004), durable resistance (Zadoks, 1993), general resistance (Brewbaker, 1983), generalized resistance (Hooker and Kim, 1973), race-non specific resistance (Nelson, 1973), partial resistance (Carson and Van Dyke, 1994; Pataky, 1994), quantitative resistance and QTL resistance (Kim, 1996, 2000; Kim *et al*., 2008).

This study aimed to understand the combining ability of new corn inbred lines bred for East Asia which parent conveyed the tolerance to *E. turcicum*. The GCA effects contributed most of the genetic variation for *E. turcicum* tolerance in these diallel studies. The presence of larger GCA effects suggests that high genetic gain could be achieved per breeding cycle and hybrid combinations.

Based on this, other information and experiences, a breeding strategy for tolerant hybrids with high yield potential for North Korea and neighboring countries particularly North Eastern China has been developed. Breeding a tolerance of crop cultivars to yield affecting biotic stresses such as *E. turcicum* would be a sustainable solution to provide a routine food aid system. This technology may be applicable to other regions.

In conclusion, abundant racial variations and different levels of NCBL infections are present in North Korea. GCA plays major role of newly bred inbred lines of corn in North Korea with polygenic control and inherited quantitatively. Recurrent selection might be the most effective way to improve the level of *E. turcicum* tolerance in breeding program. New inbred lines confer better tolerability to *E. turcicum* than the widely used inbreds such as Mo17, B73 and B14. The incorporation of new tolerant parental source for making hybrid combinations could be the safety protocol for outbreak of *E. turcicum* and shall increase staple food corn production security. One tolerant hybrid to NCLB with sustainable yield potential is better than ten hybrids with several single gene controlled race specific high resistance, most of them will be broken down one day. This principle can be applicable universally, particularly under climate change (Brewbaker *et al*., 2011; Kim *et al*., 2008).

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