

## Section 2:

### Executive Summary of the Project

A cross between At354, a salt tolerant parent and Bg352, a salt susceptible parent was made to produce recombinant inbred line (RIL) population aiming at identifying salinity tolerant QTLs. Hybridity of F<sub>1</sub> progeny was confirmed using microsatellite markers and 6 true hybrids were advanced to produce 281 lines of F<sub>5</sub> generation by single seed method.

For the investigation of salinity tolerant QTLs, nine phenotypic parameters related to salinity tolerance were assessed in randomly selected 100 RILs of F<sub>5</sub> population under hydroponics supplemented with 100 mM NaCl concentration (12 dS/m). For the genotyping of the RILs 158 SSR markers were surveyed and of them 45 markers that were polymorphic between At354 and Bg352 were used for genotype-trait association analysis. Linkage maps were constructed for chromosome 1, 3 and 4 as it was a prerequisite for linkage based QTL mapping. QTLs were identified by single marker analysis, simple interval mapping and composite interval mapping. Composite Interval mapping revealed 6 QTLs distributed in chromosome 1 and chromosome 4 namely, *qSSI1*, *qSL1*, *qSNK1*, *qSL4*, *qSNK4* and *qSSI*, explaining 8.9% to 16% of the phenotypic variations of SSI, shoot length and shoot Na<sup>+</sup>/K<sup>+</sup> ratio. In both instances of *qSSI4* and *qSL4* LOD peak laid between RM280 and RM3843 which has about 3Mbp difference, thereby suggesting to be used as potential flanking markers for breeding studies of salt tolerance. The RILs accumulated with 5 promising QTLs were identified for further analysis on agronomic traits and salinity tolerance in reproductive stage as an application of project output.