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A single gene at the heart of pod shattering

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Abstract

Pod shattering is a defining trait of legume domestication, yet the genetic routes to indehiscent pods and their geographic context remain incompletely resolved. Celebioglu et al., [1] identify repeated loss-of-function mutations in the R2R3-MYB transcription factor *PvMYB26* as important contributors to reduced pod shattering in common bean (*Phaseolus vulgaris*), and use *PvMYB26* haplotypes to pinpoint domestication centers in the Americas. Their work illustrates how a single regulatory node can couple pod wall anatomy, domestication, and agricultural origins, and raises broader questions about parallelism, constraint, and future breeding for harvest stability.

Keywords: Allele; Domestication; Shattering; Mutation; Pod

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Main text

PvMYB26 controls pod lignification and shattering

In wild legumes, explosive pod shattering is an efficient seed dispersal strategy; in crops, it represents a major barrier to harvestability [2]. Reducing shattering is therefore a central component of the domestication syndrome. Celebioglu et al., [1] dissect this trait in common bean and identify the transcription factor, *PvMYB26*, as a major regulator of pod dehiscence and a genomic marker of domestication history.

Using recombinant inbred populations from wild to domesticated crosses, the authors map pod shattering to a locus encoding an R2R3-MYB transcription factor, orthologous to *MYB26* genes previously implicated in pod dehiscence in other legumes [3]. In Middle American domesticates, Celebioglu et al., [1] identify an ~8 kb deletion that removes the *PvMYB26* promoter and transcription start site. This structural variant reduces PvMYB26 expression to <1% of wild-type levels and leads to a ~44% decrease in lignin deposition in the pod wall. Histological analyses show that the lignified fiber layer, responsible for generating tension along the suture, is poorly developed in deletion carriers, resulting in pods that remain closed under typical cultivation conditions.

Thus, modest anatomical changes in a specific tissue layer, associated with strong downregulation of

PvMYB26, may sufficient to transform a wild-type "explosive" pod into an indehiscent, farmer-friendly structure. This fits an emerging pattern in domestication genetics: targeted perturbation of transcription factors with narrow spatial domains can retune organ mechanics without grossly altering overall development.

Convergent domestication of *PvMYB26* alleles

The story becomes more striking when extended across the species' global diversity. In seed crops such as cereals, grain legumes like common bean, and certain Brassica species, three traits form the core of domestication syndromes: larger seeds, non-shattering pods, and loss of seed dormancy [4]. Among the ~12 domesticated legume crops, common bean stands out as particularly fascinating [5]. Previous studies have established that common bean underwent two independent domestication events originated from distinct wild gene pools in Mesoamerica and the central Andes. Wild common bean spans a vast natural range from northern Mexico to southern Argentina, encompassing three genetically distinct, non-overlapping populations: Northern/Middle American (Mexico to Colombia), Central/debouckii (Ecuador/northern Peru), and Southern (southern Peru, Bolivia, Argentina) [6]. Celebioglu et al., [1] analyzed a diverse panel of 327 wild and domesticated accessions from Middle American and Andean gene pools and uncover multiple, independent domestication alleles at *PvMYB26*. In the Middle American pool, the 8 kb deletion is present in nearly all domesticates and absent from wild accessions. The deletion resides in a ~125 kb hard selective sweep, suggesting strong selection during domestication.

In the Andean gene pool, however, domesticates lack the deletion and instead carry a distinct frameshift mutation that truncates the PvMYB26 protein, again reducing shattering. A third truncation allele occurs in the so-called debouckii population, which has been considered "undomesticated" but shows some domestication-like features. This suggests at least three independent domestication or proto-domestication events, all targeting *PvMYB26* but via different mutational routes.

These data add a compelling example to the growing list of parallel domestication at homologous genes. In legumes and other crops, orthologs of *MYB26* and related regulators repeatedly emerge as shattering genes, consistent with the concept of a "Vavilovian homologous series" where similar traits are modified through analogous genetic changes across related species [2]. The repeated use of *PvMYB26-like* genes raises questions about constraint: are there limited viable genetic solutions to reducing pod shattering without compromising other pod functions, or has selection simply favored the most accessible, high-effect alleles? Similar patterns have been reported in soybean and rice, where recurrent selection of orthologous shattering-related genes contributed to parallel domestication outcomes across independent lineages.

Spatial domestication of *PvMYB26* as geographical marker

Beyond trait genetics, the PvMYB26 haplotype data provide unusually sharp resolution on where domestication occurred. Because the Middle American 8 kb deletion is nearly fixed in domesticated accessions, the wild populations most closely related at the *PvMYB26* locus are likely near the center of domestication. Celebioglu et al., [1] find that these wild haplotypes cluster in eastern Jalisco and northern Michoacán, pointing to west-central Mexico as the primary domestication center for common bean in Middle America contrasting with earlier hypotheses favoring southern Mexico.

In the Andes, the distinct *PvMYB26* truncation allele is prevalent in domesticated accessions but absent in wild ones, supporting an independent domestication center in the southern Andes. The debouckii allele, found in Ecuador and northern Peru, introduces a third focal region where a domestication-like mutation has arisen but did not widely spread, suggesting a potentially distinct or less extensive domestication process.

This work exemplifies how trait-defining genes under strong selection can be used as geographic markers to refine domestication scenarios. Rather than relying solely on neutral markers or archaeological remains, a functionally characterized locus like *PvMYB26* provides a more direct link between phenotype, selection, and geography. A key future challenge is to integrate such locus-specific signals with genome-wide demographic inferences and archaeobotanical timelines to build a more coherent picture of early agriculture in the Americas.

Implications for future breeding

The *PvMYB26* story has several broader implications. First, it reinforces the idea that domestication often proceeds via changes in regulatory genes orchestrating organ anatomy. *PvMYB26* acts in a restricted cell layer but exerts a disproportionate effect on shattering. This echoes other domestication loci (e.g., in cereals and legumes) where tissue-specific transcription factors modify dispersal structures, branching patterns, or inflorescence architecture.

Second, the presence of multiple *PvMYB26* domestication alleles offers a natural laboratory for studying genotype-environment trade-offs. It remains unclear whether the Middle American deletion, Andean truncation, and debouckii allele are functionally equivalent in all environments. Some variants may be better suited to particular climates or management systems, affecting pod robustness, susceptibility to mechanical damage, or tolerance to drought and heat. Systematic phenotypic and physiological comparisons across environments could reveal whether breeders can exploit specific alleles—or combinations with other shattering loci to tailor ideotypes to future climate scenarios.

Third, the study prompts the question of how many domestication traits are controlled by similar "hotspot" genes across crops. Pod shattering, seed size, plant architecture, and flowering time all show evidence of parallelism at orthologous loci in multiple species. Identifying these hotspots systematically, and understanding why they are favored targets (large effect, limited pleiotropy, high mutational target size), could guide both the reconstruction of domestication histories and the rational design of new trait combinations.

Finally, the work underscores the power of integrating developmental genetics, anatomy, and population genomics. It is the combination of detailed anatomical characterization, expression profiling, functional validation, and dense haplotype mapping that allows *PvMYB26* to serve simultaneously as a mechanistic gene and a marker of domestication geography. Similar integrative frameworks could be applied to other domestication traits to gain both mechanistic depth and historical breadth.

Conclusion

Celebioglu et al., [1] provide an elegant demonstration of how a single transcription factor connects pod wall development, domestication syndromes, and the emergence of agriculture in the Americas. By showing that repeated, independent loss-of-function mutations in *PvMYB26* underlie reduced pod shattering in common bean and tracing the geographic footprints of these alleles, they offer a model for domestication research that is at once molecular, anatomical, and historical. Their findings invite further exploration of parallel domestication at *MYB26-like* loci across legumes and highlight domestication genes as powerful tools for both understanding the past and breeding beans for a changing future.

Data availability

Not applicable

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Not applicable

Conflict of interest

The authors declare that they have no conflict of interest.

Author Contribution

The authors confirm contribution to the paper as follows: study conception and design: AS; data collection: AS, MS; draft manuscript preparation: AS, AA; manuscript revision: MS, AA. All authors discussed the content, reviewed the results and approved the final version of the manuscript.

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