

Views on variability in *Phaseolus* beans.D. G. Debouck¹

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Agriculture today faces many challenges, especially to increase production and raise its quality, while using less expensive inputs. One way to meet these challenges directly is through genetic progress in crops. There is no genetic progress without access to a wider variability and without better knowledge of it. When I started some work on the genetic resources of *Phaseolus* beans in 1977, germplasm collections worldwide were not representative of the genetic variability present in the cultigens and in the genus. Instead of considering the variability as a fixed result of the past, or as items to accumulate on a shelf, I thought that it might be better to try to understand what caused the patterns we can observe today and to identify where the variability worth conserving can be found. The key questions were then: if you have 50 or so species (by the way, how many are there?) in a genus, why were only five domesticated? How were these five domesticated? Where? For what purposes? Particularly when dealing with autogamous crops in the context of individual plant selection in the Americas, it is not clear how variability will be kept within landraces, thus the importance of understanding the early steps of domestication and how variability could have been retained for a period of about 8,000 years.

In 1977, only four species were considered as domesticated, and most scholars saw Mexico as the likely place of origin for them, because most of the wild species then known were reported from that country. However some authors called attention to some particular patterns of variation, suggesting that the picture might be more complex. Thanks in large part to the excellent collaboration of my Latin American colleagues, I have been able to collect some 2,600 accessions for 54 taxa, some of which are new to science or have never been collected before, from Chihuahua, Mexico down to Tucuman, Argentina. And although many points remain to be studied, we are seeing changes in how to better conserve and use our bean plant genetic resources.

Origin and diversification might not have occurred at the same place; that may be equally true for species as for cultigens. There is evidence that *P. vulgaris*, *P. coccineus* and *P. polyanthus* form a syngameon. Indeed we found natural hybrids between cultivated *P. coccineus* and *P. polyanthus* in Putumayo, Colombia, and between *P. vulgaris* and *P. polyanthus* in Tolima, Colombia. While their respective wild relatives differentiated into the presently known morphotypes, they progressively occupied new ecological niches and acquired more diversity. Thus, we can explain the differences observed in the morphology, physiology, biochemical and molecular constitution in the different populations of wild common bean across its range. We cannot exclude at this stage that the variability of wild *P. vulgaris* was enriched in Mesoamerica because of the presence of the *P. coccineus* complex there (as it evolved with and

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separated from it), although so far I have been unable to find any natural hybrids between wild *P. vulgaris* and *P. coccineus*. The unique variability exhibited by wild *P. vulgaris* on the western slopes of the Andes certainly deserves further consideration; it might confirm my early feeling that there are not two groups of wild common bean but as many as there are important mountainous ranges between 30 ° lat. N and S. The complex of species in *P. coccineus* in the wild is now undergoing an active speciation process in Mexico (as is that in *P. neglectus*), and is therefore certainly the widest gene pool to work with and has much to give to *P. vulgaris* (for instance CMS sources for the production of hybrid beans). We found the wild ancestral form of *P. polyanthus* in Guatemala; perhaps this the cultigen does not have as much realized evolutionary potential as the others, but it is certainly promising.

The lima bean has still much to offer. We have discovered another group of wild forms in the western *cordilleras* of southern Ecuador and northern Peru, that were later identified as the ancestors of the Big Limas, once considered to have been domesticated in Guatemala. So two independent domestications occur in this crop, from two groups of wild ancestors that separate from each other much earlier than for the wild forms of *P. vulgaris*. The domestication of the Big Lima is probably an ancient one, and I am not sure that it was primarily domesticated for food. I had the same doubt for some groups of *P. vulgaris*, at least for those in the Southern Andes; if you have selective pressures other than for food, the diversity there might be greater.

One lesson of these studies is the presence of a founder effect, variable from one cultigen to another, and within them, variable from one region to another. Another lesson is the unique character of the variability: the wild relatives express variation along their range, and variants (in e.g. biochemical attributes, cfr the arcelin story) are often locally unique. The same is also applicable to certain landraces, for instance the *nuñas* and *chuies* in *P. vulgaris*. For each and all of these reasons, we cannot discard a group of accessions in favour of another, we have to consider variability in a genepool perspective. After the case of potato or tomato breeding, one approach to *Phaseolus* that could take us forward would be to consider the genus as the wide genepool.

Obviously we still have much to study in the variability of each cultigen, but it might be appropriate to tackle the problem from the symbiont side too. If preliminary results are confirmed, then it becomes more important to know where and when the different landraces were actually domesticated. Finding those that co-evolved for years in a certain biotic context will surely help towards a more sustainable production. But this would be incomplete if we do not study how variability has been generated within each cultigen. The so-called wild-weed-crop complex certainly helped in the formation of certain races and thus contributed to their genetic isolation. Likewise, it may have helped to increase the richness of cytoplasm within a pool (a too often neglected aspect). The second half of the crop history, particularly for *P. vulgaris*, was already marked by germplasm exchange. Have those that separated very early from their wild relatives come to an evolutionary dead-end? How is that separation reflected by genetic compatibility? What variability has been gained by the crop as it was moved from one place to another? We may now have some germplasm and the right tools especially the molecular ones to address some of these challenging questions, which will throw new light on future crop improvement.