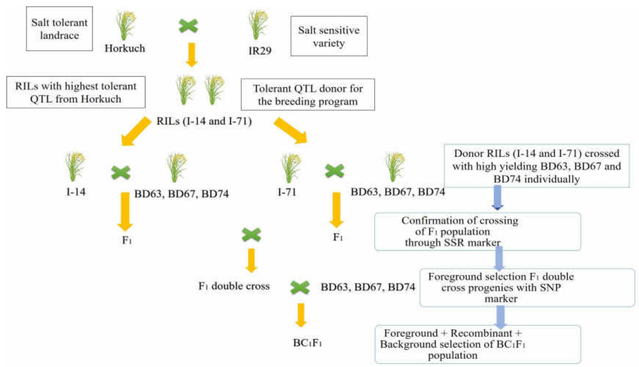
Incorporation of salt tolerant QTL in the background of high quality commercial rice variety through SNP-based KASP markers

Abstract

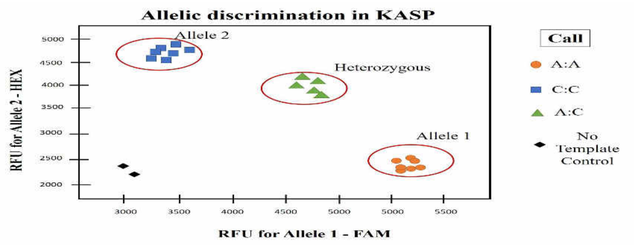
Salinity intrusion is one of the major impact of climate change which is affecting the growth of commercial rice varieties in the coastal regions of Bangladesh. To cultivate these varieties, they need to be introgressed with salt tolerant QTLs which will confer them the ability to survive in saline stress while giving high yields. SNP markers are widely distributed throughout the genome and have proven to be a promising tool for marker assisted selection. Use of fluorescent based KASP (Kompetitive Allele Specific PCR) SNP markers to establish foreground, recombinant and background loci can further shorten the time and increase the efficiency of marker assisted selection. Horkuch is a popular salt tolerant rice landrace which grows in the coastal regions of Bangladesh. Salt tolerant QTLs were identified in chromosome 1, 2 and 3 of Horkuch from crossing population of sensitive IR29 and Horkuch. These QTLs are being incorporated into popular rice varieties BD63, BD67 and BD74. KASP markers were used to select crossbreeds where the QTLs were successfully transferred. It is hoped that through this process, we will be able to produce highly salt tolerant rice having high yields at the same time.

Background

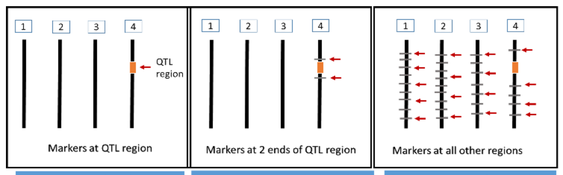


Methodology

Establishment of SNP marker through KASP detection technology

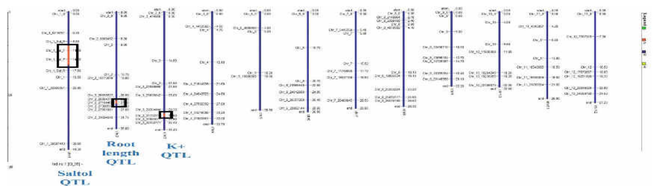


Marker Assisted Selection



In foreground selection markers tightly linked with the QTL region were used to detect the donor allele. Markers unlinked to QTL were used to reduce the donor allele only to QTL region and to recover the genotype of recipient high yielding parent.

Screening for best crossing line with multiple salt tolerant QTLs from Donor parent and genomic background of recipient high yielding parent



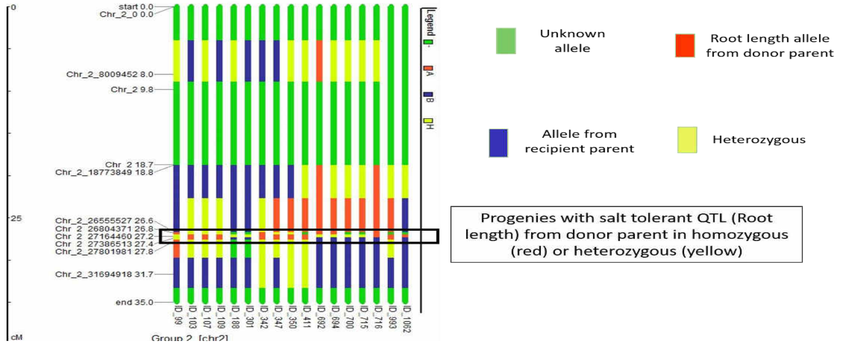
Best crossing lines would have donor allele limited only to the QTL (Saltol, Root length and Potassium QTL) regions present in Chromosome 1, 2 and 3.

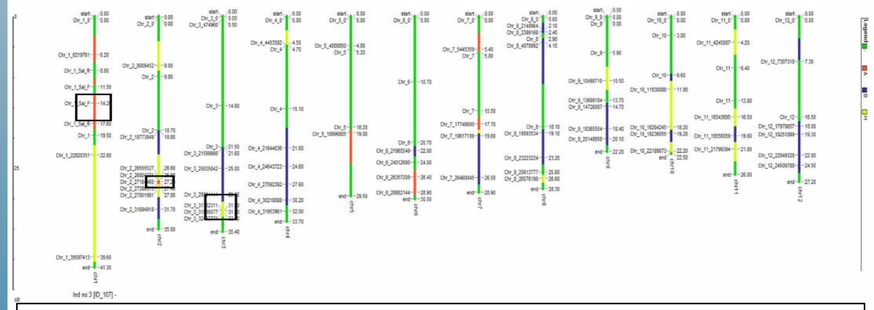
KASP: a high throughput genotyping platform of choice

- KASP technique is simple, flexible and straightforward and can be performed in any lab with regular qPCR machine and FRET capable plate readers
- KASP is cost effective requiring no expensive instruments and all the labelled components of the Universal reporting system of KASP are present in KASP master mix itself
- Data analysis of KASP is very simple. It uses 2 allele specific forward primers, tails of which are conguated to FAM and HEX dye respectively.The data generated in the reaction is analysed by a software package provided by LGC.
- KASP detection technology has high specificity and sensitivity with very low error rate.

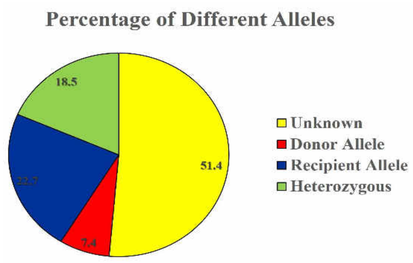
Results

Graphical Genotyping of improved lines from BC1F1 population



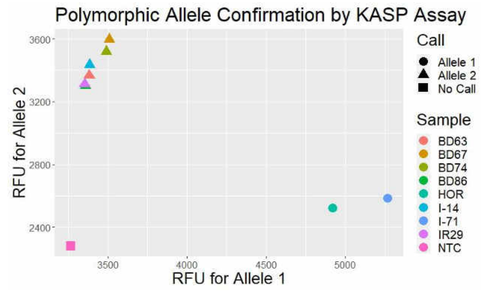


Screening for donor alleles in 976 BC1F1 population resulted in selection of 17 progenies with salt tolerant QTL (marked region of Chromosome 1, 2 and 3)



An impressive 22.7% recovery of recurrent parent genotype (recipient parent- BRRI-dhan 63, presented in blue) in one of the best selected progeny of 1st backcross line

Results



Polymorphic SNP establishment by KASP assay between recipient and donor parents for marker id1001153. I-14 and I-71 showing Allele 1 and BRRI dhan showing Allele 2. This marker can thus effectively predict alleles transferred in cross populations.

Conclusion

- High throughput molecular marker SNP made it viable to recover a maximum number of recurrent parent genotype within only 2-3 backcross generation.
- KASP assay is highly effective, sensitive, and reliable in genotyping the crossing lines for screening alleles and selecting best lines.
- Pyramiding salt tolerant QTLs originating from landrace Horkuch into commercial high yielding variety would enhance the crops survival in salt stress while not compromising yield.

Reference

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Acknowledgements

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