Fabalous Molecular Markers: Preventing Favism by Identifying Faba Bean Mutants

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Faba bean (Vicia faba L.) is an ancient legume species known for its high protein content, excellent nutritional benefits, nitrogen-fixation ability and adaptive capabilities in cool climates. However, more than 400 million people worldwide cannot consume faba beans due to a disease called favism which prevents the breakdown of vicine-convicine (VC), resulting in haemolytic anemia or even death. Faba beans with reduced VC have been discovered, but there remain challenges in quantifying VC concentration. To reduce these challenges, a molecular marker was developed to detect low VC faba bean mutants. An optimal area of the faba bean genome for marker development was first identified by aligning existing expressed sequence tags (EST) to the Medicago truncatula genome, and selecting the EST that aligned within the VC QTL region. This produced the EST Contig 4518, which was then sequenced in four faba bean genotypes to identify single nucleotide polymorphisms (SNPs) that differed between low VC and high VC genotypes. This identified 3 SNPs and therefore 3 potential molecular markers. The markers were validated with 52 faba bean genotypes through Kompetitive Allele Specific PCR (KASP) Assay. SNP 316 found in Medtr2g009270 gene was the most successful marker in terms of its ability to differentiate low VC content, high VC content, and heterozygous faba bean genotypes. This molecular marker is being used in seed selection to accelerate breeding programs. This is a vital step towards expanding the faba bean market for producers, and enabling all consumers to enjoy faba beans.

Awards Won:

Fourth Award of $500

China Association for Science and Technology (CAST): Award of $1,200