The common bean has been part of the Great American Biotic Interchange: evidence from the study of cpDNA and implications for conservation and breeding.

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Introduction

What do we know about the distribution of wild beans in North America? It is known that the common bean (Phaseolus vulgaris) has a complex history of migration and adaptation to the North American environment. The bean has been an important food source for humans for thousands of years, and its distribution has been shaped by both natural and cultural processes. The bean was first domesticated in the Americas, and its spread across the continent has been influenced by climate, geography, and human activities.

The distribution of wild common bean (Phaseolus vulgaris) from northern Mexico to northwestern South America (Fig. 1). The haplotypes can also be studied by means of Nested Clade Analysis (Templeton 1995). Here maternally inherited (Corriveau & Coleman 1988) when investigated on 106 samples of 14 chloroplast haplotypes in the tiger salamander, Ambystoma tigrinum (Templeton et al. 1995). Second, because of the current location of such sister species, it is likely that the separation took place in southern Mesopotamia, with an early migration into the northern Andes in the Pleistocene period, and the third lineage diverged by 0.6 million years ago. Gepts et al. (2000) estimated the separation of P. vulgaris from its sister species P. cocineus at 2 million years ago, and the separation of the Mesoamerican and Andean genepools at 0.5 million years ago.

Results and Discussion

The chloroplast DNA supposedly invariant within a species (see discussion by Solitis et al. 1992) and here maternally inherited (Corriveau & Coleman 1988) when investigated on 106 wild and 20 weedy forms for seven non-coding regions reveals fourteen polymorphisms or haplotypes (Chacón et al. 2005, 2007). These haplotypes are not directly related, displaying some continuous (L in Mexico, Guatemala to Colombia), or localised (E in the Pacific range, F in Costa Rica), or disjunct (A in Mexico and Bolivia) distribution (Fig. 1). The haplotypes can also be studied by means of Nested Clade Analysis (Templeton et al. 1995) and Mantel test as implemented in ARLEQUIN 2000 (Schneider et al. 2000). The haplotypes form a network (Fig. 2) linked to the sister species of Phaseolus (Freytag & Debouck 2002), P. coruscans and P. dumosus, through haplotype A that can be considered as ancestral. The haplotypes can be grouped into one- and two-step nested clades along rules established by Templeton and co-workers (1987, 1991), allowing testing into the three lineages of increased but differential speciation, and likely migration events. The first lineage differentiates little but is present in both subcontinents. The second lineage differentiates in the Pacific Andean range and from there into Central America. The third lineage differentiates in Mexico and then Central America up to Colombia.

Using ITS sequences retrieved from GenBank and divergence age estimates for legumes set by Lavin and co-workers (2005), Chacón et al. (2007) estimate that P. vulgaris separated from its sister species about 1.3 million years ago, and that the second lineage diverged by 0.6 million years ago. Gepts et al. (2000) estimated the separation of P. vulgaris from its sister species P. cocineus at 2 million years ago, and the separation of the Mesoamerican and Andean genepools at 0.5 million years ago.

These results suggest the following points for discussion. First, P. vulgaris separates from a cluster of four sister species (= its secondary genepool), confirming early results (Debouck 1999, Delgado et al. 1999). Second, because of the current location of such sister species, it is likely that the separation took place in southern Mesopotamia, with an early migration into the northern Andes in the Pleistocene period, and the third lineage diverged by 0.6 million years ago. Gepts et al. (2000) estimated the separation of P. vulgaris from its sister species P. cocineus at 2 million years ago, and the separation of the Mesoamerican and Andean genepools at 0.5 million years ago.

Literature cited


Figure 1. Geographic distribution and frequency of 14 chloroplast haplotypes (graph pies).

Figure 2. Unrooted network of chloroplast haplotypes using ARLEQUIN 2000. Observed haplotypes with capital letter (in a dotted box when interior), with a black dot when missing (extinct). One-indicated 1-1 and 1-8) and two-step (2-1 and 2-3) clades are indicated by boxes, dotted and solid lines, respectively.

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