

STUDIES ON EPIGENETIC ASPECTS OF *lpa1-241* TRAIT IN MAIZE

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Phytic acid is a nearly ubiquitous component of plant seeds, supplying both phosphate (P) and cations during germination. However, during digestion, the phytic acid form of P is not bio-available for monogastric animals. A possible solution to this problem is the isolation of cereal mutants accumulating less phytic P and more free P and cations in the seed (low phytic acid, *lpa*).

Several mutants have been isolated in recent years in maize, barley (*Hordeum vulgare* L.), rice (*Oryza sativa* L.) and soybean (*Glycine max* L.). These low phytic acid (*lpa*) mutants produce seeds in which the chemistry of seed P, but not the total amount of P, was greatly altered.

All *lpa1* mutations affect the first committed step in inositol biosynthesis, i.e. the production of *myo*-inositol-3-phosphate (Ins3P) from glucose-6-phosphate (G6P), catalysed by the enzyme *myo*-inositol-3-phosphate synthase (Ins3P synthase, MIPS).

In previously published studies, we described a single, recessive *lpa* mutation (originally named *lpa241*) in maize (*Zea mays* L.) mapping on chromosome 1S, which resulted allelic to the *lpa1* mutant, showing a decrease in the expression of the *myo*-inositol-3-phosphate synthase located on the short arm of the chromosome 1 (*MIPS1S*).

In this work, we present some genetic and molecular analyses of the *lpa1-241* trait that may indicate an epigenetic origin of the mutation.

Some families show a Mendelian segregation of the *lpa* phenotype, while others seem to produce more mutant individuals than expected. We measured this phenomenon on both backcross and BC₁F₁ families.

Also, a high rate of spontaneous occurrence of this mutation was found and its value has been estimated for different families belonging two different inbred lines.

The analysis of the coding region of the *MIPS1S* gene using MS-PCR (methylation-sensitive PCR) showed many methylated sites at its 3' portion. So far, we could not find noticeable differences between the *lpa1-241* mutant and the wild type.

Further details on *MIPS1S* gene methylation pattern, as well as the genetic segregation of the trait, will be presented.