

---

Oral sessions | Abiotic Stress for Crop Production | P33: Salinity

## [O33] Salinity

Chair: Yoshihiko Hirai (Okayama University, Japan)

Chair: Sakae Agarie (Kyushu University, Japan)

Chair: Glenn Borja Gregorio (Southeast Asian Regional Center for Graduate Study and Research in Agriculture (SEARCA), Philippines)

Thu. Sep 9, 2021 5:00 PM - 7:00 PM Room 3 (Oral) (Abiotic Stress for Crop Production)

---

5:40 PM - 5:55 PM

### [O33-03] Morphological and Microsatellite Marker Assisted Genetic Diversity Analysis of Wheat Genotypes for Salinity Tolerance

\*Nominated for Presentation Awards

○ Sayma Farabi<sup>1</sup>, Nihar Ranjan Saha<sup>2</sup>, Md. Hasanuzzaman<sup>3</sup>, Md. Shahidul Haque<sup>4</sup>, Mirza Mofazzal Islam<sup>5</sup>  
(1. Department of Biotechnology, Bangladesh Agricultural University, Bangladesh, 2. Department of Biotechnology, Bangladesh Agricultural University, Bangladesh, 3. Department of Biotechnology, Bangladesh Agricultural University, Bangladesh, 4. Department of Biotechnology, Bangladesh Agricultural University, Bangladesh, 5. Plant Breeding Division, Bangladesh Institute of Nuclear Agriculture, Bangladesh)

Salt affected soils can be better utilized by developing and growing salt tolerant wheat varieties. To find out the genetic diversity, screening was conducted to evaluate the salt tolerance capacity of 46 (24 Bangladeshi and 22 exotic) wheat genotypes in Hoagland's hydroponic nutrient solution under four different salt concentrations (control, 9, 12 and 15 dS/m) on the basis of salt tolerant index (STI) and microsatellite markers. The experiment was conducted with a Completely Randomized Design (CRD) with 2 replications. The results showed that different levels of salinity significantly affected the growth attributes by reducing the length, dry and fresh weight of roots and shoots. The highest STI was shown in nine tolerant genotypes namely ESWYT P-2 Borkot, ESWYT P-5, Agroni, ESWYT P-8, BARI-23, ESWYT P-30, ESWYT P-19, ESWYT P-12. The molecular analysis of the wheat genotypes was carried out with 30 SSR markers related to salt tolerance. A total of 128 alleles were detected among the 46 wheat genotypes with an average of 4.47 alleles per locus for salt related SSR marker. The highest polymorphism information content (PIC) and Nei's (1973) gene diversity, 0.7408 and 0.7760 were produced by the marker Xtxp-12 in this experiment. Similarity indices based cluster analysis separated 46 genotypes into seven different clusters. Considering the above facts, the salt tolerant varieties and inbred lines identified in this study could be used as parents to incorporate salt tolerance in future wheat cultivars. Further research is underway.