MODULATION OF PHYTIC ACID CONTENT IN THE SEED OF COMMON BEAN (PHASEOLUS VULGARIS L.)

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The major form in which phosphorus occurs in plants is myo-inositol-1,2,3,4,5,6-hexakisphosphate, commonly referred to as phytic acid or InsP6. This compound forms mixed salts with various mineral cations, e.g. potassium, magnesium, iron and zinc (phytates), therefore affecting the nutritional quality of food. Minerals, when bound to InsP6, are hardly or not absorbed in the intestine and are largely excreted, resulting in iron and zinc deficiencies, (1).

Recent studies have shown that dietary InsP6 might also have beneficial health effects, for example as an anticancer agent and anti-oxidant (2). At present, modulation of phytic acid content in the seed, particularly its reduction, is one of the major goals in seed crop genetic improvement (1).

Although in common bean phytic acid content is a serious problem for human nutrition, particularly in developing countries (1) no improved varieties are yet available for this character. In this context, we are testing the possibility to produce, by chemical mutagenesis, mutants with an altered content of phytic acid.

We treated with ethyl-methanesulphonate solutions 7,000 F5 seeds of a breeding line under development. Seed germination was about 50% and only 2,028 plants were able to produce seeds. The analysis for identification of mutants is in progress and is based on a measure of free Pi, taking into account that a reduced phytate content is positively correlated with an increase in free Pi (3).

We also started the isolation and characterisation of the seed specific form of MIPS. In fact, it has recently been reported in soybean seeds that the mutation of the gene encoding for MIPS is correlated with a significant reduction in phytates and raffinosaccharide content (4).

By RT-PCR, a cDNA coding for the seed MIPS has been isolated from mRNA of early maturing cotyledons. This gene is about 74 % identical to a P. vulgaris MIPS gene expressed in vegetative tissues (PVU38920) and about 94% identical to the soybean seed gene we used as a reference. A Southern blot analysis of MIPS gene organisation indicates that no more than three genes are present. The gene is highly expressed very early during cotyledon development, before synthesis of storage proteins mRNAs. MIPS cDNA is now being assembled to express in E. coli the recombinant protein for antibodies production.