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On the Origin of the Common Bean (*Phaseolus vulgaris* L.)

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ABSTRACT

Phylogeographic methods provide the tools to accurately access the geographic origin and diversification of crop species. In the present commentary, I urge the common bean community to face those methods and a tree-thinking mentality with regards to the long standing debate of the origin of common bean. Such efforts will ultimately bring back interest into wild bean studies and reinforce the uniqueness of this species as a system to study diversification, domestication and adaptive processes across the two most diverse hotspots in the world.

Keywords: Phylogeography; Domestication; Bottlenecks; Outgroups; Andes; Mesoamerica

1. Introduction

Wild bean is thought to have diversified in South and Central America, after which domestication in the southern and northern ends of each region gave independent origin to the Andean and Mesoamerican domesticates. Additional structure within each of these genepools accounts for up to 10 different races. Both genepools followed parallel pathways of dissemination through the world, generating new secondary centers of diversity in Africa and Asia [1].

Several recent works defended a Mesoamerican origin of the common bean [2,3]. This was mainly based on the extensive diversity and population structure within the Mesoamerican genepool, and the signature of predomestication bottlenecks in the south of the Andes detected in 5 genes across 102 wild accessions. However, these two main lines of evidence are not only circumstantial, but do not exclude an Andean origin of common bean. Extensive population structure does not necessarily correlate with origin, and may also be the result of widespread local adaptation and unparalleled genetic drift across the Mexican and Guatemalan valleys [1,4]. Meanwhile, demographic bottlenecks in the south of the Andes may have occurred during colonization either from Mesoamerica or from Ecuador and North Peru, and therefore do not exclude the possibility that the origin of common bean is in the latter region with the absence of strong bottle-necks during the northern radiation.

Several arguments against a phenetic approach, as the one that has been repeatedly applied to address the origin of beans, must also be considered. In the first place, there are no living ancestral populations or lineages because each one has had the same period of quasi-independent evolution since divergence [5]. Therefore, in the absence of outgroups it is not possible to reconstruct ancestral character states and areas. It will only be possible to identify ancestral alleles, and to differentiate the two competitive hypotheses regarding the origin of common bean if the previous surveys had been combined with a set of carefully chosen *Phaseolus* species (**Figure 1**). This would provide a rooted cladogram and an appropriate phylogenetic inference. Nowadays, wild beans are still being discovered [6] and further expeditions in the west slopes of the Ecuadorian and Northern and Central Peruvian Andes are urgently required. A clearer picture of the distribution of the wild accessions is essential to carry out an accurate reconstruction of ancestral areas. Furthermore, archeological clues are much older in the Andes than in Mesoamerica, and therefore its inclusion is crucial for an accurate reconstruction of areas. Secondly, the genetic proximity between some accessions from the south of the Andes and some from central Mexico may not be due to incomplete linage sorting of ancestral polymorphism, but instead to homoplasy or ancestral introgression [7]. The first option seems particularly plausible in the previous works because they did not use character-state tree reconstruction methods, but distance methods; even though the former methods are the ones that incorporate the nucleotide mutation processes into the phylogenetic inference [8].

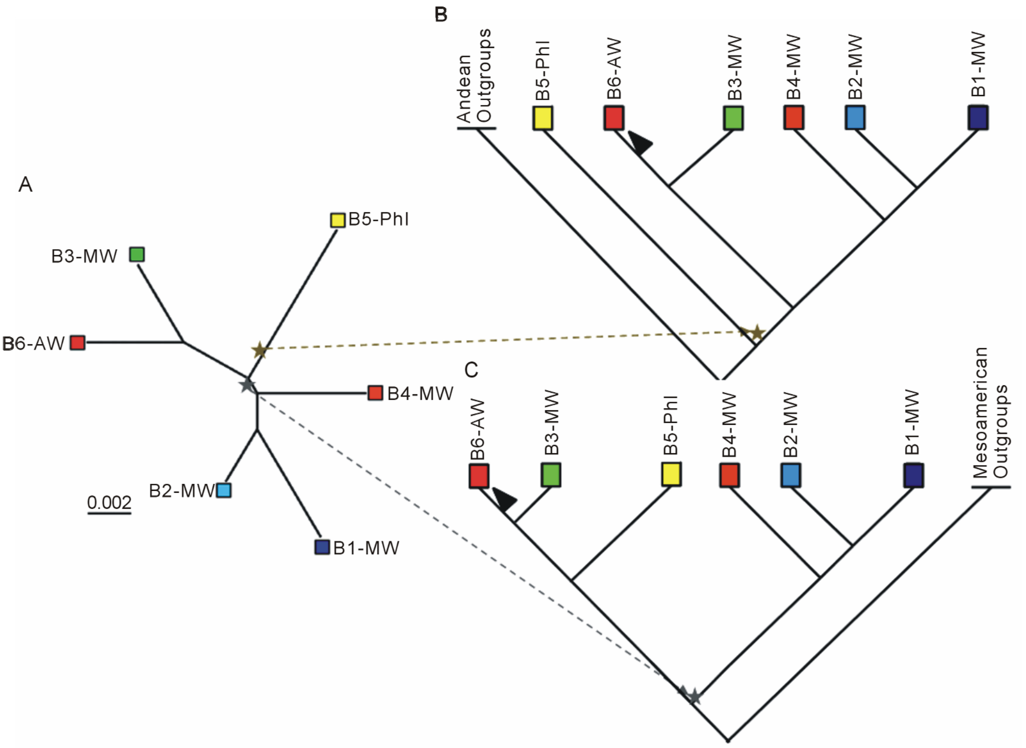

Figure 1. The importance of outgroups (other *Phaseolus* species) and a tree-thinking mentality (2) to address the origin of the common bean. Outgroups give polarity to unrooted trees and allow reconstructing ancestral character states and areas. Previous works [2] (A) are fully congruent with both an Andean (B) and a Mesoamerican (C) origin of the common bean depending on how its relationship with a hypothetical outgroup is. A is an unrooted dendogram. On the other hand, B and C are rooted cladograms reconstructed after considering Andean (B) or Mesoamerican (C) outgroups. Dashed lines display where the root of the tree is placed. Black triangles represent the occurrence of an Andean bottleneck, which is also compatible with both hypotheses because it happens only in one branch of the tree. Abbreviations: MW—Mesoamerican wild, AW—Andean wild, B1-6: within-genepool populations as previously defined [2].

2. Conclusion

Phylogeographic methods provide the tools to accurately access the geographic origin and diversification of species. I urge the common bean community to face those methods and a tree-thinking mentality with regards to the long standing debate of the origin of this species. Such efforts will ultimately bring back interest into wild bean studies and reinforce the uniqueness of these species as a system to study diversification, domestication and adaptive processes across the two most diverse hotspots in the world: the Andes and Mesoamerica [9].

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