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SHORT COMMUNICATION

INFLUENCE OF SALINITY ON SEEDLING GROWTH AND METABOLISM IN MAIZE GENOTYPES

A.K. SINGH*, R.A. SINGH AND SUNIL KUMAR

Department of Botany and Plant Physiology, Rajendra Agricultural University, Pusa-848 125, Bihar

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Twelve maize (*Zea mays* L.) genotypes were evaluated under different levels of salinity (<0.0, 8.0, 12.0 dSm^{-1}) by growing in sand culture with Hoagland solution (control) and Hoagland solution enriched with salts (NaCl : $CaCl_2$: Na_2SO_4) for 20 days. After primary screening on dry weight basis, two most tolerant (Sabour sel 9 (a) and Jogia local – (x)- S_3-12-1-16) and two most susceptible (Pant 7421-(x)-S_3-129-1 and AB(w)-S_4-4-3-#) genotypes were further grown under similar test condition to investigate the physiological basis of salinity tolerance. At maximum salinity stress (12.0 dSm^{-1}), there were comparatively more accumulation of sugars, chlorophylls, carotenoids and free amino acids alongwith higher catalase and peroxidase activities. Possibly, some of these indices might be useful for improving maize genotypes against salinity stress.

Key words: **Dry weight, hydrolytic enzyme, oxidative enzyme, photosynthetic pigment, sugar.**

Salt affecting soil is a world wide problem. While high concentrations of salt have detrimental effect on plant growth (Mer *et al*. 2000), excessive amounts cause death of growing plants. Such soils are poor in fertility with low available nutrients, high osmotic pressure, poor air and water movement and low microbial activity. The problem of soil salinity is further increasing because of the use of poor quality water for irrigation and poor drainage. Therefore, it poses serious problem to food security in developing countries like India due to high rate of population growth and stagnation due to declining crop productivity in high productivity areas (Kamaluddin and Abdin 2006). However, plant species differ in their tolerance to salt (Brady and Weil 1996) to sustain growth. The identification of suitable genotypes for this purpose requires an efficient screening to breed salt-tolerant genotypes to sustain crop productivity and achieve food security (Chinnusamy *et al.* 2005).

The mechanism which imparts salt tolerance to some genotypes and sensitivity to others, has not been fully worked out in maize. Hence, the present work was planned to find out some useful physiological and biochemical parameters for screening tolerant/ susceptible maize genotypes against salinity stress and to understand the mechanism of salt tolerance in maize during seedling growth to elucidate the basis for improvement of the genotypes.

Seeds of maize (*Zea mays* L.) genotypes, viz. Jogia local- (x)-S_3-12-1-16, Sabour sel 9(a), Pant 7421 –(x)-S_3-129-1, AB (w)-S_4-4-3-#, M_9 – (x)-S_4-37-1-52, M_9 – (x)-S_4-37-3-54, Pool 28 sequia best syn., Tyl DMR-Pool-C_2, Santa Rosa-8079-1-4-(x)6-f-(x)-1-H, (M_9xCM 601)-(x)-S_4-7, Pop-45-S_3-HC-7-1-1-2-1-f and Pant 7421–(x)-S_3-16-1 were received from All India Coordinated Maize Improvement Project (AICMIP), Department of Plant Breeding, Tirhut College of Agriculture, Dholi (Bihar).

*Corresponding author, E-mail: drak_s@sify.com

Seeds were stored at a seed moisture of about 10% in a sealed container along with carbon bisulfide as disinfectant. Seeds at the time of conduct of the experiment were tested to have more than eighty per cent germination.

The stock salt solution was prepared by taking NaCl, $CaCl_2$ and Na_2SO_4 in the ratio of 7:2:1 and this solution was used for maintaining Hoagland nutrient medium at different salinity levels. The nutrient medium for sand culture was prepared after Arnon and Hoagland (1940). The nutrient (Hoagland) medium as such served as control. For preparing nutrient medium of different salinity, viz. 8.0 and 12.0 dSm^{-1}, stock salt solution was added to the medium and different salinity levels were adjusted on direct reading conductivity meter (Systronics, Model-303). These salt enriched nutrient solutions were used for seedling growth.

Seeds were surface sterilized with 0.1 per cent $HgCl_2$ solution for one minute and then thoroughly washed with distilled water. These healthy and surface sterilized seeds were taken for experimental purpose and were grown in sand culture at different levels of salinity stress, viz. 8.0 and 12.0 dSm^{-1} by using Hoagland nutrient solution with corresponding stress. Plant grown under Hoagland nutrient solution (without salt enrichment) were taken as control. The experiments were carried out in completely randomized design in three replications. On 20^{th} day, the experiment was terminated and shoots samples were subjected to various analyses.

Total sugars and total free amino acids were quantified in dry samples by the method of Miller (1959) and Lee and Takahashi (1966), respectively. Photosynthetic pigments (total chlorophylls and carotenoids) as well as enzymes, *viz* protease catalase and peroxidase were assayed in fresh samples by the method of Arnon (1949). Dubey and Rani (1990), Kar and Mishra (1976) and Palmiano and Juliano (1973), respectively.

Twelve maize (*Zea mays* L.) genotypes were subjected to primary screening on dry weight basis at seedling growth stage. Out of which Sabour sel 9(a) and Jogia local (x)-S_3-12-1-16 were identified as most tolerant, whereas Pant 7421-(x)-S_3-129-1 and AB(w)-S_4-4-3-# were categorized as the most susceptible genotypes. These four selected genotypes were further grown under similar test condition to investigate the physiological parameters attributing to their tolerance.

As regards dry weight of shoot, gradual reduction was recorded in all the four genotypes with increasing level of salinity (Table 1). At maximum salinity (12.0 dSm^{-1}), minimum reduction in growth was observed in Sabour sel 9(a) and Jogia local-(x)-S_3-12-1-16, whereas maximum reduction was recorded in Pant 7421-(x)-S_3-129-1 and AB (w)-S_4-4-3-#. The genotype and stress interaction was found significant. This reduction under salt stress may be due to inhibition of hydrolysis of reserve/ synthesizing food or/ and its translocation to the growing axis (Singh and Singh 1999).

Further, the total chlorophylls deceased in the genotypes with the increase in salt stress and the decrease being more in Pant 7421-(x)-S_3-129-1 and AB (w)-S_4-4-3-# (susceptible genotypes). Similar reports were made by earlier workers (Sudhakar *et al.*1991, Singh and Singh 1999) and this is attributed to the increased chlorophyllase activity and also partly due to the interference of salt ions with the *de novo* synthesis of proteins, the structural component of chloroplast (Sadhakar *et al.* 1991). The less reduction of chlorophyll pigments in tolerant genotypes might have caused more dry matter accumulation in maize genotypes.

As regards carotenoids content under salt stress, tolerant maize genotypes recorded maximum value (showing minimum reduction in comparison to control) at 12.0 dSm^{-1}, whereas minimum value of carotenoids was observed in susceptible genotypes (Table 1). Changes in carotenoids content under salinity has earlier been reported (Ramanjubu *et al.*1993, Singh and Singh 1999). Comparatively more accumulation of carotenoids in tolerant genotypes enabled them to perform better under salt stress because of antioxidant properties of carotenoids.

Total soluble sugars declined in all the four genotypes with increasing salinity stress (Table 1). Significant differences were observed between the genotypes of tolerant and susceptible groups for total sugars. The reduction in sugar content under salinity stress might be

Table 1. Effect on salinity levels on dry weight, total chlorophylls, carotenoids and total soluble sugars in 20-day-old maize genotypes

Genotypes	Salinity (dSm^{-1})	Dry wt. of shoot (mg)	Total chlorophylls (mg g^{-1} fw)	Carotenoids (mg g^{-1} fw)	Total sugars (mg g^{-1} dw)
Sabour sel 9(a) (T)	0.0 (control)	77.60	0.497	0.235	28.16
	8.0	66.26	0.446	0.196	24.66
	12.0	53.60	0.369	0.156	20.16
Jogia local –(x)-S_3-12-1-16 (T)	0.0 (control)	89.06	0.481	0.217	28.40
	8.0	81.53	0.425	0.187	24.80
	12.0	63.50	0.329	0.141	20.56
Pant 7421-(x)-S_3-129-1 (S)	0.0(control)	70.83	0.402	0.114	23.50
	8.0	51.23	0.292	0.092	17.66
	12.0	37.50	0.169	0.055	14.96
AB(w)-S_4-4-3-# (S)	0.0 (control)	75.10	0.387	0.079	24.16
	8.0	41.73	0.255	0.065	19.50
	12.0	30.50	0.152	0.044	15.83

C.D. at 5%	Stress (S)	Genotypes (G)	SxG
Dry weight	1.970	2.275	3.941
Total Chlorophylls	0.018	0.021	0.048
Carotenoids	0.005	0.006	0.010
Total sugars	1.472	1.700	2.945

T= Tolerant ; S=Susceptible

due to lower amylase activity which causes reduced hydrolysis of reserve polysaccharides in the cotylendons. Salt induced reduction in sugar content has earlier been reported (Ashraf and McNeilly 2004, Singh and Kumari 2006). At maximum salinity levels, comparatively more accumulation of sugar was recorded in tolerant maize genotypes in comparison to susceptible genotypes. More accumulation of sugar, a compatible solute, lowers the osmotic potential in the cytoplasm and thus increasing the ability of the cytoplasm to retain water under reduced water supply in tolerant genotyhpes (Abede *et al.* 2003). Another possible role of sugar might be a readily available energy source.

Total free amino acids content showed a declining trend in both the tolerant and susceptible genotypes (Table 2). These findings are in consonance with the earlier reports (Levitt 1972). Comparatively higher value of free amino acids in tolerant genotypes might be due to high protease activity under the test condition. Levitt (1972) suggested that decreased availability of amino acids might also be due to denaturation of enzymes involved in the amino acid formation. Increasing trends of protease activity have been observed in both tolerant and susceptible genotypes (Table 2). Higher activity of protease in tolerant genotypes may provide more free amino acids for the synthesis of new desired proteins for the plant growth. Similar findings of protease activity have been reported earlier (Dubey 1984, Singh *et al.* 2001).

Salinity induces reactive oxygen species (ROS) production and leads to oxidative damage. These toxic species may react with proteins and lipid component of membranes causing damage through lipid peroxidation. Among antioxidative enzymes, activity of catalase was recorded under salt stress condition (Table 2). The activity was more in Sabour sel 9(a) (170.20 units) and Jogia local –(x)-S_3-12-1-16 (171.52 units) in comparison to Pant 7421-(x)-S_3-129-1 (106.28 units) and AB (w)-

Table 2. Effect on salinity levels on total free amino acids, protease, catalase and peroxidase in 20-day-old maize genotypes

Genotypes	Salinity (dSm^{-1})	Free amino acid (mg g^{-1} dw)	Protease (units g^{-1} fw)	Catalase (units g^{-1} fw)	Peroxidase (units g^{-1} fw)
Sabour sel 9(a) (T)	0.0 (control)	37.91	61.0	110.43	264.33
	8.0	32.58	82.4	142.51	283.33
	12.0	26.45	130.0	170.20	305.66
Jogia local –(x)-S_3-12-1-16 (T)	0.0 (control)	35.83	55.0	109.73	231.00
	8.0	29.37	75.1	139.69	260.00
	12.0	22.28	120.0	171.52	289.00
Pant 7421-(x)-S_3-129-1 (S)	0.0 (control)	26.45	66.2	145.18	227.66
	8.0	18.75	66.4	130.03	200.00
	12.0	10.62	71.2	106.28	172.33
AB(w)-S_4-4-3-# (S)	0.0 (control)	23.74	63.1	169.90	251.00
	8.0	13.75	69.3	132.78	223.33
	12.0	10.00	75.1	98.73	195.66

C.D. at 5%	Stress (S)	Genotypes (G)	SxG
Free Amino Acids	1.081	1.248	2.162
Protease	0.568	0.655	1.136
Catalase	1.511	1.745	3.023
Peroxidase	13.561	15.659	27.122

T= Tolerant ; S=Susceptible

S_4-4-3-# (98.73 units) at 12.0 dSm^{-1}. Similar reports have earlier been reported (Singh *et al*. 2001, Singh 2004). Higher activity of catalase in tolerant genotypes may help in protecting the membrane from lipid peroxidation due to H_2O_2, which is a toxic metabolite produced by plants in various ways. Peroxidase, another H_2O_2 scavenging enzyme, behaved differently in both the groups with increase in salinity. In contrast to the susceptible lines, the peroxidase activity increased in tolerant genotypes (Table 2). This result is comparable with the earlier findings (Singh 2004, Singh and Kumari 2006). The higher peroxidase activity indicates that salt tolerant lines had an increased ability to decompose H_2O_2. Possibly, some of these indices might prove useful to plant breeders for improving maize genotypes to withstand salinity.

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