

# Exploring The Salinity Tolerant Variety Of Rice

Mansoor A. Malik<sup>1</sup>, Mehrajud Din Talie<sup>2</sup>, Tajmul Islam<sup>3</sup>, Juniad A. Magray<sup>4</sup>, Purnima Shrivastava<sup>5</sup>

<sup>1,5</sup>Research Scholar, Department of Botany, Bhagwant University, Ajmeer

<sup>2,3,4</sup>Research Scholar, Department of Botany, University of Kashmir, (190006)

Email: <sup>1</sup>malikmansoor011@gmail.com

**Abstract :** Soil salinity affects several physiological and biochemical processes in plants. Plant culture of mixed composition and different concentrations of salt treatments were applied for 10 days to detect the response of the salinity tolerant variety of Rice regarding growth, survival, plant height, leaf area, leaf injury, relative growth rate. In vitro superoxide dismutase (SOD), ascorbate peroxidase (APX) and catalase (CAT) activities in the leaves are also screened. Most influenced genotype was IR-64 in terms of growth and dry matter and PB-1 for root length. Maximum SOD activity was recorded in PB-1 followed by IR-64. However, HKR-127 the minimum SOD activity was recorded. APX activity showed large variation in rice genotypes following Sodium chloride (NaCl) treatment. APX activity increased significantly in PB-1 over control in dose dependent manner in all the treated samples. The maximum (25.0%) APX activity was observed in PB-1 at T4 treatment over control. Salt treatment remarkably increased the APX activity in IR-64 up to T3 level of NaCl treatment. In HKR-127 genotype at all levels of treatments there was non-significant increase in its activity. Moreover, Catalase activity in PB-1 increased significantly with all the treatments. The difference among treatments was significant at all levels the highest activity (26.3%) was at T4 level of treatment in PB-1 genotype. IR-64 genotype showed increased catalase activity up to T3 level while in HKR-127 increased non-significantly in CAT at all treatments. The data are discussed in regard to implications of salt stress.

**Key Words:** Salinity, Physiological, Resistance, Rice, Salt tolerance

## 1. INTRODUCTION

Soil salinity is one of the most prevailing abiotic stresses that adversely affect crop productivity and quality of main food crops including rice in the world, particularly in arid and semi-arid areas (Hernandez 2019; Mansuri et al., 2020). It affects every aspect of the physiological and biochemical processes of plants, and significantly reduces growth (Flowers et al. 1977).

The agronomical parameters used for salt tolerance are growth, survival, plant height, leaf area, leaf injury, relative growth rate and relative growth reduction (Ashraf and Harris 2004). Accumulation of sodium salts may lead to soil sodicity which binds to negatively charged clay particles, making the soil unfavorable for crop growth (Chinnusamy et al. 2005). The deleterious effects of salt stress on plant growth are related with low osmotic potential or water stress, salt stress and nutritional imbalance (Ashraf 1994). With the onset and development of salt stress within a plant, all the major processes viz. photosynthesis,

respiration, lipid metabolism and protein biosynthesis are affected (Chen et al., 2018; Hussain et al. (2018). All these responses to salinity contribute to deleterious effects on plants, although there are tolerant plants to NaCl that can implement a series of adaptations to acclimate to salinity that can help their survival. These adaptation mechanisms include morphological, physiological, biochemical, and molecular changes (Acosta-Motos et al 2017).

Resistance to environmental stress occurs when a plant stands the imposed stress that may arise from either tolerance or an escape mechanism from the situation. Escape mechanism can contribute to the prevention of stress during the life cycle of plant, also tolerance can take place at the cellular level. Plants are either dormant during the salt stress or there must be cellular adjustment (Yokoi et al. 2002).

Conventional methods of breeding have been applied to improve salt stress in various crop plants. Most of these techniques have been unsuccessful in transferring salinity tolerance to the target species (Ashraf 2002). Hence, development of salt tolerant varieties become increasingly popular as a means of battling salt-related yield losses (Winicov 1998).

Keeping in view, the above adverse effects of salt stress to various crops such as rice the present study entitled "Exploring the Salinity Tolerant Variety of Rice" was undertaken to develop salinity tolerant cultivars of rice in order to combating salt-related growth circumstances in Pusa-BAS-1, IR-64 and HKR-127 genotypes of Rice.

## 2. MATERIALS AND METHODS

### *Study species*

Rice was taken as plant material for this study. Cultivated rice is generally considered as a semiaquatic annual grass, although in the tropics it can survive as a perennial plant. Following Rice genotypes were selected for the present investigation and were purchased from Indian Council of Agricultural Research (ICAR), New Delhi (110001).

1. Pusa-BAS-1
2. IR-64
3. HKR-127

### *Plant culture*

The seeds were sterilized in 0.1% mercuric chloride solution for 1 min, then thoroughly washed in double distilled water (DDW). These were then germinated in soilrite under dark conditions. After three days of proper germination, young seedlings of uniform size were transferred to the 250 mL plastic containers containing one fourth strength Hoagland's solution (pH 6.8) with the required composition of macro and micronutrients for a week. Growth conditions in hydroponic chamber were maintained. Day/night temperatures about 28°C/25°C, light/dark period 16/8 hours, light intensity ( $300 \mu \text{mol m}^{-2} \text{s}^{-1}$ ) and relative humidity 70%. After growing plants in the growth chamber for 7 day with the above environmental conditions, plants were again supplemented with fresh nutrient solution by replacing the one-fourth strength of the Hoagland's solution with the half strength in order to support the increasing nutrient demand of the young growing seedlings. The seedlings were allowed to grow for three days more in the nutrient solution.

### *Treatments*

After ten days, following treatments of NaCl were given to the seedlings: T0 = 0mM; T1 = 25mM; T2 = 50mM; T3 = 75mM; T4 = 100mM. Growth, enzymatic antioxidants and non-enzymatic antioxidants were studied in samples collected at 7th day of NaCl treatment. The following parameters were analyzed:

*Plant fresh matter and plant dry matter*

Root and shoot were measured with a metric scale and expressed in centimeters. Plants were cut at the root-shoot junction and the petiole-stem junction in order to divide them into root, stem and leaves. The separated plants were dried separately in a hot air oven at  $65^{\circ}\text{C}\pm 20^{\circ}\text{C}$  for 72 h. The samples were weighed on an electronic top pan balance (Sartorius BL-210S, Germany) so as to obtain the dry weight of roots, stem and leaves independently, which was expressed in grams per plant.

*Chlorophyll content*

Chlorophyll content was estimated in the fresh leaf samples by the method given by (Hiscox and Israelstan 1997).

*Soluble protein content*

The total soluble protein content of the leaves was estimated following the method of (Bradford 1976).

*In vitro assay of superoxide dismutase activity*

In vitro assay of superoxide dismutase (EC 1.15.1.1) activity was estimated by the method (Beyer and Fridovich 1987).

*In vitro assay of ascorbate peroxidase activity*

In vitro assay of ascorbate peroxidase (L-Ascorbate:  $\text{H}_2\text{O}_2$  oxidoreductase EC1.11.1.1) activity was estimated by the method (Nanko and Asada 1981).

*In vitro assay of Catalase Activity*

In vitro activity (ED 1.11.1.6) of catalase was determined by the method of (Aebi 1984).

### 3. RESULTS

It was revealed from the results that NaCl treatments affect one or the other ways to all the genotypes of rice under investigation. The statistical analysis tool used during the present study was one-Way ANOVA.

*Plant fresh matter*

It was revealed from the results (Fig. 1) that large variability among the Rice genotypes for the sensitiveness to the levels and duration of NaCl treatments was observed. While the minimum reduction in the fresh matter was reported in PB-1 genotype. NaCl treatment up to the level of 75 mM (T1-T3) showed a slight effect on the fresh matter of IR-64. However, NaCl treatment reduced the fresh matter of HKR-127 genotype significantly at all levels of treatments.

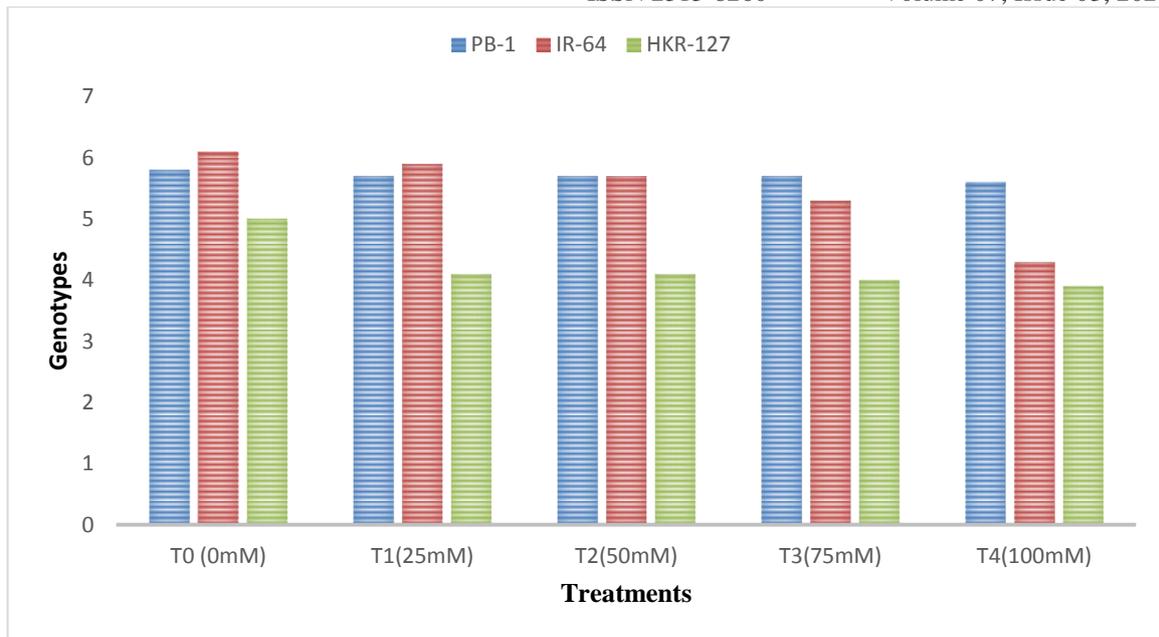


Fig. 1. Showing plant fresh matter (g) of various genotypes of rice as influenced by various levels of NaCl treatments.

#### *Plant dry matter*

It was revealed from the results (Fig. 2) that dry matter of rice genotypes was affected at various levels of NaCl treatments. Dry matter of PB-1 genotypes underwent non-significant reduction at all the NaCl treatments. However, NaCl treatment significantly affected the dry matter of IR-64 at T4 level. While as in HKR-127 genotype plant dry matter reduced at selected days of sampling.

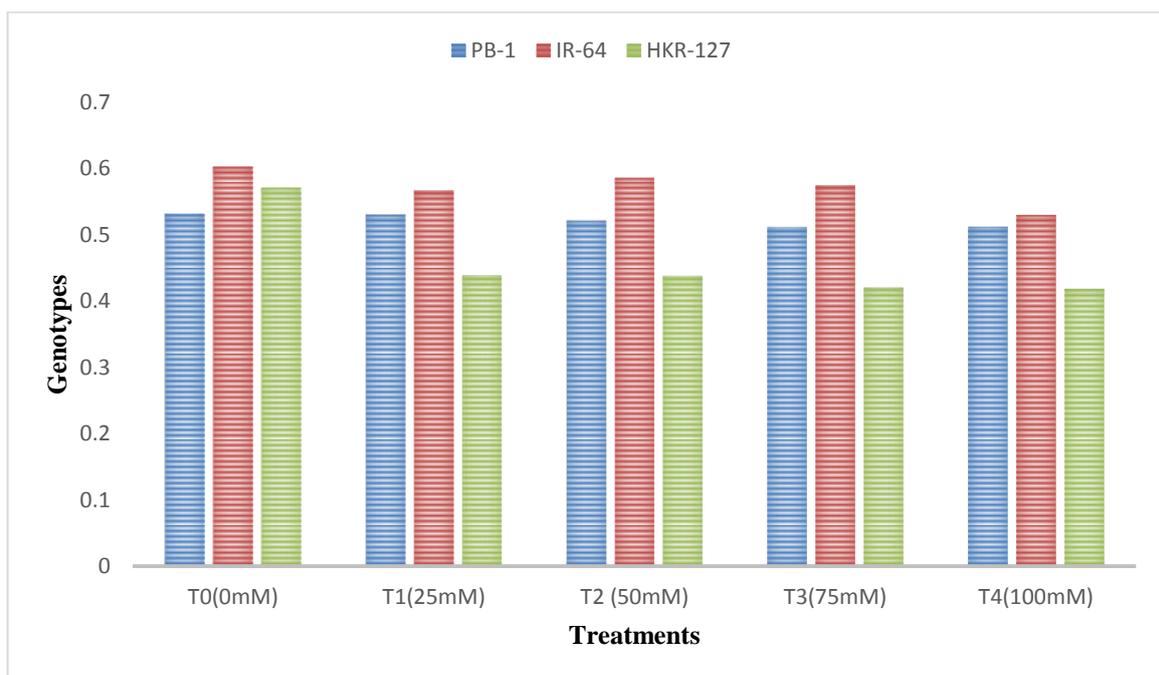


Fig. 2. Showing results of plant dry matter (mg) of various genotypes of rice as influenced by different levels of NaCl treatments

### Root length

Data of the root length of rice genotypes as influenced by various doses of NaCl treatment are presented in (Fig. 3). The observations revealed that there was no significant effect on IR-64. However, in case of PB-1 and HKR-127 genotypes root length reduced significantly by NaCl treatments at all days.

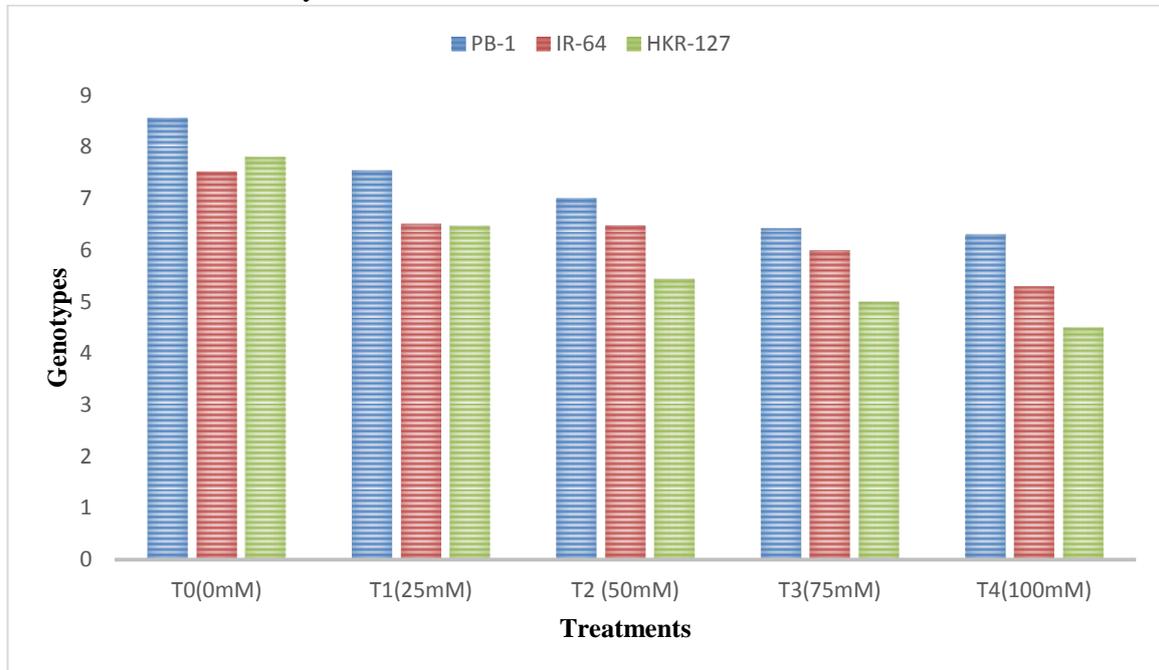


Fig. 3. Plant root length (cm) of various genotypes of rice as influenced by various levels of NaCl treatments

### Shoot length

Results revealed (Fig. 4) that shoot length of rice genotypes was reduced by all the levels of NaCl treatments. However, IR-64 and PB-1 genotypes tolerate the NaCl exposure up to 75mM (T3) level but the maximum reduction was recorded in HKR-127 when compared to control.

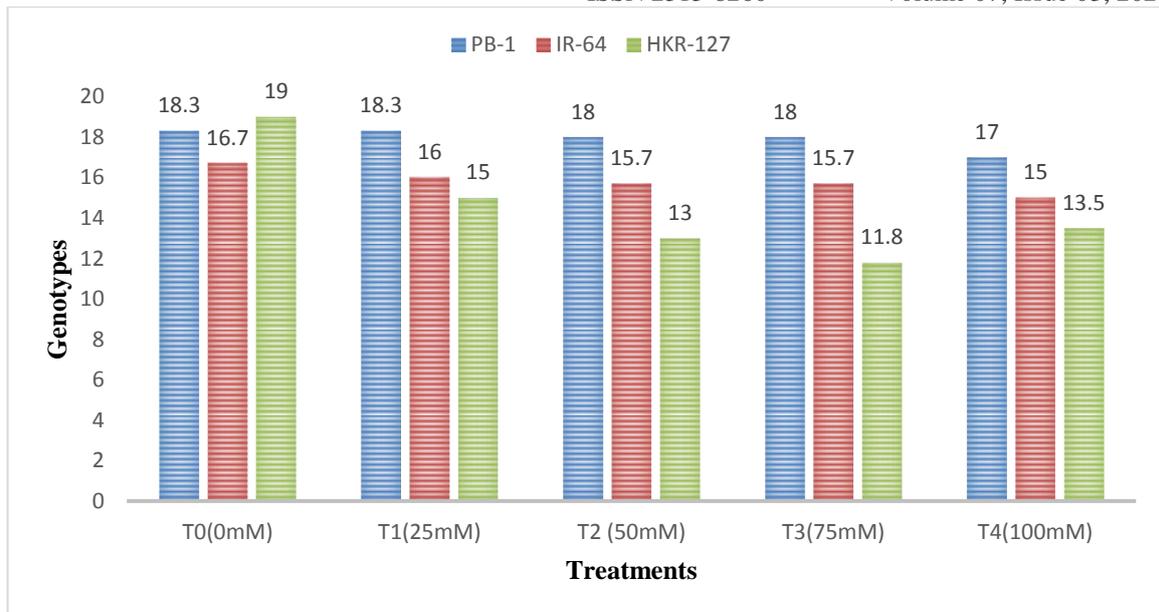


Fig. 4. Plant shoot length (cm) of various genotypes of rice as influenced by various levels of NaCl treatments

#### *Chlorophyll content*

It was observed from the results (Fig. 5) that various concentrations and duration of NaCl treatments resulted in a decline in the total chlorophyll content in the all genotypes. The minimum reduction in chlorophyll content was observed in PB-1. However, the chlorophyll content of IR-64 was reduced significantly at T4 NaCl treatments. Similarly, in case of HKR-127 genotype there was significant reduction in chlorophyll content at all the levels of treatments.

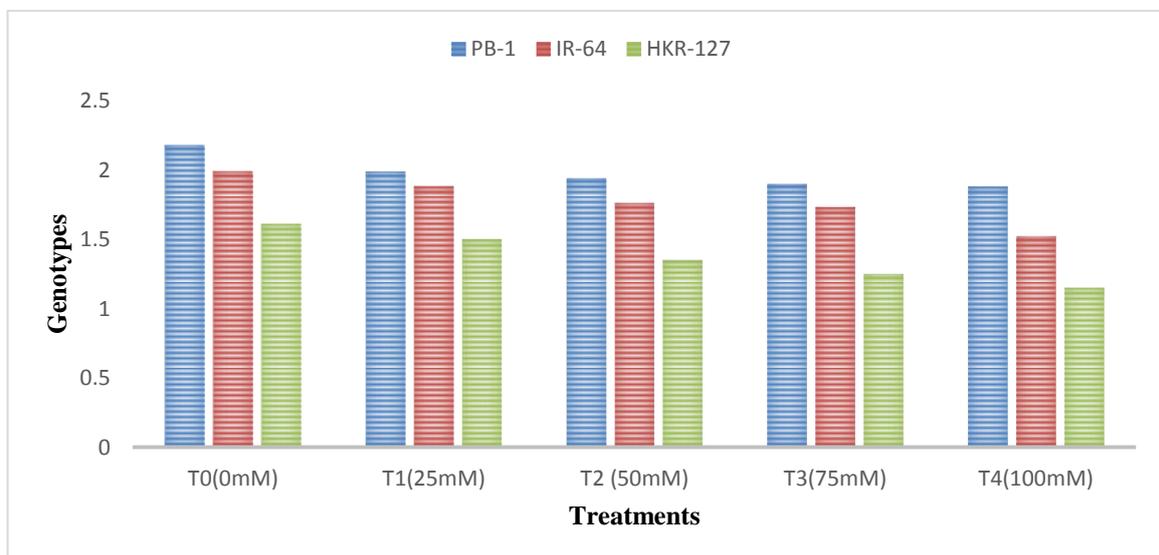


Fig. 5. Showing results of chlorophyll content of various rice genotypes as influenced by various levels of NaCl treatments

#### *Soluble protein content*

Results (Fig. 6) revealed that NaCl treatments caused reduction in soluble protein content which differed with genotypes under investigation. The reduction in soluble protein content of PB-1 by all NaCl treatment was not significant. However, soluble protein content of IR-64

was reduced at T4 treatment. Furthermore, HKR-127 genotype showed significant reduction in soluble protein content at all NaCl treatments.

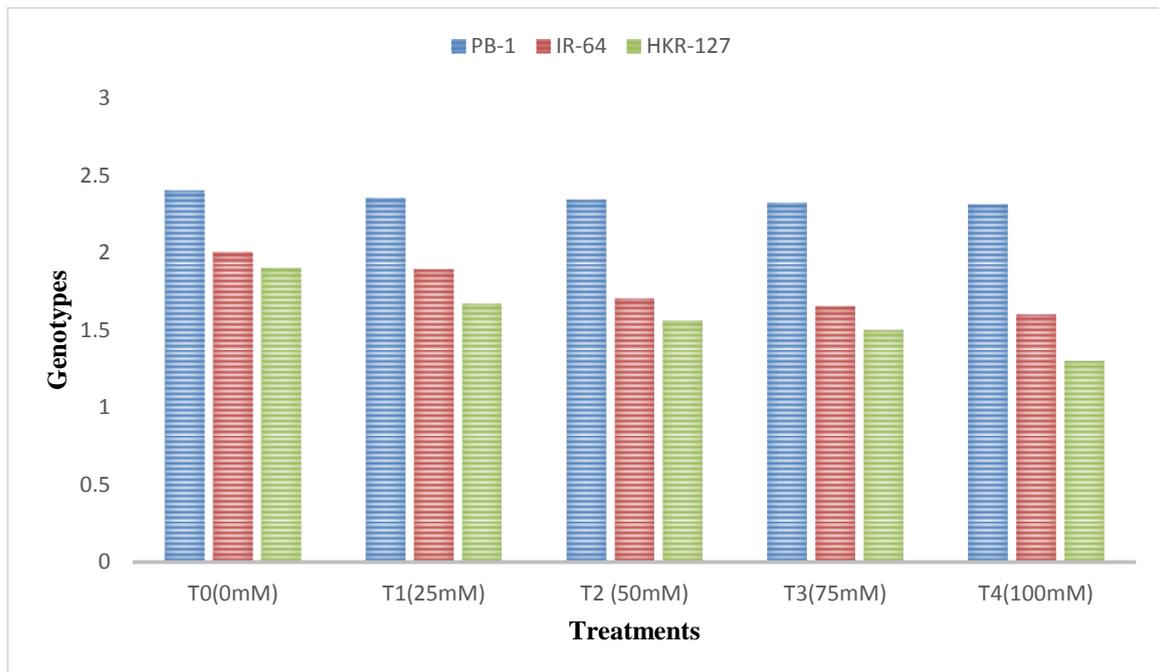


Fig. Soluble protein content of various genotypes of rice as influenced by various levels of NaCl treatments

#### *Superoxide dismutase activity*

It was revealed from the results (Fig. 7) that SOD activity showed large variation in all genotypes at various levels of NaCl treatments. The highest SOD activity was recorded in PB-1. NaCl treatment inclined the SOD activity of PB-1 in dose dependent manner. Similarly, the NaCl treatments showed the rise in SOD activity in IR-64 genotype. However, in HKR-127 genotype the minimum activity was recorded.

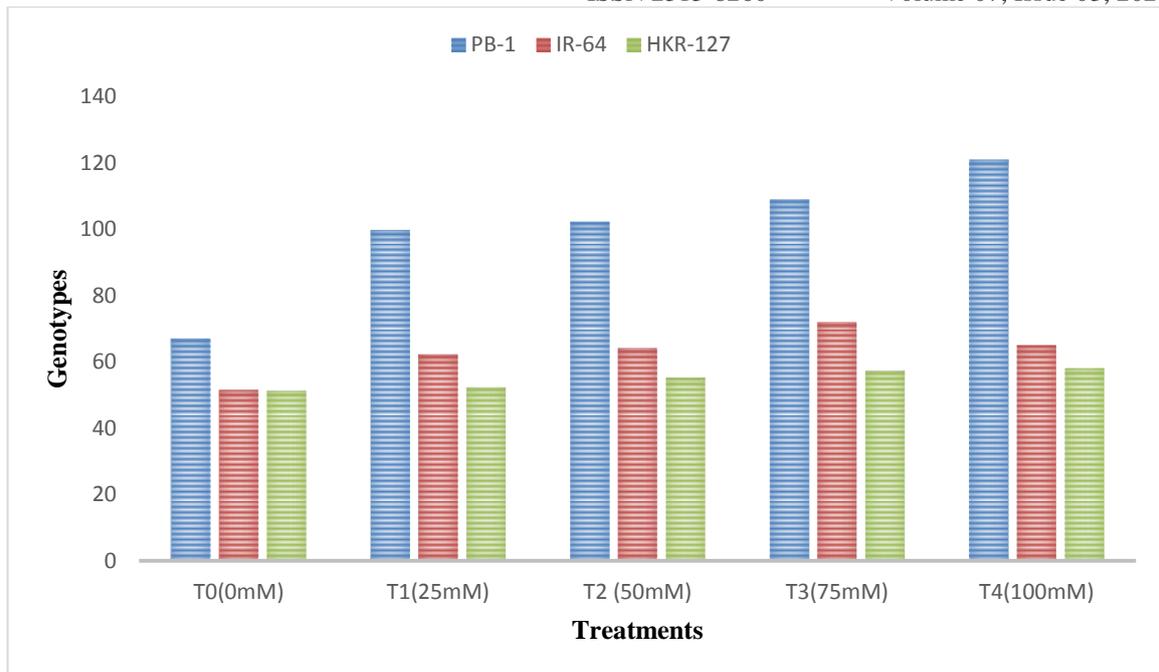


Fig. 7. Results showing Superoxide dismutase activity of various genotypes of rice as influenced by various levels of NaCl treatments

#### *Ascorbate peroxidase activity*

It was observed from the results (Fig. 8) that Ascorbate peroxidase (APX) activity showed large variation in rice genotypes following NaCl treatment. APX activity in genotype of PB-1 increased significantly over the control in dose dependent manner in all the treated samples. NaCl treatment remarkably increased the APX activity in genotype IR-64 up to T3 level of NaCl treatment. However, in case of HKR-127 genotype at all levels of treatments there was non-significant increased activity.

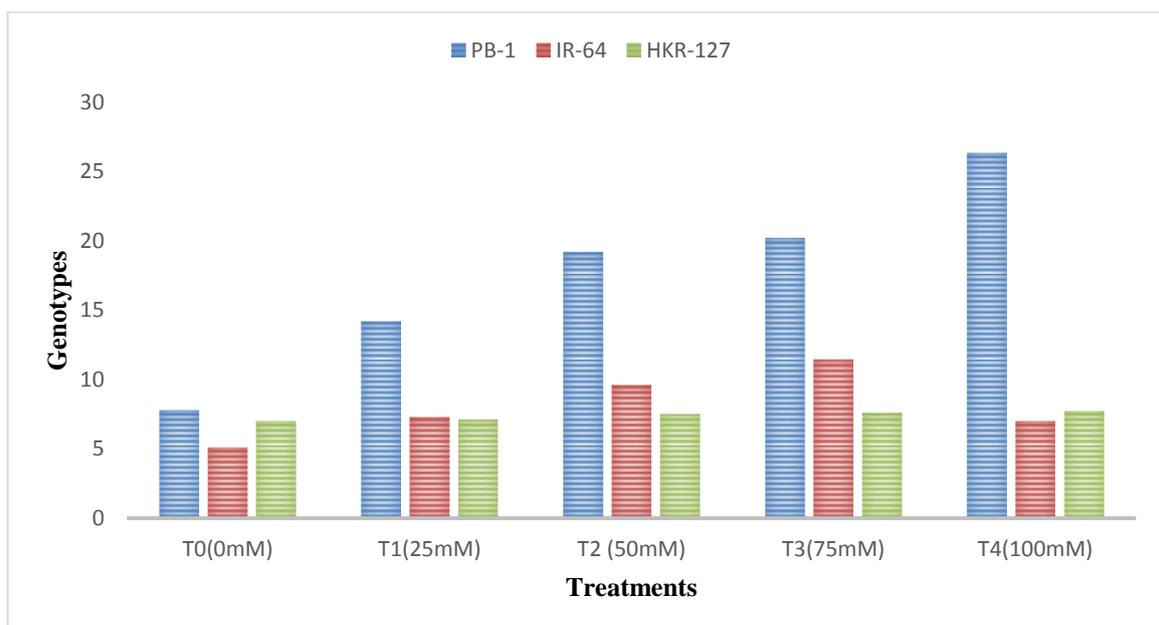


Fig. 8. Results showing APX activity of various genotypes of rice as influenced by various levels of NaCl treatments

*Catalase activity*

It was revealed from the results (Fig. 9) that salt treatments induced the CAT activity differentially in rice genotypes. Catalase activity in PB-1 was increased significantly with all the NaCl treatments. However, IR-64 genotype showed increase in catalase activity up to T3 treatment level, while as HKR-127 genotypes showed non-significant increases in CAT activity at all levels of treatments.

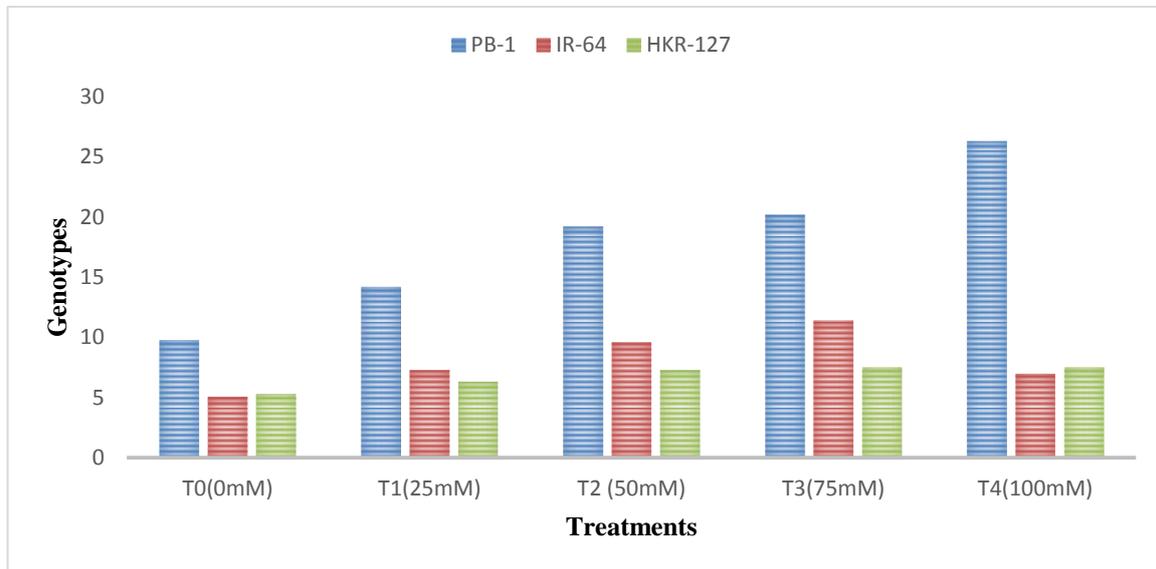


Fig. 9. Results showing Catalytic activity of various genotypes of rice as influenced by various levels of NaCl treatments

#### 4. DISCUSSION

The ability of plants to tolerate salinity is determined by multiple biochemical pathways that assist retention or acquisition of water, protect chloroplast functions and maintain ion homeostasis. Essential pathways include those that lead to synthesis of osmotically active metabolites, specific proteins and certain free radical enzymes to control ion and water flux and support scavenging of oxygen radicals (Parvaiz and Satyawati 2008; Chen et al., 2018). Salt stress significantly influence the growth of three genotypes under investigation in terms of biomass production, soluble protein content, SOD, APX and catalase activities. Genotype IR-64 shows good response in terms of fresh and dry matter against all the concentrations of salt treatment. Shoot length, Chlorophyll and soluble protein contents were increased in PB-1 genotype. Superoxide Dismutase, Ascorbate peroxidase and catalase activity were also positively influenced in genotype PB-1. Kakar et al. (2019) screened Seventy-four rice genotypes at three salinity treatments. Several shoot and root morpho-physiological traits were measured and a wide range of variability was observed among genotypes for measured traits with root traits being identified as the best descriptors for tolerance to salt stress conditions. Among these 74 rice genotypes, FED 473 and IR85427 were identified as the most salt tolerant and salt sensitive, respectively. Similarly, Chuamnakhong et al. (2019) studied the physiological responses of two rice genotypes to different pH levels under high saline stress. The results revealed that FL478 is relatively saline-alkaline tolerant compared to IR29 genotype.

A higher content of soluble proteins has been observed in salt tolerant cultivars of rice during the present study. The same trend has been reported in case of barley, sunflower, finger millet, and rice (Ashraf and Harris 2004). Similarly, Hussain et al. (2018) reported the protein profiling under different salinity conditions and identified a total of 5340 proteins

with 1% FDR in NPBA and LYP9 rice genotypes. It was also suggested that the differentially expressed proteins are mainly involved in regulation of salt stress responses, oxidation-reduction responses, photosynthesis, and carbohydrate metabolism in rice genotypes. These findings are in accordance with the present study. However, Agastian et al. (2000) have reported that soluble protein increases at low salinity and decreases at high salinity in mulberry cultivars.

Several factors associated with salinity stress can lead to an increase in reactive oxygen species (Asada, 1999). Free radical scavenging systems such as superoxide dismutase can be a critical component of salinity tolerance (Bohnert and Jensen, 1996) because of their protection of chloroplast function as was revealed during the present study. In leaves of rice plant, salt stress preferentially enhances the content of H<sub>2</sub>O<sub>2</sub> and the activities of SOD, APX, and GPX, whereas it decreases catalase activity (Lee et al. 2001). Lechno et al. (1997) reported that NaCl treatment increases the activities of the antioxidative enzyme catalase and glutathione reductase and the content of the antioxidants such as ascorbic acid and reduced glutathione but does not affect the activity of SOD in cucumber plants. However, it was revealed from the present study that increase in SOD activity was found in case of PB-1 in dose dependent manner followed by genotype IR-64 and HKR-127 respectively. Furthermore, Muchate et al. (2019) also reported that in case of Spinach (*Spinacia oleracea* L.) in vitro shoot cultures showed enhanced SOD, APX and CAT activities with an increase in salt stress. The same trend has been observed in case of PB-1 genotype during the present investigation.

The present study also supports the work of (Lin and Kao 2000) who reported a significant increase in APX activity in salt-treated rice seedlings and concluded that this could be due to the oxidation of ascorbate (AsA) in controlling H<sub>2</sub>O<sub>2</sub> under stress. However, in case of HKR-127 genotype at all levels of treatment there was non-significant increase in APX activity.

## 5. CONCLUSION

Three genotypes of rice PB-1, IR-64 and HKR-127 were selected to see the response against the different concentrations of salt treatment. A total of nine parameters were selected and the three genotypes of rice for all the parameters were treated with T0 (0mM), T1 (25mM), T2 (50mM), T3 (75mM) and T4 (100mM) NaCl concentrations. Genotype IR-64 shows good response in terms of fresh and dry matter against all the concentrations of salt treatment. Shoot length Chlorophyll and soluble protein content were increased in PB-1. Superoxide Dismutase, Ascorbate peroxidase and catalase activity were also positively influenced in genotype PB-1.

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### **Conflict of interest**

The authors have declared that there is no conflict of interest

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