Characterization of common bean wild populations for their *in situ* conservation in Northwestern Argentina

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Abstract

In situ conservation of wild species is a method of conservation that allows keeping populations in their natural environments, and set the strategies for maintaining the natural populations. The Active Bank of Northwestern Argentina (BANOA) is in charge of the *in situ* conservation of wild populations of common bean (*Phaseolus vulgaris* L.) in Northwestern Argentina (NOA), and has an *ex situ* collection of 401 landraces and 221 wild accessions from the NOA. We evaluated the phenotypic diversity of 68 common bean wild populations from the NOA both in protected and unprotected areas, finding a moderate variation among them. Ten phenotypic reproductive characteristics related to pod and seed displayed significant differences in the analysis of variance, these traits together with the seed weight were the basis for the multivariate analysis. The cluster analysis ordered the populations in 12 groups but not trends in geographical distribution or phenotypical variation were recognized. For the conservation *in situ* of the wild bean populations their diversity should be considered. Two types of populations can be highlighted: i) candidates for *in situ* conservation in order to preserve the novel variation generated by convergence with cultivated sympatric germplasm (populations 433, 437, 471, 509, 513 and 517) and ii) those whose phenotype represent clearly the wild status and should be preserved *in situ* as them in their current status (populations 480, 495, 496, 525 and 533).

Key words: breeding; domestication; genetic diversity; germplasm; *Phaseolus vulgaris*

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Introduction

Genetic resources for agricultural development and future food security are constantly threatened; therefore their conservation is imperative. *In situ* conservation ensures continuity of the dynamic processes in which species develop under environmental changes and co-evolve with biotic and abiotic factors, so the processes of evolution and adaptation are maintained and the generation of new genotypes is guaranteed as well as the genetic integrity of the wild or natural populations. On the other hand, *ex situ* conservation of cultivated plants and their wild relatives in genebanks has some constraints but ensures the long-term conservation of them. *Ex situ* collections are important to provide relatively easy access to germplasm by researchers and plant breeders.

The common bean is the most important grain legume for direct human consumption on a global scale. Among the main food crops, the common bean shows the greatest variation in growth habit, seed characteristics (size, shape and colour) and maturation time. This variability enables its production in a wide range of cropping systems and environments as diverse as the Americas, Africa, the Middle East, China and Europe. Despite being cultivated for its fresh pods and grains, beans are produced and consumed mainly as dry legume. The current integration of genomic data into genebank documentation systems and its combination with genetic and phenotypic data will open a new era for the valorization of the common bean genetic resources (Schmutz et al. 2014; Vlasova et al. 2016).

This crop has spread from The Americas to every continent over the past centuries, which resulted in a complex genetic structure of the bean germplasm outside its areas of origin and domestication (South and Central America) (De Ron et al. 2015). The diffusion of the common bean out of the American domestication centers appears to have been very complex, and involved numerous introductions into different continents and countries. Several of these have been proposed as secondary centers of diversification, such as Europe (Santalla et al. 2002; Angioi et al. 2010; Gioia et al. 2013), central-eastern and southern Africa, Brazil and China (Bellucci et al. 2014).

Andean domesticated common bean germplasm is notable diverse in plant and seed morphology and agroecological adaptation, but it has been proved to have a narrow genetic base on the basis of molecular analysis (Beebe et al. 2001; Bitocchi et al. 2013) as compared to Mesoamerican germplasm. The genetic structure of common bean landraces reflects the structure of the wild beans; hence a narrow genetic variability for biochemical analysis in Andean domesticated germplasm was also found in wild germplasm (Koenig and Gepts 1989; Cattán-Toupan et al. 1998).

The precise region of domestication for the Andean common bean gene pool as well as the number of domestication events has been controversial although previous studies have indicated that Bolivia is the most likely candidate as the primary domestication site of the Andean gene pool of common bean (Beebe et al. 2001; Bitocchi et al. 2013). In this area there is still a considerable amount of genetic diversity in many wild populations and also in the cultivated varieties, owing to the small size of the farms in these areas and the persistence of traditional methods of agriculture. Argentinean domesticated germplasm includes mostly bean populations of races Nueva Granada and Peru. However, race Chile and Mesoamerica have also been found (Singh et al. 1991) which could be due to a limited germplasm exchange in pre-Columbian times between Mesoamerica and South-America although more extensive seed movement occurred after the 1500s.

Wild beans of South America are very small seeded compared with their corresponding domesticated forms. Common bean has evolved during domestication from small- to large-seeded forms, from extreme indeterminate climbing types to determinate bush types, from seed dormancy and water impermeability of the seed coat to lack of dormancy and water permeable seed coat and from highly fibrous pod wall and shattering forms to lack of fibres and no shattering types (Brücher and Brücher 1976; Smartt 1988; Gepts and Debouck 1991). There was a change of seed coat pigmentation and a reduction of the content in toxic materials, which have probably improved the flavour and caused the loss of seed protection against predators (Smartt 1988). The domesticated forms of the common bean have important traits that distinguish them from the wild forms, such as reduced and loss of the dissemination mechanisms, loss of seed dormancy and photoperiod insensitivity (Quiroga et al. 2015), greater seed size, and determinate growth habit. The main effect of domestication of this species was a reduction in the genetic diversity in the domesticated forms which was threefold greater in Mesoamerica compared with the Andes. This appears to be a result of a bottleneck that occurred before domestication in the Andes, which strongly impoverished this wild germplasm, leading to the minor effect of the subsequent domestication bottleneck (i.e. sequential bottleneck) (Bitocchi et al. 2013) and selection at loci controlling domestication traits. (De Ron et al. 2015).

These marked phenotypic differences, named the domestication syndrome (Hammer 1984; Koinange et al. 1996), resulted from selection during several thousands of years for adaptation to cultivated environments. Moreover, wild bean populations are believed to represent more genetic variability than domesticated beans (Gepts et al. 1986; Koenig et al. 1990). This evidence suggests a founder effect in the domestication process (Ladizinsky, 1985), which could have excluded valuable genetic variability of wild beans from domesticated populations (Schoonhoven et al. 1983; Debouck and Tohme 1989). In addition, the tendency towards increased selfing upon domestication might have limited gene flow between landraces and neighbouring wild common bean populations.

Wild germplasm remains important for the genetic improvement of domesticated types (Cattan-Toupance et al. 1998; Singh 2001) since hybrids between wild and domesticated beans are fully fertile and have no major barriers (Singh et al. 1995). Their potential as a source of genetic diversity can be illustrated by the arcelin seed protein, which is responsible for resistance to bruchids (*Zabrotes subfasciatus*). This resistance is absent in mostly of cultivated varieties of common bean (Schoonhoven and Cardona 1982), while only a few wild bean populations from Mexico were highly resistant (Acosta-Gallegos et al. 1998). Studies of Andean germplasm including wild and domesticated germplasm will provide sources of diversity to broaden the genetic base of Andean common bean germplasm which is obviously important due to the Andean beans have been more difficult to improve for yield potential (White et al. 1992; Kornegay et al. 1992).

According to De la Fuente et al. (2013) Argentinian domesticated accessions present a substantial genetic variation with a considerable number of unique haplotypes and private alleles and seem to constitute two homogeneous and distinct groups (Tohme et al. 1996; De Ron et al. 2004; Santalla et al. 2004; Galván et al. 2006). De la Fuente et al. (2013) also observed a strong reduction in genetic diversity between wild and domesticated accessions from Argentina; most of the alleles of the domesticated accessions were found in the wild accessions, and some loci showing more variation in domesticated versus wild accessions. In the same study, these authors also examined phenotypical variables between wild types and landraces; wild accessions flowered earlier and had smaller seeds and pods, pigmented flowers and seeds and higher yields (by pods per plant and seeds per pod) than domesticated

types. Additionally, Rodriguez et al. (2016) by analysing the genetic spatial patterns of the wild common bean documented the existence of several genetic groups and the occurrence of variable degrees of diversity in Mesoamerica and the Andes; these findings are of paramount importance for the conservation of the genetic diversity within this species.

Different collecting missions involving common bean primitive landraces and wild populations were carried out in the NOA since the 70's (Menéndez-Sevillano 2002) to increase the availability of regional genetic diversity that could be used as a source of genes to introduce in current cultivars (Singh et al. 1995). The BANOA is one of the genebanks of the INTA Genetic Resources Network where the common bean collection that includes 221 wild and 401 primitive landraces is the main germplasm collection of that genebank. The INTA as research institute could contribute to decision-makers (Ministries of National and Provincial Environment) and the BANOA can monitor populations to confirm their status. The knowledge of the phenotypic variation of the wild common bean germplasm is a prerequisite for their *in situ* conservation that means to preserve as far as possible the genetic integrity of the wild populations as a relevant natural resource.

The objective of this research was to evaluate the presence and phenotypic diversity of wild populations of common bean in the NOA both in protected and unprotected areas and to assess about their *in situ* conservation.

Material and methods

Collecting missions

The missions for collect the wild bean populations from the NOA included in the present study were carried out from 2007 to 2013, in the Argentinean provinces of Salta, Jujuy, Tucumán, Catamarca and Córdoba (figure 1). The missions were performed during the austral autumn (June) due to the biological cycle of the wild plants and to avoid severe adverse environmental conditions during the missions. The table 1 shows the 68 wild populations sampled in these missions together with the geographical reference. The populations were sampled in the following geographical interval: 22° 14' - 27° 47' S / 63° 42' - 65° 58' W / 896 – 1910 meters above sea level (masl), isoetes 550 – 2000 L/year rainfall.

Mostly of the studied populations grow in the Yungas ecoregion, a narrow strip in the slopes of the Andean mountains in the provinces of Salta, Jujuy, Tucumán and Catamarca reaching heights of up to 3000 masl. The climate is warm and humid with summer rains and frost in winter, annual rainfall reaches 2500 mm. It is a region of mountains, canyons and plains with forest acid soils with its three characteristic horizons: humifer, topsoil and mineral earth. The region includes several microclimates that result in a forest transition: 1) from 350 to 500 masl with rainfall of 700-1000 mm annual extends from Salta to Tucuman, 2) mountain jungle eastern slopes of the mountains of NOA from Bolivia to Catamarca limit between 550 and 1600 masl, it is a rainforest, 3) the montane forest is the highest part of the region between 1200-3000 masl with a more cold weather with snowfalls are very rainy summers and dry winters (Cabrera 1976). The studied populations were also located with respect to isoetes: most populations were distributed among the isoetes 1000 and 2000 mm of annual rainfall, although two of them namely 480 y 433 were found between 600 and 800 mm, corresponding to the dry Chaco ecoregion. The location of each wild population was georeferenced in vector format that allows spatially locate them and define the ecoregion where they grow.

Phenotypic characterization

From each population pods and seeds were collected and the growth habit and flower colour was observed. Pod and seed morphological traits were recorded as follows in the 68 wild populations studied. Pod length, width and thickness, expressed in millimeters and number of seeds per pod, were measured in a random sample of 20 pods in each population. From these data the index $K = \text{thickness}/\text{width}$ (Puerta Romero 1961) indicative of the shape of the pod was calculated, considering flat pods when $K \approx 0.5$ and rounded pods when $K \approx 1.0$. Seed length, width and thickness, expressed in millimeters, were measured in a random sample of 30 seeds in each population. From these data the indexes $J = \text{length}/\text{width}$ and $H = \text{thickness}/\text{width}$ (Puerta Romero 1961) indicative of the shape of the seed were calculated, considering the seed shape according to these indexes as follows. J index: spherical 1.16-1.42; elliptical 1.43-1.65; oblong - short kidney 1.66-1.85; oblong - medium kidney 1.86-2.00 and oblong - long kidney >2.00 . H index: flat ≤ 0.69 ; semi-filled 0.70-0.79 and full ≥ 0.80 . Seed weight expressed in grams was measured in a sample of 100 seeds in each population and the seed colour was recorded.

Statistical analysis

Mean, standard deviation, standard error, coefficient of variation and range of variation were calculated for all the traits in the 68 populations studied and analyses of variance (ANOVA) were performed by the usual method (Steel et al. 1997) for 10 quantitative traits studied over the 68 populations, using the statistical package INFOSTAT. Multivariate analysis of the variation in the populations was performed by cluster analysis according the UPGMA (unweighted pair-group method using arithmetic averages) method, using the statistical package INFOSTAT. The multivariate analysis was based in the quantitative traits that had significant differences in the ANOVA, and the seed weight.

Results and Discussion

In situ conservation of crop wild relatives is a priority to maintain the genetic integrity of the species and the potential gene pool for the future. Therefore, it is essential to study these wild populations to gather information about their variability, their degree of conservation and their potential use for the genetic improvement of cultivated varieties of the species. However, their study has restrictions, since it is necessary to avoid impacts on the wild population as the genetic erosion that can be derived from the sampling by removing individuals from the population. For this reason, sampling has been limited to the reproductive parts of the plant, fruit (pod) and seed. These reproductive parts of the plant provide sufficient information for a phenotypic characterization of a population.

The qualitative characters observed were basically homogeneous in all the populations: growth habit type IV indeterminate climbing (CIAT 1984), coloured flowers and coloured seeds. The mottled seed coat pattern in Argentinean wild bean seeds was considered (Brücher 1988) as a phylogenetically ancient feature with a marked selection advantage because mottled seeds are nearly invisible to animals such as birds and rats when they fall onto a debris-covered soil. On the other hand, domesticated common bean populations in the NOA, considered as primitive landraces, are high variable in these qualitative traits (Menéndez-Sevillano 2002; De Ron et al. 1999), maybe as consequence of the evolution of the species after domestication and its coexistence with wild ancestral forms. Debouck (1989) suggested that the current diversity observed in the bean landraces in the NOA is derived from non-food uses of the dry seeds; therefore “aesthetic” selection could have been the principal force for

bean evolution is this area. This aesthetic selection would have lasted for several millennia resulting in types with a wide variation in seed colours and colour patterns absent in the wild populations. Burkart (1945) also reported this aesthetic use of beans since the use of as a children toy of vividly coloured seeds called “chuis” was observed in Bolivia. Selection for food purposes of wild and domesticated beans must also be considered as a relevant evolutionary factor of the species in this area. Bean is a component of traditional Argentinean food such as the “locro”, a high nutritive local recipe that incorporates corn, meat, cucurbit, and bean (usually white but also coloured). Besides the wild bean was reported as an emergency food when other sources fail (Debouck 1990).

The ANOVA was performed over 10 traits with repeated measures in each population that excludes 100 seeds weight that was determined over one seed sample in each population. Differences among populations were highly significant in all the traits analysed. The table 2 displays the mean, range of variation, standard deviation and coefficient of variation of the traits studied in the 68 wild bean populations.

Regarding seed dimensions (length, width and thickness), the ranges of variation and the coefficients of variation indicates a moderate variability in these traits. The most variable was the thickness of the seed, in which the maximum is almost double the minimum and the CV is close to 10%. In average the seeds were elliptical and flat in shape, with a mean value of 1.51 for the J index and 0.58 for the H index although in this trait the CV has a score of 7.30 that indicated certain variation. The longest seeds correspond to the populations 472 (9.52 mm) and 437 (9.01 mm). Eight populations displayed seeds longer than 8.50 mm while 13 populations had seeds smaller than 7.50 mm, in particular 525 had a small seed only 6.97 mm long. De Ron et al. (2004) in a study of 83 domesticated population from the NOA reported an average seed length of 13.0 mm, with a minimum value of 9.9 mm, close to the longest seeds of the studied wild bean populations. It could indicate that there is some degree of evolution of the wild populations that are sympatric with domesticated beans (landraces and commercial varieties) and that outcrossing could play a role in this process as indicated by Gepts et al. (2000) in Mexican wild and cultivated bean populations and Mumba and Galwey (1999) in Mesoamerican and Andean germplasm in different evolutionary bean types (wild, landrace and improved).

The population 513 had the highest seed weight (16.3 g 100 seeds), eight populations scored over 10.0 g 100 seeds, and 13 populations had values under 7.0 g 100 seeds, including the population 487 that displayed a low value of 5.3 g. Some of the populations displayed high values for seed weight, seed length and pod length, such as 437, 513 and 517. The populations 399, 421 and 437 had values of seed weight over 10 g 100 seeds and 6.0 or more seeds per pod. These results agree with those by Galván et al. (2006) that reported 100 seed weight values from 7.0 to 14.0 g 100 seeds. In this trait the maximum value is quite far of the minimum value of 28.9 g 100 seeds in the study of primitive landraces by De Ron et al. (2004) but Singh et al. (1995) reported mean values of 14.7 and 14.8 g 100 seeds in lines derived from crosses wild x cultivated beans. According to this, the seed dimensions and the seed weight are relevant when considering the evolution of the wild populations and their convergence with the sympatric domesticated landraces.

Regarding the pod traits, is notable that the shape is in average round, with a mean value of the K index of 0.92. Some populations displayed long pods, for instance 437 (95.5 mm) and 527 (90.4 mm). Nine populations displayed values greater than 85.0 mm while 22 of them were smaller than 75.0 mm. The number of seeds per pod averaged 5.7, and a CV with a value of 11.1% that indicated variation in this trait. Seven populations had more than 6.5

seeds per pod while eight ones had less than 5.0. The range of variation of the pod length was 66.0-95.5 mm in agreement with the results by Galván et al. (2006) that displayed a range of variation 57.4-89.4 mm. When comparing with primitive domesticated landraces from the NOA, De Ron et al. (2004) reported a wide range of variation (86.3-147.8 mm) whose minimum value overlap the maximum value of the wild populations studied.

According to these results, six populations must be pointed out due to their relatively high scores in some characters such as 100 seeds weight, seed length and pod length when compared with the rest of the populations studied. These characters are key traits in order to assess about the possible convergence with sympatric domesticated beans (landraces or commercial varieties) indicated by a trend to gigantism of the six populations within all the wild populations studied. These six populations, namely 433 (from Higuierillas), 437 (Higuierillas), 471 (Cuesta de Clavillo), 509 (Los Toldos), 513 (Los Toldos) and 517 (Los Toldos) are reflected in the table 3 (A) as candidates for special attention for their *in situ* conservation in order to preserve the integrity of the novel variation generated. It is notable that none of them were sampled in protected areas and that there is not a trend among them regarding geographical situation and rainfall.

Based also in those key traits, 100 seeds weight, seed length and pod length, five populations must be highlighted, namely 480 (Cuesta de Clavillo), 495 (National Park El Rey), 496 (National Park El Rey), 525 (Los Toldos) and 533 (Los Toldos) and are displayed in the table 3 (B). These populations are very small seeded with short seed or pod when compared with the rest of the populations, this phenotype representing clearly the wild status, thus these populations must be preserved as them in their current status. It is notable that 495 and 496 were sampled in a protected area, but that there is not a trend among them regarding geographical situation and rainfall.

The dendrogram from the cluster analysis (figure 2), according to the dissimilarity coefficient based on the Euclidean distance, allowed to order the 68 populations studied in 12 groups (table 4). Group 1 includes only population 513, which, by its characteristics, could be the result of the crossing with domesticated germplasm, like the populations 509 from group 2, and 437, 471 and 517 from group 4. Group 5 comprises population 480, which should be protected *in situ* for presenting a clear wild phenotype, like population 525 from group 8. Group 10, with five populations, incorporate 433, also a possible product of convergence with cultivated sympatric germplasm. Group 11 is the most numerous, with 25 populations, among which is 495 that has a clear wild phenotype, and group 12 includes 16 populations, with 496 and 533, included among those that should be preserved *in situ* for its wild status.

The cluster analysis did not detect a geographical trend when ordering the populations. The 11 populations from Quebrada de Escoipe (Salta) are distributed in groups 7, 11 and 12; the 12 populations from Cuesta de Clavillo (Tucumán and Catamarca) are located in the groups 3, 4, 5, 6, 9 and 12, including population 480 proposed for *in situ* conservation. Seven populations originated in Higuierillas (Salta) are distributed in the groups 4, 10, 11 and 12, including 433 and 437, product of crossing with cultivated sympatric germplasm. The eight populations from Provincial Park Potrero de Yala (Jujuy) are distributed in groups 6, 11 and 12, while the 12 populations from National Park El Rey (Salta) are located in the groups 3, 11 and 12, being 495 and 496 populations that merit conservation *in situ*. From Hualinchay (Tucumán) five populations are distributed in the groups 2, 10, 11 and 12. Finally, 13 populations from Los Toldos (Salta), are located in the groups 1, 2, 4, 8, 10, 11 and 12, and population 533 is relevant for *in situ* preservation because its wild characteristics.

There is no clear distribution of the phenotypic diversity in the studied populations according to the results of the cluster analysis. In the present research this diversity is distributed among all the groups that arise from the analysis of groups. The *in situ* conservation of wild populations should be related to their diversity (Singh et al. 1995), although some of them, due to their special phenotypic characteristics deserve more attention, as already mentioned.

As a conclusion, we evaluated the presence and phenotypic diversity of common bean wild populations from the NOA both in protected and unprotected areas, finding a moderate variation among them. Wild populations candidates to be preserved in protected areas are those both with introgression from domesticated nearby either primitive or commercial types, because it creates a new important variation, but it is also true that in this way will lose the genetically unique wild diversity so it is important to look for locations far from domesticated varieties to preserve the original genetic heritage by *in situ* conservation. The risks to wild populations are the advance of the agricultural frontier, the climate change, the wild and domestic livestock that find palatable their leaves and grains, the advance of civilization (such as highways, roads and housing developments) and clearing the bench, because the wild bean is very heliophilous and abounds on the sides of roads and environments modified by human activities.

Two types of populations can be highlighted: i) the candidates for special attention for their *in situ* conservation in order to preserve the novel variation generated by convergence with cultivated sympatric germplasm and ii) those whose phenotype represent clearly the wild status and should be preserved *in situ* as them in their current status. In both cases is necessary to keep a sample of these population for *ex situ* conservation in order to preserve the genetic constitution of the wild and the intermediate populations in the moment of its identification, because they will continue evolving and changing the genetic structure in time.

Further studies according to the research by Bitocchi et al. (2012; 2013) and Rodriguez et al. (2016) about the organization of the genetic variation of the common bean in its centres of domestication should be applied to the Andean pool and will be adequate to go further on the knowledge of the genetic structure of the Andean wild bean populations to contribute to their conservation *in situ* supporting the conclusions of the present research.

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504 Table 1. Origin of the 68 wild bean populations studied.
505
506 Table 2. Mean, range of variation, standard deviation (SD) and coefficient of variation (CV)
507 of the quantitative traits in the 68 wild bean populations studied.
508
509 Table 3. Wild bean populations candidates to be supported for their *in situ* conservation: A)
510 phenotype suggesting tentative convergence with sympatric cultivated landraces, B)
511 phenotype representing clearly the wild status.
512
513 Table 4. Clustering by the UPGMA method of the 68 wild bean populations studied and their
514 average phenotypic characteristics.
515
516 Figure 1. Sampling area of the 68 wild bean populations from the NOA included in the study.
517
518 Figure 2. Dendrogram of the clustering of the 68 wild bean populations studied using the
519 UPGMA method.