



Review

Diversity maintenance and use of *Vicia faba* L. genetic resources

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ABSTRACT

The faba bean (*Vicia faba* L.) is an ancient crop that is represented in collections by cultivated forms only. Botanic and molecular data suggest that the wild ancestor of this species has not yet been discovered or has become extinct. This fact makes *ex situ* collections more crucial for the present and future breeding activities of this crop, especially when the modernization of agriculture reduces genetic diversity.

At the world level, more than 38,000 accession entries are included in at least 37 listed collections. The partial allogamous status of this crop makes maintenance activity of genotypes more expensive and difficult. In addition to the requirement of fixed genotypes to support new association genetics strategies, there is a need for more research on pollinators and maintenance of genetic diversity within populations.

A large genetic variability has already been identified in *V. faba* in terms of floral biology, seed size and composition, and also tolerance to several biotic and abiotic stresses. More knowledge is needed on the interactions of *V. faba* with parasitic and pollinator insects, on traits related to environmental adaptation and impacts, on nitrogen fixation in interaction with soil *Rhizobia* and on bioenergy potential, which strengthens the demand for new and large phenotyping actions. Diversity analysis through genotyping is just beginning. The use of amplified fragment length polymorphism (AFLP) or simple sequence repeat (SSR) markers has allowed genetic resources to be distinguished according to their geographic origin and the structuring of collections. Conservation of gene sequences among legume species and the rapid discovery of genes (particularly in the model species *Medicago truncatula* and *Lotus japonicus*), together with robotic developments in molecular biology, offer new possibilities for the analysis of sequence diversity for *V. faba* genes and to evaluate their impact on phenotypic traits. Combined genotyping and phenotyping projects must continue on *V. faba* so that core collections can be defined; these will help in the discovery of genes and alleles of interest for breeders.

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1. Introduction

Faba bean (*Vicia faba* L.) – sometimes referred to as broad bean, horse bean or field bean – is a major food and feed legume because of the high nutritional value of its seeds, which are rich in protein and starch. Seeds are consumed dry, fresh, frozen or canned. The 2005 world production of faba beans was 4.9 Mt from 2.8 Mha (FAOSTAT, 2005), which is small compared with soybean and pea world production (220 Mt and 12 Mt respectively) (FAOSTAT, 2005). The main faba bean producers are China (2 Mt), Europe (1 Mt—principally U.K., France, Spain, Portugal and Greece), Ethiopia (0.4 Mt), Egypt (0.4 Mt) and Australia (0.2 Mt). The feed market for dry seeds has mostly been developed in Europe (0.7 Mt consumed by pigs and poultry); in addition, straw or silage is sometimes used to feed ruminant animals. *V. faba* represents a crucial source of protein for foods, especially for Mediterranean countries and China. The geographic distribution and objectives of the breeding programs developed for this species therefore reflect where consumption is highest. In relation to the size of the market and in comparison with soybean, the faba bean selection programs are few and small. They partly rely on genebanks for providing genitors and alleles of interest. The role of the *ex situ* and on-farm collections is even stronger for this crop due to the absence of a natural reservoir of wild accessions and of the modernization of agriculture, which progressively phases out numerous landraces.

2. Origin and evolution

The faba bean is an ancient crop. Plant traces of this species have been associated with early crop domestication in archaeological deposits of the Stone, Bronze and Iron Ages in the Near East and Mediterranean basin: in Spain, Italy, France, Switzerland and Germany. The name *faba* originates from one of the forms of the Greek verb φάγέω – “to eat” – which highlights its use for food and feed by the ancient Greeks and Romans (Muratova, 1931; Hopf, 1973).

Despite numerous studies, little is known of the origin and domestication of faba bean (Maxted et al., 1991). Cubero (1973, 1974) postulated the Near East as its center of origin, with four different routes radiating from this center: (1) to Europe; (2) along the north African coast to Spain; (3) along the Nile to Ethiopia; (4) from Mesopotamia to India. Secondary centers of diversity are postulated to have occurred in Afghanistan and Ethiopia. However, Ladizinsky (1975) reported the origin to be in central Asia. According to Muratova (1931) and Maxted (1995) the center of origin for the genus *Vicia* is southeastern Europe and southwestern Asia.

Trait analyses have distinguished two groups: the small-seeded forms in southwestern Asia, including India, Afghanistan and adjoining regions of Bukhara and Kashmir; and large-seeded forms in the West. The Eastern group is very ancient, and can be traced back to the Neolithic culture; this group has the greatest number of endemic forms and the greatest diversity of characteristics, having many specific traits that are lacking in other groups (few pairs and many pairs of leaflets, their glaucous and grey-green colour, presence of tender and of coarse valves of the pod, wide range of variation of the maturity period, size, colour and shape of seeds, dimensions of leaflets, height and branching of stem, etc.), and they

are found over a large area (from Spain to the Himalayas) (Muratova, 1931). Until recently, this group was considered to originate from the 7th Millennium BC, as small faba seed remains have been found in an archaeological excavation in Israel, dated 6800–6500 BC (Kislev, 1985; Garfinkel, 1987). However, recent archaeological findings at Tell el-Kerkh, in north-west Syria, indicate a date of origin for faba bean during the late 10th Millennium BC (Tanno and Willcox, 2006). All these data point to southwestern Asia as the principle center of *V. faba* origin. The Mediterranean region, with the concentration of large-seeded forms, is considered to be a secondary center (Muratova, 1931). Numerous archaeological data testify that this group has a much younger age. Remains of *V. faba* in archaeological excavations in the Mediterranean basin and central Europe are dated to the 2nd to 3rd Millennia BC (Bond, 1976; Cubero, 1973; Witcombe, 1982). Broad bean (*major* types, more than 1 g per seed) is thought to have originated only after 500 AD (Hanelt, 1972). The earliest archaeological finds of *major* types come from Iraq and are dated at around 1000 AD (Schultze-Motel, 1972).

According to Muratova (1931), *V. faba* spread from the principle center to Ethiopia, and from the Mediterranean region to Europe to form a third center of importance. The migration of faba beans towards South America, especially the Andean Region, probably occurred in the 15th century, helped by Spanish and Portuguese ship travelers. This resulted in Peruvian and Bolivian landraces displaying a large variability e.g. in seed size, color and shape. In recent history, Bond and Crofton (1999) described the development of winter faba beans in the 19th century in Europe; these were bred from Russian and French small-seeded winter hardy populations.

The timing of the introduction of faba bean to China is uncertain, but there are several historical documents that recorded the origin and usage of faba bean in China from 300 AD. According to Zheng et al. (1997), faba bean (*V. faba* var. *major*) was first introduced to the northern part of China from the Middle East 2100 years ago through the Silk Road. However, a faba bean seed image on ancient pottery was found in a historical site in the Guanghe county of Gansu province in northern China (spring sowing area) in 1973, which was dated to 4000–5000 years ago (Ye et al., 2003). Faba bean grain fossils indicated that faba bean has been grown in southern China (winter sowing area) for more than 4000–5000 years (Ye et al., 2003). China is likely to be another secondary center of diversity for faba bean genetic resources, as well as having been reproductively isolated from the European and west Asian gene pools, especially the Chinese winter gene pool (Zong et al., 2009a).

As no wild faba bean has ever been found and because *V. faba* does not cross with other *Vicia* species, the wild ancestor of *V. faba* remains unknown (Muratova, 1931; Hanelt et al., 1972). This is an important issue as, consequently, we do not know how much diversity has been lost. The closest wild relative of *V. faba* is considered to be *V. pliniana* (Trabut) Murat. from Algeria (Muratova, 1931). Differences from *V. faba* in morphological characters – such as a broad arillus, the anatomical structure of the seed coat and its weak swelling – allowed Muratova to classify it as an independent species, *V. pliniana*. Pods of this wild form which has slightly different morphology from that of *V. faba* beans, were used for cooking (Trabut, 1911).

Another presumed ancestor is *V. faba paucijuga*, which was found by the traveler Slagintwein in Tybet and Pendjeb (Alefeld, 1866). *V. faba paucijuga* has a short stem, a small number of leaflets per leaf and very small seeds (Cubero and Suso, 1981). Hopf (1973) proposed that *V. narbonensis* L. is a probable wild ancestor of *V. faba*. These two species have many morphological similarities and coincide in their distribution. However, Ladizinsky (1975) and Birch et al. (1985) argued against considering *V. narbonensis* and other wild species as immediate ancestors of the cultivated *V. faba*. Although *V. narbonensis*, *V. johannis* and *V. bithynica* all cross well with each other, many attempts to cross *V. faba* with any of its relatives have failed (Cubero, 1982; Bond et al., 1985; Hanelt and Mettin, 1989). In attempted hybrids with *V. narbonensis* as female, the ovules stopped growing 9 days after pollination, whereas in the reciprocal cross they stopped growing after 15 days (Raupakias, 1986). Hybrid tissues from crosses with *V. melanops* and *V. lutea* developed further than those from crosses with *V. johannis*, but all embryos aborted (Ramsay and Pickersgill, 1986).

All close *V. faba* relatives are diploids with 14 chromosomes, whereas *V. faba* is diploid with only 12 chromosomes. The chromosome morphology of *V. faba* differs from the other species of the genus, which are mainly homogenous (Perrino and Pignone, 1981). By studying nuclear DNA amounts and the chromosome number of 56 *Vicia* species, Raina and Rees (1983) have shown that *V. faba* has a high content of DNA, and the presence of a large metacentric pair of chromosomes, which are twice the size of the remaining five pairs of acrocentrics. This large chromosome is probably derived from an ancestral fusion of two acrocentrics (Fuchs et al., 1998). The size of the *V. faba* genome (1C = 13.3 pg) is very different from that of *V. sativa* (1C = 2.3 pg), *V. narbonensis* (1C = 8 pg) (Raina and Rees, 1983; Pearce et al., 1996) and the model species for legume genomics, *Medicago truncatula* (1C = 0.48 pg). Modern classifications of the genus *Vicia* put *V. faba* into the species classification *faba* (Ball, 1968; Kupicha, 1976; Maxted et al., 1991; Maxted, 1993).

Molecular investigations have indicated the independence of *V. faba* and its large genetic difference from the *V. narbonensis* complex (van de Ven et al., 1993, 1996; Przybylska and Zimniak-Przybylska, 1997; Raina and Ogihara, 1994; Jaaska, 1997; Sanz et al., 2007). Restriction-fragment length polymorphism data has divided the *Vicia* gene pool into the following species – *narbonensis*, *peregrinae* and *faba* – which is in good agreement with the classification by Maxted et al. (1991). However, it has also been suggested that *V. faba* is more closely aligned to species from the genus *Hypechusa* and the genus *Peregrinae* than to those in the *V. narbonensis* complex (van de Ven et al., 1993, 1996). Phylogenetic relationships between *V. faba* and related species inferred from chloroplast *trnL* sequences have also shown that *V. faba* appears to be more distant from the *narbonensis* species than from the *hypechusa* and *peregrinae* species. All these data testify to a wide genetical distance between *V. faba* and other *Vicia* species, and support placing *V. faba* in the monospecific species *faba* (Fennell et al., 1998).

3. Existing *ex situ* collections of *V. faba* in the world

To reduce and slow down erosion of genetic resources of *V. faba*, scientists and breeders have developed *ex situ* genebanks, during the 20th century. This has resulted in several valuable collections, which are alive and continue to be maintained. Our present world inventory (Table 1) identified 37 collections, with approximately 38,000 accessions being publicly available.

The holdings of *V. faba* germplasm were estimated at 17% of total grain legume accessions kept by genebanks at the world level (Suso et al., 2005). Along with the European collections, which

Table 1
Vicia faba ex situ collections worldwide in 2008.

Country	Institute/city	No. of accessions
Europe		
Austria	Gene BFL/Vienna	110
	AAHFS/Linz	86
Azerbaijan	GRI-ANAS/Baku	17
	RICH/Baku	10
Bulgaria	IIPGR/Sadovo	692
Cyprus	ARI/Nicosia	100
France	INRA/Dijon	1900
Germany	Genebank IPK/Gatersleben	1920
Greece	Genebank Tessaloniki/Thermi	150
	Agric. Univ./Athens	55
Hungary	Inst Agrobot./Tapioszele	341
Israel	Genebank/Dagan	343
Italy	Genebank/Bari	1876
The Netherlands	DLO/Wageningen	726
Poland	PBAI/Radzikow	856
	IOPG-PAS/Poznan	1258
Portugal	INRB-IP/Oeiras	788
Russia	VIR/St Petersburg	1881
Spain	CNR/Madrid	1622
	Germplasm/Zaragoza	43
Slovakia	SCPV-RIPP/Piestany	60
Slovenia	AIS/Ljubljana	41
Sweden	Nordic Gene Bank/Alnarp	72
The Czech Republic	AGRITEC/Sumperk	392
	RICP/Prague	46
Turkey	AARI/Izmir	373
United Kingdom	JIC/Norwich	168
	NIAB/Cambridge	180
Ukraine	YIPB/Kharkof	114
Total Europe	30 collections	18,076
Syria	ICARDA/Aleppo	9000
China	CAAS/Beijing	5200
Australia	DPI/Victoria	2445
Morocco	INRA/Rabat	1715
Ethiopia	PGRC/Addis Ababa	1118
USA	USDA/Pullman	575
Canada	PGRC/Saskatchewan	231
Other: Afghanistan, Egypt, India, Iran, Iraq, Peru, Pakistan	Unknown	Unknown
Total world	37 known collections	38,360 known accessions

consist of 50% of the faba bean world accessions, the other large collections are at the International Center for Agricultural Research in the Dry Areas (ICARDA) Syria, CAAS China, DPI Australia and INRA Morocco (Table 1). Most accessions of European collections are listed in a database on the ECPGR website, together with their passport data (Duc et al., 2001, http://www.ecpgr.cgiar.org/databases/Crops/vicia_faba.htm). These collections mostly contain cultivars and farmer's populations. A total of 30% have cultivar names, 17% are of unknown geographic origin and 52% are of European origin. Some websites provide phenotypic data.¹

¹ <http://www2.dpi.qld.gov.au/extra/asp/auspgris/>, <http://sgrp.cgiar.org/InTrust-Collections/SINGER.htm>, <http://vir.nw.ru/data/dbf.htm>, http://www.ars-grin.gov/npgs/acc/acc_queries.html, http://icgr.caas.net.cn/cgris_english.html, <http://193.50.15.18/legumbase/>.

At the world level, 50% of curators described the maintenance of *V. faba* collections in open pollination, which is a concern for the conservation of landrace identity in such a partially allogamous crop (Suso et al., 2005). Over total accessions, the mean estimated delay between two successive renewals is 12.7 years, with a wide range of variation of 3–35 years. This delay is related to the conditions of seed conservation and their ability to maintain germination capacity. Only a few curators have developed a long-term storage method.

Recently various curators have prioritized participation in the development of core collections and further assembly into a joint composite collection. This action has been initiated through the 2007 Generation Challenge Program of CGIAR building a composite collection of 1000 accessions from world origins which is presently under genotypic characterisation with microsatellite markers (Sadiki et al., 2006).

4. Methodologies of germplasm management *ex situ* and on farm

Ex situ conservation entails the actual removal of genetic resources from their natural habitats and their maintenance in special facilities called genebanks. The genetic resources of *ex situ* collections are local landraces and mass selections from landraces, open pollinated populations and synthetics, and inbred lines and hybrids.

Three basic strategies of management of *ex situ* germplasm are used to conserve genetic diversity—as populations, inbred lines and as gene pools (Perrino et al., 1991). Each technique presents its own advantages and limitations. Populations are particularly appropriate for the proper maintenance of genetic variation that is initially present in accessions. Inbred lines allow conservation of identity in uniform lines; however, this technique significantly erodes any original variability within the accession (Nadal et al., 2003). Gene pools consist of accessions mixed in equal proportions and maintained as bulk focusing on a number of selected essential agronomic traits. Terzopoulos et al. (2003) proposed a five steps procedure for grouping accessions to handle faba bean germplasm. Maintenance in the form of a gene pool and/or inbred lines does not exclude the necessity of maintaining the original populations from which they were derived.

One of the most difficult aspects of regeneration in genebanks is the proper maintenance of genetic variation that is initially present in accessions. There are two risks during regeneration of accessions (1) loss of diversity which requires critical care about minimum population size (Vencovsky and Crossa, 1999) and about the environmental conditions; (2) loss of identity due to migration among accessions. The major constraint is avoiding contamination between accessions by foreign pollen. Based on the assumption for insect-pollinated outcrossing species, strategies other than distance could be used to ensure isolation (Ellstrand and Hoffman, 1990). Suso et al. (2006) demonstrated that planting particular barriers surrounding the plots (e.g. *Vicia narbonensis*, a male sterile line or a tetraploid genotype of *V. faba*) rather than using a non-cultivated area between plots seemed effective for preventing inter-plot gene flow, depending on the genotype and the location. A more recent investigation (Suso et al., 2008) has identified floral traits associated with pollen-mediated gene flow that could be used to determine outcrossing distances for low and high outcrossers, and hence decrease between-plot gene flow.

The main challenges and priorities for improving *ex situ* and *in situ* conservation have been assessed in an online consultation hosted by the European Cooperative Programme for Crop Genetic Resources (ECPGR) secretariat (reported on the webpage of the ECPGR Oil and Protein crops; [http://www.ecpgr.cgiar.org/Net-](http://www.ecpgr.cgiar.org/Net-works/Grain_legumes/grain_legumes.htm)

[works/Grain_legumes/grain_legumes.htm](http://www.ecpgr.cgiar.org/Net-works/Grain_legumes/grain_legumes.htm)) and in a meeting of experts assembled by the Global Diversity Trust in ICARDA. Pre-breeding strategies with bee pollination were encouraged to obtain mass-reservoir populations for enhanced adaptability and conservation of biodiversity. These could be implemented to target conservation of diversity from specific agro-ecological regions (e.g. with very low rainfall for drought tolerance, or from high altitudes for frost tolerance).

Populations can be used either as a conservation tool or as a breeding tool. Through a dynamic management of populations, 24 mass reservoir populations were built from elite breeding lines at INRA France, each reservoir being a bulk of genotypes homogeneous for a specific trait (i.e. disease resistance, earliness, height, tannin content). Some of these populations include a dominant nuclear male sterility in order to promote mating within each, and provide sources of parents for breeding programs (Duc et al., 1985). These mass-reservoir populations would also be available for on-farm conservation and participatory breeding.

Similarly trait targeted populations of landraces could contribute to the implementation of the International Treaty for Plant Genetic Resources for Food and Agriculture. On-farm conservation of diversity helps to directly address the diversity assessment to farmers' perception of geographic adaptation. This strategy can promote participatory breeding with on-farm enhancement of local varieties, or the production of prebreeding pools adapted to local agronomic practices. Linking the *in situ* and *ex situ* conservation strategies will create a network facilitating valuable cooperation with different individuals—curators, breeders and farmers. A research priority could address the biological mechanisms that are relevant to the co-evolutionary three-level interaction of crop/pollinator/farmer complexes that shape the genetic diversity and adaptability of landraces.

5. Diversity analysis through phenotyping

5.1. Trait variation

As an ancient domesticated crop adapted to a huge range of latitudes and altitudes, grown in the seasons of winter and spring, and having a diversity of food and feed uses, *V. faba* offers an enormous genetic variability for breeding purposes. Selection for adaptation over a wide range of agri-ecological environments has retained genes determining biotic and abiotic stress tolerance, efficiency of symbiotic nitrogen fixation, yield potential and seed composition.

The evaluation of *ex situ* germplasm collections of crop landraces (traditional farmers' varieties) is critical to the utilization of genetic resources for crop improvement (Maxted et al., 2000). Passport data describing the sites where landraces are collected, and species identification, provide basic data on accessions in germplasm collections. Much value is added to these collections when agronomic, biotic/abiotic stress, grain yield and quality data are available for individual accessions, enabling plant breeders to better target and exploit genetic resources in plant breeding programs (Redden et al., 2007).

Large investments in the discovery of genetic variability and also in breeding activity for traits of agronomic interest have been made for faba bean at the end of the 20th century in European countries and also at ICARDA Syria (Bond et al., 1985; Hebblethwaite, 1983; Duc, 1997; Ambrose et al., 2006; Link, 2006). Cytoplasmic and nuclear determinisms of male sterility, various flower architectures or colors, and various levels of autofertility and attractivity for pollinating insects, were described; this could help to manipulate the levels of outcrossing (Duc, 1997; Link et al., 1994; Link, 2006).

A wide diversity of earliness and length of flowering period, of stem architectures (internode length, branching, determinate growth, stiff stem) offer the possibility of adapting the crop to diverse agronomic practices (for example, winter/spring sowings, inter-cropping) and climatic zones. High levels of freezing tolerance have been found in French and German landraces (Arbaoui and Link, 2006; Arbaoui et al., 2008; Stoddard et al., this issue); this has been useful for the breeding of winter cultivars, reducing drought stress at flowering via earlier maturity, and increasing cultivation areas towards more continental zones. Drought-tolerant genotypes have also been described—this is a crucial requirement in Mediterranean areas that are facing significant climatic change. Variability for nitrogen-fixing activity has been revealed for some genotypes or some genotypes \times *Rhizobium* strain interactions (El-Sherbeeney et al., 1977; Duc et al., 1987).

Genitors for resistance or tolerance to major biotic stresses were reviewed by Duc (1997), Torres et al. (2006), Link (2006), Sillero et al. (this issue) and Pérez-de-Luque et al. (this issue). Resistance to major pathogen fungi were described (*Botrytis fabae*, *Ascochyta fabae*, *Uromyces viciae-fabae*, *Fusarium* sp., *Microsploaera pennicillata*, *Erysiphe polygoni*) and some of these were used in breeding programs. There are moderate levels of resistance to Bean Leaf Roll Virus and Bean Yellow Mosaic virus. Tolerance to broomrape (*Orobancha crenata* Forsk.) has been identified; this is valuable in breeding programs dedicated to the Mediterranean zone (Rubiales et al., 2006). *V. faba* can be infested by nematodes (*Ditylenchus dipsaci*), and a few genotypes were shown to be resistant (Caubel and Leclercq, 1989).

Of the major pests attacking the faba bean crop, some partial resistance *Aphis fabae* has been identified (Holt and Wratten, 1986) whereas no variability was described for *Sitona lineatus* or *Bruchus rafinamus*, although resistances to similar pests has been found in other legumes (Redden et al., 2005; Sharma et al., 2007; Stevenson et al., 2007).

According to genotype, single seed weight varies from 0.2 to 2.6 g and a single pod carries 2–10 ovules. Composition of the seed is also diverse for protein content, ranging from 25 to 37% of the seed dry matter with quantitative inheritance, whereas oligogenic determinations of zero tannin trait and low vicine and convicine contents in the seed were identified (Duc et al., 1999; Link et al., 2005).

ICARDA has an extensive faba bean collection exceeding 2470 landrace accessions (The System-wide Information Network for Genetic Resources (SINGER, 2007). Through selfing for up to five generations, 1–5 bean pure lines (BPLs) have been obtained from individual landraces. Although this process reduces within accession variance, these BPL accessions are homogenous and could be evaluated across uniform seed generations for biotic stresses and agronomic traits (Robertson and Holly, 1993). This characterization followed the standardized rating system of IBPGR faba bean descriptors (Anon., 1985) and highlighted a wide diversity. Rating systems for phenotypic traits may be growth-stage dependent; e.g. stem pigmentation at flowering time, leaf size on fully expanded leaves at the intermediate flowering nodes, lodging score; pod characteristics may also differ on green immature compared with mature pods (pod angle, shape, color and surface reflectance); therefore data must be footnoted with the associated growth stage. Repeated disease ratings are advisable during the growth cycle, both to characterize differences in disease duration, and to ensure that observations are made before interference from abiotic stresses or another disease (e.g. drought-induced leaf senescence, sclerotinia or aphid-transmitted viruses).

5.2. Regional variation in phenotypes

At ICARDA, 840 BPL accessions (derived from landraces from 41 countries) were evaluated using IBPGR descriptors in 1985–1986 (Robertson and El-Sherbeeney, 1991). Wide phenotypic variation was expressed for stem pigmentation, leaflet size and shape, lodging, flower colors on the wing and the standard petal, pod angle/shape/surface/color and distribution, and seed color/testa pattern/shape and hilum color. Different patterns of trait combinations were found for eight BPL regional origins; low stem pigmentation in the Nile Valley and Ethiopia, a high frequency of small leaves in North Europe versus a low frequency in the Nile valley, severe lodging in Ethiopia versus the least in North Europe, erect pods in the Indian subcontinent but pendant in South Europe, and dark pods in Ethiopia (Robertson and El-Sherbeeney, 1991).

The above ICARDA study did not include germplasm from China. Li-juan et al. (1993) analyzed agronomic and yield traits for 1500 germplasm from different provinces in China, and a cluster analysis showed two main groups corresponding to the separation of provinces into winter and spring types of faba bean. Seeds per pod ranged from 1.7 to 2.9 with >2 from Zhejiang, Gansu, Fujian, Sha'anxi, Guizhou and Shanghai provinces. All pod lengths were <10 cm, and 24% exceeded 7.6 cm, mainly from Zhejiang, Fujian, Gansu, Qinghai and Shanghai provinces. Fresh seed color varied as 46% white–yellow or white, 27% light green, 12% green, 4% dark green, 5% brown/red and others 6%.

Recently Terzopoulos et al. (2008) and Keneni et al. (2005) described large diversity for morpho-agronomic traits in Greek and Ethiopian landraces.

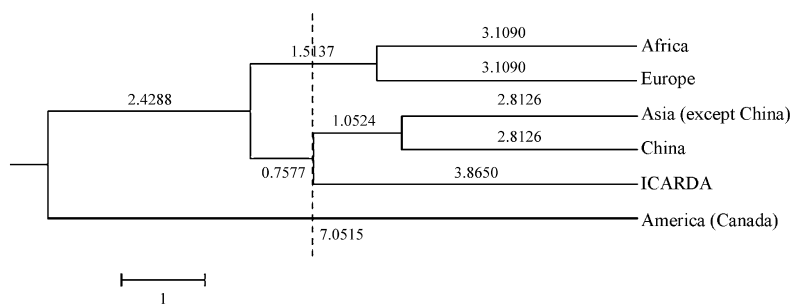
Thus diverse morphological trait combinations were associated with diverse regional origins, and it was also the case for some abiotic or biotic stress tolerance traits.

Expressions of salinity tolerance were found in some accessions from Zhejiang, Fujian, Gansu and Sha'anxi provinces, which have extensive alkali–saline soils (Li-juan et al., 1993). In the screening for salinity tolerance of 504 worldwide sources of landraces and breeding lines in Australia (Redden et al., 2006, unpublished), only 16 lines were tolerant from China, Greece, Egypt and Australia (breeding lines).

Li-juan et al. (1993) also screened 500 accessions for resistance to blight (*A. fabae*) and to chocolate spot (*B. fabae*). Only 6% of accessions, originating from the middle–lower Yangtze river basin, showed moderate resistance to both diseases. Accessions from China were rated for *Ascochyta* blight in 2006 at the University of Adelaide (ACIAR, 2007). The accessions were heterogenous, with selections for resistance equivalent to the Ascot check variety made from accessions from Guangxi, Jiangsu and Gansu provinces (Kimber et al., 2006). In Europe a major source of *Ascochyta* resistance is the line '29H' (Sillero et al., 2001). Thus diverse sources of genetic diversity for *Ascochyta* resistance are available in faba bean, both within accessions and among diverse agro-ecological sources which may be combined to contribute to more durable genetic resistance.

5.3. Documentation

In partnership with ICARDA, the ATFCC has helped to develop a search/query online interrogation database for descriptor traits of faba bean. This is an adaptation of the International Crop Information System database (Portugal et al., 2007). The 'central' for this International Faba Bean Information System (IFIS) is at ICARDA, with ATFCC as a secondary node. The database enables multiple queries on traits selected by the client (usually a plant breeder, student or academic), for selection of germplasm that can be requested online. The IFIS also searches databases of different



¹ Number of accessions per group; Africa 12, Europe 43, Asia (except China) 24, China 39, ICARDA 41, Canada 6.

Fig. 1. Dendrogram of spring faba bean germplasm (number of accessions per group; Africa 12, Europe 43, Asia (except China) 24, China 39, ICARDA 41 and Canada 6) from diverse origins based on characterization with 12 AFLP markers.

collections, and can be refined to target geographic origins identified as ‘hot spots’ for abiotic/biotic stress incidences.

The extent to which germplasm collections have been characterized and evaluated is far from complete in many instances. Alternative uses of faba bean are becoming increasingly important; the Report of the ECPGR Oil and Protein Crops Network Coordinating Committee Meeting (Ambrose et al., 2006) supported the need of evaluating new traits such as those related to climate change tolerance, mating system and the relationship between plant and pollinator, and to new uses such as biorefineries for non-food uses.

6. Diversity analysis through genotyping

At the cytoplasmic level, no variability could be detected on chloroplastic DNA among *V. faba* genotypes that appeared to be highly conserved during domestication, with a narrow variability at the origin (Shiran and Mashayek, 2004). In contrast, mitochondrial DNA displays variability in sequence and plasmid size; in some cases, associated with diversity in nuclear genomes (Flamand et al., 1992, 1993).

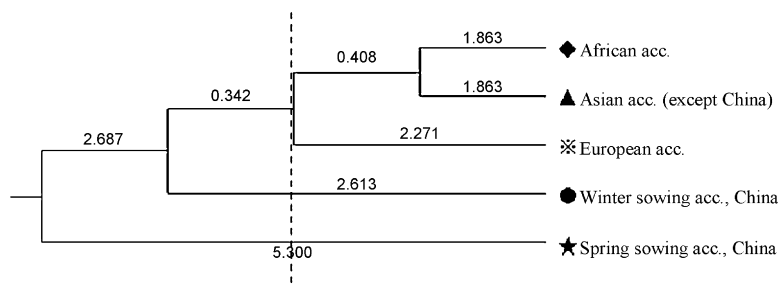
The nuclear genome of *V. faba* is enormous, with more than 13,000 Mbp in comparison to the legume model species *M. truncatula*, which is estimated to be 470 Mbp (Young et al., 2003). This large size may be largely explained by a high number of retrotransposon copies (Pearce et al., 1996). These retrotransposons, microsatellites and genes are the basis of the sequence variability that can be explored in genomes. Random amplified polymorphic DNA (RAPD) markers (Link et al., 1995), amplified-fragment length polymorphism (AFLP) markers (Zeid et al., 2003)

and inter-simple sequence repeats (ISSR) markers (Terzopoulos and Bebeli, 2008) were successfully used to characterize the genetic variability among faba bean genotypes. Long Terminal Repeat sequence retrotransposon base markers or sequence-specific amplification polymorphism markers (Sanz et al., 2007) could distinguish between geographic origins of *V. faba* genotypes, but not between *paucijuga*, *minor*, *equina* or *major* types. Molecular markers (Avila et al., 2004; Gutierrez et al., 2006; Torres et al., 2006, this issue) were successfully developed to support marker assisted selection strategies for biotic stress tolerance or seed composition traits of *V. faba* within breeding populations.

The genetic diversity of faba bean landraces from different provinces in China was compared with germplasm from the rest of the world, using AFLP analyses of 459 accessions. Winter (Zong et al., 2009a) and spring (Zong et al., 2009b) germplasm were separately analyzed using 12 primer pairs.

A dendrogram of the data for spring faba bean showed the most diverse set of accessions to be from Canada (Zong et al., 2009b). These derive from a recent small seeded breeding program for feed in Western Canada (Fig. 1) and show both narrow diversity and differential adaptation from other regions. The second most distinct set was from ICARDA (Fig. 1), these being selections made at ICARDA from breeding programs initiated in China. Other landraces were in four gene pools—a separation of Asian/Chinese from European/African accessions, and further separation between China and Asia, and between Africa and Europe (Fig. 1).

The winter faba bean from China was found to be distinct from the winter gene pools in the rest of the world and from the spring types in China (Fig. 2, Zong et al., 2009b). African and Asian faba



¹ Number of accessions per group: Africa 14, Asia (except China) 16, Europe 9, China winter grown 201, China spring grown 3.

Fig. 2. Dendrogram of different ecological regions based on 12 AFLP marker showing genetic relationships among groups (number of accessions per group: Africa 14, Asia (except China) 16, Europe 9, China winter grown 201 and China spring grown 3) of winter and three spring types.

bean landraces showed some affinity in the dendrogram clustering, and these were broadly associated with European sources (Fig. 2). Within the winter gene pool in China, accessions from Yunnan were the most distinct followed by those from Sha'anxi (Bao et al., 2006).

Another type of neutral markers that are helpful for characterizing genetic variability are genomic microsatellites (SSRs). This strategy has been launched within the Generation Challenge Program (B. Furman and M. Baum, Personal Communication; Sadiki et al., 2006). A global composite collection of 1000 accessions of faba bean was developed in collaboration between ICARDA-Aleppo-Syria, INRA-Dijon-France and CSIC-Cordoba-Spain. A preliminary test made with 2 primers designed for genomic SSR motifs and applied to 750 genotypes, has revealed 127 alleles which indicates a high level of polymorphism between faba bean accessions.

Gene sequence homologies and syntenies between *M. truncatula* and *V. faba* have not been documented up to now, but can be predicted from comparisons already made between papilionoidae species (Choi et al., 2004; Young et al., 2003). In the near future, on the basis of these similarities, the knowledge acquired about genomic data of *M. truncatula* will help to discover the allelic diversity of many *V. faba* genes, thereby supporting association genetics strategies. For this purpose, a molecular methodology called 'Ecotilling'² has recently been proposed to reveal a diversity of sequence for a given gene, among numerous genetic resources (Comai et al., 2004).

Because of the technical difficulties of achieving interspecific crosses or of producing transgenic lines with *V. faba*, only natural variability or induced by mutagenesis is available to breeders, but it is wide and still underexploited. Its analysis by genotyping and phenotyping will be of great benefit to breeders' work.

7. Conclusions

The conservation, maintenance, evaluation and utilization of faba bean genetic resources have particular challenges as *V. faba* may be insect cross-pollinated. Inbred lines are preferred for germplasm evaluation and for molecular characterization. Combined genotyping and phenotyping projects must amplify faba beans on fixed material, in order to define core collections and prompt the discovery of genitors and alleles of interest for breeders. Collaborations between curators and breeders at an international level will certainly help to concentrate on joint composite collections and promote multi-trait evaluations.

However, the partially allogamous reproduction of *V. faba* can also be utilized to provide selected gene pools. Dynamic management of *ex situ* genetic resources supplements the static conservation of seed in cold storage and needs to be prompted. Pre-breeding strategies based on mass-reservoir populations with enhanced adaptability, show the added value of conserving biodiversity in suitable habitats. These mass-reservoir populations would also be available for on-farm conservation and participatory breeding, and would contribute to the implementation of the International Treaty for Plant Genetic Resources for Food and Agriculture.

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² Ecotilling: on natural genetic resources, the strategy of targeting induced local lesions in genomes.

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