

IDENTIFICATION AND CHARACTERIZATION IN COMMON BEAN OF A PUTATIVE HOMOLOGUE TO THE ARABIDOPSIS INDEHISCENT GENE

GIOIA T.*, LOGOZZO G.*, KAMI J.***, SPAGNOLETTI ZEULI P.*, GEPTS P.**

*) Dipartimento di Biologia, Difesa e Biotecnologie Agro-forestali, Università degli Studi della Basilicata, Viale dell'Ateneo Lucano 10, 85100 Potenza (Italy)

***) Department of Plant Sciences/MS1, University of California, 1 Shields Avenue, Davis, CA 95616-8780 (USA)

Phaseolus vulgaris, candidate gene, nucleotide diversity, seed dispersal, basic helix-loop-helix (bHLH)

Pod shattering represents a key component of the domestication syndrome in common bean, because it makes this species dependent upon the farmer for seed dispersal. Attempts to elucidate the genetic control of this process have led to the identification of a major gene (*St*) linked to the presence of pod suture fibers involved in pod shattering. Although *St* has been placed on the common bean genetic map, the sequence and the specific functions of this gene remain unknown. The purpose of the current study was to identify a candidate gene for *St*. *Arabidopsis thaliana* *INDEHISCENT* gene (*IND*) is the primary factory required for silique shattering. A sequence homologous to *IND* was successfully amplified in *Phaseolus vulgaris* and mapped on the common bean map using two recombinant inbred population (BAT93 x Jalo EEP558; Midas x G12873). Although *PvIND* maps near the *St* locus, the lack of complete co-segregation between *PvIND* and *St* and the lack of polymorphisms at the *PvIND* locus correlating with the dehiscent/indehiscent phenotype suggests that *PvIND* may be not directly involved in pod shattering and may not be the gene underlying the *St* locus. Alternatively, a more precise phenotyping method needs to be developed to more accurately map the *St* locus.