# Genetic analysis of bean mutants lacking seed α-amylase inhibitor.

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Recent characterization of the protein product of the lectin-like gene (1) and N-terminal sequencing of the α-amylase inhibitor (2) have indicated identity between the two proteins.

α-Amylase inhibitor (αAI) is made up by products of a single proteolytic event on a precursor molecule. Each of the two resulting fragments, however, show electrophoretic polymorphism due to different extent in their glycosylation.

Using antibodies raised against lectin-like protein synthesized in E. coli, four bean mutants lacking αAI were identified (3).

Genetic bases of the mutation have been investigated.

Tests of allelism showed that the presence of αAI was not restored in crosses between the mutants. No different behaviour was found in the reciprocal crosses.

F1 progenies of crosses between cv.s Pinto UI 111 and Greensleeves, which αAI have different polypeptide composition, showed the intermediate electrophoretic banding pattern for αAI, indicating gene codominance. A similar trend had been observed for seed lectins and storage proteins.

In F1 progenies of crosses between these two cv.s and the four mutants, no new αAI polypeptides were present, suggesting the mutation might be at the level of the structural gene(s) or cis-acting regulatory loci. Furthermore, two mutants yielded αAI with polypeptide patterns simpler than those of the parents, the fully glycosylated subunits being absent.

The reason for the lower extent of αAI glycosylation in these crosses is under investigation.

1) Ceriotti, A. et al. (1989) FEBS Lett. 255, 157-160.
2) Moreno, J. and M.J. Chrispeels (1989) Proc. Natl. Acad. Sci. USA 86, 7885-7889.
3) Bollini, R. et al. (1989) Ann. Rept. Bean Imp. Coop. 32, 27.