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MYO-INOSITOL-1-PHOSPHATE SYNTASE: THE FIRST GENE IN PHYTIC ACID METABOLIC PATHWAY, ISOLATION AND CHARACTERZATION

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Phytic acid, *myo*-inositol 1,2,3,4,5,6-hexakisphosphate, is the major storage form of phosphorus in the seed where is deposited in protein bodies as a mixed salt of mineral cations, such as potassium, magnesium, iron, and zinc. Minerals, when bound to InsP6, are hardly or not absorbed in the intestine and are largely excreted, resulting in iron and zinc deficiencies affecting the nutritional quality of food.

Recent studies have shown that dietary InsP6 might also have beneficial health effects, for example as an anticancer agent and anti-oxidant. Therefore, modulation of phytic acid content in the seed, particularly its reduction, is one of the major goals in seed crop genetic improvement.

The phytic acid biosynthetic pathway is still not completely clear, but the first known step is the conversion of D-Glucose-6-phosphate to D-*myo*-inositol-1-phosphate by the isomerase D-*myo*-inositol-1-phosphate synthase (MIPS). Manipulation of phytic acid content in the seed, particularly if achieved by genetic engineering, requires knowledge of how the key enzymes of the biosynthetic pathway are regulated. Therefore we decided to focus on the charcterisation of MIPS from bean, which is the most important legume for human consumption.

The cDNA encoding for MIPS was isolated from developing *P. vulgaris* seeds (cv Taylor's Horticultural) and its expression was analysed in different tissues and developing stages of the seed. In order to make a deeper characterisation of the MIPS gene we used a 6x *Phaseolus vulgaris* BAC library to isolate the MIPS gene and its regualtory region/s. Screening of the BAC library resulted in the identification of only one positive BAC clone, suggesting a simple single locus organisation for this gene. The BAC clone was further analysed to identify the genomic region containing the MIPS gene. Sequence analysis showed that MIPS gene consists of 10 exons and 9 introns. In addition, a fragment of about 3.5 Kpb upstream the transcription start site was identified and sequenced. The analysis of such fragment using plant promoter prediction programs is in progress.