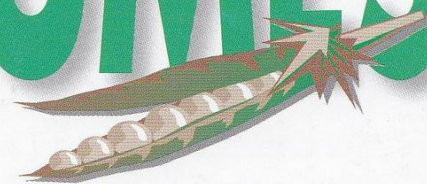


GRAIN LEGUMES



The magazine of the European Association for Grain Legume Research
Le magazine de l'Association Européenne de recherche sur les Protéagineux

ISSUE No. 51

January 2009

Vavilovia formosa,
an intriguing *Pisum* relative

Resistance to rust in pea

GL-TTP and AEP:
Together we stand, divided we fall!

Faba beans in Mexico

Legumes: the bright side of the world
Echoes of the Second GL-TTP Workshop in Novi Sad





On behalf of the International Steering Committee,
the European Association for the Grain Legume Research (AEP)
cordially invites you to participate in the

**7th European Conference on Grain Legumes &
5th International Food Legume Research Conference
(AEP VII & IFLRC V)**

LEGUMES FOR GLOBAL HEALTH

Legume crops and products for food, feed and environmental benefits

that will be held in
the Kervansaray Hotel Lara (Convention Centre), Antalya, Turkey
from 26th to 30th April 2010

The world's two major grain legume conferences will hold a joint meeting, bringing together the latest scientific information on all aspects of grain legumes in the context of their global impact on food, feed and environmental benefits.

The conference will be multidisciplinary and will include invited keynote presentations by leading international scientists on current topics of interest to the global research community, including:

- 1) The Future of Grain Legumes;
- 2) Seed Biology;
- 3) Human Health and Grain Legumes;
- 4) Biofortification of Grain Legumes;

- 5) Management of Genetic Resources;
- 6) Grain Legumes and Environment;
- 7) New Uses of Grain Legumes in Feeds;
- 8) New Uses of Grain Legumes for Foods;
- 9) the Position of Legumes in Agro-Energy and Non-Food Use;
- 10) Innovations in Genetics;
- 11) Innovations in Pathology;
- 12) Communicating the Benefits of Legumes;
- 13) Adapting Grain Legumes to Climatic Changes;
- 14) Innovations in Agronomy.

The participation of students and early-career researchers is strongly encouraged.

Please visit the conference web site at <http://www.iflrc-ecgl.org>

AEP conference representatives:

Diego Rubiales, AEP President (CSIC-IAS, Spain)
Álvaro Ramos-Monreal, AEP Past President (INIA, Spain)
Gérard Duc (INRA-Dijon, France)
Judith Burstin (INRA-Dijon, France)

Noel Ellis (JIC, UK)
Christophe Salon (INRA-Dijon, Dijon, France)
Carlota Vaz Patto (ITQB, Portugal)
Aleksandar Mikić (IFVCNS, Serbia)

Grain Legumes is a quarterly magazine aiming to promote better communication within the scientific community and between researchers, extension workers and end-users. Traditionally it covered only grain legumes, but its scope will be extended to forage legumes also, fulfilling a demand of the community.

As a consequence of recent financial troubles, edition of GLM was frozen during 2008. As readers might be aware, AEP has no longer a permanent office at Paris and has not technical secretary at all. AEP and GLM have no longer the support of their traditional sponsors. All current activities are based on heroic efforts of AEP volunteers. We should here publicly acknowledge their valuable contribution. Four issues of GLM will be produced during 2009 thanks to the efforts of different voluntary teams. Here we present GLM51 especially devoted to the outcomes of 2nd GL-TTP Workshop hold at Novi Sad, Serbia. This issue was possible thanks to the constancy of our colleague Aleksandar Mikić who coordinated an editorial team composed by Noel Ellis, Tom Warkentin and Kevin PcPhee. This will soon be followed by GLM52 devoted to Pea, coordinated by Judith Burstin; then by GLM53 devoted to Model Legumes coordinated by Richard Thompson and Nicolas Rispaill; and finally by GLM54 devoted to Lathyrus coordinated by Carlota Vaz Patto and Diego Rubiales. Ideas for 2010 issues are most welcome.

These issues will be printed thanks to various sponsorships that will be acknowledged in its issue. Any possible sponsorships will be most valuable and widely acknowledged. Printed issues will be freely distributed to AEP members only. One year after their production, pdf versions will be publicly available in AEP website.

Diego RUBIALES
Managing Editor

Carte blanche

- 4 This is the time for grain and forage legumes to come back! (D. Rubiales)

News

- 5 A renaissance of legumes (T. H. N. Ellis and Á. Ramos Monreal)
6 IV International Conference on Legume Genomics and Genetics (P. Smýkal)
7 12th International Lupin Conference (G. D. Hill)

Events

Research

- 8 *Vavilovia formosa*, an intriguing *Pisum* relative (G. Kenicer and colleagues)
9 Development of Kunitz-free soybean genotypes (M. Srebrić and V. Perić)

PhD Thesis

- 10 Control of broomrape (*Orobancha crenata*) in legumes by genetic resistance and alternative control methods (M. Fernández-Aparicio)
11 Resistance to rust (*Uromyces pisi*) in pea (E. Barilli)
12 Study of genetic erosion during conservation of pea (*Pisum sativum* L.) genetic resources based on microsatellite markers analysis (J. Cieslarová)

Legume periodicals

Special report

Legumes: the bright side of the world (Echoes of the Second GL-TTP Workshop)

- 13 Introduction
14 Legume genetics and breeding: the example of pea (T. H. N. Ellis)
16 Perspective of soybean in Europe (V. Đorđević)
18 Some burning questions for lucerne breeders (P. Annicchiarico and C. Scotti)
20 Black locust improvement in Serbia (B. Kovačević and colleagues)
22 Pea genetic diversity studies for better breeding (P. Smýkal)
24 Disease resistance in faba bean (D. Rubiales and J. C. Silero)
26 GL-TTP and AEP: *Together we stand, divided we fall!* (GL-TTP GA report)

Crops, uses and markets

- 28 Market situation of faba beans and field peas in the EU from a breeder's perspective (O. Sass)
30 Breeding forage legumes for enhanced seed production (Đ. Karagić and colleagues)

Around the world

- 31 Faba bean in Egypt (A. A. Emeran and colleagues)
32 Faba beans (*Vicia faba* L.) in Mexico (R. Díaz-Ruiz and A. Escalante-Estrada)

Art

- 34 Legumes in the work of J. R. R. Tolkien (A. Mikić and F. L. Stoddard)

Carte blanche
to...



Diego Rubiales

This is the time for grain and forage legumes to come back!

Legumes have always been acknowledged for their beneficial role in the rotation improving soil fertility. However, legumes did not enter into modern agriculture at the right speed and cultivation of most legumes has declined continuously in most countries, particularly in Europe. In spite of the subsidies to the farmers and of the good research generated, legume cultivation keeps declining in Europe. This is not the case with legume consumption, both for food and feed, so Europe imports legumes although exports legume related science. Obviously a reformulation of the strategies is needed here.

Now, with the increasing concerns on food security, energy prices and greenhouse gas production, the need for legumes in agriculture is more evident than ever. The current economic crisis has revealed the vulnerability of systems and the need for innovation. Renewing systems implies defining new solutions and changing innovation processes by creating new bonds between research and society. This is a time of opportunity for legumes and we ought to go for it.

Substantial efforts have been and are being made in legume research, so we can now proudly state that legumes have entered the post-genomics era. However we still face the challenge of translating this outstanding science into practice. Associations like AEP and GL-TTP have critical roles to play in this endeavour of stimulating legume research and enhancing its application. AEP and GL-TTP are now more needed than ever. Particularly under this period of crisis, support to such associations is a most refundable investment. ■

A renaissance of legumes

by T. H. Noel ELLIS* and Álvaro RAMOS MONREAL**

This is a time of opportunity for legumes. There is a heightened awareness of the need for food security and of the benefits of lowering inputs to agriculture. While the instability and potential for increase in oil and energy prices will favour crops that do not demand nitrogen fertiliser, the consequences for agriculture seem hard to predict.

The great increase that occurred in the area of legume production in Europe during the last 20 years would seem to be ready for a continuation or even expansion. However, this period of expansion was also an opportunity for pests and pathogens, *Aphanomyces*, *Ascochyta*, Bruchid beetles and broomrapes have had devastating effects, building disease pressures have led to a reduction of production area. While this creates an impetus for research and breeding activities, the reduction in crop area in France has had a negative impact on our founding organisation and major sustaining member, UNIP.

A consequence of these financial troubles has been the cessation of function of the AEP office at Georges V and in consequence this year we no longer have the support of our long term energiser, Anne Schneider. As former Presidents we are somewhat in awe of the energy that Diego Rubiales has been able to direct towards AEP relocating its office in Córdoba.

AEP now has to find its own way and the membership rather than the Head Office needs to provide the energy and commitment to maintain the cohesion and interdisciplinary that has characterised AEP activities since its inception.

The challenge to us is to undertake and coordinate those research activities that will enable legume crops to meet the challenges of the pests and diseases that assail them. If we can succeed in this endeavour we will see an increase in legume crops that will contribute to food security and environmental stewardship, but that will also indirectly rebuild the support for our founding organisation and thus properly repay that nurturing of our association from which we have all benefited. ■

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**Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Madrid, Spain

IV International Conference on Legume Genomics and Genetics (Puerto Vallarta, Mexico, 7-12 December 2008)

Legumes (*Fabaceae*) are historically tightly linked to advent of genetics. Thus it is not surprising, that there is an international community working on various aspects of legume genetics and biology, which decided in 2002 to start biannual meetings. The conference, attended by over 350 scientists from about 55 countries of all continents, had 11 sessions.

Whole genome: structure and comparison

This section has to cover and reflect upon three legume genome sequencing projects. Of *Medicago truncatula* genome given by Nevin Young from University of Minnesota, of *Lotus japonicus* by Shusei Sato, Kazusa Institute, Japan, and soybean by Jeremy Schmutz, Joint Genome Institute, USA. One of my personal highlights was a talk given by Jiří Macas, from IPMB České Budějovice, who presented opposite genome landscape of not gene-based, by repeat-based using pea genome as model.

Defining gene function

Genomic tools to reveal gene functions such as insertion mutagenesis, presented for *Medicago truncatula* by Pascal Rattet, CNRS, France, and for soybean shown by Meksem Khalid, Southern Illinois University, USA, has dominated this section. Excellent talk (as usual) was given by Julie Hofer, JIC, UK, on tendril formation and branching in legume leaves.

Pathogenesis and disease resistance

Biotic stresses are one of the major focal points of practical as well as basic research. Gene responsible for bluegreen aphid resistance has been determined in Mt by Singh Karam, CSIRO, Australia. Interesting talk was given by Ben Rosen from University of California, USA. This lab looked at numerous and highly variable NBS-LRR type of disease resistance genes.

Genome enabled agriculture

In this section one of the highlights was talk given by Francisco Aragao, EMBRAPA, Brazil, on development and marketing of virus (BGMV) resistant common bean. Another brilliant talk was given by Tom Clemente, University of Nebraska, USA, on soybean oil modification for feed and fuel, rising oleic acid content to 85% increases tank life, mitigates NOx emission. Finally, from other side of the globe, Australian ARC Centre, Brisbane, Paul Scott presented *Pongamia pinnata*, a tropical/subtropical tree as very promising source of bio fuel.

Source: Petr Smýkal, Agritec Plant Research Ltd., Šumperk, Czech Republic (smykal@agritec.cz)

Abiotic stress

There were numerous talks on these aspects on bean, soybean and model *Medicago truncatula* species.

Development

An astonishing „Hollywood style“ presentation was given by Robert Goldberg from University of California, USA, focusing on how many genes are required to make a soybean/legume seed? Another talk drew attention: Elisabeth Dun from Christine Beveridge laboratory, ARC Centre, Brisbane, Australia, presented a novel class of phytohormones, strigolactones, recently published in *Nature*.

Translational genomics

Douglas Cook, the organizer of next conference to be held in California in 2010, showed his vision on genomic being used to deduce evolution of *Papilionoideae* genomes as well as to develop tools for applied legume genomics.

Whole genome expression analysis

Truncatunix software was presented by Helge Küster from University of Hannover, Germany. How candidates might more closely screened using QTL mapping and genome knowledge was presented by Randy Schoemaker, USDA-ARS, USA.

Evolution and diversity

The talk by Jeff Doyle from Cornell University, USA, on soybean relatives evolution provided link also to Darwinian question of fitness as shown by photosynthetic capacity.

Symbiosis

The complicated but finely tuned interplay of kinases and associated phosphatases cascades was shown by Peter Gresshoff from ARC for Integrative Legume Research, Australia.

Recognition and signalling

Cascades similar to shoot meristem CLAVATA3 pathway are currently revealed, as shown by Jens Stougaard, University of Aarhus, Denmark, or Peter Gresshoff. As calcium signalling plays an important role was presented by Giles Oldroyd, JIC, UK.

All together, there were 74 plenary lectures with 136 posters. The organizers received a large applause at the end. Most of the participants left Mexico with warm wishes for bright legume future. ■

12th International Lupin Conference (Fremantle, Australia, 14-18 September 2008)

The International Lupin Conference had last convened in Western Australia in Geraldton in 1986. Western Australia was a very appropriate venue as the state grows the largest area of lupins, predominately *Lupinus angustifolius*, in the world.

Both health and wealth

The conference theme was 'Lupins for Health and Wealth'. A very full scientific programme was presented and over one hundred papers were presented on the cultivation and utilisation of lupins. On the Wednesday of the conference there were field trips (see photos) to the Wongan Hills Research Station to the North East of Perth to observe lupin trials and to lupin processing plants in and around Perth. A pleasing aspect of the conference was the presence of a number of farmers from both Western Australia and from overseas. Among papers presented there was a special session on the potential role of lupin seed in human diets to reduce the incidence of obesity and diabetes.

2011 Poland: the next Lupin Odyssey

At the General Assembly of the International Lupin Association, held during the conference, it was decided to accept an offer from the Polish Lupin Association to host the 13th International Lupin Conference in 2011 was accepted. Italian delegates expressed an interest in hosting the 14th meeting in 2014.

Overall it was a highly successful conference. In particular the Western Australian organising committee are to be congratulated for its smooth execution, a well constructed program and social events and getting the proceedings published prior to the conference. ■



Source: George D. Hill, Lincoln University, Canterbury, New Zealand
(George.Hill@lincoln.ac.nz)

EVENTS

April 26-30, 2010

5th International Food Legume Research Conference &
7th European Conference on Grain Legumes

Antalya, Turkey

<http://www.iflrc-ecgl.org>

May 26-28, 2010

XII International Symposium on Forage Crops

Kruševac, Serbia

<http://www.symposium.ikbks.com>

August 29 – September 2, 2010

23rd General Meeting of the European Grassland
Federation

Kiel, Germany

<http://www.grassland-organicfarming.uni-kiel.de/egf2010>

August 29 – September 4, 2010

XIth European Society for Agronomy Congress
Montpellier, France

<http://www.agropolis.fr/agro2010>

September 6-10, 2010

9th European Nitrogen Fixation Conference

Geneva, Switzerland

<http://www.enfc2010.ch>

Vavilovia formosa, an intriguing *Pisum* relative

by Gregory KENICER*, Petr SMÝKAL**, Margarita VISHNYAKOVA*** and Aleksandar MIKIĆ****

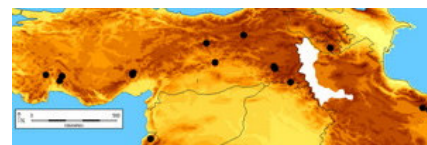
The tribe *Fabeae* (formerly *Vicieae*) contains five genera, including some of the most important grain legumes: *Lathyrus* (sweet pea and chickling vetches/vetchlings), *Lens* (lentils), *Pisum* (peas) and *Vicia* (vetches). The remaining monotypic genus, *Vavilovia*, is obscure and intriguing.

Beautiful from the beginning

Vavilovia formosa (Steven) Fed., a small, patch-forming perennial found in upper-alpine screes of the Caucasus, eastern Turkey, northern parts of Iraq, Iran, Syria and Lebanon. First described by Steven in 1813, the plant was assigned to the now defunct genus *Orobis* L., with the specific epithet *formosus* (meaning 'beautiful') (1). Later it was associated with two other genera in tribe *Fabeae*, *Lathyrus* and *Pisum* (1) and came to be known as the perennial pea (*Pisum formosum* (Steven) Alef.). Fedorov (1939) revised the taxonomy in his monograph (2) and, based on morphological characteristics, such as shape of the flower and stipule, presence of creeping, thread-like rhizomes, as well as characteristics of disjunctive distribution range, ecology and perennial habit, he established *Vavilovia* Fed. The name honors N. I. Vavilov, the Russian scientist who pioneered the study of cultivated plants and first recognized the importance of their wild relatives.

Hybridization with pea

Vavilovia and *Pisum* share a spatulate style with reflexed margins. Unlike *Pisum*, the leaflets of *Vavilovia* unroll rather than unfolding (supervolute rather than conduplicate vernation), and it is a perennial, rhizomatous plant. In these respects and in its ecology, *Vavilovia* markedly differs from wild and cultivated *Pisum* and resembles *Lathyrus*. These three genera have been shown to be monophyletic with respect to *Vicia* and *Lens* (3). Among the traits that support a closer relationship to pea are: 1) the same number of chromosomes ($2n=14$), of which two usually have satellites in both taxa; 2) susceptibility to the pea-specialized fungi *Uromyces pisi* and *Ascochyta pisi* (4); 3) a possible hybridization with pea. The hybridization of ♀ *V. formosa* × ♂ *P. sativum* produced hybrids that withered before flowering, with several basal branches, long internodes and trifoliolate leaves. The hybridization of ♀ *P. sativum* × ♂ *V. formosa* gave hybrids with significantly greater height than both parents, numerous basal and lateral branches, flowers and pods; however, all seeds aborted or had truncated development (1). In this respect, interspecific crosses of *Vavilovia* with *Pisum* may be a potential source of new traits for pea improvement.



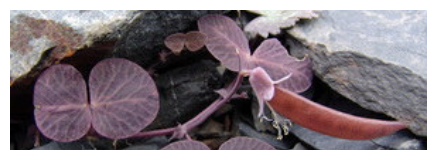
The geographical distribution of *vavilovia* in Armenia, Azerbaijan, Iran, Lebanon and Turkey

Molecular taxonomy: a genus of its own

Until now molecular phylogenetics has not been used to determine anything regarding *Vavilovia*'s relationship to *Pisum* and *Lathyrus*. Species relationships were determined for 31 species of tribe *Fabeae* using sequences for four regions known to be informative for the group (3); the maturase K, trnL-F and trnS-G spacer regions of chloroplast DNA, and the internal transcribed spacer (ITS) region of nuclear DNA. Maximum parsimony and Bayesian analysis of combined sequence data confirmed *Vavilovia* as a separate group positioned between *Lathyrus* and *Pisum*. ■



A *vavilovia* population from Dagestan, Russia (photos by A. Ivanov)



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Development of Kunitz-free soybean genotypes

by Mirjana SREBRIĆ* and Vesna PERIĆ*

Soybean is an important leguminous crop as a protein source and for industrial uses. The main utilization of soybean meal certainly is for animal feed. The soybean seeds contain approximately 40% protein and 20% oil (1). Like other legumes, mature soybean grain also contains antinutritive components. Several of these factors, such as the trypsin inhibitor, hemagglutinin, saponins, lipoxygenase, phytic acid and urease have been investigated. One of the most unfavorable is the trypsin inhibitor.

The way trypsin inhibitors work

Two types of trypsin inhibitor were found in soybean grain: the Kunitz trypsin (KTI) inhibitor and the Bowman-Birk inhibitor. Trypsin inhibitors inhibit the activity of trypsin. The ingestion of raw soybean meal by monogastric animals causes protease hyper-production and pancreatic hypertrophy, and at the same time growth rate decreased. Mature grain of conventional soybean varieties requires heat processing to break down trypsin inhibitor activity before using as food or animal feed.



At the same time, protein denaturation and other qualitative changes occur in soybean grain, especially if the temperature of heating is excessive (2). About 6% of whole soybean seed proteins belong to KTI, which results in 30-50% of the trypsin inhibitor activity.

Four inhibitor forms

Thousands of seed samples from the USDA soybean germplasm collection were screened for variation in the KTI. Four different Kunitz-trypsin inhibitor (*Ti*) forms were determined. The three types of KTI (*Tia*, *Tib* and *Tic*) are inherited as codominant alleles in a multiple allelic system at a single locus. The absence of KTI is inherited as a recessive allele and has been designated *ti*. (3). The recessive form, found in soybean germplasm samples PI 157440 and PI 196168, lacks the KTI. The germplasm PI 157440 was a parent of the first developed Kunitz-free genotype Williams 82.



From a flower to a cultivar: removal of stamens in female flowers (above) and corolla in male flowers (right) and the comparative field trials in Zemun Polje (left)

Achievements in Serbia

A section of the soybean breeding programme at the Maize Research Institute was aimed at reducing trypsin inhibitor activity. The variety Kunitz, which was developed by backcrossing with the variety Williams 82, has been used as a donor of this desirable character. Kunitz-free lines were developed from a few cross combinations between Kunitz soybean variety and adapted high yielding genotypes. Identification of Kunitz-free individual plants was done in segregating generations. Two registered Kunitz-free varieties Lana and Laura are the result of this soybean breeding programme.

Lana is a late maturing cultivar from maturity group II, while Laura belongs to maturity group I. Grain yield of these varieties is equal to high yielding varieties from the same maturity groups. Soybean grain without KTI can be processed at a lower temperature and for a shorter period of time. In this case, we save energy, which is of interest in industrial processing, and preserve the valuable nutritional composition of soybean grain. This trait makes them also suitable for direct feeding in adult non-ruminant animals without previous thermal processing. ■

(1) Singh, R. J. and Hymowitz T. (1999) *Genome* **42**, 605-616.

(2) Vollman J. *et al.* (2003) *J. Sci. Food Agric.* **83**, 1581-1586.



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Control of broomrape (*Orobancha crenata*) in legumes by genetic resistance and alternative control methods

by Mónica FERNÁNDEZ-APARICIO*

The weedy root parasite *Orobancha crenata* constitutes a serious threat to grain and forage legumes in the Mediterranean and Western Asia. Control strategies have centred around agronomic practices and the use of herbicides. Resistance breeding is hampered by scarcity of proper sources of resistance and of a reliable and practical screening procedure. In this PhD project we identified sources of resistance and studied the defense reactions involved both in the field, in pot, and in mini-rhizotron experiments and studied the possibility of control by intercropping.

A wide range of responses to crenate broomrape were identified both in cultivated lentil (7) and in wild *Lens* relatives (10), although complete resistance was not detected. Low infection seemed to be based on a combination of various escape and resistance mechanisms from lower root density, lower induction of *Orobancha* seed germination, and reduced establishment of broomrape radicles. Resistance was also identified in vetch (5). In order to identify alternative systems for genetic and genomic analysis, we studied early stages of the interaction between *Medicago truncatula* accessions and a range of *Orobancha* species. We found significant differences in the induction of germination and in the number of attachments supported (3).

Root exudate of 22 plant species was applied separately to seeds of 9 broomrape species, finding various levels of specialisation in the *Orobancha* species (9). A wide range of species are described as potential trap crops due to their ability to induce germination on several *Orobancha* species to which they are resistant. Many of the species that stimulate the germination of these last two groups of broomrapes are not infected, being resistant in a later stage of the infection process, representing interesting examples of trap crops. The crude root exudate of fenugreek stimulated both *O. ramosa* and *O. crenata* seed germination. Active fractions of root exudate stimulated germination of broomrape species in a differential pattern (8). Germination of some *Orobancha* species was stimulated also by the toxins ophiobolin and some fusicoccin derivatives (6).

Our field experiments show that *O. crenata* infection on faba bean and pea is reduced when these host crops are intercropped with oat (2) and with fenugreek (4) (*Trigonella foenum-graecum*). Inhibition of *O. crenata* seed germination by allelochemicals released by oat and fenugreek roots is thought to be the mechanism for reducing *O. crenata* infection. Fenugreek root exudates were extracted with organic solvent and fractionated giving several fractions, two of which showed moderate and strong inhibition of *O. crenata* seed germination. The most active metabolite is a new monosubstituted trioxazonane, affectionately renamed by us as trigoxazonane (1). ■

*PhD Thesis, 18 January 2008, University of Córdoba, co-supervised by D. Rubiales and A. Pérez-de-Luque.

This thesis received the 2008 PhD Prize by the University of Córdoba for the Macro Area of Natural and Experimental Sciences.

- (1) Evidente *et al.*, 2007. *Phytochemistry* **68**, 2487-2492.
- (2) Fernández-Aparicio *et al.*, 2007. *Crop Protection* **26**, 1166-1172.
- (3) Fernández-Aparicio *et al.*, 2008. *Annals of Applied Biology* **153**, 117-126.
- (4) Fernández-Aparicio *et al.*, 2008. *Crop Protection* **27**, 653-659.
- (5) Fernández-Aparicio *et al.*, 2008. *Crop Protection* **28**, 7-12.
- (6) Fernández-Aparicio *et al.*, 2008. *Journal of Agricultural and Food Chemistry* **56**, 8343-8347.
- (7) Fernández-Aparicio *et al.*, 2008. *Weed Research* **48**, 85-94.
- (8) Fernández-Aparicio *et al.*, 2008. *Weed Research* **48**, 163-168.
- (9) Fernández-Aparicio *et al.*, 2009. *Annals of Botany* **103**, 423-431.
- (10) Fernández-Aparicio *et al.*, 2009. *Plant Breeding*, **128**, 266-270.

Resistance to rust (*Uromyces pisi*) in pea

Resistencia genética a roya (*Uromyces pisi*) en guisante

by Eleonora BARILLI*

The purpose of this study was to identify and characterise sources of resistance to pea rust (*Uromyces pisi*) in *Pisum* spp. and to describe the host range of the pathogen. Resistance to pea rust was investigated in a collection of 2759 accessions of *Pisum* spp. under field and growth chamber conditions (2). Resistance of the most promising accessions was further macroscopically and microscopically characterised.

Various levels of incomplete resistance (partial resistance), not associated with hypersensitive response were identified. No hypersensitivity was observed. Under both field and growth chamber conditions, partial resistance characterised by a compatible infection type and reduced disease progress, was based on a prolonged latency period and a reduced infection frequency compared to a susceptible check. Microscopically, this was associated with a reduction in intercellular hyphal growth and in cell penetration, resulting in less and smaller colonies (4).

Genetic control of the resistance to *U. pisi* was characterised in the most promising accession *P. fulvum* P660. A genetic map was developed from a population of 94 recombinant inbred lines from a cross between susceptible and resistant *P. fulvum* accessions, covering 1283 cM. It included 146 markers (144 RAPDs markers and 2 STSs markers) distributed in 9 linkage groups. Two QTLs for resistance to pea rust were detected. A QTL identified against *U. pisi* in seedlings under growth chamber conditions explained 63% of the phenotypic variance and was placed on LG3. It was also detected in mature plants in the field. Another QTL was detected for resistance only in mature plants under field conditions, explaining 66% of the phenotypic variance and placed on LG6.

Systemic acquired resistance was induced by exogenous application of DL-3-aminobutyric-acid (BABA), benzothiadiazole (BTH) and salicylic acid (SA) causing a reduction in infection frequency in non-treated leaves, which implies the systemic translocation of the induction signal (3, 5).

Pea accessions could be infected by other *Uromyces* species besides *U. pisi*, including *U. viciae-fabae* (1) and *U. striatus*, which caused compatible infection type and considerable disease development under growth chamber conditions, but not in the field. *U. pisi* proved to have a wide host range, including pea, chickpea, carob bean, faba bean, lentil and grass pea which implies difficulty in interrupting its life cycle and, consequently, eradicating the disease.

ITS (Internal Transcribed Spacers) studies on 50 isolates of various species of *Uromyces* allowed the formation of 5 different groups. *U. pisi* isolates formed a monophyletic group, clearly separated from the remaining *Uromyces* species.

In this thesis we studied both the pathogen and its principal host under several aspects. Our aim was to increase the knowledge about the pathosystem pea-*U. pisi* in order to design an integrated control package in which several strategies were combined. ■

*PhD Thesis, University of Córdoba, 23 November 2007, supervised by D. Rubiales, J. C. Sillero and A. M^a. Torres.

(1) Barilli *et al.*, 2009. Crop Prot. **28**, 980-986.
 (2) Barilli *et al.*, 2009. Field Crops Res. **114**, 198-203.
 (3) Barilli *et al.*, 2009. J. Phytopath., in press.
 (4) Barilli *et al.*, 2009. Plant Breed., in press.
 (5) Barilli *et al.*, accepted. Eur. J. Plant Pathol.

Study of genetic erosion during conservation of pea (*Pisum sativum* L.) genetic resources based on microsatellite markers analysis

by J. CIESLAROVÁ*

Ex situ conservation of crop genetic resources is a key element in long-term conservation of genetic diversity. However, periodic regeneration of germplasm is often performed with limited trial space and with a small number of individuals, which increases the risk of genetic drift and decreased or loss of genetic diversity.

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The aim of our work was to determine the extent of genetic erosion during the conservation and regeneration in ex-situ seed collections of genetic resources of pea (*Pisum sativum* L.) using molecular markers.

Five accessions of registered pea varieties ('Bohatýr', 'Raman', 'Klatovský zelený', 'Arvika', 'Viktoria 75') were studied. Two samples composed of 20 individual plants for each accession, spanning a period of 40 years since their release, were investigated and compared for 10 microsatellite loci. The aim of the study was: 1) to determine the effect of genetic drift during the process of maintenance and regeneration of accessions in ex situ seed collections of pea genetic resources, and 2) study the intra-accession variation, mutability and speed of evolution of repetitive (SSR) sequences. In case of three accessions (Bohatýr, Arvika, Raman), evidence of genetic drift and intra-accession variation were clearly detected. ■

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Bean Improvement Cooperative Annual Report

<http://www.css.msu.edu/bic/Reports.cfm>

Journal of Lentil Research

lentilresearch@rediffmail.com

Lathyrus Lathyrism Newsletter

<http://www.clima.uwa.edu.au/news/lathyrus>

Legume Research

<http://www.indianjournals.com/ijor.aspx?target=ijor:lr&type=home>

Pisum Genetics

<http://hermes.bionet.nsc.ru/pg/>

Soybean Genetics Newsletter

<http://www.soygenetics.org>

Legumes: the bright side of the world



GL
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Echoes of the Second GL-TTP Workshop

Despite the rough times grain legume research and production have had, especially in Europe, the Grain Legumes Technology Transfer Platform (GL-TTP) successfully overcame numerous difficulties and kept on working on the fulfillment of its primary goal: to enhance the exploitation of the revolutionary results provided by the FP6 Grain Legumes Integrated Project (GLIP) in breeding and other applied research.

As a satellite meeting of the International Conference on Breeding Field and Vegetable Crops, BREEDING08, the Second GL-TTP Workshop was held on 27 and 28 November 2008 at the Master Congress Centre in Novi Sad, Serbia. Under the title of *Integrating Legume Science and Crop Breeding*, it gathered together more than 50 scientists dealing with genetics, genomics and breeding of all economically important legume species from 24 countries.

In total, 59 contributions were presented as either talks or posters, comprised within six main topics, namely

- 1) *Achievements and Challenges in Legume Breeding*,
- 2) *Legume Breeding and Biodiversity*,
- 3) *Status and Requirements of Legume Breeding*,
- 4) *Fundamentals of Legume Breeding*,
- 5) *Aims and Methods of Legume Breeding and*
- 6) *Legume Breeding, Symbiosis and Stress*.

This Special Report brings forth the seminal contributions of the event, witnessing that GL-TTP shares the same strategic aim with AEP: to integrate diverse legume research communities, such as those of soybean, other grain legumes, forage legumes and tree legumes, that often were unaware of each other's results, into an efficient and sustainable network to the mutual and lasting benefit of each of its members.

Legume genetics and breeding: the example of pea

by T. H. Noel ELLIS*

In the UK, the vining pea crop (for freezing and vegetable use) and the combining crop (mainly for animal feed) have a similar total economic value, but of course the combining (or field pea) crop grown for dry seed has the larger area and so has the larger potential for the provision of public goods. The impact of this crop is essentially to lower the input cost and environmental footprint of agriculture. However, public goods are necessarily independent of market driven factors, but it is the market that determines farmers' choice of crop.

It seems clear that the rise of genomics has not been correlated with an increase in the competitiveness of the pea crop. We should ask what underlies the declining trend in the pea crop area. Presumably there are many factors. Typically the pea price is about twice that of wheat, and the yields are about 45% of wheat and have remained (on average) stable for several years. These economic factors will certainly guide farmers' choices, but a 50-fold preference for wheat seems remarkable. Seeding rates are high (pea seeds are bigger than wheat grains) so the initial outlay for a farmer is high and the management regime for the crop is different. A farmer, therefore, needs a significant investment in order to plant a pea crop successfully. Peas still have a reputation for yield loss and crop failure, mainly due to lodging in the UK conditions, however, yield stability year on year suggests either that this is simply a problem of perception, or that catastrophic yield losses are not recorded.

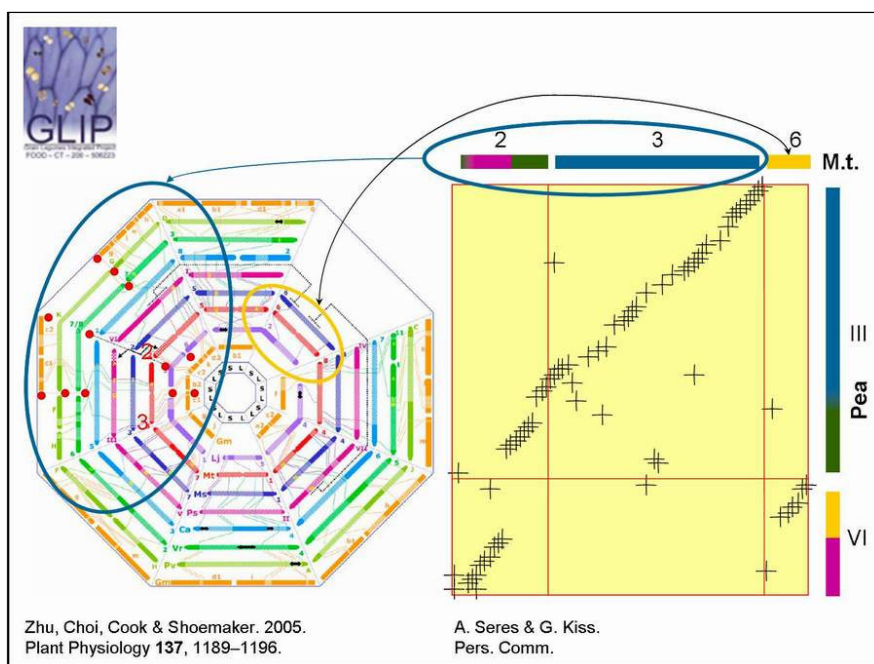
These are typical gloomy expressions for those interested in legumes, however, we should see in this that there are some real opportunities. Pea yields are nearly 50% that of wheat and the crop value is about twice. The cost of input nitrogen is rising because of rising energy costs. The environmental impact if nitrogen fertilizer is large - and can be more than 50% of the energy cost of some crops.

What do we know about pea genomics?

The pea genome is large and much of the genome is comprised of repetitive sequences (4) with nearly 50% identified as LTR retrotransposons from a 454 sequencing strategy.

Studies of the genetics and diversity of the insertion sites for these elements (2, 5, 6) have shown that in general these are highly polymorphic, with few insertion sites fixed in *Pisum* as a whole or indeed within subtaxa of *Pisum*. This can be interpreted in two complimentary ways:

1. The pea genome, on average, contains relatively few retrotransposon insertions: most sites are empty in most individuals.
2. The pea genome is vast with an interminable number of insertion sites: if we included all occupied sites then the genome would be very much larger than the genome of a single individual.



Pea and *Medicago truncatula* comparative maps

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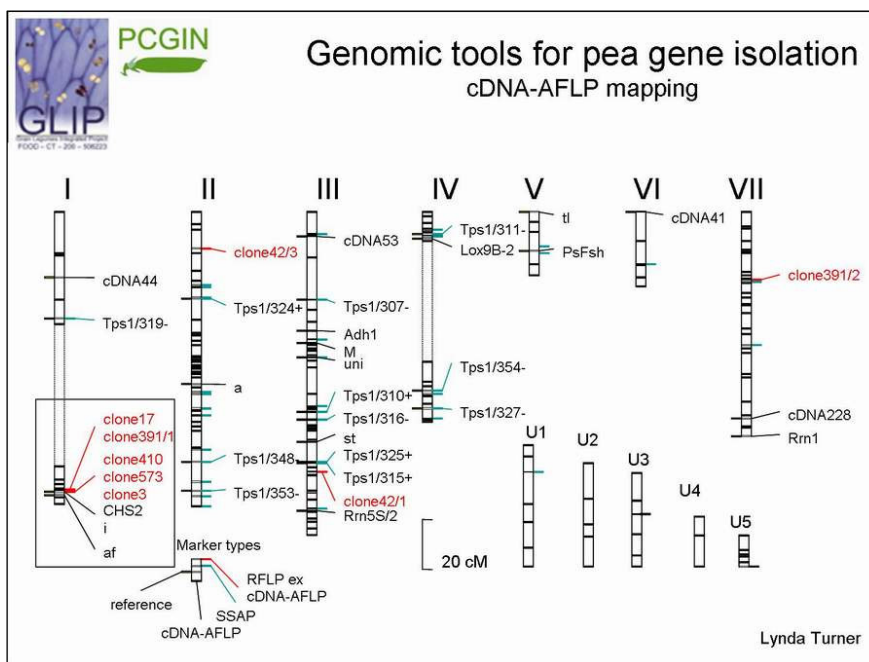
Multiplexed genetic markers can be added directly to the pea genetic map by using cDNA from a segregating population as a template

These may seem strangely contradictory statements, but they are in fact consistent with one another and are a consequence of the abundance and polymorphism of these elements. Interestingly the former view suggests that the pea genome, on average (but in no particular instance) looks something like the model for the genome of *Medicago truncatula*. This view is in turn consistent with the observed syntenic relationship between the gene content of pea and especially *Medicago truncatula* (3).

All this suggests that despite the relatively small amount of publically available DNA sequence for pea there are many resources to draw upon, and the good news is that within *Pisum* there is an abundance of polymorphism for both molecular markers and the genes that underlie phenotypic variation.

How is genetic variation partitioned in *Pisum*?

We know that retrotransposon insertion site polymorphism can be used as a system of genetic markers to infer patterns of relationship among *Pisum* accessions (5, 6). The main message from these studies is that *Pisum* is relatively poorly differentiated with a great deal of mixing of alleles between diverse types, and this has been borne out by a more recent analysis of nucleotide polymorphism within genes. There is, therefore, an abundance of genetic diversity available in *Pisum* as a resource for breeders, but accessing useful alleles from non-adapted material is problematic for breeders. Accordingly, a search among adapted material for contrasting lines with respect to (neutral) molecular markers and the establishment of recombinant inbred populations from this material would seem worthwhile.



Novel genetic variation

For breeders, it is not always feasible to find suitable genetic variation within accessible germplasm. In pea the search for sources of resistance to *Aphanomyces* has been a notorious case in point. The generation of transgenic plants has been touted as one possible approach to overcome this type of limitation, and methods for pea transformation are available, but this general approach has not (yet) led to the development of varieties that can be used in agriculture, in part for technical reasons, but sadly also because of non-scientific difficulties. The more traditional source of induced variation was called 'mutation breeding' and this has recently seen a resurgence with the advent of systematic mutant populations such as Fast Neutron induced deletions that can be used in forward genetic screens or TILLING (<http://urgv.evry.inra.fr/UTILLdb>) for which a platform has been established in pea (1) that allows a reverse genetic screen. We can anticipate, therefore, that the studies of the many model systems will identify candidate genes which are expected, when mutant, to confer an interesting or useful phenotype, and access to resources such as

that developed by Bendahmane and colleagues will provide direct access to the corresponding plant types.

What does the pea crop need?

The pea crop requires some improvement, and the targets such as disease resistance or standing ability are relatively clear. The application of genomic resources to partition genetic variation in germplasm or breeding material is a viable approach as is the use of both forward and reverse genetic tools to access novel variation. Marker assisted selection could be feasible because of the abundant molecular marker diversity in pea. What is needed though, is a low cost procedure to incorporate such approaches in breeding programmes. ■

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Perspective of soybean in Europe

by Vuk ĐORĐEVIĆ*

European countries require more than 20 million tons of soybean meal and other soybean products per year. The European soybean production is inadequate to supply all soybean consumers, since production of soybean is less than 10% of its requirements. Large soybean producing countries are Italy, France, Serbia and Romania. There is also a notable production decrease in last 20 years in old European countries (Italy and France), but Romania and Serbia have constant production in the same period. In contrast, there is a growing interest for soybean in Ukraine. In this country, there is 10-fold soybean area increase in the last decade. Unfortunately, the soybean yield in Ukraine is relatively low and even with a great yield and area increment, there will still be a gap between production and demand. This situation pushes European soybean consumers to find soybean on world market – the import from Argentina, US and Brazil is worth over 4 billion \$. Generally, European countries are depending on import, but there are some special markets where European producers can find their place. There are constant demands for organic production and soybean is a very useful crop for converting the conventional to organic production. The implementation of special varieties with altered chemical content could be very beneficial for the processing industry. Modification of protein functional properties in plants is the most economical way to supply the processing industry.

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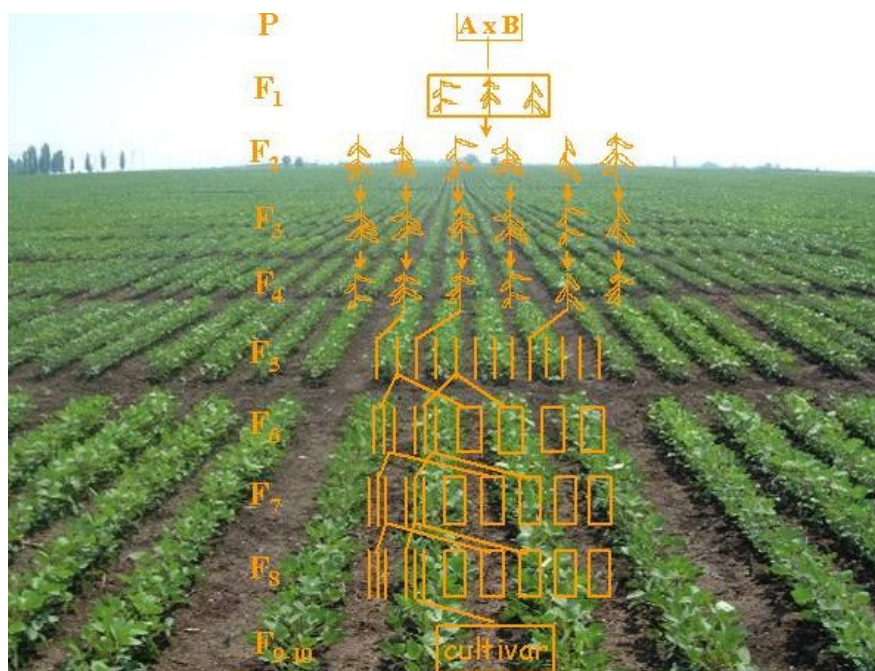
Special-use soybean varieties

The soybean seed, which contains about 40% of protein and 20% of oil on dry basis, provides approximately 60% of world supply of vegetative protein and about 30% of the oil. The majority of seed is processed in purpose of separation of the protein and oil fraction. Protein is primarily used as livestock feed, but it is also important for various food products and industrial application. Due to a well-balanced amino acid content of soybean proteins, it provides nearly all the essential amino acid requirements of swine and poultry. Soybean oil is used for human consumption and different industrial application. Several soybean products like soymilk, livestock feed and oil, can be improved by processing raw material from special soybean varieties developed by conventional plant breeding. Alternation of seed chemical compositions and employment of specially used varieties can improve the quality of final products and decrease costs during processing. Several variety types, with altered protein composition or fatty acids, are available. Seed lipoxygenase enzymes are mainly responsible for beany off-flavor of some soybean products such as soymilk and tofu. Through conventional breeding, it is possible to eliminate all three lipoxygenase isozymes from soybean seed (triple null *lox* or lipoxygenase-free varieties) without influencing the other technological and agronomical properties of soybean. Trypsin inhibitors (Kunitz and Bowman-Brick trypsin inhibitors) are a thermo-labile anti-nutritional factor regularly present in soybean seed. Thermal processing and solvent extraction inactivate trypsin inhibitors and

other thermo-labile anti-nutritional factors. Varieties lacking Kunitz inhibitor can be processed with saving energy during production of soybean meal. The growing rate of monogastric animals fed by raw Kunitz-free soybean is still inferior in comparison to soybean meal. Unfortunately, up to date there has been no soybean variety without the requirements for thermal processing, lacking anti-nutritional factor other than trypsin inhibitor. This type of varieties is suitable for small farms with direct feed production and animal growing. Altered fatty acid composition by conventional soybean breeding is prosperous and successful. Low linoleic soybean variety contains 1% linoleic acid in contrast to conventional varieties which contains about 8%. Linolenic acid is responsible for making soybean oil prone to rapid spoiling, prompting the use of partial hydrogenation to increase stability and shelf life. Due to better oil sources on European market and low human consumption of soybean oil, this type of varieties is not so interesting for European growers and processors.

Perspectives of soybean breeding

Even for conventional and organic production, or special type varieties, soybean breeding is the first essential step. Yield is the most important trait and a lot of effort is done to increase yield potential. The most common soybean breeding method is single seed descent. Plant breeding usually considers selecting the superior genotype from large and variable plant populations. Molecular markers are very popular and a



useful tool to increase efficiency of soybean breeding programs. Considering simply inherited traits, such as disease resistance, the usage of molecular markers has proved to be a successful story. Minimizing phenotypic screening with simple tracking of marker transmission, transferring the desired genes into a new genetic background, the breeders get predictable results. Transferring the same gene into another genetic background will also generate same results. With a complex trait, such as yield and other agronomical important traits, the usage of molecular markers is much more difficult. Widespread use of molecular markers in studies of complex, quantitative traits has an inadequate application in plant breeding. Reasons for this disproportion lie in the nature of complex traits. Main concepts of application molecular markers in soybean breeding consider QTL detection, developing procedure for marker based selection and estimates of QTL effect. Success of appropriate molecular marker application concept possesses several challenges: type of molecular markers, quality of phenotypic data, epistasis, GxE interaction, QTL x environment and QTL x genetic background interactions. Due to inconsistency of QTLs, simple transfer of QTLs into a new soybean

variety is very difficult and uncertain. Even closely related biparental populations, with one common genotype have different QTLs for complex traits. According to this fact, the breeding procedure needs to involve QTL analysis with simultaneous selection of superior progeny. Soybean genome is covered by more than 4,000 different types of markers, it is the precondition for successful mapping of complex traits and marker assisted selection. Using such a large set of markers in the breeding program is almost impossible. It is necessary to reduce the number of markers which are suitable for marker assisted selection of complex traits. The simplest way is to use polymorphic markers in the same interval spaced all over the genome. Mapping resolution depends of marker density and length of the interval. Another way of reducing the number of markers is searching for genomic hotspots. From previous studies, researchers can choose potential markers and increase marker density in some genomic regions of interest. Associated studies on elite germplasm can be very beneficial for identifying favorable alleles. Still, QTL analysis is necessary to confirm and validate the effect of desired QTL in actual genetic background. Genetic basis of soybean is very

narrow, and according to the pedigree data only 26 ancestral genotypes contribute about 80% of gene pool. This unfavorable fact can be useful in searching of genomic hotspots. During the last century of soybean breeding, the goal of breeding program was yield. We can say that the history of soybean breeding is in the recurrent selection of yield. Keep in that in mind, allele frequencies change between the starting gene pool and present elite lines, which makes potential genomic hotspots easy to trace. However marker number reduction is done, it is crucial to find the appropriate phase of breeding process for implementation of marker analysis. Standard QTL analysis considers multi-year and multi-location field trials of segregating population and marker analysis of all population members. This approach has proved to be impractical for breeding. Different modifications of breeding scheme are available, balancing between effective population size, accuracy of phenotypic data, number of crosses and capacities for marker analysis. Mapping and QTL analysis should be done as early as possible in the breeding process, in order to guarantee a sufficiently large number of individuals for precise analysis and to reduce further testing of unsuccessful genotypes. One possibility is to increase population size in earlier phases of breeding process and then conduct mapping and QTL analysis. Based on these findings, only a small number of potentially superior lines would be advanced for further examination. One time embedded linkage between molecular markers and QTL can be used for screening seed remnant of that bi parental population. Quantitative genetics and statistical methods entered plant breeding in the middle of the last century and today they are conceptual parts of plant breeding process. As biotechnology goes forward, we are witnessing a new influence of technology and knowledge in plant breeding. ■

Some burning questions for lucerne breeders

by Paolo ANNICCHIARICO* and Carla SCOTTI*

Lucerne has displayed low rates of forage yield gain compared with other crops (e.g. maize), owing to several biological characteristics which hinder its breeding work (autotetraploidy, open pollination, high gene interaction, perennial growth cycle, and high genotype \times environment interaction). We are pointing out some questions which we feel are crucial for breeding of this crop.

Which is the most efficient selection scheme for synthetic varieties?

A number of schemes have been proposed, but empirical comparisons have been rare and limited to just a few schemes, whereas theoretical comparisons are hindered by the absence of reliable estimation for relevant genetic parameters. A large-scale comparison of nine major selection schemes, including clonal selection and genotypic selection with and without intra-family selection based on half-sib families and families from one (S1) or two (S2) selfing generations, is on-going in Lodi. The efficiency of selection schemes will be compared according to actual selection gains of the synthetics selected according to each scheme. The genetic base includes 125 potential parents issued by a preliminary stage of phenotypic selection carried out on a large base population. The ability of genotypes to be cloned or to produce S1 seed was widespread. Production of S2 seed confirmed to restrain the genetic base, being insufficient for 26% of the parent germplasm.

How to exploit heterosis?

Non additive genetic variation, which is at the basis of heterosis, could be exploited by free hybrids (alias semi-hybrids) in which both hybrid seed (derived from between-population crossing) and non-hybrid seed (derived from within-population crossing) are present (3). Two procedures are currently being tested in Lodi. In the first one, the final product is a double hybrid (DH) variety obtained by crossing multiplied simple hybrids (SH) (7). In practice, we have tested several sets of SHs derived from crossing of partially inbred families, applying strong selection for dry matter yield along with two selfing generations under sward conditions (250-400 plants/m²). The best SHs represented the basic modules for variety development. In fact, they could either be polycrossed to obtain synthetic varieties, or multiplied separately and finally crossed to give DHs (Figure 1). In two independent two-year experiments, DHs yielded 133-145% more than the respective best parent. The best-yielding DHs outyielded the corresponding synthetic by 10-25%. This yield gain could only be due to better exploitation of heterosis by DHs, as DHs and synthetics shared the same four S2 constituents. Parental SHs are also an effective way of storing genetic diversity and

handling it to promptly face diversified selection challenges.

A second, less complex procedure implies the assessment of two-way or three-way free-hybrids derived from three narrowly-based pools issued from two cycles of phenotypic selection, namely: i) one locally top-performing landrace from northern Italy; ii) one selection from a collection of Egyptian germplasm selected for winter hardiness; iii) one selection from semi-erect germplasm originated from Eastern Europe and from Spanish "Mielga" populations. The three-way free hybrid would contemplate a 50% genetic background for the local landrace. Free-hybrids will be compared with the synthetic variety obtained by selection within the local landrace, to verify whether the increase of heterosis provided by hybridization with exotic material could offset the lower richness in locally-useful adaptive genes. The allegedly higher yield stability of the free-hybrid material (3) will also be assessed.

Can we breed very drought-tolerant varieties?

We first investigated drought tolerance because of its impact on the large genotype \times location (GL) interaction effects observed for lucerne material across northern Italy.

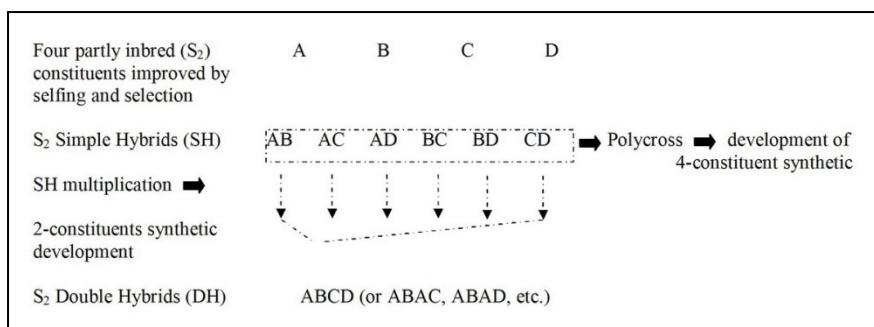


Figure 1. Scheme for constructing free-hybrids with four constituents

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Four artificial environments created by the factorial combination of drought stress (almost nil or high) and soil type (sandy-loam or silty-clay) successfully reproduced the GL effects observed across agricultural environments (2). A close relationship emerged between drought tolerance and the level of summer drought stress: i) in the evolution environment, for landraces; ii) in the evolution environment of the parental germplasm and/or the selection environment, for varieties (2). Large roots featured material specifically adapted to favourable environments (1), probably because of its special importance for storing nitrogen reserves under severe intra-specific competition, while the large investment of photosynthate required for an extensive root system may not repay the additional water uptake in water-limited Mediterranean-climate environments.

Tolerance to more severe drought stress levels is gaining interest as a consequence of climate change. Information for this context is being generated by the EU-funded project PERMED, which contemplates the assessment of adaptation and drought tolerance for a number of populations across several south-European and north-African environments, followed by the investigation of morphophysiological traits associated with drought tolerance in separate physiological studies. Preliminary results suggest the presence of two adaptation strategies for drought-tolerant cultivars. One implies drought avoidance through a water-conservation strategy (implying more water available in late, severe stressed periods), while the other is likely to rely on physiological mechanisms of drought resistance. A large root system is being confirmed as typical of material specifically adapted to favourable environments.

How to improve forage quality?

Early mowing has a major impact on forage quality, but requires varieties which tolerate early cutting (at 5% blooming). Selection for modified stem morphology, such as increased internode number and decreased internode length, can

contribute to forage quality by increasing the leaf/stem ratio, which is the main trait affecting protein content. Indeed, we found limited protein content variation in healthy, green leaves of different material (28-30%), while finding wide variation in stems (from 10-11 to 16-20%) which mainly depended on the different age of the internodes overtopping to form the mature stem. Two experimental synthetics obtained from positive selection for dry matter yield, stem height and diameter and divergent selection for stem morphology (short internodes, SI vs. long internodes, LI) along two selfing generations exhibited significant differences across summer cuttings for internode length and number, leaf/stem ratio (0.80 for SI, 0.76 for LI and 0.70 for some control cultivars), and protein production per plant (0.61 for SI, 0.56 for LI and 0.54 for cultivars) (8). The conventional simultaneous improvement of forage yield and leaf/stem ratio is also possible on the basis of the slight inverse genetic correlation that we found between these traits.

Which opportunities for marker-assisted selection?

Various linkage maps for tetraploid lucerne are available now. Results from US trials indicated that useful markers for forage yield are markedly site-specific and inconsistent across cropping years (6), suggesting that their use may be envisaged in the context of a definite adaptation target for the future variety. Useful markers have reportedly been located for traits less complex than forage yield, although their inference space (and, hence, their usefulness for breeding) may be limited when based on progenies of one biparental cross. Methods based on the analysis of shifts in marker allele frequency in selected material relative to unselected material, which allows for widening of the inference space of the results, seem particularly useful in breeding for stress tolerance (4).

How to exploit genetic tools from *M. truncatula*?

Most SSR molecular markers (64 out of 73) used in Lodi for estimating the genetic

diversity of lucerne material derived from *M. truncatula* EST and genomic libraries. There is concern that information on marker-trait associations for forage yield or tolerance to abiotic stresses obtained from *M. truncatula* may be only marginally exploitable in lucerne, owing to physiological differences arising from perenniality and possible differences due to gene function or gene structure in the genome (9). We have established mutant collections of *M. truncatula* by insertional and chemical mutagenesis in cooperation with IGV-CNR of Perugia (5). They allow complementary approaches of forward (phenotypic screening, and identification of the gene(s) affected by the mutation *via* the known inserted sequences) and reverse genetics (screening for Single Nucleotide Polymorphisms in gene(s) of interest, and phenotypic study of the progenies carrying the mutations). We are targeting secondary metabolite pathways which are conserved in the *Medicago* complex and, in particular, the triterpenic saponin pathway, owing to the interest of saponin biological activities (natural biocide, probiotic, and pharmacological activity). We have found a mutant plant lacking haemolytic saponins and identified the responsible gene, which is currently being characterized. ■

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Black locust improvement in Serbia

by Branislav KOVAČEVIĆ*, Saša ORLOVIĆ* and Andrej PILIPOVIĆ*

Black locust (*Robinia pseudoacacia* L.) is an important leguminous tree species that originated from North America and was introduced to Europe in 1601. That was the achievement of Jean Robin (1550-1629), famous arborist of the Kings of France, so the genus *Robinia* was named after him. Nowadays, it is widely spread in the world, especially in areas with a dry climate. It is mainly used for fixing sands, afforestation of abandoned agricultural lands, wood production for industry and energy, honey and forage production. The first serious project in which the black locust was utilized at the territory of Serbia was afforestation of the Deliblato sands. This project was started in 1817 by the Austro-Hungarian monarchy and continued until now. The introduction of black locust in the 1850s was a breakthrough in that event (1). It is estimated that there are currently more than 50,000 ha of black locust stands in Serbia, and half of it in Vojvodina. Black locust is usually planted on sands, along roads and railways as shelterbelts, within settlements, but also as plantations dedicated to wood and biomass production, and bee-keeping. Black locust is a very adaptable

species. Its best performance is on sandy-loamy soils, with adequate moisture, where it can grow up to 35 m high and with 50 cm of breast height diameter. It also tolerates extremely dry, salty soils where it is less productive but still viable. The majority of black locust stands are established on less favorable soils.

How to develop a genotype

There were many black locust breeding programs, but the most interesting programs were in United States and Hungary. The usual methods were provenance tests, clonal selections within stands, selection among and within half-sib and full-sib families. The interest in this species was related to its high adaptability, drought tolerance, abundant and frequent seed crop, excellent sprouting ability, early and abundant flowering, fast growth and relatively high timber yield, tolerance to pests and diseases. Beside the US and Hungary, nowadays there is increased interest in black locust in Mediterranean countries (Italy, Greece, Spain and Turkey), and Asia (China and Korea).

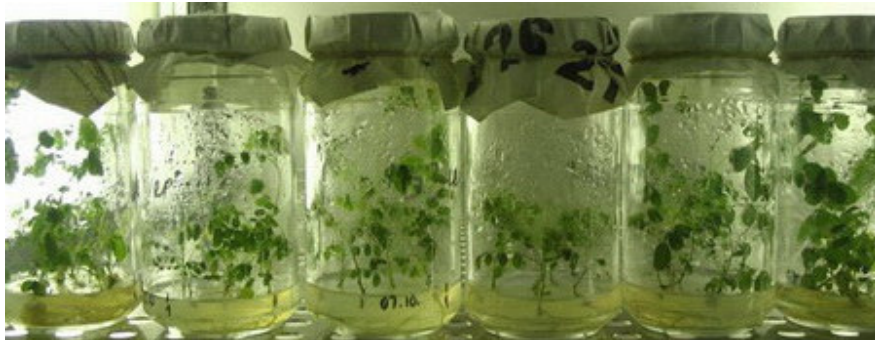
In Serbia, the program on the improvement of black locust production started in the 1980s, at the Institute of lowland forestry and environment in Novi Sad. Initially, some Hungarian clones were introduced, such as Jászkiséri, Nyírségi, Ülloi, Zalai, Appalachia and Rosaszin-AC. Until now, more than 150 superior genotypes were collected from seed grown stands and propagated vegetatively (root cuttings, green cuttings, micropropagation, grafting). They are preserved in genotype archives at the Institute's experimental estate near Novi Sad.

The efforts are concentrated in the improvement of tree shape (straight), wood quality (for industrial purpose), long flowering and high nectar production. However, the production of clonal material is not valued enough, because the black locust timber is rarely used by the wood processing industry. Thus, we use these clones in the establishment of new seed orchards, in order to improve their genetic potential for the quality of wood material and tolerance to pests, diseases and changing ecological conditions. Also, many high quality stands throughout Serbia are registered to be dedicated to seed production. In the near future we are hoping the selected clones will be used for the establishment of plantations dedicated to biomass production and bee-keeping, as well as for horticultural purposes.

Some recent attempts include selection among and within half-sib families. The selection process starts within families from the juvenile phase in nursery tests (good rooting, vigor and pest and diseases tolerance characteristics). The selection among families is rather weak and starts later, in the adult phase, in order to preserve variability within species.

The variability of important black locust anatomical, physiological and morphological traits is studied in our Institute. Contemporary international research includes work on identification of biochemical and molecular markers that are important for variability studies and protection of authorship, as well as identification of quantitative trait loci that could be used in marker assisted selection.

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Micropropagation of interesting black locust genotypes

By both seed and root

Black locust plants are commonly multiplied by seed or by root cuttings. Growing trees from *seed* is a relatively simple method for reliably producing seedlings on a large scale under a variety of circumstances. There are more than ten registered stands dedicated to seed production in Serbia. The seed viability and germination should be tested, and seed scarified before sowing. Two hundred to two hundred fifty thousand one-year old seedlings of good quality could be raised on one hectare.

Vegetative propagation is suitable for reproduction of superior genotypes in order to preserve superior traits. Production of plants in this way demands more care than raising seedlings from seeds. The most common way is by root cuttings (root pieces cut into 8–10 cm lengths), and rarely by softwood cuttings, for which root promoting hormones should be used (Kevrešan et al, 2007). Also, clones of black locust are propagated by means of micropropagation or grafting. Plant tissue culture methods provide us with new means to speed up vegetative propagation of recently selected clones and give us the opportunity to establish new clone trials and a seed orchard with them. Also, some clones of horticultural value are propagated in tissue culture too.

Black locust as a power plant

Considering the contemporary rising demands for energy and the importance of renewable sources of energy, especially biomass, the interest in wood energy production plantations becomes considerable. Black locust is a promising tree species for this purpose, since it has excellent

energy production properties, such as:

- vigorous growing potential in juvenile phase;
- excellent coppicing ability;
- high density of the wood;
- high dry matter production;
- favorable combustibility of the wood;
- relatively fast drying;
- easy harvesting and wood processing.

The way of introduction of such production in regular agricultural practice is seen through agroforestry systems, in that the coppicing ability of black locust is of high interest. Advantages of energy forests of coppice origin are that the cost of establishment is low compared to that of soil preparation, plantation and cultivation. From the developed root system of the previous stand, a large dendromass can be produced within a short time period. Disadvantages of these forests are that the area distribution of trees in coppice stands is not as uniform as in plantations optimized for energy production. In coppice stands the quantity of the produced dendromass is lower and the length of growing time is highly influenced by the uneven distribution of stems.

A bee forage and a beauty

In recent years interest has increased in the establishment of plantations dedicated to bee-keeping. They would be established as a mixture of numerous clones with good vitality and growing habits but differing in flowering phenology (Guzina and Tomovic, 1997). In that way, the longer, less weather-dependent bee forage would be insured. Beside other good qualities these genotypes should have good flowering and nectar production.

There are several varieties and species forms that are widely used in horticultural purposes like: R.p. var. *umbraquifera*, with globul tree shape, R.p. var. *pyramidalis* with pyramidal tree shape, R.p. var. *inermis* without thorns, R.p. var. *monophylla* with single-leaf leaf-type (just one leaf blade).

A recipe for high yields

Black locust requires deep, well-drained soils with adequate moisture until the associated nitrogen-fixing *Rhizobium* bacteria are able to thrive. Thus, soil preparation to improve aeration and the soil water regime and tilling of the inter-row space is necessary.

Black locust afforestation and artificial regeneration may utilize one year old seedlings that are coppiced immediately after the planting in order to improve vitality of the plant and avoid branching caused by tip necrosis. Black locust stands are often regenerated by coppice (from root suckers) too. In young stands of coppice origin, a cleaning should be carried out to adjust spacing when the stands are 3–6 years old.

Height growth peaks within the first five years, while diameter growth culminates in the first decade. The peak of current annual increment is at about the age of 20, whereas that of the mean annual increment is at about the age of 35–40 years.

Thinning and pruning of crop trees are regular operations tending operations in order to achieve optimal growth and wood volume production results. The usual annual wood volume increment in our black locust stands is 8–9 m³/ha/yr. ■

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Pea genetic diversity studies for better breeding

by Petr SMÝKAL*

The process of plant domestication had consequences on plant genetic makeup. More than 250,000 higher plant species are described at the moment, but only about 500 have been cultivated at one time or another. Crop genetic diversity, being crucial for feeding humanity as well as for the environment, continues to be reduced.

It is not surprising that demand for high productivity and homogeneity in crops has resulted in a limited number of standard, high-yielding varieties at the expense of heterogeneous traditional local varieties. Traditional local varieties and landraces preserve much of the diversity within a species and comprise the genetic resources for breeding new crop varieties to cope with environmental and demographic changes. The study of genetic diversity for both germplasm management and breeding has received a considerable amount of attention, especially with the introduction of the core collection concept.

The largest resources of pea

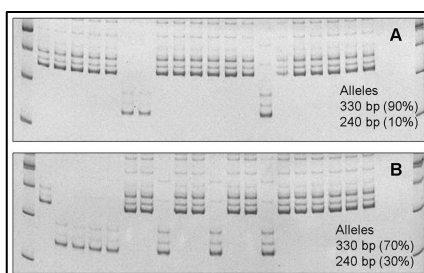
Pea (*Pisum sativum* L.), as one of the oldest domesticated crops, ranks as the fourth most widely grown food legume. Its seeds serve as a protein-rich food and feed source. Adapted to a wide range of climates, accessions of pea have been collected and maintained within several major collections worldwide. These include: John Innes Centre (JIC), UK (3,194), Nordic Gene Bank (NGB), Sweden (2,724), United States Department of Agriculture (USDA), USA (3,710), International Center for Agricultural Research in the Dry Areas (ICARDA), Syria

(6,105), Instituto del Germoplasma (BAR), Italy (4,297), Leibnitz Institute of Plant Genetics and Crop Plant Research (IPK), Germany (5,336), Australian Temperate Field Crops Collection (ATFC), Australia (6,567), Vavilov Institute of Plant Industry (VIR), Russia (6,790) and the National Genebank of China (NGC), China (3,837 accessions).

Forming the core collections

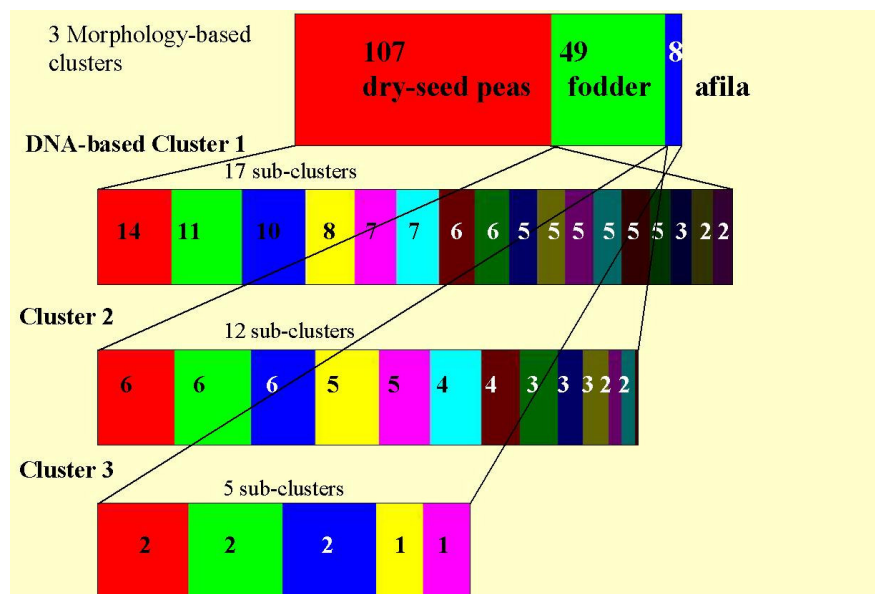
Many studies have been conducted on *Pisum* germplasm collections to investigate genetic and trait diversity. It is also important for breeders to know the genetic basis of cultivars, especially whether they have become too narrow in diversity to render the crop vulnerable to disease or pests. Accessions most genetically distinct from others are likely to contain the greatest number of novel alleles. Morphological descriptors are still widely used in defining germplasm groups and remain the only legitimate marker type accepted by UPOV (Union for the Protection of New Varieties of Plants) for new variety registration. Morphological traits often represent the action of numerous genes; however, trait manifestation can be substantially influenced by environment. Genetic structure of defined populations have been investigated by various molecular marker approaches, including microsatellite and retrotransposon-based markers (1, 4, 6, 8, 10).

In particular, Simple Sequence Repeats (SSRs or microsatellites) have been popular for assessing *Pisum* diversity because of their high polymorphism and information content, co-dominance and reproducibility (1, 5). A potential but largely neglected problem using SSRs for characterizing highly diverse germplasm, is size homoplasy and possibility of back-mutation exhibited by this marker type. Alternatively, marker systems based on retrotransposon insertion polymorphism have been used for phylogeny and genetic relationship studies in pea. Retrotransposon-based insertional polymorphism (RBIP) provides a highly specific, reproducible and easily scoreable method based on presence and absence of specific insertions suitable for in depth phylogeny and germplasm diversity studies (4). Using these markers, several major world pea germplasm collections have been analyzed and core collections formed: over 2,000 accessions of the Chinese collection have been analyzed by 21 SSR loci (10), 310 USDA pea accessions have been assessed by 37 RAPD and 15 SSR markers (2), INRA France used an extensive set of 121 protein and SSR markers to genotype 148 INRA accessions (1, 5). The CDC Canada pea collection (~100 accessions) was studied by RAPD, ISSR and SSR (8), the entire JIC pea germplasm (~ 3,500 accessions), comprised largely of expedition collections, was analyzed using 45 RBIP markers (Jing *et al.* in preparation) and over 1,400 pea accessions of the Czech National Pea Germplasm collection were genotyped using a combination of RBIP and SSRs (6).



SSR analysis of AD141 locus performed on 8% PAGE-TBE gel, EtBr stained/UV visualized; Twenty individual seeds of sample from 1963 year (A) and 2004 (B); 100 bp marker

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This latter study has shown that both SSRs and RBIPs have similarly high information content, and offer comparable diversity measurements. This is an important finding, as SSRs in spite of having multiple alleles, are more difficult to transfer between labs, while essentially binary RBIPs are simpler.

Marker methods improvement

Although the above mentioned marker types are used widely, their potential is limited. With advances in model legume sequencing and our increased genomic knowledge, there is a shift to gene-based markers. This trend can be expected to further proliferate in line with rapid advances in high throughput single-nucleotide polymorphism (SNP) generation and detection assays, such as next generation sequencing technologies.

Improvements in marker methods have been accompanied by refinements in computational methods to convert original raw data into useful representation of diversity and genetic structure. The initially and still largely used distance-based methods have been challenged by model-based Bayesian approaches. The incorporation of probability, measures of support, ability to accommodate complex models and various data types make them more attractive and powerful.

A virtual world pea collection

A large amount of polymorphic data points have been produced. However, after data processing, further use of such data is limited, especially in the absence of cross-comparison between collections. Furthermore, most of these accessions have been evaluated for morphological, agronomic and phytopathological traits, thus the data has great potential application for basic science and breeding. An international initiative was formed to coordinate the international *Pisum* research community (3, 7) in order to foster combining available data sets into a virtual global collection and the development of a dispersed international reference collection. We feel the time is right for establishment of a virtual, pea world core collection combining suitable molecular platforms with robust morphological parameters to address population structure and allow better cross-comparison between collections. Such a collection would provide a useful and powerful resource for next generation markers such as single nucleotide polymorphism (SNPs) and, more importantly, for phenotypic analysis of agronomic traits. These would act as toolkits for association mapping, as a strategy to gain insight on genes and genomic regions underlying desired traits (9). Compared to conventional linkage-mapping based on

Model-based analysis of genetic structure

time-consuming mapping population development, linkage disequilibrium (LD) - mapping using the non-random associations of loci in haplotypes is a powerful high-resolution tool for complex quantitative traits. In contrast to biparental crosses, the higher resolution and the possibility of historical trait data exploitation indicate that this approach has enormous potential in crop breeding and genetics. The prerequisites include a collection of accessions with a wide representation of the available and existing genetic diversity, recording the phenotypic characteristics and finally genome-wide genotyping.

A database for the future

One very important, if not critical, issue is the deposition and availability of molecular, agronomic, and morphological trait data. There is an attempt to develop and use a database system that will bring together passport, morphological and genotypic data that will improve germplasm management as well as enable data exploration across a wide range of data types. Defining a pea core together with a set of markers SSR, RBIP and for the future – SNPs, can provide a basis for comparison of phenotypic and molecular analysis. ■

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Disease resistance in faba bean

by Diego RUBIALES* and Josefina C. SILERO**

Faba bean (*Vicia faba* L.) is one of the oldest legume crops grown as a valuable protein rich food and for animal feed. It is an excellent candidate crop to provide nitrogen input into temperate agricultural systems. Priorities for faba bean breeding include the development of cultivars resistant to diseases. The key diseases of faba bean are Ascochyta blight, chocolate spot, rust, downy mildew, foot and root rot complex, broomrape, stem nematode and various viruses. Different control methods have been proposed against these diseases, ranging from cultural practices to the use of chemical and biological control methods, although the use of genetic resistance is the most economical and environmentally friendly control method. However, to date no efficient sources of resistance have been described to most faba bean diseases, or resistance is complex in nature, making necessary the implementation of other control measures. Still, significant genetic variation for these traits exists for faba bean, with numerous germplasm lines maintained, providing an excellent resource for plant breeders. Many of these traits have already been incorporated into modern cultivars, but several others, many of which are controlled quantitatively by multiple genes, have been more difficult to manipulate. We will briefly revise and critically discuss current and future strategies on breeding faba bean for resistance against important diseases.

Ascochyta blight

Ascochyta fabae is a common disease that causes up to 90% yield losses in susceptible cultivars when environmental conditions are favourable for disease development. The fungus infects all above-ground plant parts including seeds and the damage includes reduction in photosynthetic area, lodging following stem girdling, pod and seed abortion, and seed infection. Ascochyta control through crop rotation, clean seeds, and chemical treatment has not been completely effective and the development of resistant cultivars is widely recognized as the most efficient method of control. Different methods of disease assessment have been used but only incomplete resistance has been identified so far (5, 9). Physiological specialization has been suggested but firm definition of true races of *A. fabae* is still controversial and standardisation of the inoculation and evaluation methods and development of a unique differential set is needed.

Chocolate spot

Botrytis fabae is especially severe in humid areas. The major constraint for faba bean breeding for chocolate spot resistance is the

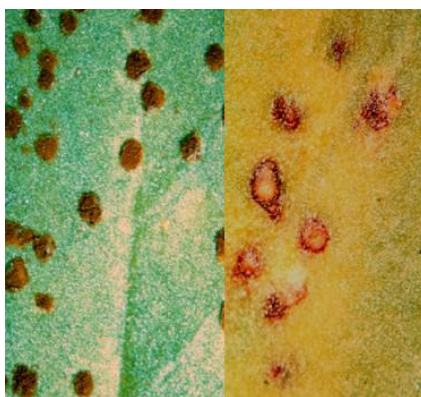
lack of high levels of resistance. Although there is some resistant germplasm, most has yet to be introduced into the agricultural market. Several methods of screening are being used (9). It is remarkable to notice that resistant germplasm originates mainly from the Andean region of Colombia and Ecuador (1). Molecular markers have not been associated so far with chocolate spot resistance.

Downy mildew

Peronospora viciae occurs in most faba bean production areas, but is most frequent and severe in north-western Europe. Soil-borne oospores cause systemic infection of emerging plants. These produce wind dispersed conidia which give rise to cycles of secondary or localised infection. Epidemics can develop rapidly, and yield losses are highest when infection increases during early flowering or before flowering. Cultivars with high levels of partial resistance have been described (6), however, large scale evaluations are required given the increased importance of the disease in major growing areas, and the relatively high cost of fungicide control. In parallel, investigation of variation in the pathogen population is needed.

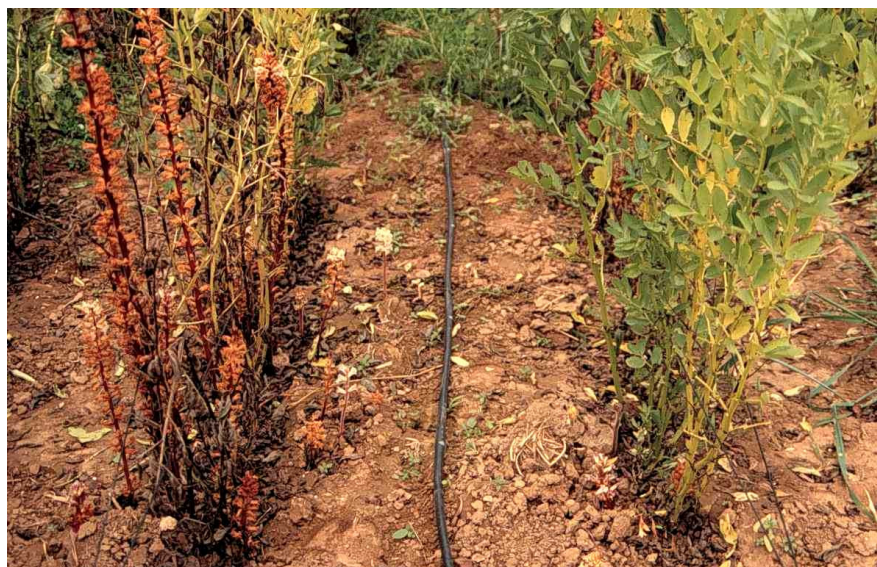
Faba bean rust

(*Uromyces viciae-fabae*) is a major disease in the Middle East, North Africa, Europe and China. Different control methods have been proposed ranging from cultural practices to the use of chemical and biological control methods. Several sources of resistance against rust have been reported in faba bean in the last decades. Incomplete resistance is



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common whereas hypersensitive resistance has only recently been reported (7). Only incomplete levels of hypersensitive resistance were identified, causing intermediate infection types. However, the evidence of physiologic specialisation in *U. viciae-fabae* suggests that the use of single resistance genes in cultivars would not result in long time rust control, so strategies to prolong the durability should be implemented.

Foot and root rot

A number of pathogens have been associated with this complex faba beans including various species of *Fusarium*. Some other fungi may also be present, including *Rhizoctonia solani*, *Pythium* spp., *Phoma* spp. and *Aphanomyces euteiches*. Different screening methods have been recommended (2), but the wide range of possible causal agents complicates the screening. It is important to identify the major agent in each area and to screen for resistance against it.

Stem nematode

Ditylenchus dipsaci is the most common and damaging nematode of faba bean, particularly the 'Giant' race. Screening procedures have been developed to estimate resistance in faba bean in pots under controlled environment conditions and in nematode-infested fields (8). Resistance has been reported but no information is so far available on the genetics of resistance.

Broomrape (*Orobanchae* spp.)

Faba bean can be parasitized by three different species of broomrape, namely crenate broomrape (*Orobanchae crenata*), foetida broomrape (*O. foetida*) and Egyptian broomrape (*O. aegyptiaca* (syn. *Phelipanche aegyptiaca*). The only way to cope with the weedy root parasites is through an integrated approach, employing a variety of measures in a concerted manner, starting with containment and sanitation, direct and indirect measures to prevent the damage caused by the parasites, and finally eradicating the parasite seed bank in soil. Breeding for resistance is the most economic, feasible and environmental friendly method of control, however appropriate screening methods and effective selection indices are needed to ensure success. Resistance against broomrape in faba bean is difficult to access, scarce, of complex nature and of low heritability, making breeding for resistance a difficult task. This has made selection more difficult and has slowed the breeding process, but the quantitative resistance resulting from tedious selection procedures has resulted in the release of cultivars with useful levels of incomplete resistance combined with a degree of tolerance (4).

Susceptible versus incomplete resistance to crenate broomrape

Viruses

Several viruses may damage faba bean, including bean yellow mosaic virus (BYMV), pea enation mosaic virus (PEMV), bean leaf roll virus (BLRV), faba bean necrotic yellows virus (FBNYV), true broad bean mosaic virus (TBBMV), broad bean mottle virus (BBMV) and broad bean stain virus (BBSV). Some resistance has been identified against BYMV, BLRV and BYMV (3).

The adaptability and productivity of faba bean are limited by major diseases. Successful application of biotechnology to disease resistance in faba bean will require both a good biological knowledge of faba bean and the mechanisms underlying resistance. Effectiveness of MAS might soon increase with the adoption of new improvements in marker technology, together with the integration of comparative mapping and functional genomics. Comprehensive studies on host status and virulence of the causal agents are often missing, and in most of the examples listed above, there is little agreement on the existence of races and on their distribution. Scarce information on levels and mechanisms of resistance is a major limitation for any breeding programme. ■

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GL-TTP and AEP: *Together we stand, divided we fall!*

GL-TTP General Assembly, Master Congress Centre, Novi Sad, Serbia, 28 November 2008

The GL-TTP originated as a component of the Grain Legumes Integrated Project (GLIP). This FP6 EU project was founded to help to promote European feed protein production. Its biological activities were built up mainly on the model legume species *Medicago truncatula* with its extension to crop legumes and integrated agronomy, genetics, genomics, physiology, crop protection, and end use. The goal of GL-TTP was the transfer of results and applications generated from research activities of GLIP to plant breeders and the grain legume industry. As an EU project, GLIP and GL-TTP were bound by legal agreements within the consortium and with the European Commission. With substantial financial support from GLIP, GL-TTP was managed by a full time scientific manager until the end of 2007. In January 2008, new Executive Committee members were elected and assumed the leadership activities. The GL-TTP website (www.gl-ttp.com) is maintained within the AEP website (www.grainlegumes.com).

In an effort to coordinate the GL-TTP with other international pulse organizations such as the International Conference on Legume Genomics and Genetics (ICLGG), the International Food Legume Research Conference (IFLRC), and the European Association for Grain Legume Research (AEP), the question whether there is an excessive proliferation of legal entities involved in pulse crop

research. The primary question is: “Should GL-TTP continue as a legal entity, should it continue under AEP, or under an entirely new organization”? In recent times, GL-TTP and AEP have endeavoured to address the broader community of not only grain legumes, but all diverse representatives of the large *Fabaceae* family, including economically important forage legumes and leguminous trees.

There are currently 27 member organizations. Many new members from eastern European countries joined this past year. The membership categories were reduced from three to one, with a membership fee of 250 euros per organization per year of which 100 euros were spent on organization of the workshop.

A proposal regarding future plans for GL-TTP was outlined at the meeting in November 2008 as follows: There are numerous organizations in Europe and worldwide that have a long term interest in legume oriented research and development. In addition, there are numerous well known and accepted reasons to retain legumes in agriculture. The importance of legumes to world agriculture and economies underscore the need to have a strong organization which could effectively present scientific results with a single voice to the scientific community and funding organizations. Moreover, the idea of technology transfer to end-users remains an important need.



However, the shift in Europe to long term dependency on imports of plant derived protein has resulted in a negative effect on legume cultivation in Europe (3% versus 30% legumes in cropping systems in North America), end-users' and breeders' interest is steadily declining. On the

other hand, with the current economic recession and sustainability becoming a primary goal in agriculture, the economic situation may become more favourable for legume cultivation in Europe.

Arising from these considerations, the GL-TTP Executive Committee proposed to its members that it should have the power to act to promote the wider interest of grain legumes. Based on the above-mentioned reasons and the fact that the legal status of GL-TTP is precarious due to the GLIP project ending in 2008, the Executive Committee proposed dissolution of GL-TTP to be executed by ballot with at least $\frac{3}{4}$ of the members present at the General Assembly.

Proposal: "That the membership of the GL-TTP empowers its executive committee to negotiate a merger of functions with the European Grain Legumes Association (AEP). For clarity we anticipate that this could be either as a new legal entity or with the functions of the GL-TTP as an interest group in AEP."

A vote was taken, with 21 of 27 members actually present. The participants unanimously supported the proposal, with 21 in favour, and 0 who opposed, and that was sufficient to confirm the decisions that have been made.

The current GL-TTP executive committee was challenged to implement the proposal by the end of 2009. ■

GL-TTP Executive Committee members:

- Petr Smýkal (Agritec Plant Research Ltd., Šumperk, Czech Republic), President;
- Noel Ellis (John Innes Centre, Norwich, UK), Past President;
- Anne-Marie Bochard (Limagrain, Riom, France), Treasurer;
- Tom Warkentin (University of Saskatchewan, Saskatoon, Canada), First Vice-President;
- Aleksandar Mikić (Institute of Field and Vegetable Crops, Novi Sad, Serbia), Second Vice-President.

Market situation of faba beans and field peas in the EU from a breeder's perspective

by Olaf SASS*

When looking at the development of the acreages of faba beans and field peas during the last decade, the trend for each crop followed a different pattern. Of course this is mainly determined by the developments in the countries with the largest acreage. Therefore a closer look at the situation within those countries shall be undertaken. Figures demonstrate the cumulative area of spring and winter faba beans in the UK and France, as well as the pea growing area in the countries with the largest area in the EU which are France, Germany and the UK. The trends can be described as follows.

1. Field peas: there is a steady reduction in acreage during the respective years with a quite drastic decline in France from over 600.000 in 1998 to about 115.000 in 2008. Germany and the UK have moved in the same direction.

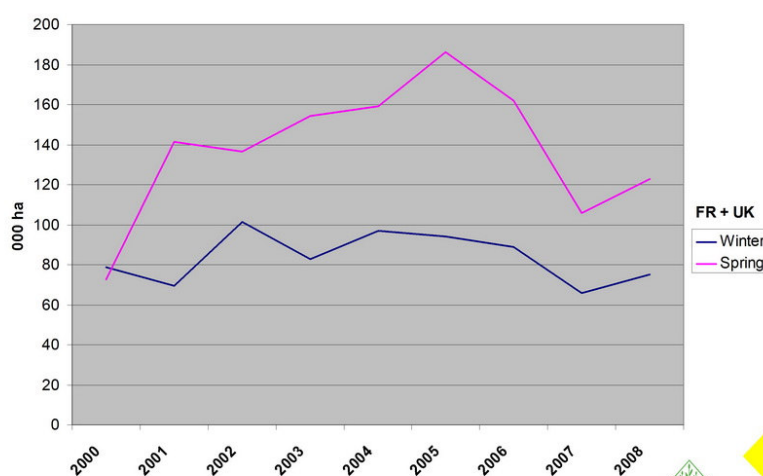
2. Faba beans: for the spring beans there is a slight expansion of the area, for winter faba beans this has been stable. However, the overall amount of the acreage is at a relatively low level.

Why are the trends different? The decline in field pea production in France has various reasons one of which is the appearance and spread of the soil borne root rot disease caused by *Aphanomyces euteiches*. Fields with a severe infection are not suited to pea production for a long time. Another point is the fact that peas are mainly used as components in animal feed. There they

substitute protein from soybean and starch from cereals or other energy providing fodder components. Many of these components especially soybeans are generally cheaply available on the world market and prevent home grown protein crops from capturing higher prices. For peas there are hardly any premium sectors in the market in which higher prices could be achieved. In the UK, there are a few of them with production of large blue or marrowfat peas. These are quite small and require special breeding efforts. The constant production levels of faba beans in the UK is partly due to some agronomic circumstances. In certain areas there are some very heavy soils. On these soils it can be difficult to establish winter oilseed rape as one of the most common broad leaved crops in crop rotations. Winter

oilseed rape requires a fine seed bed in August which may be quite difficult on these soils especially in dry summers. Faba beans can deal with such soil conditions and can take on the role as one the main crops in cereal rotations. In addition, there is an opportunity for the farmer to get a premium for his crop. Faba beans with smooth seeds, white hilum, free of spots, cracks and holes caused by bruchid seed beetles, can be exported into Egypt and neighbouring countries for human consumption. When this quality is achieved there can be a bonus of 3-5 Euro/100 kg compared to the basic fodder price. A reasonable acreage, like in the UK, together with a good extension service which maintains a good know-how about the whole production process, also stabilises faba bean yields.

FABA BEANS Acreage development 2000 – 2008

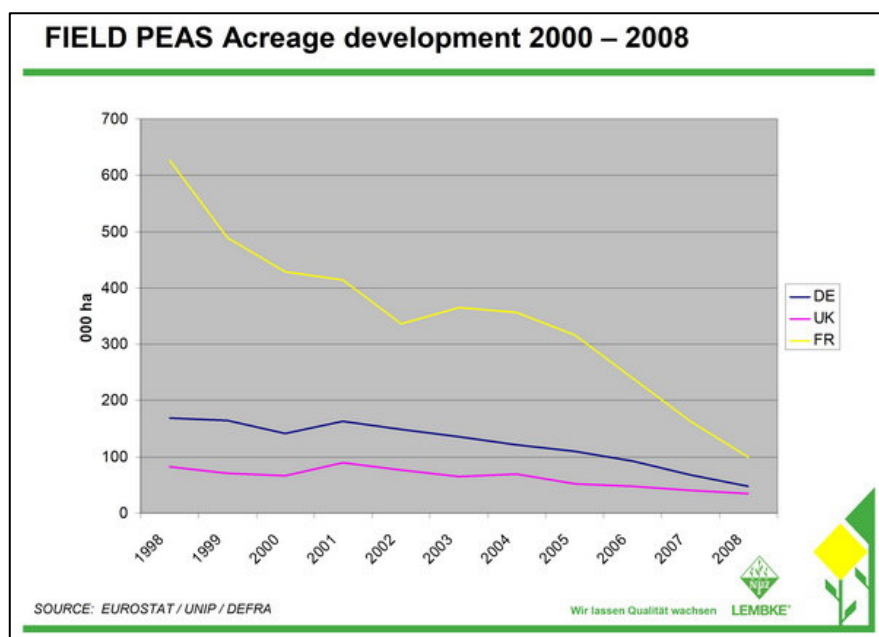


SOURCE: UNIP / DEFRA / W&S

Wir lassen Qualität wachsen LEMBKE



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The developments shown are negatively correlated with the willingness of the farmers to buy certified seed. With the decline of pea production and the urge to save costs the use of certified seed is reduced even more. According to our internal calculations the market for certified seed in the EU-15 for faba beans is about 16.000-18.000 tonnes, which may yield 1.2 to 1.5 million Euro in royalties per year. This includes both winter and spring types. For peas our internal calculations are 30.000- 35.000 tonnes of certified seed with total royalties of 2.0-2.5 million Euro. It is evident that to bring up these numbers the overall acreage and the use of certified seed needs to be significantly increased. A full sized breeding program costs 450.000-500.000 Euro per year. The royalties also have to cover all marketing and advertising costs. Certainly a breeder never can calculate having the whole market. Finally a breeding company of course does not only want to cover costs but to have some sustainable financial gain from this business.

Looking at the actual input in private breeding to our knowledge in spring faba bean there is one larger program plus 3 programs with minor input in Europe. In the pea area there are still 5 full programs active plus 2-3 with lower intensity. In winter faba beans there are 2 programs with lower input and in winter peas one full program and 2 with minor input.

As a conclusion it can be stated that the level of faba bean production in the EU is basically constant, which is mainly due to the situation in UK. The level of the overall acreage is not very high and unfortunately split into winter and spring types which require separate breeding programs. There are no signs for any larger positive movements. The breeding activity in Europe has more or less adapted to this market situation.

For the peas the trend is negative and the number of breeders active still seems to be too high to survive, based on the existing markets. Generally it must be stated that the overall breeding input into these crops is certainly too low to make significant genetic improvements in the medium-term perspective. The gap between the genetic improvement of pulse crops and the other large arable crops will inevitably grow. To maintain pulse crops in EU rotations, they need additional financial support, which pays tribute to their important contribution to extend crop rotations, reduce reliance on nitrogen fertilizers, and improve biodiversity. The fact of being self sustainable for mineral nitrogen reflects about 200 litres of crude mineral oil per ha which is not used with the respective saving of carbon dioxide emissions. All these positive contributions to the environment must be rewarded and at the moment there are slight signs in France and Germany that this is politically recognized. ■

Breeding forage legumes for enhanced seed production

by Đura KARAGIĆ*, Slobodan KATIĆ*, Vojislav MIHAILOVIĆ* and Branko MILOŠEVIĆ*

It is true that the most important forage legume species, such as lucerne, red clover, pea and vetches, have considerable genetic potential for seed yield. However, their plant morphology often leads to significant losses in seed production. By this reason, breeding programs for these species must always incorporate reliable seed yields as an equally important strategic goal to forage yield and quality. In that way, seed losses will be decreased to an acceptable level and make the newly developed cultivars suitable to answer market demands.

The main use of forage legumes, especially those cultivated as field crops, is the production of feed, such as green forage, hay and haylage. As a consequence, forage legume breeding leads to the development of cultivars with high forage yield, high leaf proportion in the total yield and slender and soft stems with high digestibility. However, such plant morphology, the chemical composition of cell walls and intercellular space, predispose the plant to significant susceptibility to lodging.

To improve standing ability

It is lodging that represents the major problem in the seed production of all forage legumes in diverse agroecological conditions of Europe, including Serbia. The seed producers try to prolong and improve the standing ability of each forage legume cultivar by the regionalisation of production and various agronomic practices, such as mode and time of sowing of vetch and pea and the cutting schedule in lucerne and red

clover. Nevertheless, the effects of these measures are limited and cultivars with improved standing ability are needed. Therefore, forage legume breeders should make an acceptable compromise between forage yield and quality on one side and standing ability on another side. The latter could be improved by shortening the internodes and increasing the number of nodes. Breeding has successfully solved the problem of lodging by reducing plant height from 130-170 cm in most wild or locally grown forage pea populations to 60-80 cm in all modern dry pea cultivars.

To improve seed characteristics and crop physiology

However, in some dry pea cultivars a new problem of a thin and insufficiently elastic seed coat that breaks easily during maturation and harvest is the reason for a significantly lower viability in comparison to those with a more elastic seed coat.

Thousand seed mass is an important factor in dry pea cultivation, since it is directly correlated with the cost of sowing. Large thousand seed mass (250-300 g) which often equates to high grain yields and desirable protein production is undesirable with regard to seed cost and often results in a doubling of expenses compared to dry pea cultivars with a thousand seed mass of 150 g. It is considered by many that the upper limit of a desirable thousand seed mass in modern dry pea cultivars should not exceed 230 g.

Increasing the uniformity of flowering in forage legume varieties, especially red clover and vetch, could shorten the period of maturation and significantly decrease seed losses in harvest, thus having a rather positive impact on the increased seed yields. Moreover, breeding should decrease the susceptibility to pod dehiscence and seed shattering, especially in vetches, as well as to decrease the susceptibility of protein pea to powdery mildew and aphids. ■



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Faba bean in Egypt

by Amero A. EMERAN*, Walid M. EL-RODANY** and Diego RUBIALES***

Faba bean (*Vicia faba* L.) is one of the main winter grain legumes grown for seed in Egypt. It is known as the principal traditional meal for the majority of Egyptian people, being consumed almost daily. The most popular dishes in Egypt for breakfast are named *Fol medames* and *Tamia* (also called *Falafel*) which can be eaten as such or as sandwiches (Fig. 1).

Total area devoted to faba bean cultivation annually is about 100.000 ha (Fig. 2) with produces about 300.000 tonnes (Fig. 3) and supplies about 65 % of Egyptian consumption, thus requiring annual imports of more than 150.000 tonnes (2). This makes Egypt one of the major faba bean importers (1). These imports used to be made from Australia, but now arise mainly from France and UK who harvest earlier and are geographically closer. Interestingly, imported seeds are sold far cheaper at local markets (0.4 €/kg) than locally produced faba beans (1 €/kg), and are less appreciated by consumers as they do not meet local preferences for culinary quality.

Unfortunately, even when Egypt is deficient in faba bean production, the total area of faba bean production decreased substantially between 2000-2006 due to biotic and abiotic stresses which limited the realization of full yield potential and caused instability in yield. In Egypt, the most important biotic stress on faba bean is caused by broomrape (*Orobanche crenata*). This is an obligate parasitic weed which markedly reduces yield and might cause total crop loss.

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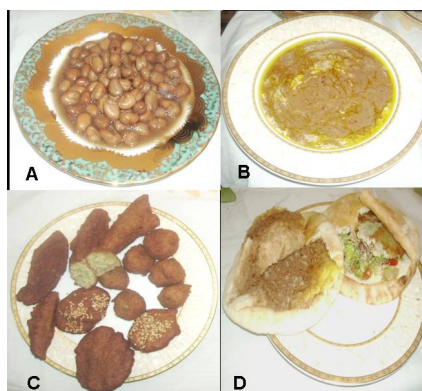


Fig.1: (A) *Fol medames* before preparing, (B) *Fol medames* ready for eating, (C) *Tamia*, (D) *Fol medames* and *Tamia* as sandwich

Fig2:Faba bean total cultivation area(1000ha.) in Egypt

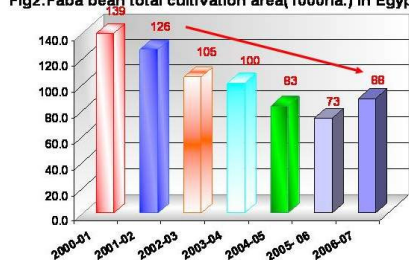
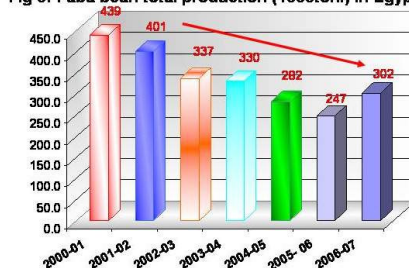


Fig 3: Faba bean total production (1000ton.) in Egypt



Area of faba bean cultivation decreased by about 30% in the last decade because of *O. crenata* infestations. Chocolate spot, incited by the fungus *Botrytis fabae*, is the most serious leaf disease of faba bean crops in Egypt, followed in importance by rust (*Uromyces viciae-fabae*). Losses due to these foliar diseases might reach 55% in susceptible cultivars.

A wide variety of approaches including physical, cultural, chemical and biological have been explored against these diseases. However, the most effective method is the use of resistant cultivars. Egyptian researchers strive to release cultivars to meet farmer requests (table). Most of the varieties released bear some resistance to foliar diseases but little to broomrape. Only 'Misr 1' and 'Giza 843' are sufficiently resistant against broomrape as to be recommended in the infested area. *Field Crops Research Institute* is releasing good varieties and is continuously screening for sources of resistance. Extension programs are used to transfer new knowledge of faba bean production to farmers, but there is still need for technical advice to farmers and need to renew planting seed every year. ■

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(2) MALR (2007). Ministry of Agriculture and Land Reclamation, Administration Center for Agr. con. Statistics, Statistical brochure (2006/2007).

Released in	Cultivar	Earliness	Foliar Diseases reaction	<i>Orobanche</i> reaction
1997	Giza 3	Moderate	Moderately resistant	Susceptible
1998	Giza 843	Late	Moderately resistant	Resistant
1998	Giza 716	Early	Resistant	Susceptible
2001	Sakha 1	Early	Resistant	Susceptible
2001	Masr 1	Late	Susceptible	Resistant
2001	Nubari 1	Late	Resistant	Highly Susceptible
2003	Sakha 2	Late	Resistant	Highly Susceptible
2005	Sakha 3	Late	Resistant	Susceptible
2006	Wadi 1	Early	Resistant	Susceptible

Faba beans (*Vicia faba* L.) in Mexico

by Ramón DÍAZ-RUIZ* and Alberto ESCALANTE-ESTRADA**

In Mexico, faba bean is an important crop grown in the upland regions, up to 3,000 masl. In 2005, the area sown for grain production was 20,737 ha, 19,305 ha under rainfed conditions and 1,432.5 ha with irrigation. The production obtained was 21,223 t, which gave a yield of 1,02 t/ha (1). Under rainfed conditions production was 17,576 t and with irrigation 3,648 t. The yield per hectare under rainfed conditions was lower (0,91 t/ha) than under irrigation (2.5 t/ha). The area of faba beans grown for immature pods was smaller than the area for grain production: 9,521 ha produced 50,587 t and the average yield was 5.3 t/ha. The Central Plateau is considered to be the most important region for faba bean production. The crop is sown principally because of its resistance to frost, and it provides farmers with a major economic income. Faba bean can be sown as a single crop or associated with maize. It is sown in rotation with maize or wheat. The young pods of faba bean acquire a good price on the market, and faba bean produced for grain or vegetable provides a greater economic income to the farmers than other crops such as maize.

Sowing and frost resistance

Faba bean for grain is sown in February in regions located between 2,800 and 3,000 masl, and in April in regions located between 2,400 and 2,600 masl. Faba beans for young pods are sown in November in regions that have areas of residual humidity. The plants are resistant if there is frost during the vegetative stage, but faba beans are susceptible to frost during the reproductive stage, when flowers and fruits can display severe damage. However, during this stage the frosts are not very frequent. When frosts coincide with the reproductive stage of the crop the flowers and fruits die, but if humidity exists in the soil, plants return to flowering and form fruits, although the total yield is limited.

Farmers sow faba bean seed in rows 70 cm apart, and with 50 cm between the bushes. In every bush there are two plants. In general the crop is not fertilised and it is harvested by farmers without machinery. During harvest the grain is cleaned in the field and separated from the pods with the help of the wind before being moved to the granary. The seed of faba bean used by farmers for sowing is one year old, but we have shown that the native seed stored for eight years often has a germination rate in excess of 90%, and so it can be used for sowing.

Seed coat colours of faba bean in México



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Reproductive state of *Vicia faba*

Pest and disease damage can be severe

The principal pest that attacks faba bean in the field and glasshouse is the aphid (*Aphis fabae* L.), which may produce severe damage under dry conditions. Aphids appear on the new leaves and after five days they produce a sticky substance that looks like spots of honey. Chocolate spot (*Botrytis fabae*) appears when the relative humidity is high, so it is more frequent in regions with altitudes between 2,800 and 3,000 masl, than at altitudes between 2400 and 2600 masl. Rust (*Uromyces fabae*) is more frequent at low altitudes than at high ones. It can spread by different means (wind, human, and insects) and it infects the crop quickly causing severe damage. Losses can be higher than 80% and the crop can be lost if the rust is not controlled when the first symptoms appear. The aphids and diseases must be controlled immediately, otherwise the loss in grain yield is significant. Nowadays, the crop is protected from pests and diseases by preventive applications of different insecticides and fungicides.

Abundant germplasm diversity

The seed of faba bean has been grouped into four seed coat colour classes: yellow, white, spotty brown and purple, and the predominant colour is yellow (2). The diversity inside each colour group is abundant in terms of characters such as time to flowering, content of pigments in the stem, number of stems, number of pods, number of grains, weight of grain and yield of grain. The diversity shown is attributed to the high percentage of crossing which depends on the position of the flower on the plant, the type of population, the type of pollinator, the density of the population, the compatibility and the extent of male sterility (3). In general, farmers maintain the germplasm of faba bean as populations. The variability presented in the populations guarantees production in conditions of intense or limited rain. In glasshouse conditions, native self-fertile varieties have been identified, and these will be used to produce varieties for regions with few species of insect pollinators. The self-pollinating lines have the advantage of increasing their yield in the presence of pollinators (4).

Genetics and breeding

The majority of varieties sown in Mexico are native. They produce high yields of grain in a specific region and they belong to the farmers. Every year farmers select the seed for sowing, considering the healthiness and size of the seed. It is necessary for technical personnel and researchers to offer training in the way of selecting plants *in situ* in order to increase the grain yield of these varieties.

In addition, there are breeding projects being developed for faba bean in order to obtain improved varieties for the region considering the existing native germplasm and the incorporation of varieties belonging to other regions of the country. New varieties have to express desirable characters for farmers and the industry such as resistance to pests and diseases, high protein content and low tannin content. In addition, varieties suitable for production of vegetable faba bean, for the production of grain and also for dual purposes are required. The methods used are classic breeding methods and molecular tools.

While faba bean is very important for Mexican farmers due to its frost resistance and generation of significant economic income, new varieties are necessary for improved grain yields. To aid this, Mexico has faba bean germplasm diversely adapted to the environment that can be used in the generation of new varieties for different purposes and new crop strategies. ■

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Legumes in the work of J. R. R. Tolkien

by Aleksandar MIKIĆ* and Frederick L. STODDARD**

John Ronald Reuel Tolkien (1892-1973), an English writer, poet and linguist, is best known for his creation of the extensive imaginary world called Arda, depicted in his works, such as *The Lord of the Rings*. Tolkien reveled in the use of languages and was fascinated by their diversity.

One of the explanations for the huge success of Tolkien's works may be the extremely subtle development and usage of many invented languages, of which the Elvish ones, such as Quenya and Sindarin, are the most renown. Quenya owes its roots to Finnish, and Sindarin to Welsh.

How Elves addressed legumes

The word denoting pea (*Pisum sativum*) in the earliest form of Quenya, called Qenya, is *orivaine*, or, written in the Tolkien-invented Tengwar script, *ṙṙṙṙṙ*, and is derived from the words *orë*, 'seed, grain', and *vaine*, 'sheath, pod'. Another Qenya legume name is *kamilot*, *ḡḡḡḡḡ*, denoting red clover (*Trifolium pratense*), derived from *kanwa*, 'dark red', and *-lot*, 'flower'. This is similar to a descriptive nature of the origin of many plant names in the real world (2).

The remaining two Qenya legume names are *belilokte*, *ḡḡḡḡḡ*, denoting wisteria (*Wisteria* spp.), and *lindelokte*, *ḡḡḡḡḡ*, denoting laburnum (*Laburnum* spp.), both containing *loctë*, denoting blossom and literally meaning *purple cluster* and *singing cluster*. All of these words are not far from *Lotus* and *Melilotus*.

The only legume name found in Sindarin is *aeglos*, *ḡḡḡḡḡ*, denoting a shrub very similar to gorse (*Ulex* spp.), but larger and with white flowers, and with an additional meaning of *icicle*, probably due to a unique and impressive whiteness of its blossom.

It may be noteworthy that there is a Quenya word that denotes a plant organ closely related to the members of the tribe *Fabeae*, especially pea and vetches (*Vicia* spp.): it is *liantë*, *ḡḡḡḡḡ*, and it denotes tendril, also having a descriptive nature, since it also denotes both spider and vine.

Hobbits admired legumes too

In their more realistic, or, better to say, Latin or English form, plants, including legumes, are present in the Hobbit personal names, especially the female ones, so among Rosies, Lobelias, Belladonnas, Primulas and Daisies, one may encounter Melilot, too.

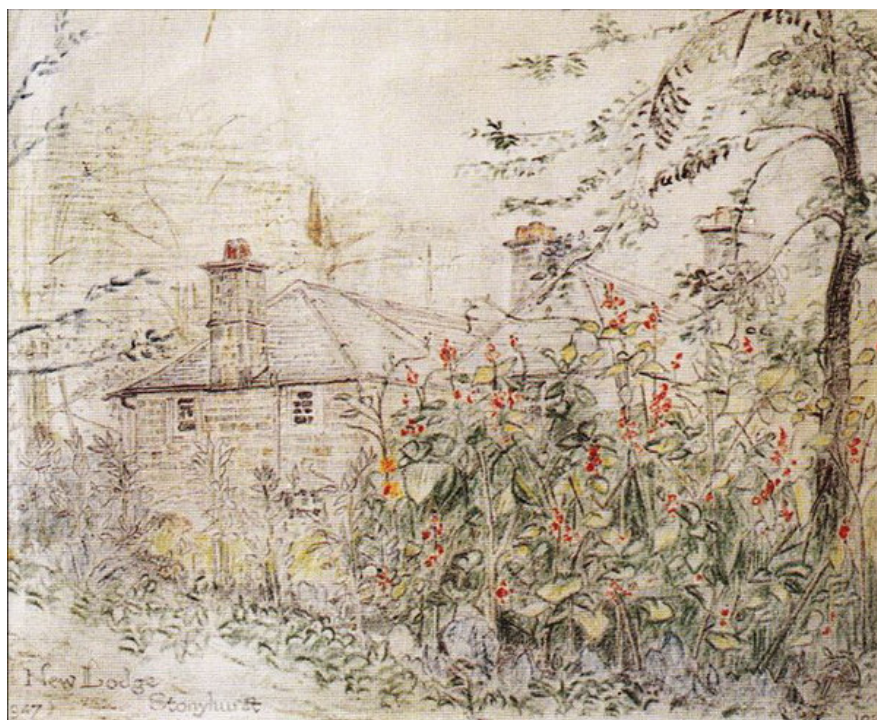
In the end, Tolkien left numerous drawings and paintings of both the real and his invented worlds: on one of them, given below, the poles with runner bean (*Phaseolus coccineus*) and faba bean (*Vicia faba*), both in full flower, may be seen, resembling perhaps (1) Frodo's view from Tom Bombadil's house, as described in the Chapter 7 of *The Fellowship of the Ring*.

'The sky spoke of rain to come; but the light was broadening quickly, and the red flowers on the beans began to glow against the wet green leaves'. ■

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In memory of Aleksandar B. Popović (1973-1999).



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