Fluorescence based Kompetitive (competitive) Allele specific PCR (KASP) for high-throughput SNP marker detection and validation

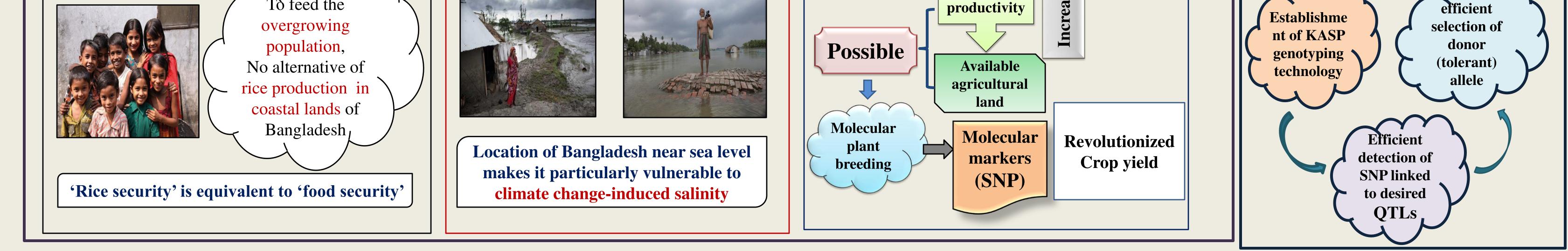
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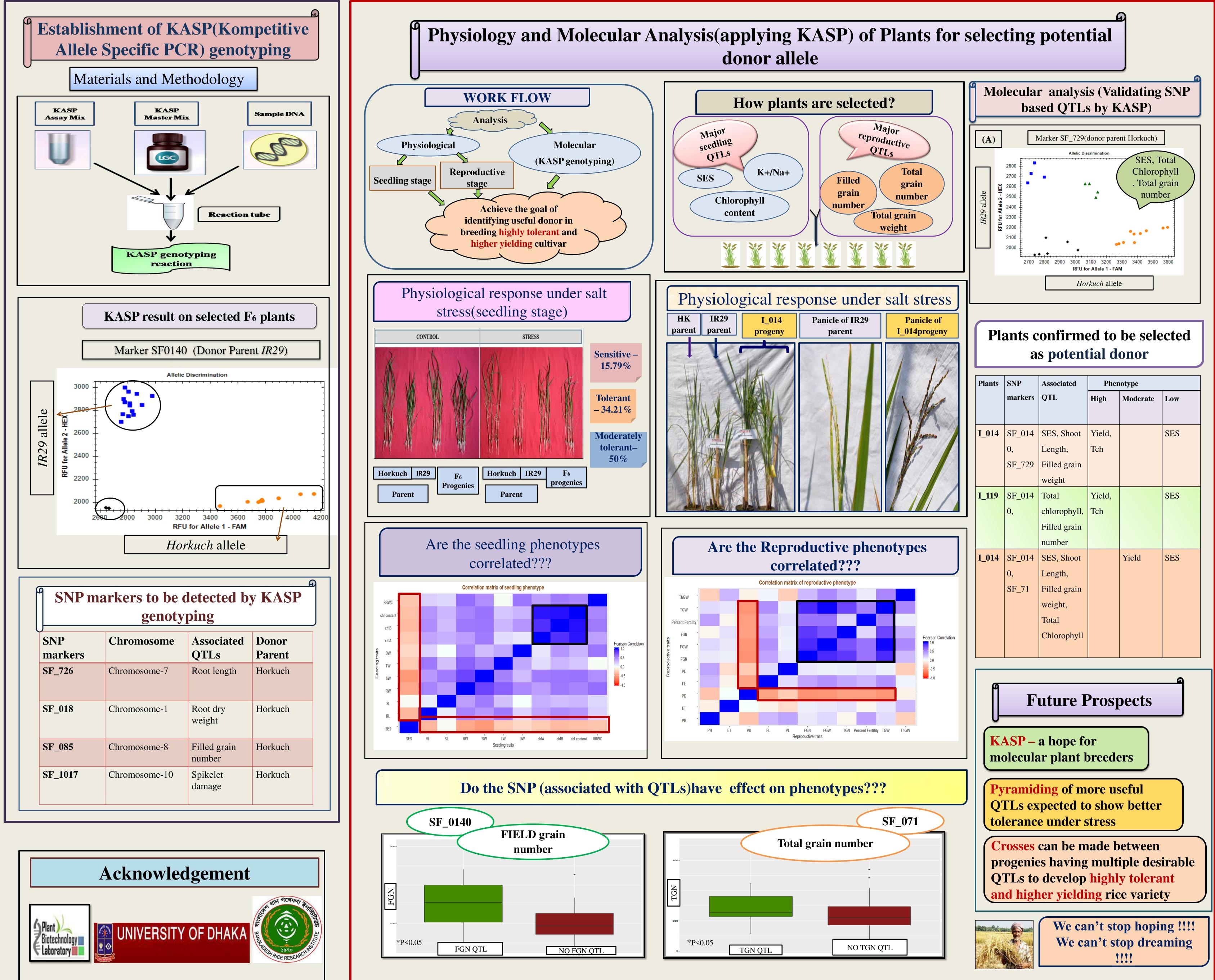
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Abstract:

Considering the enormous potential of DNA markers in plant breeding and recent advances in single nucleotide polymorphism (SNP) genotyping for its promising role in crop improvement, it has become inevitable for the plant breeders to adopt the capacity of SNP marker development and marker assisted selection (MAS). While, gene cloning allows insertion of a single gene, MAS enables insertion of multiple loci for pyramiding of different tolerance mechanisms, leading to a higher level of tolerance. Cost of utilizing high throughput SNP detection system is possibly the major hindrance in implementing marker assisted selection (MAS). In the current work, we have attempted to establish fluorescence-based Kompetitive Allele Specific PCR (KASP) technology for easy and efficient detection of SNP alleles. KASP was applied for the validation of the identified salt tolerance quantitative trait loci (QTL) with an aim to select potential donor (tolerant) allele/plant for use in marker-assisted breeding. A mapping population at F_6 and F_7 with the salt tolerant rice landrace Horkuch and sensitive but high yielding IR29, was used to establish KASP genotyping. Specific salt tolerance SNP-based QTLs had been previously identified at the F_{2-3} stage from this mapping population, with IR29 (\mathcal{P}) and Horkuch (\mathcal{J}).KASP markers were designed for these loci and F₇ population for molecular validation. Physiological analysis was also done in both seedling and reproductive stages. Later correlation analysis of both physiological and molecular data was done to select appropriate donor plant. KASP genotyping was successfully established as fluorescence based SNP detection method by detecting seven out of eight SNPs. From the correlation between physiology and molecular analysis few F₆plants have been found as potential donors multiple traits or QTLs. In the overall study KASP genotyping method was found more suitable as a marker validation system than other methods due to its speed, high accuracy, low cost, flexibility in assay design and fluorescence based detection method. The method is now being used in a breeding program for introgression of multiple QTLs in a commercial Rice variety.

Background	Major Purposes of this study





SF_018Chromosome-1Root dry weightHorkuchSF_085Chromosome-8Filled grain numberHorkuchSF_1017Chromosome-10Spikelet damageHorkuch	SF_726	Chromosome-7	Root length	Horkuch
SF_1017Chromosome-10SpikeletHorkuch	SF_018	Chromosome-1	•	Horkuch
	SF_085	Chromosome-8	-	Horkuch
	SF_1017	Chromosome-10	-	Horkuch