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Maintenance, evaluation and use of faba bean germplasm collections: problems and prospects

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SUMMARY - After a short survey on the distribution and importance of faba bean (*Vicia faba* L.) in the world, theoretical and practical aspects for the maintenance of its germplasm collections are discussed. Main strategies for maintenance and utilization of the collections already existing in major centres are also discussed along with needs for studies in the field of resistance to biotic and abiotic stresses.

*RESUME - "Conservation, évaluation et utilisation des collections de germoplasme de fève : problématique et perspectives". Après une brève étude concernant la répartition et l'importance de la fève (*Vicia faba* L.) dans le monde, nous discutons des aspects théoriques et pratiques relatifs à la conservation des collections de germoplasme. Les principales stratégies pour le maintien et l'utilisation des collections déjà existantes dans les centres les plus importants sont également envisagées, ainsi que le besoin d'effectuer des recherches dans le domaine de la résistance à des conditions biotiques et abiotiques adverses.*

Introduction

Both the Centre of Origin of faba bean (*Vicia faba* L.) and its wild ancestor are still unknown. It is a crop of the Old World but any region could be designated as a centre of diversity (Cubero and Suso, 1981); therefore, germplasm from Mediterranean countries, the Near East, Afghanistan, India and China is equally important. Crosses with postulated relatives of *V. faba* and especially with the *V. narbonensis* group and other species of the section Faba have failed (Ladizinsky, 1975). Chemotaxonomic studies (Perrino *et al.*, 1986, 1989) have shown that *V. faba* is quite distinct from other species of the same section. Thus, at the present time the gene pool of *V. faba* is still restricted to itself.

Fortunately, the genetic variability of the species is quite large (Abdalla, 1976; De Pace, 1979; Filippetti, 1979; Porceddu *et al.*, 1979; Scarascia Mugnozza and De Pace, 1979), and though most researchers refer to four botanical varieties, namely: *V. faba major, V. faba equina, V. faba minor* and *V. faba paucijuga*, in practice a continuous variation for most seed, pod, plant, chemical and physiological traits has been observed.

The existence of a high genetic variation within the species, together with some other factors, may explain why the crop has spread throughout the world (Table 1). In fact, though faba bean is much more cultivated in Asia, Africa and Europe (the original home of the crop), the harvested area in South America is nearly two thirds (207000 ha) of the European one (321000 ha) and if the total area of the New World is considered, this is only slightly lower (290000 ha) than that of Europe. However, yield per hectare and total production in Central and North America are consistently lower than those obtained in Europe.

The harvested area in Oceania is very small (37000 ha) when compared with that of Asia (1769000 ha) and even with that of North and Central America (83000 ha), but in 6 years (from 1981 to 1987) it has increased more than three times (from 11000 to 37000 ha); in addition, the yield per hectare has tripled (from 533 to 1703 kg/ha), and it is second in the world, after Europe (2030 kg/ha); consequently, the total production in the same period has increased tenfold (from 6000 to 63000 t) and

Table 1. Area harvested, yield and production of faba beans, dry, in the world.

	Area harv. (000 ha)		Yield (t/ha)		Production (000 t)	
	1979-81	1987	1979-81	1987	1979-81	1987
Asia	2318	1769	1.171	1.395	2716	2466
Africa	739	851	1.233	1.298	912	1105
Europe	354	321	1.355	2.030	480	653
South America	200	207	0.458	0.536	92	111
N.C. America	63	83	1.242	0.989	79	82
Oceania	11	37	0.533	1.703	6	63
World	3685	3268	1.162	1.371	4285	4479

Source: FAO yearbook (1987)

is therefore very close to the total production of North and Central America (82000 t) where, on the contrary, the harvested area is much larger (83000 against 37000 ha).

Thus, although cultivation of the crop in America and Oceania is of a relatively recent origin, the breeding system of the species may allow further adaptation and new diversification of the species.

Table 1 also shows a consistent decline in cultivation of the crop in Asia, where a decrease of the harvested area (from 2318000 to 1769000 ha) has been accompanied by a decrease in total production (from 2716000 to 2466000 t). From a genetic resources point of view, this may mean that in Asia there is not much breeding activity, no much introduction of new varieties, and therefore local germplasm should still be available. This situation would suggest the need for further collection of germplasm in key areas of Asia.

In the Mediterranean region (Table 2), faba bean harvested area (765000 ha) and total production (1069000 t) are about 21-22% of the world value. In general, the common trend is towards a slight increase of the area, yield per hectare and total production, but this is mainly due to the contribution of France, Egypt and Morocco, while in other countries the tendency is towards a slight reduction of the harvested area with no appreciable changes in yield and production. However, the good results obtained in France, Egypt, Morocco and Oceania, suggest that faba bean germplasm can be further exploited for increasing yield, not only in other Mediterranean countries, but also in Asia, Ethiopia, other African countries, the New World and especially South America.

A contribution for the improvement of the crop can be given by making more use of the germplasm collections already assembled in gene banks (Table 3) or to be collected in some key areas of the Mediterranean region, Near East, Afghanistan, India, China, etc.

Table 2. Area harvested, yield and production of faba beans, dry, in the Mediterranean.

	Area harv. (000 ha)		Yield (t/ha)		Production (000 t)	
	1979-81	1987	1979-81	1987	1979-81	1987
Morocco	165	200	0.560	0.850	97	170
Italy	161	128	1.277	1.359	205	175
Egypt	103	120	2.134	2.692	219	323
Spain	79	49	0.972	1.020	78	50
Tunisia	69	48	0.682	0.729	47	35
Algeria	48	82	0.573	0.429	27	35
Portugal	36	27	0.586	0.735	21	20
Turkey	30	49	1.748	1.796	53	88
France	23	37	3.063	3.730	70	138
Syria	8	9	1.772	1.775	14	16
Libya	7	9	1.007	1.000	7	9
Greece	5	3	2.048	1.627	11	6
Cyprus	1	1	1.429	1.224	2	2
Yugoslavia	*	3	*	0.578	*	2
Palestine	*	*	0.200	0.500	*	*
Lebanon	*	*	1.500	1.238	*	*
Total	735	765	1.158	1.397	851	1069

*Missing data
Source: FAO yearbook (1987)

Table 3. Major collections of *Vicia faba*.

Country	Institute	No. of accessions
Syria	ICARDA, Aleppo	8305 *Vicia faba*
USSR	N.I. Vavilov, IAPI, Leningrad	2525 *Vicia faba*
Italy	IDG, CNR, Bari	1951 *Vicia faba*
China	CAAS, Beijing	1900 *Vicia faba*
FRG	IPP, Braunschweig	1840 *Vicia faba*
Spain	INIA, Cordoba	1256 *Vicia faba*
GDR	ZGK, Gatersleben	1140 *Vicia faba*
Ethiopia	PGRC, Addis Ababa	1018 *Vicia faba*
France	INRA, Dijon	1000 *Vicia faba*
Netherlands	SVP, Wageningen	700 *Vicia faba*
Czechoslovakia	PBRICL, Tumenice	500 *Vicia faba*
Morocco	INRA, Rabat	309 *Vicia faba*
India	Unknown	– *Vicia faba*
Iran	Unknown	– *Vicia faba*
Pakistan	Unknown	– *Vicia faba*
Afghanistan	Unknown	– *Vicia faba*
Iraq	Unknown	– *Vicia faba*

Maintenance and its scientific background

Once genetic variability has been collected and preserved, the main objective of gene banks is to avoid loss of genetic integrity of single accessions, or entries, or populations.

Regeneration of seed stocks is directly linked to the genetical characteristics of the species, its reproductive mechanism and effects of the environment on these features. Thus, some information on the breeding system, amount of out-crossing and inter-crossing, gene frequency and percentage of homozygotes in *V. faba* will be provided before proposing any solutions to the problems of maintenance and use of germplasm.

Breeding system

Genetic variation in faba bean is mainly due to the partially cross-pollinated habit of the crop. In fact, open-pollination varies widely from 15 to 46% (Porceddu *et al.*, 1980) and though higher values of 61% (Poulsen, 1975) and even 70% (Holden and Bond, 1960) have been reported, it is accepted that the most likely out-crossing values are in the range of 0 to 50% (Frusciante and Monti, 1980).

In general, a population of faba bean is composed by 1/3 of hybrid plants and 2/3 of inbred ones (Scarascia Mugnozza and De Pace, 1979). The hybrid plants are autofertile, whereas the inbreds (Drayner, 1959; Kambal *et al.*, 1976) are partly (1/2) autofertile and partly (1/2) autosterile. Autosterility may be due to two different mechanical barriers (Kambal *et al.*, 1976) which can be broken by insect pollination or repeated tripping. Thus, in general the identity of a population of faba bean is maintained only if inbreeding and outbreeding within the population reach an equilibrium.

Out-crossing and inter-crossing

Throughout this paper out-crossing will refer to open-pollination among plants of the same accession and inter-crossing to open-pollination among plants of different accessions. The result of inter-crossing is that, after a certain number of generations, two accessions lose their identity and become identical. The rate of inter-crossing depends on the rate of out-crossing and the degree of isolation between accessions. In practice, because of physical distance between plants belonging to different accessions, inter-crossing is always lower than out-crossing which, as already said, may range from 0 to 50%. Thus, in the worst case, inter-crossing can reach a maximum value of 50%.

Gene-frequency

Consequences of seed regenerations, such as changes in allele frequency and the determination of the number of generations required for an allele to be less present, or to be lost under environmental conditions different from those existing where the population evolved, are described by De Pace *et al.* (1982).

Considering a simple model (Witcombe, 1984), in which two accessions differ completely for a single locus so that their initial difference in gene frequency is 1, even in the extreme case of 50% inter-crossing, it takes six generations for the two accessions to become identical (Fig. 1) and three generations to become very similar (0.1). As already stressed, in faba bean gene flow is always less than 50%. Assuming an inter-crossing of 25%, which is more likely than 50%, it takes 12 or more generations for two accessions to become identical and more than 24 generations if the rate of inter-crossing is 10%. It is clear then if inter-crossing is reduced below 25%, or even better, below 10%, it takes many generations for two accessions to become similar and even more to become identical.

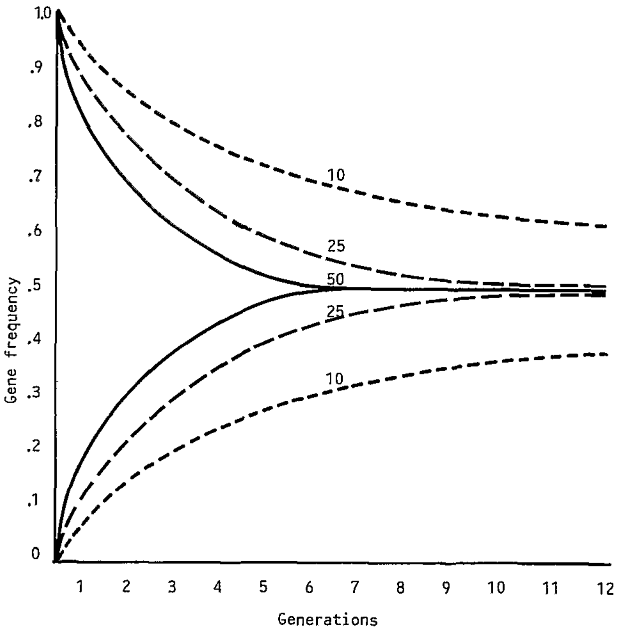


Fig. 1. The rate at which two accessions, initally differing for one gene become identical at 50, 25 and 10% of inter-crossing (from Witcombe, 1984).

Percentage of homozygotes

Assuming that a given accession differs from all the others and that it inter-crosses with other entries at rate of 10%, which is the most probable in many cases, the allele 'A' will be found in other accessions with a probability that is very low or almost non-existent after one generation (Fig. 2). Nevertheless, after six generations, the frequency of that allele at that locus is less than 0.6. After six generations the gene frequency goes down very slowly and it will need 21 generations to reach the frequency of 0.1, which means that in the presence of genetic drift it can be completely lost. The situation is even worse for recessive genes which can be seen or recognized only when they are in an homozygous state and only 1% of the genotypes of the original accession may be in this situation after 20 generations.

Both models (Fig. 1 and 2) show that when the rate of inter-crossing is as low or lower than 10%, the effects of inter-crossing are only very strong after many generations. This means that a certain degree of inter-crossing can be tolerated in germplasm collections without losing the identity of single accessions.

Main strategies for regeneration of germplasm collections

As a consequence of the breeding system, partial outcrossing, rate of inter-crossing, gene frequency, etc., three main ways of maintaining faba bean germplasm collections have been suggested (a) as populations, (b) inbred lines and (c) gene pools.

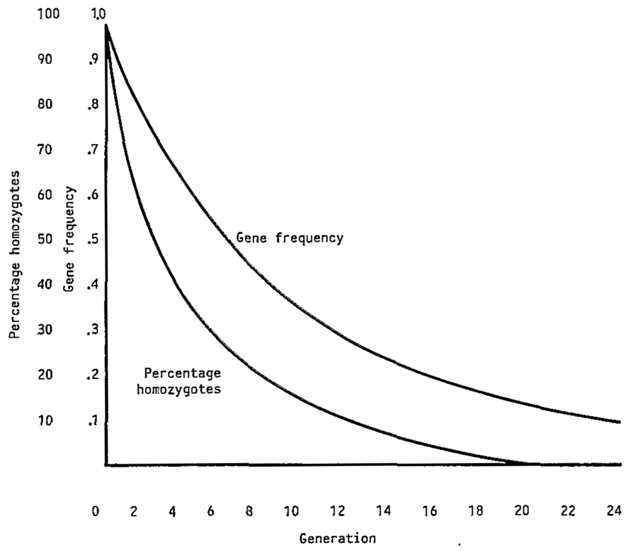


Fig. 2. The rate at which an accession loses a gene when all other accessions are different at one locus, at 10% of intercrossing (from Witcombe, 1984).

Populations

The rate at which different populations become identical can be reduced by reducing inter-crossing and the number of generations.

Reducing inter-crossing

Inter-crossing can be reduced considering different factors, such as distance between plots, the size of plots, plant density and pod position on the plant.

In general, when the distance between plots is around 10 m, inter-crossing is around 10%, if the border plants are discarded. An increase in the size of the plots can have a large effect in reducing the rate of inter-crossing (Table 4), whereas any further increase in distance between plots after a minimum of 11 m can only still be effective in reducing the rate of inter-crossing for plants growing in the centre of the plot.

When only small seed samples are available, small plots should be surrounded by crops like *Brassica napus*. In this way the insects passing from an accession of faba bean to the next one will very likely lose the faba bean pollen by visiting the oil seed rape flowers. Plants of triticale and other species may be suggested, but in this case they will act only as a physical barrier.

Plant density is another important factor. Experimental data (Porceddu *et al.*, 1980) indicate that if plant density increases from 20 to 80 plants/m^2 (Table 5), inter-crossing may increase respectively from about 15 to 31% at pod level and from about 9 to 16% at plant level. Inter-crossing can then be reduced by a factor of a half if plant density is reduced to 1/4 (from 80 to 20 plants/m^2).

Pod position along with plant density can also play an important role. Some experimental data (Porceddu *et al.*, 1980) show that if basal pods, in particular the first

Table 4. Inter-crossing in faba bean (adapted from Hawtin and Omar, 1980).

	Mean inter-crossing between plots (%)		
	Border	Centre	Whole
Plot size 16 m sq.	14.7	10.1	14.2
Plot size 28 m sq.	9.5	6.7	8.9
Average inter-plot distance 11.0 m	12.3	10.4	11.6
Average inter-plot distance 14.3 m	11.8	6.1	10.9

Table 5. Frequency of out-crossing events in faba bean. Plants grown at two localities and at different densities (adapted from Porceddu *et al.*, 1980).

Locality	Plants/m^2 (no.)	Mother plant pods with out-crossing offspring (%)	Plants from out-crossing (%)
Torre Lama	20	15	9
	40	26	13
	80	24	12
Scalera	20	18	8
	40	24	13
	80	31	16

5 fruit clusters, are discarded, inter-crossing is further and significantly reduced at any plant density, but especially at the lowest one, where inter-crossing of the apical pods is nearly half of the basal ones. In fact, for apical pods it ranges from 10 to 14% when pods with cross-fertilized seeds are considered (Table 6) or is even lower (7%) at the plant level (Table 7).

Reducing the number of generations

Another way to reduce inter-crossing is to reduce the number of generations (Fig. 3). From collecting or exchange of accessions seed samples are generally small and need at least one or two multiplications before enough seed is available to create a base collection for long term storage. In very few cases seed samples from collecting are large enough to allow a direct long term storage. There are also cases in which more than two multiplications are required before a seed sample enters into a base collection. Once the base collection at -20 °C has been established, the base (foundation) collection at 0 °C can be used to supply seed samples (active collections to the breeders), but this requires further multiplication of single accessions. In this way the base collection at -20 °C does not undergo further generations and the risk to lose genetic identity of the original collection is avoided. However, a certain number of generations cannot be completely eliminated, since this depends on the longevity of the seeds in the base collection, though fortunately faba bean seed is long lived.

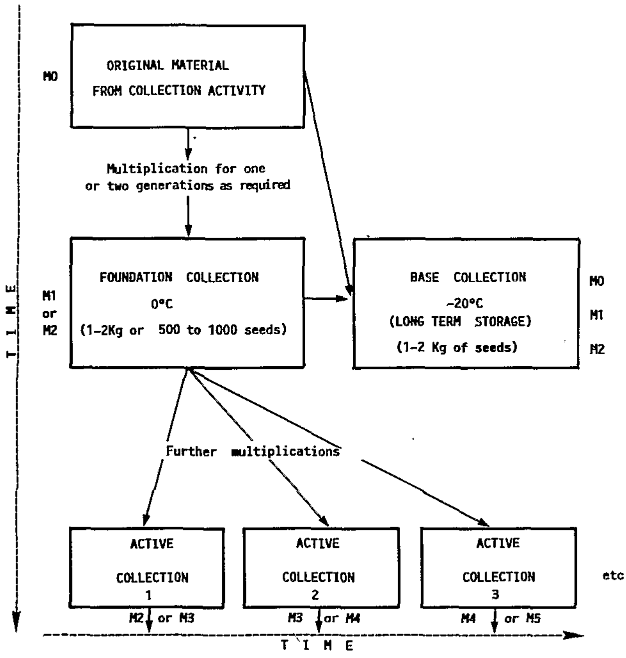


Fig. 3. Flow diagram for reducing the number of generations in *Vicia faba* germplasm maintained as open-pollinated populations (adapted from Witcombe, 1984).

Table 6. Frequency of out-crossing in the basal pods (1st - 5th clusters) as distinct from the others (adapted from Porceddu *et al.*, 1980).

Locality	Plants/m^2 (no.)	Mother plant pods with out-crossing offsprings (%)	
		1st-5th fruit clusters	Other fruit clusters
Torre Lama	20	21	10
	40	30	18
	80	26	18
Scalera	20	21	14
	40	26	21
	80	32	28

Table 7. Frequencies of allogamous offspring coming from the first five fruit clusters (starting from the bottom of the plants) and from the remaining ones of the mother plants (adapted from Porceddu *et al.*, 1980).

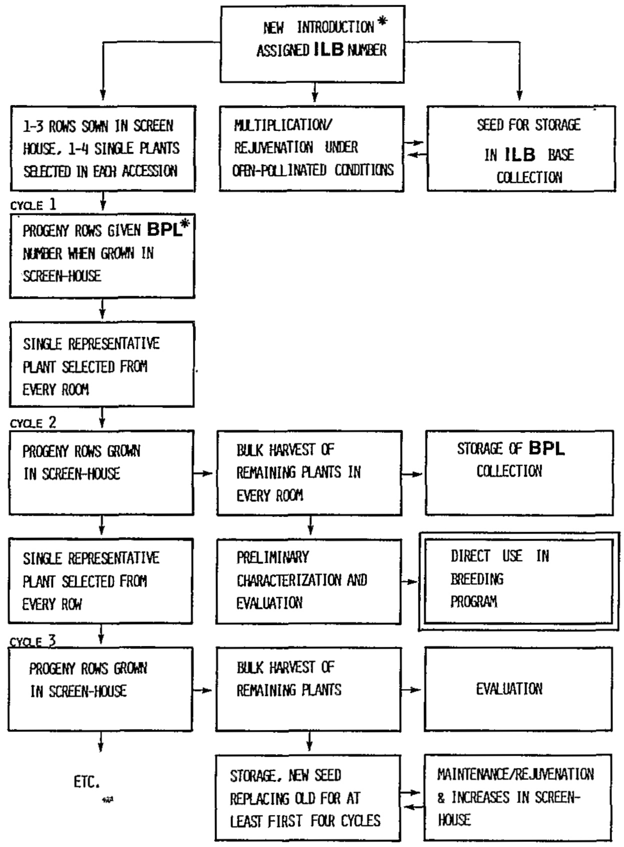
Locality	Plants/m^2 (no.)	Allogamous offsprings (%)	
		1st-5th fruit clusters	Other fruit clusters
Torre Lama	20	10	7
	40	14	11
	80	13	8
Scalera	20	8	7
	40	14	10
	80	16	16

Inbred lines

Another approach to maintain cross-pollinated germplasm accessions is as inbred lines (Burton, 1979). This simplifies seed maintenace because lines can easily be maintained as inbred lines in screenhouse, though tripping may be required for some of them. This way, thousands of genetically different lines can be maintained with their identity. A critical factor is that selfing uncovers many recesive genes. After evaluation, seed requests for inbred lines can be easily met, while those for open-pollinated lines would seriously erode the original collection.

At ICARDA, because of this difficulty of maintaining and evaluating open-pollinated accessions, a pure-line collection has been derived from the original heterogeneous, heterozygous accessions (Hawtin and Omar, 1980). This system is detailed in Fig. 4.

The original accession as received at ICARDA is given an ILB (International Legume Bean) accession number. Through a process of selfing, one to four lines (based on variability in the original accession) are developed as pure line BPL accessions (Bean Pure Line) from each ILB line. The process involves growing each ILB line in one to three rows in the screenhouse where one to four plants are selected for growing a progeny row the next year when each progeny row is given a BPL accession number. This whole process is done under screenhouse to insure self pollination. The second year one representative plant is selected for growing in a progeny row the next year. This continues till five cycles of selfing when maintenance is well established. Evaluation may start during the second cycle of selfing.



*ILB BASE COLLECTION IDENTIFIER (INTERNATIONAL LEGUME BEAN)
BPL PURE LINE COLLECTION IDENTIFIER (BEAN PURE LINE)

Fig. 4. Flow of faba bean germplasm at ICARDA.

Gene-pools

The germplasm collection of faba bean can be divided into different gene pools on the basis of morphological traits and country, or region of origin. The first step is to evaluate each accession for characters with a reasonably high heritability. The results of this kind of evaluation can be used to create specific gene-pools based on such characteristics as maturity, seed size, height and growth habit.

In this respect multivariate analysis of data can provide a useful tool. A first analysis can pool on the basis of a whole range of characters and a second one can separate accessions into geographic groups (Murphy and Witcombe, 1981; Polignano and Spagnoletti, 1985).

Thus, each gene pool may consist of a number of selected accessions which are mixed in equal proportions and maintained as a bulk by growing them as a single population. In this way a collection of around 2000 accessions, like the one in Bari could be reduced to about 100-200, or even less, gene pools. Within each germplasm pool, since linkages are broken, the total phenotypic variance may even increase and recessive genes may be less exposed to genetic drift. Gene pools can then be distributed, and used as source populations for selecting special lines.

Maintenance in the form of gene-pools and or inbred lines, does not exclude the necessity of maintaining, in base collections, the original populations from which they were derived. The main problem of these two additional ways of maintenance is additional cost. Thus they are welcome only when breeders have clear ideas on utilization of germplasm collections and more than one breeder, country and institution are interested.

Conservation

Storage conditions and seed size are also two important factors for the maintenance of germplasm collections. Long term storage is possible at 5-6% seed moisture and -20 °C; under these conditions longevity of *V. faba* seeds is very high (Roberts, 1975). These are the conditions for Bari collections. Medium term storage at low relative humidity (35-40%) and low temperatures (5 °C to 10 °C) still provides very high longevity. In Bari seed samples of active collections are stored at 5-6% seed moisture, closed under vacuum in alluminium follium bags at 0 °C with 35-40% of relative humidity. Under these conditions active collections can be stored for more than 10 years.

As for the seed size, since a considerable portion of the variability is maintained over several accessions and useful genes are likely to be found at a high frequency, a pratical number of 1000 seeds per accessions can be recommended instead of 12000 suggested by the IBPGR.

Evaluation and use

An important stage in germplasm management is evaluation and utilization, without this step the collection is a useless museum. Preliminary evaluation data, including characterization, is produced by genetic resources centres, and usually consists of a short list of descriptors to provide some preliminary information on the germplasm collection. Such preliminary evaluation data can be used to select special lines or to bulk similar accessions from the same geographical area in order to form the so called gene pools or trait specific gene pools (Witcombe, 1984).

Agronomical traits and seed protein content

In Bari all the collection, consisting of about 2000 accessions from more than 37 countries (Table 8), has been characterized for 11 agronomical traits (Table 9) which were recommended by a pannel of experts during a workshop held in Bari in 1983. The frequency distribution (Fig. 5) of the 11 characters over all the collection, neglecting the origin, shows that most of the accessions flower around 95 days (calculated from 1st January), have green stem colour, narrow leaf shape, medium leaf dimension, low pod density, central-basal distribution, pendent pods, medium plant height, three flowers per cluster, and one pod per node. A very low number of accessions flower within 83 days or later than 150 days, have large and big leaves, high pod density, apical pod distribution, tall plants, horizontal and erect pods, more than 5 flowers (from 5 to 8) per cluster and more than two pods (from 3 to 5) per node. This frequency distribution shows that genetic variation is present for almost all characters and that there is the possibility to select the desired lines in different combinations with other characters. The frequency distribution shown in Fig. 5 does not show the variation existing within populations which often is high but with different frequency distributions according to characters and place of origin.

At ICARDA 840 pure line accessions (BPL) were evaluated for 43 descriptors as per the IBPGR/ICARDA descriptor list (Robertson and El-Sherbeeny, 1988). There was considerable variation for flowering date, plant height, branches per plant, height of lowest pod-bearing node, stem thickness, leaflets per leaf, pods per plant, seeds per pod, pod length, seed yield, biological yield, harvest index, 100–seed weight, autofertility, and protein content. Even thought these were highly inbred lines, seed yield ranged from 0 to 7.5 t/ha, with a mean

Table 8. Germplasm collection of *Vicia faba* maintained at the Germplasm Institute of CNR, Bari, Italy.

Origin	No. of accessions
Italy	319
Egypt	186
Canada	124
Cyprus	106
Turkey	105
Afghanistan	91
Spain	91
Ethiopia	89
Sweden	66
England	65
Iraq	61
Greece	52
Tunisia	51
Syria	41
Iran	38
Lebanon	35
Algeria	34
Netherlands	32
Morocco	32
Yemen	26
Sudan	23
Yugoslavia	17
Libya	16
France	10
Jordan	7
Hungary	7
USA	7
China	6
Germany	6
USSR	6
Portugal	5
India	4
Japan	4
Pakistan	3
Palestine	2
Bulgaria	1
Poland	1
Unknown	182
Total	1951

Table 9. List of traits used for characterizing the *Vicia faba* collection of the Germplasm Institute in Bari, Italy.

Characters	Number and description of character states
1. Flowering date	Recorded when 50% of plants had flowered
2. Flower colour	5: white, violet, dark brown, violet with spots
3. Stem colour	3: green, green with violet venations, violet
4. Flower N.	From 2 to 8
5. Leaf shape	3: narrow, medium, large
6. Leaf dimension	3: small, medium, big
7. Pod density	4: very low, low, medium, high
8. Pod distribution	5: basal, central-basal, central-apical, apical, uniform
9. No. of pods per node	5: from 1 to 5
10. Pod angle	3: pendent, horizontal, erect
11. Plant height	3: short, medium, high

of 3.6 t/ha, and there were 25 accessions with seed yields greater than 6 t/ha. Seed weight ranged from ca. 21 to 193 g/100 seed.

An analysis of the seed protein content, seed weight, number of pods per plant and number of seeds per pod, carried out on 753 accessions of faba bean obtained from 15 different European, Mediterranean and Asiatic countries (Polignano *et al.*, 1979) showed that accessions from Ethiopia, Egypt and Afghanistan had the highest protein content variation. The Italian material was representative of most of the variation found in each individual country. In all, the protein content varied from 19 to 34%, the 100-seed weight from 130 to 203 g, the number of pods per plant from 1 to 140 and finally the number of seeds per pod from 1 to 6.

An analysis of 41 characters carried out on 123 accessions (Polignano and Olita, 1981; Perrino, 1988) from different Mediterranean countries and the Near East showed a considerable variation for at least 12 characters (Table 10). For each character it is possible to choose the country of origin with the highest frequency for the lowest and for the highest value. This can help in increasing the probability to detect the material with the desired character. For example, looking for plants with even less than 5 stems per plant, the germplasm accessions with the highest frequency (54%) for this character are from Egypt, while the highest number of stems per plant (more than 15) is more frequent (28%) in the accessions from Greece; early flowering types (less than 75 days) are more frequent (82%) in the material from Iraq and the latest flowering (more than 80 days) are more frequent (63%) in the material from Spain; the less productive (less than 50 g) come from Egypt and the most productive ones (150 g) from Italy. This does not mean that yield per hectare is lower in Egypt and higher in Italy since yield per hectare depends also on many other factors, like crop density, use of the crop, and environment grown in. In a series of analyses of 10 traits carried out on 131 accessions (Polignano and Uggenti, 1984) these results were confirmed.

Source of resistance

At ICARDA sources of resistance for various pathogens such as *Botrytis fabae, Ascochyta fabae, Uromyces fabae,* and *Ditylenchus dipsaci,* have been found in the faba bean pure line (BPL) collection (Hanounik and Robertson, 1988; Hanounik and Robertson, 1989).

Lines resistant to *Orobanche crenata* and to *Uromyces fabae* have been also found in Bari (Perrino *et al.*, 1988; Perrino and Monti, 1988) and in the Rabat collection. Concerning *Orobanche,* more studies are needed to understand the mechanism of tolerance and/or resistance. Tolerant lines are defined as those which can provide more yield in the presence of broomrape (Perrino *et al.*, 1988) while resistant ones are those which provide yield but do not allow broomrape to develop.

A collection of 600 accessions of the German Democratic Republic was screened (Rollowitz and Schimdt, 1982) for resistance to bean yellow mosaic virus (BYMV) and pea enation virus. Many accessions were also screened for reactions to broad bean true mosaic virus, alfalfa mosaic virus, and broad bean wilt virus. As a result, one line was found very resistant to 14 isolates of BYMV and other lines were found tolerant to the other four viruses.

Breeding activity

At ICARDA many crosses are now being made for resistance to various pathogens using resistant lines found in the germplasm collection. Since many requests for resistant lines from several countries have been received, a germplasm catalog should be developed following the example of Hanounik (1982) for *Botrytis fabae.* The publication of evaluation data, especially pathogens resistance, frost tolerance, unique plant type, etc., is fundamental if the goal is to increase the utilization of faba bean germplasm collections.

Conclusions

Faba bean is cultivated on more than 3 million of hectares in the world, including more than half million in the Mediterranean region. These figures justify the interest of breeders and international organizations, like ICARDA, FAO, CEE, etc. to make more efforts for im-

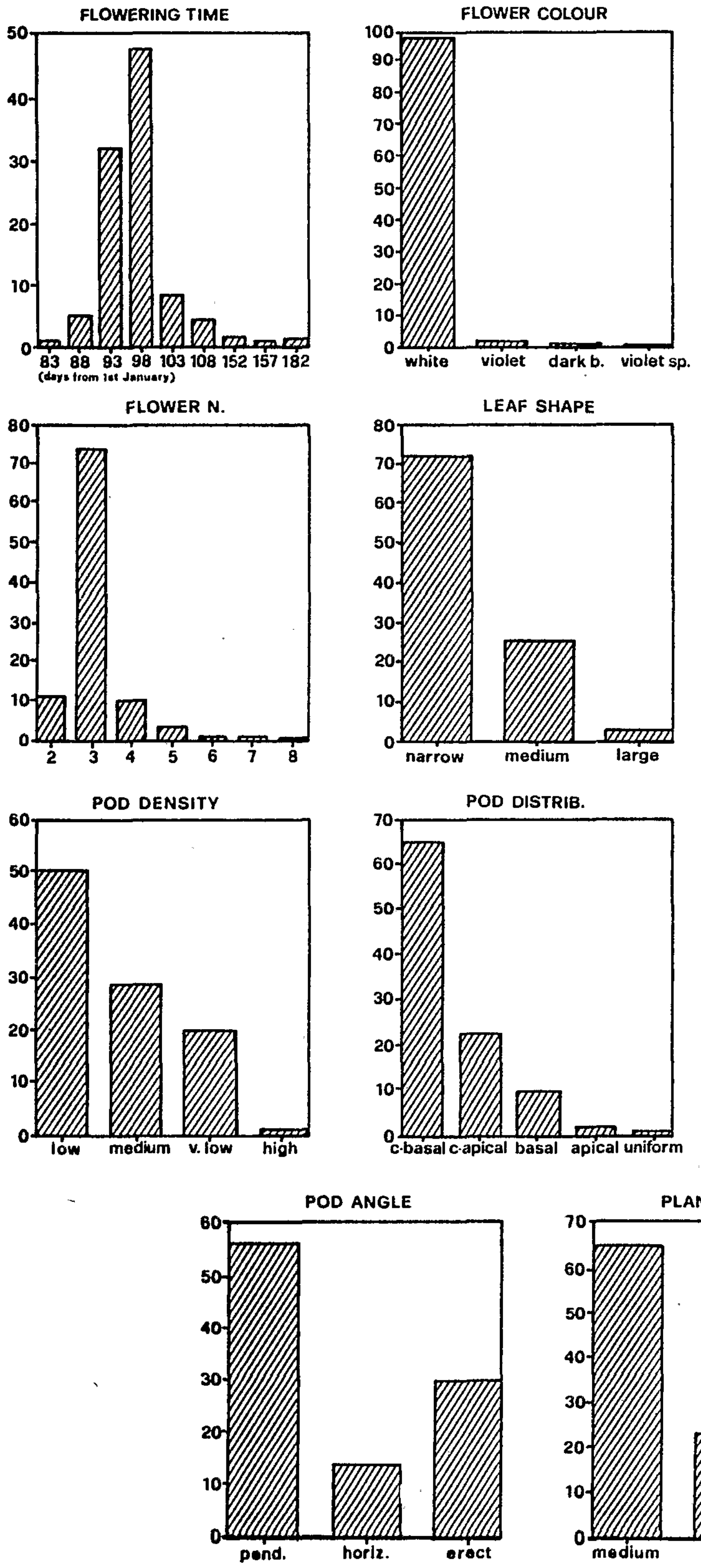


Fig. 5. Frequency distribution of 11 characters used for the characterization or preliminary evaluation of the *Vicia faba* germplasm collection at the Germplasm Institute of CNR in Bari.

Table 10. Variability for 12 characters observed on 123 accessions of faba bean from different Mediterranean countries plus, Iran and Iraq.

Characters	Range of variability		Countries with the highest percentage			
	Minimum value	Maximum value	Minimum value		Maximum value	
Stems/plant (No.)	< 5	> 15	Egypt	(54%)	Greece	(28%)
Plant height (cm)	< 40	> 100	Spain	(20%)	Greece	(17%)
Lowest node bearing pods (No.)	< 2	> 6	Italy	(9%)	Iran	(13%)
Nodes on the main stem with pods (No.)	< 5	> 15	Greece	(46%)	Tunisia	(21%)
Flowering time (from January 1st)	< 75	> 80	Iraq	(82%)	Spain	(63%)
Pod angle[a]	1	3	Lebanon	(51%)	Greece	(92%)
Mean weight of seed (g)	< 1	> 2	Egypt	(86%)	Algeria	(5%)
Seeds per pod (No.)	< 6	> 12	Iran	(97%)	Iran	(2%)
Pods per plant (No.)	< 20	> 60	Egypt	(63%)	Italy	(8%)
Yield of pods per plant (g)	< 20	> 100	Egypt	(41%)	Greece	(21%)
Seeds per plant (No.)	< 50	> 200	Egypt	(40%)	Italy	(15%)
Yield of seeds per plant	< 50	> 150	Egypt	(65%)	Italy	(23%)

[a] 1 erect, 2 horizontal, 3 pendent
Source: Perrino (1987)

proving the yield and utilization of the crop, both for human and animal consumption and for further collecting activity in some key areas of the Mediterranean region, Near East, Afghanistan, India, China, etc.

Maintenance of germplasm collections in the main genetic resource centres may be of three kinds. All centres should maintain local collections as populations and evaluate them for a minimum number of agronomical traits; computerization, production and distribution of catalogs with a minimum passport data and mean values for the scored traits should also take place. More advanced centres, like that of ICARDA, should also be in a position to concentrate on creating pure line collections with inbred lines and screen them for biotic and abiotic stresses, in collaboration with breeders, pathologists and physiologists, according to local agricultural needs. All centres, but especially those that cannot afford the management of large collections, could maintain trait specific gene pools and distribute them on request to faba bean breeders for selection and breeding programs.

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