had no relation to their geographical origin. Ht-monogenic sources, inbred NAI-147 and composite Girija, were among the genoypes that expressed resistance to the disease.

The 65 entries were sown in Augmented Block Design along with 4 checks (viz., Super-1, C_6, C_{14}, and C_{15}) within 3-rowed plots having inter- and intra-row spacing of 70 and 25 cm, respectively. Moderate doses of nitrogen were applied. Nitrogen in too low or too high quantity leads to increased and decreased disease severity, respectively, as cited by Bimla (Ann. Biol. 18(2):137-141, 2002) and Sharma and Mishra (1989). Artificial inoculation in the field was performed at the 6-8 leaf stage per Ivanova (Ras. Nauki 20(6):119-123, 1983). Plantings during the 2 years were altered by one month so as to mitigate the influence of early maturation on disease severity. Similarly, inoculation under controlled plot conditions was done at the 2- and 4-leaf growth stages to rule out the effects of juvenile sensitivity. Disease intensity was calculated according to modified McKinney rapid technique as applied by Horsfall and Heuberger (Phytopathology 32:226-232, 1942). This technique is based on individually scoring the leaves of a plant into 10 grades depending upon the percentage of leaf area infected. The severity (%) was calculated as $\{\sum (nV) / (NG)\} \times 100$, where 'n' is the number of infected leaves in each grade (1-10, which corresponds to 10-100% diseased area); 'V' is the numerical value of each grade; 'N' is the total number of leaves examined; and 'G' is the maximum numerical value of infection grades (i.e., 10). Based on disease intensity, genotypes were categorized into 5 groups as follows (Jeffers, personal communication): 0.1-5% = resistant; 6-25% = moderately resistant; 26-50% = moderately susceptible; 51-75% = susceptible; >75% = highly susceptible.

The results of screening germplasm over the two years indicated that *turcicum* leaf blight (TLB) disease intensity at the field level exhibited very high correlations (0.81** and 0.72**) with those calculated under controlled pot grown conditions. Genotypes at serial numbers 47, 48 and 62 (Girija) showed disease intensity less than 10% at field level. The genotype Girija recorded absolute resistance to the disease under both the screening environments (Table 1) with disease intensity percentages of 2.99 (0.48) and 4.26 (0.63) under field and controlled conditions, respectively. This genotype ranked only 6th for grain yield per hectare with 5.61 tons. The variability ranged from 2.99 to 76.29 and 4.26 to 57.68 percent for disease intensity and from 50 to 99 days for 50% silk emergence. At least 22 genotypes were found superior to check composite C6 with respect to disease log score. The genotypes showing moderate resistance under both the environments included RS-14, Ht-1, Ht-2, Ht-3, NAI-104, NAI-112, NAI-147, NAI-155, and Vivek-9. Smith and Kinsey (Plant Dis. 64:779-781, 1980) suggested the conferring of resistance by Ht-gene backgrounds. These Ht-monogenic sources have expressed resistance under controlled conditions in demonstrations by Leath and Pedersen (Plant Dis. 70:529-531, 1986), and with the exception of Ht-N, are known to display the chlorotic type of resistance (Leonard et al., Plant Dis. 79:776, 1989) observed in the present study. Populations NAC-6002 and NAC-6004, procured from the National Turcicum Leaf blight Nursery, Mysore, were found to be moderately resistant to TLB under field conditions, which has also been reported by Prabhakar et al. (Current Res. 32:63-66, 2003). The land races and most of the exotic materials succumbed to the disease. Disease intensity at the field level was negatively correlated to yield, which corresponds to the findings of Satyanarayana (Madras Agric. J. 82(40):249-251, 1995), and Sharma and Misra (Indian Phytopathol. 36(2):255-256, 1983). As expected, early maturing varieties tend to be more susceptible to disease than full season ones. This is because late summer conditions coincide with the log growth phase of early varieties where 70% or more of the leaf area was infested by the disease. This agrees with the findings of Patil (Mysore J. Agric. Sci. 13(1):1-4, 1979) that indicate genetic linkage between TLB resistance and late maturity traits. Thus there remains a possibility of selecting for early-maturing resistant lines among the recombinant generations of late-maturing resistant and early-maturing susceptible crosses. The varieties Girija, NAI-147, NAI-155 and Vivek-9, showing resistant to moderately resistant reactions to TLB in the present study, are all late season varieties that could be used as parents in backcross breeding to adaptable, high-yielding (average 50 qha^{-1}), susceptible checks C_{15}, C_6, C_{14} and Super-1.

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Evaluation of salinity tolerance at the seedling stage in maize (*Zea mays* L.)

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Maize (*Zea mays* L.) is the third most important cereal in the world after wheat and rice, and it grows under a wide range of climatic conditions. It is moderately sensitive to salinity and considered the most salt-sensitive of the cereals (Maas and Hoffman, J. Irrig. Drain Div. ASCE 103:115-134, 1977). Maize contains enormous variability (Paterniani, Crit. Rev. Plant Sci. 9:125-154, 1990) in which salinity tolerance may exist. Based on reports for many crops (Ashraf and McNeally, J. Agron. Crop Sci. 159:269-277, 1987; Ashraf and McNeally, Plant Breed. 104(2):101-107, 1990; Maiti et al., J. Plant Physiol. 148:741-744, 1996), selection for tolerance to salinity at the seedling stage appears useful in selecting for tolerance in saline soils. Previous papers indicate the effects of salinity treatments on the development of the maize coleoptile and radicle were considerable (Cicek and Cakirlar, Bulgarian J. Plant Physiol. 28:66-74, 2002).

This paper examines the presence of genetic variability in salt treatment of maize seedlings in thirteen populations and eighteen inbred lines of maize. Seeds were surface sterilized in 1% sodium hypoclorite solution for 5 minutes, then rinsed with distilled water. Six caryopses of each genotype were germinated between absorbent paper in plastic trays. The paper was moistened with either distilled water (control) or 150 mM NaCl. Each treatment was replicated two times. A completely randomized block design was used. Experiments were carried out in a controlled environmental room at 25ºC, with 16 h day length and with a relative humidity of 60%. After 12 days of treatment, the seedlings were harvested. The length for shoot and radicle (LS and LR, respectively) and the number of leaves (LN) were recorded. Shoot and radicle were separated, and the samples were dried for two days until constant weight, for dry weight determinations (DS and DR, respectively).

The mean values for all traits were compared using the least significance differences test at a 5% level. Five groups of variation were found for LS and DR, four for radicle length, and three for LN and DS (Tables 1 and 2). Length of shoot and dry weight of radicle were useful in identifying a discriminative response to salinity for the genotypes used.

Table 1. Average length of shoot (LS), length of radicle (LR) and leaf number (LN) for each genotype.

LS			LR			LN		
Genotype	Mean	Groups	Genotype	Mean	Groups	Genotype	Mean	Groups
5	14.5	A	5	18.8	A	16	1.2	A
6	14.0	AB	1	18.0	AB	4	0.9	AB
11	13.2	ABC	19	16.4	ABC	23	0.8	ABC
25	12.5	ABCD	28	16.4	ABC	6	0.7	ABC
16	11.4	ABCDE	6	16.4	ABC	22	0.7	ABC
23	11.3	ABCDE	24	16.3	ABC	5	0.6	ABC
29	11.2	ABCDE	2	16.0	ABCD	8	0.6	ABC
8	10.8	ABCDE	22	15.5	ABCD	1	0.4	ABC
28	10.6	ABCDE	13	15.1	ABCD	25	0.4	ABC
10	10.6	ABCDE	25	14.7	ABCD	10	0.3	BC
31	10.5	ABCDE	29	14.6	ABCD	11	0.3	BC
4	10.5	ABCDE	10	13.7	ABCD	26	0.3	BC
13	10.4	ABCDE	26	13.6	ABCD	24	0.2	BC
24	10.4	ABCDE	23	13.6	ABCD	27	0.2	BC
2	8.8	ABCDE	31	13.2	ABCD	20	0.2	BC
1	8.8	ABCDE	27	13.1	ABCD	31	0.2	BC
26	8.6	ABCDE	18	12.9	ABCD	2	0.1	BC
22	8.6	ABCDE	30	12.5	ABCD	7	0.1	BC
19	8.2	ABCDE	8	12.5	ABCD	13	0.1	BC
15	7.8	ABCDE	11	11.8	ABCD	17	0.1	BC
21	7.7	ABCDE	14	11.7	ABCD	3	0.0	C
9	7.3	BCDE	4	11.0	ABCD	9	0.0	C
27	7.1	BCDE	12	10.9	ABCD	12	0.0	C
20	6.8	CDE	20	9.9	ABCD	14	0.0	C
30	6.5	CDE	7	9.8	ABCD	15	0.0	C
17	6.1	CDE	9	9.8	ABCD	18	0.0	C
18	6.0	DE	16	9.1	ABCD	19	0.0	C
14	5.6	DE	21	7.7	BCD	21	0.0	C
7	5.3	E	3	6.7	CD	28	0.0	C
3	4.9	E	15	5.5	D	29	0.0	C
12	4.3	E	17	5.2	D	30	0.0	C

Genotypes with the similar letters are not significantly different at the 5% level

Table 2. Average dry weight of shoot (DS) and dry weight of radicle (DR) for each genotype.

DS			DR		
Genotype	Mean	Groups	Genotype	Mean	Groups
11	544.4	A	4	283.9	A
6	542.4	A	24	198.9	AB
4	528.8	A	31	190.6	ABC
5	494.9	AB	6	184.2	ABC
24	481.9	ABC	28	182.9	ABCD
29	473.5	ABC	14	176.8	ABCD
28	467.7	ABC	8	164.0	ABCDE
8	435.4	ABC	25	154.7	BCDE
23	428.5	ABC	5	148.6	BCDE
13	418.6	ABC	19	146.6	BCDE
10	416.2	ABC	13	144.4	BCDE
16	408.1	ABC	11	140.7	BCDE
25	404.3	ABC	23	135.7	BCDE
31	362.6	ABC	29	128.5	BCDE
21	357.8	ABC	30	127.1	BCDE
2	349.6	ABC	21	125.2	BCDE
1	318.2	ABC	7	119.8	BCDE
26	308.6	ABC	22	111.9	BCDE
19	306.1	ABC	16	102.7	BCDE
20	287.3	ABC	1	95.0	BCDE
30	285.6	ABC	20	90.1	BCDE
7	278.0	ABC	10	87.0	BCDE
15	266.4	ABC	3	86.8	BCDE
27	265.2	ABC	2	85.0	BCDE
9	255.0	ABC	26	78.4	BCDE
22	233.6	BC	27	72.7	CDE
14	214.4	BC	12	72.3	CDE
12	210.1	BC	15	69.6	CDE
17	207.1	BC	9	66.8	CDE
18	203.3	BC	17	58.8	DE
3	197.8	C	18	42.5	E

Genotypes with the similar letters are not significantly different at the 5% level

The technique employed at seedling stages provides a rapid, accurate and inexpensive method for preliminary screening of a large number of accessions. Our results allowed the identification of genotypes with tolerance to saline soils that could be utilized to understand the genetic basis of tolerance and to accelerate a breeding programme in the maize.

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Additional results from candidate-gene-based association mapping in teosinte

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Our previous association mapping study in teosinte was successful in detecting associations between genetic variation in major regulatory genes in maize and trait variation in teosinte (Weber et al., Genetics 177:2349-2359, 2007). Encouraged by this initial success, we have expanded this study by assaying 163 single nucleotide polymorphisms (SNPs) in 68 additional candidate genes in these same individuals. These candidate genes represent genes that have been characterized in maize or genes homologous by sequence to genes characterized in other plant species. We have also included four kernel composition traits (free lysine content, derived starch content, protein content, and oil content) in addition to the 13 traits included in our previous analysis.

Methods were identical to those outlined previously (Weber et al., Genetics 177:2349-2359, 2007). As before, not all marker-trait pairs were tested; instead, prior knowledge was used to determine which marker-trait pairs to test. Supplementary materials including the candidate gene list, trait definitions, and a list of marker-trait pairs tested, as well as all of our data files (genotypes, phenotypes, seed source information, principal components and the kinship matrix) are available for download at http://www.panzea.org.

Of the 1017 marker-trait pairs tested, only 47 (4.6%) had a *P*-value of less than 0.05, similar to the expectation under the null hypothesis (~5%). Of the 47 detected associations, two withstand correction for multiple testing by the false discovery rate ($Q < 0.1$, Table 1). A marker in *waxy1* and a marker in *pbf1* significantly associate with fruitcase weight (FCWT). Both of these associations are biologically plausible given what is known about these candidate genes. *waxy1* is a granule-bound starch synthase that accounts for all amylose production in the kernel (Nelson and Rines, Biochem. Biophys. Res. Commun. 9:297-300, 1962; Shure et al., Cell 35:225-233, 1983). It is possible that the association of *waxy1* and fruitcase weight is due to its role in amylose production. *pbf1* is a prolamin binding factor hypothesized to be a transcriptional activator of storage proteins in maize (Vicente-Carbajosa et

Table 1. List of significant marker-trait pairs after correction for multiple testing.

Trait‡	Gene	Marker	N[a]	R^2	$2a/\sigma_P$	d/a	P	FDR Q value
FCWT	*waxy1*	PZB00547.3	506	0.014	2.15	-0.339	0.0044	0.0770
FCWT	*pbf1*	pbf1.3	483	0.014	0.975	-0.304	0.0077	0.0770

[a]Number of individuals with both trait and marker data.