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# INTERROGATION OF *SALTOL* LOCI FROM FL 478 TO ELITE VARIETY BG 352: EARLY SCREENING DATA

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Soil salinization significantly affects local rice production, posing a dual threat to the country's economy and food security due to the high sensitivity of rice to salinity. The cultivation of salt-sensitive rice varieties intensifies the above situation. Thus, genetic improvement of elite rice varieties for salinity tolerance is significant. The *SalTol* Quantitative Trait Loci (QTL) is collocated with the *OsHKT1;5,* a gene encoding a high-affinity Potassium transporter that is associated with salinity tolerance at the seedling stage. The objective of the present study was to introgress *SalTol* QTL from rice variety FL 478 into popular high-yielding rice variety Bg352. A backcrossing program was initiated using FL 478 and Bg 352, respectively, as the donor and the recurrent parent. The plants were manually crossed, and the F1 generation was advanced to BC1F1. Leaf samples were collected from the individual seedlings of the BC1F1 population, DNA was extracted, and Polymerase Chain Reaction was performed using RM 493 (*SalTol* linked SSR marker). The success rate of the manual crossing program was 90.5%. BC1F1 population was similar to the recurrent parent in plant height, architecture, and days to flowering, with a high uniformity within the population. From 38 BC1F1 plants studied, nine were heterozygous for *SalTol*. The nine plants where *SalTol* was successfully introgressed were advanced to BC2F1. The use of QTL linked RM 493 marker was effective, improved breeding efficiency and accuracy, and accelerated the breeding process. Further, backcrossing and marker-assisted selection are needed for the recipient genome recovery.

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**Keywords:** Marker-assisted Backcross Breeding, Rice, Salinity Tolerance, *SalTol,* Soil Salinization.