

A BIOCHEMICAL TRAIT HELPS TO RECOGNIZE PHASEOLUS PARVIFOLIUS FREYTAG IN THE GENE POOL OF TEPARY BEAN

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Introduction

The section of *Phaseolus* currently including the tepary bean, i.e. the *Acutifolii*, consists of two species: *Phaseolus acutifolius* A. Gray (with three varieties: var. *acutifolius*, var. *latifolius* and var. *tenuifolius*) and *P. parvifolius* Freytag (Freytag & Debouck 2002). Schinkel & Gepts (1989) could not separate these varieties by nine allozyme assays. Garvin & Weeden (1994a) reported limited polymorphism for aconitase, apparently with no relationship with foliar attributes. Jaaska (1996) found a unique electromorph for three out of six accessions of var. *tenuifolius*, now classified in CIAT as '*parvifolius*'. In a study of 91 accessions with ten enzyme systems, Florez (1996) found that the allele *Aat-2⁹⁵* uniquely separates the twelve '*parvifolius*' materials from the rest of wild teparies. Zink & Nagl (1998) reported a minor difference in banding pattern of microsatellites between *P. parvifolius* and accessions of *P. acutifolius*. Muñoz et al. (2002) found in a diversity study with help of AFLPs that *P. parvifolius* forms a group separating from other wild teparies at the level of separation of common bean genepools. The purpose of this study was to find a biochemical marker ("diagnostic isoenzyme") for the recognition of either one of the varieties of tepary bean.

Materials and Methods

We analyzed 100 accessions (26 cultivated, 72 wild and 2 "escaped") of *P. acutifolius* from the world collection held at CIAT. These accessions represent the geographic, ecological, and morphoagronomic variability, as well as the variation of seed proteins found in tepary bean. Ten enzyme systems assayed by means of polyacrylamide and starch gel electrophoresis from different tissues were evaluated. The methodology for isozyme extraction, running and staining was the one reported by Ramirez et al. (1987). Globulin patterns (seed storage proteins) were analyzed by SDS-PAGE as in Gepts et al. (1986). For each allozyme, loci and alleles were designated as described by Koenig & Gepts (1989).

Results and Discussion

Out of all enzymatic complexes analyzed, the aspartate aminotransferase (AAT; E. C. 2.6.1.1) system obtained from root tips and polyacrylamide gel electrophoresis displayed alleles in *P. parvifolius* that were absent in the other varieties (Figure 1). In agreement with genetics of Aat isozyme (Garvin & Weeden 1994b; Garvin et al. 1989), the Aat-2 locus has three alleles (93, 95 and 100), all of them homozygous in the accessions evaluated. The allele *Aat-2⁹⁵* is present exclusively in *P. parvifolius* (Table 1). Only three patterns (IX, X and XII) of globulins were found in *P. parvifolius*. The "XII" type is dominant (present in all accessions), whereas in the other botanical varieties it appears with low frequency (4,1 % in wild var. *acutifolius* and 9,3 % in wild var. *tenuifolius*) (Florez, 1996).

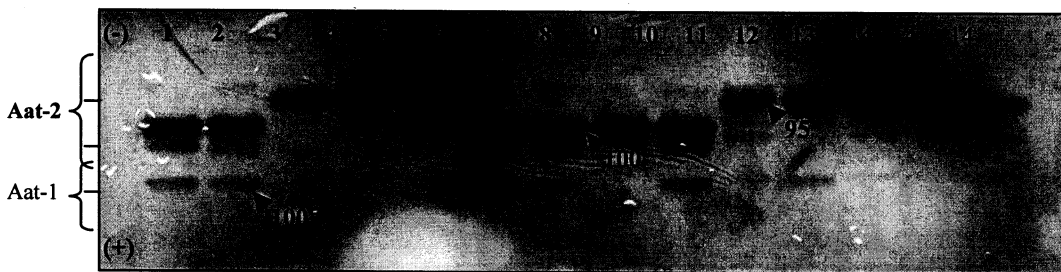


Fig. 1. Polyacrylamide gel phenotypes observed for aspartate aminotransferase (AAT). Individuals in lanes 1 and 2 are cultivated (var. *acutifolius*), individuals 6 and 7 are wild var. *acutifolius*, and individuals 8 and 9 are wild var. *tenuifolius*. The rest are classified as *P. parvifolius* (lane 3, 4, 5, 10, 11, 12, 13, and 14).

Table 1. Distribution of electromorphs found for AAT isozyme¹ in varieties of *P. acutifolius* and *P. parvifolius*

Botanical variety	Biological Status	Loci/ alleles/ individuals				
		Aat-1		Aat-2		
		100/	n/n ²	93/100	95/95	100/100
var. <i>acutifolius</i>	Cultivated	12	14	1	-	25
var. <i>acutifolius</i>	Wild	23	5	-	-	28
var. <i>tenuifolius</i>	Wild	21	3	1	-	23
<i>P. parvifolius</i>	Wild	20	-	-	20	-
Weedy forms	Intermediate	2	-	-	-	2

¹ The genetics of AAT isozyme has been reported by Garvin and Weeden (1994b), with three zones of migration observed. Nevertheless, we observed only two zones of migration (Florez, 1996).

² A null allele has been reported in tepary bean.

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