GRAIN LEGUMES

AEP

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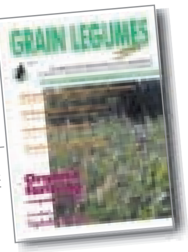

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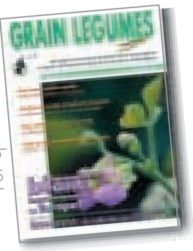

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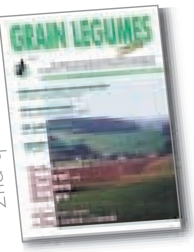

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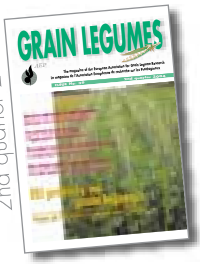

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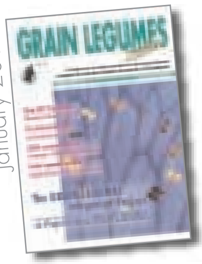

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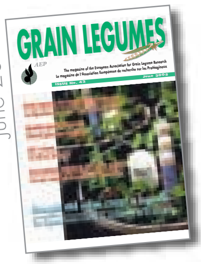

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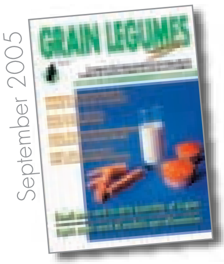

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EDITORIAL

As scientific knowledge requires increased specialisation to investigate in more detail the complexity of biological systems, and when technologies have even greater capacity for data generation, it becomes increasingly vital to aggregate and integrate the different results, techniques and specific areas of expertise to progress the general understanding. This is the challenge faced by global research approaches such as that of the EU project GLIP, and our special report illustrates some of its integrative activities.

At the same time, meeting this challenge will facilitate the exploitation of knowledge for the benefit of regional bio-economies, and this is more and more urgent in order to demonstrate that scientific research can meet agricultural needs and those of society, at a time when agriculture is experiencing drastic changes and increased market forces, and when funding bodies favour research linked to economic applications.

EUROCROP, the coming EU concerted action on arable crops set up to define future research needs for this agricultural sector, will be an interesting forum for anticipating the future context and requirements, and for proposing relevant strategies. Nitrogen-fixing crops appear to be necessary key components for sustainable agricultural development but this does not seem to be well known and we should demonstrate and publicise it further.

Anne SCHNEIDER
Managing Editor

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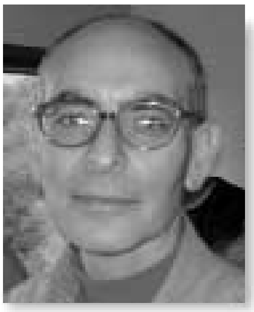

Nevin D. Young*

A reference genome for grain legume researchers

Grain legume researchers are about to receive one the best presents imaginable – the genome sequence for a reference legume. By the end of 2006, the first 'pseudomolecules' representing the chromosomes of Medicago truncatula *will be released. They will contain the draft DNA sequence for most of the gene-containing portion of the Medicago genome, an achievement that has taken nearly eight years and the efforts of labs in eight countries worldwide. This first release of Medicago's sequence will just be the beginning. Further sequencing is planned over the next three years, eventually bringing the genome from 'draft' stage to an essentially finished and complete version.*

To sequence Medicago, scientists had to break the chromosomes down into smaller, more manageable pieces (clones), each large enough to hold about 20 genes. A combination of human and robotic manipulation revealed the sequence for each of these clones, which then had to be stitched together to reconstruct the sequence of Medicago's chromosomes. This is the reason the final products are 'pseudo' molecules. In the draft form, many gaps remain (probably about 33% of the gene-containing portion of the Medicago genome). By the time the sequence is finished, researchers anticipate more than 95% will be complete.

Scientists will work with the Medicago genome mainly through large sequence databases (like Genbank and EMBL[1]), supplemented by specialised websites with visualisation and data search tools. MIPS[2], TIGR[3], and the Universities of Minnesota and Oklahoma are examples of bioinformatics sites. Researchers will move along Medicago chromosomes easily, viewing genes that have been predicted, those that are transcribed and expressed as well as those that are highly conserved with other plants.

The Medicago sequence, along with that of a second reference legume, Lotus japonicus, *will enable researchers to quickly discover candidate genes for important phenotypes, uncover genome regions that control gene expression, and design better DNA microarrays for analysis of gene function. One of the most important phenotypes that will be targeted will be symbiotic nodulation and nitrogen fixation. But there will be many other important targets: responses to biotic and abiotic stress, root and shoot development, flower and seed morphology.*

Because of Medicago's taxonomic position, the work of all legume scientists is certain to be transformed by the availability of such a profound genomic resource. ■

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*University of Minnesota, St Paul, USA.
(neviny@umn.edu)

[1] European Molecular Biology Lab; [2] Munich Information Center for Protein Sequences; [3] The Institute for Genomic Research.

GL-Pro in Brussels in May 2006: a Dissemination Event to inform decision-makers

"It is both profitable and environment friendly to include grain legumes in crop rotations and, in each European region, it is possible to grow at least one grain legume species adapted to the conditions of the region." These are the simple messages that summarise the main conclusions of the studies conducted by GL-Pro[1], and which were disseminated, with quantified assessments, to 90 participants at the recent Brussels event 'Benefits of grain legumes for European agriculture and environment: new results and prospects' organised on 3–4 May in association with GLIP (EU GRAIN LEGUMES Integrated Project).

Indeed, the GL-Pro surveys and analyses carried out in different European regions to compare typical crop rotations with rotations including grain legumes, especially pea, have provided quantified evidence of their economic and environmental value[2] to be disseminated among, and discussed with, local stakeholders as well as regional, national and European decision-makers.

(Photo AEP, Paris, France)

GL-Pro Dissemination Event at the Renaissance Hotel, Brussels.

Profitability and environmental values

With the introduction of peas or faba beans, the economic profitability of the crop rotations is maintained because inputs, especially N-fertilisers, for the grain legume and also for the following crop, generally wheat, are saved; the yield of the following wheat is also increased. On the agronomic side, disease and weed management is facilitated due to the increased length of the rotation and the introduction of the break crop. This reduction of pest pressure leads to a lower pesticide requirement, but also to the increased sustainability of the cropping system and its mid- and long-term profitability.

Life cycle assessments (LCA) have shown the value of legume crops, which do not need N fertilisers, both in terms of their use of fossil-energy and their lower level of greenhouse gas emissions. The introduction of a grain legume in a crop rotation composed of 75% cereals and 25% oil crops can save, on a per hectare per year basis, about 10% of the non-renewable energy sources and greenhouse gas emissions. Their value is greater when introduced in intensive cropping systems that require many inputs.

As the carbon market is likely to have openings for agriculture, this could provide an economic benefit to complement the environmental value of grain legumes.

A European impetus

GL-Pro experts believe that grain legumes have a role to play in the future of European agriculture whose new rules target both competitiveness and sustainability. They also believe that currently, a European impetus, activated jointly by the political, professional and technical players of the agricultural economic supply chain, can make this a reality. The GL-Pro experts gave some examples where decision-makers could have an impact on current developments:

– maintaining active breeding programmes in order that new improved grain legume varieties continue to be developed;

– settling common European registration files for plant protection products in order to facilitate the registrations at the national level and suppress the disparities between countries;

– supporting the dissemination of technical know-how to farmers, as well as facilitating the organisation of these recent agricultural economic integrated chains, from producers to end-users in each producing country.

New ideas for the future

R&D brainstorming sessions during the second day of the event provided an opportunity to discuss the prospects for grain legumes, and consider innovative approaches to exploit still further the value of grain legumes in future agricultural systems. For example, the energy market, for producing heat and electricity through combustion, fermentation or bio-refining, is developing quickly and, in addition to their major outlet value as a valuable component of animal feed, grain legumes could play a major role for this energy sector in coming years, because of their high energy efficiency (high energy production: consumption ratio).

Innovations in legume breeding were presented and the best ways to facilitate the transfer of these advances to the production sector were discussed, with assessments of the characters of interest to be targeted per species and region. Experience and results concerning the value and management of minimum soil tillage systems for grain legumes were exchanged.

The concept of 'ecosystems services', i.e. that agricultural systems such as the ones including legumes provide environmental services for society in addition to producing end-products was debated with a view to developing this argument in an innovative scientific approach. ■

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[1] The project GL-PRO (QLK5-CT-2002-02418) is coordinated by UNIP (Union Nationale Interprofessionnelle des Plantes riches en Protéines - France) and supported by the European Commission (FP5). The meeting taking place in Brussels was organised and supported by GLIP (European consortium of 60 scientific teams), UNIP (France), Pro-Plant (Germany), ITAcyl (Spain) and AEP (European Association for Grain Legume Research).

[2] Some results were presented in the special report of our previous issue: 'Economic and environmental value of European cropping systems including grain legumes', *Grain Legumes* **45**, 13–22. In addition, full GL-Pro analyses reports are currently being prepared by the project consortium and will be available from the AEP office.

Source: Anne Schneider, AEP (a.schneider-aep@prolea.com) and Gaëtan Dubois, GL-Pro (g.dubois@prolea.com)

Second AEL Conference

The Second Conference of the Spanish Legumes Association (AEL), entitled ‘New challenges and opportunities for legumes in the Spanish food and feed sectors’, was held in Cuenca on 25–27 April, 2006. The conference attracted fifty-one papers with the most recent Spanish results on agronomy, biotic and abiotic stresses, genetic resources, breeding, production, commercial strategies, technological application and new uses of legumes species in Spain.

The opening lecture ‘Legumes: potential sources of bioactive components’ was presented by Dr Francisco Millán, Director of the Instituto de la Grasa (Fats Institute) of Seville. Sixteen papers were selected for oral presentation in four round-table sessions. Thirty communications were presented as posters. The subjects of the round tables and main lectures were:

Round table 1: Legumes production in Spain. ‘The role of legume crops in Mediterranean sustainable agriculture: reality or illusion’, lecture by Dr Luis López Bellido, Professor at Córdoba University.

Round table 2: Genetic resources and breeding of legume crops in Spain. ‘Rules for the control, certification and trade of legume seeds’, lecture by Dr Daniel Palmero, Technical Department of Varieties Evaluation (INIA).

Round table 3: Legume research in a European framework, biotechnological aspects. ‘Research on grain legumes in the European Union’, lecture by Dr Álvaro Ramos, President of AEP.

Round table 4: Technological applications and commercial strategies for the legume sector. ‘Science, innovation and technological development’, lecture by Dr Alfredo Tiemblo, Vice-president of the Confederation of Spanish Scientific Societies (COSCE).

All the participants were very active in the round-table discussions and in the poster session, thus meeting the main objective of AEL conferences: to be a forum for discussion between the different groups associated with legumes: researchers, farmers, enterprises and administration.

The local government of Castilla La Mancha and the Mayor of Cuenca afforded the event a very warm reception and closing ceremony. A great effort was made to obtain good local dissemination, and the event was presented on many TV channels, in newspapers and in agricultural magazines. The organisation and subject of the GLIP project were also disseminated through a poster in Spanish elaborated by members of Workpackage 8.1 (Dissemination of knowledge) and some of their results were presented by Spanish members of this consortium.

Another of the activities of this Conference was the AEL General Assembly where the Executive Committee was re-elected. The composition of this Committee is:

President: Antonio de Ron (CSIC)

Vice-president: Mercedes Muzquiz (INIA)

Secretary: Paula Rodiño (CSIC)

Past-president: Celia de la Cuadra (INIA)

Members: Marcelino de los Mozos (CIA Albaladejito); Antonio Ortiz (GRUCOL, S.A.); Constantino Caminero (ITACYL) and Vidal Mate (Bean D.O. label Lourenzá). ■

Source: Celia de la Cuadra and Lucía de la Rosa, INIA, Spain. (rosa@inia.es)

(Photo L. de la Rosa, INIA, Madrid, Spain)

Delegates at the Second AEL conference.

Insert

Asociación Española de Leguminosas (AEL)

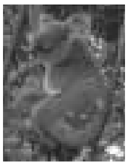
Objectives: To promote the development of Spanish legumes; to coordinate researchers in the agricultural sector; to be a forum for discussion between the agricultural sector, researchers and social communicators; to defend legume variability and to encourage new legumes uses.

Basic tools: Publications, databases, electronic agendas; web pages (www.uco.es/asociaciones/leguminosas); leaflets; technical publications and advertising through sectorial magazines and mass media contacts and AEL conferences (Córdoba, 16–17/12/03 and Cuenca, 25–27/04/06).

National links: Ministry of Science and Technology, Ministry of Agriculture, Food and Fish; Nutritional and Health National Network; Confederation of Spanish Scientific Associations (COSCE); Spanish Seed Grower Association; Farmers and Rural Development Associations.

International links: European Association for Grain Legume Research (AEP); Iberian Bean Research Group; Embassy of Canada in Spain; Plant Science Group of the University of Lincoln (New Zealand). Participation in EU projects: PHASELIEU Concerted Action (1997–2000) and the GRAIN LEGUMES Integrated Project (2004–2008).

Legume genomes and genetics 2006: down under in Brisbane



The third International Conference on Legume Genomics and Genetics (ICLGG3) was held in Brisbane, Australia on 9–13 April, 2006. A strong display of oral presentations (55) and posters (147) meant that the 230 delegates from 27 different countries received a valuable update and integration of new developments in the field.

Where does one start to summarise such a meeting? Clearly, legume genomics and genetics are an active field of research, demonstrated by the enthusiasm of researchers, the strong representation by young scientists, and the quality of the research. ICLGG3 presentations foreshadowed several key discoveries and supporting publications in high impact journals. The maturity of legume genomics was demonstrated by the multitude of interactions, amalgamating various research expertise, approaches and knowledge.

Significant for crop production, the genomic and genetic basis of organ development in legumes was described in detail. Substantial advances were described for the genetic control of flowering, nodulation, lateral branching, pollen and seed development and embryogenesis. Over the last 10,000 years selection of plant morphology has been a major contributor to increases in plant productivity.

The meeting highlighted a lot of genomic analysis of legume nodulation, leading to nitrogen fixation. In a world of increased fuel costs and increased demands for protein, this symbiotic process has both practical as well as scientific importance.

Flower morphology and leaf shape mutants (namely *Lotus japonicus* and pea) were isolated, and by application of high-throughput genomics, comparative genomics and sequencing, several candidate genes in crop legumes may now become available. Again we look forward to the publication of these findings.

A large amount of both genomic and EST DNA sequence is now public, aiding the analysis of crop genomes. Genomic information derived by comparative genomics has repeatedly directed gene discovery and plant breeding in other legumes.

Using a combination of high quality and fast-scan sequencing, it appears that most of the gene space of the model legumes *Lotus japonicus* and *Medicago truncatula* and soon soyabean will be sequenced. The *Lotus* gene space is nearly sequenced; this is exciting news and we look forward to publications in printed and electronic databases. In addition the *Medicago* genome is approaching completion. These are exciting times as it allows us to compare legume genomes, to cross reference molecular markers for targeted analysis in other crops.

Reverse genetics of legumes is becoming more common place. TILLING (targeting induced local lesions in genomes) in soyabean, *Lotus*, pea and *Medicago* is possible now, as is the application of RNA interference to determine the physiological role of critical genes. We are seeing more application of the hairy root transformation system, creating composite plants in which candidate genes are tested in transgenic roots.

The GLIP programme in Europe was strongly represented with over 10 major speakers and an AEP sponsored session. The mission of the genomic research that is the eventual application of gene technology for crop improvement remained a constant theme and was featured by some plenary sessions on the health, nutritional and environmental benefits of legume crops.

Legumes continue to be a plant family of great significance. Both protein- and fuel-security issues affect us. New infectious diseases such as the avian flu and BSE have heightened the interest in legume crops. An ever-increasing crude oil price, associated with increasing nitrogen fertiliser costs and the progressive acceptance of diesel engines, have made biodiesel a common household term. How will we be able to grow the legumes that supply both the protein and oil for these requirements?

Legume genomics and genetics, both as a conference and as a field of research are 'healthy' and growing. Potential for expansion and increased benefit to real world outcomes affecting agriculture as well as food and industrial products from legumes is now supported by the availability of sophisticated genomic tools. These include large bioinformatics capabilities, forward and reverse genetics, recognition of developmental interactions during vegetative and reproductive phases, and increased understanding of regulatory circuits involving novel bioactive molecules such as flavones, and peptides and micro-RNAs.

We can look forward to another powerful as well as enjoyable meeting to be held in Mexico in 2008 (organised by Gina Hernandez and Jaime Mora). ■

Source: Peter M. Gresshoff, ARC Centre for Integrative Legume Research, University of Queensland, Brisbane, Australia. (p.gresshoff@botany.uq.edu.au)

UK seed specialists, Wherry & Sons Ltd, celebrate 200th anniversary

In June 2006 Wherry & Sons Ltd of Bourne, Lincolnshire, UK celebrated 200 years (1806–2006) as specialist producers of pulses for food use around the world. In support of this the company has its own breeding programmes for peas and beans.

When the PBI (Plant Breeding Institute), Cambridge discontinued breeding faba beans in 1999 the programme was purchased by Wherry & Sons Ltd and they are now the major breeders of winter faba beans in the UK, although this represents only a small proportion of their interests and activities. The company also has a small marrowfat spring pea programme.

The faba bean programme is currently under the control of Mr James Wherry and managed by Mr Peter Smith with Mr Mervyn Pope, the former PBI pulse breeder, acting as consultant to the company.

PBI attempted to breed F1 hybrid beans in the 1960s and 1970s but the male-sterile genes proved difficult to manage. Hence, since then nearly all winter bean varieties have been composites, comprised of three to six lines. All current varieties have been evaluated independently in Ministry trials for inclusion in the UK National List and have also been recommended by NIAB.

Improvements have been made in resistance to *Ascochyta*, yield, shortness of straw, straw length and quality in terms of hilum and testa colour. The current NIAB recommended winter bean varieties are Clipper, Wizard and Griffin. ■

Source: James Wherry (jameswherry@wherryandsons.com) and David A. Bond, Cambridge, UK.

Lupinus mariae-josephi H. Pascual – a new lupin species adapted to calcareous soils[1]

Lupinus mariae-josephi *H. Pascual – une nouvelle espèce de lupin adaptée aux sols calcaires*[1]

by Higinio Pascual*, Natalia Bellostas** and Guillaume Laberge***

In the Iberian Peninsula, the genus *Lupinus* has traditionally included only eight species that normally live on acidic or neutral soils (1). Six of these species are native to the Peninsula and two of them, *Lupinus albus* and *L. polyphyllus*, have been introduced. *L. albus* is used as a forage legume and for human consumption, whereas *L. polyphyllus* is used exclusively as an ornamental species. Among the endemic species of the peninsula, *L. luteus* and *L. angustifolius* are used as legume forage, whereas *L. micranthus* is used only as an ornamental plant. *Lupinus mariae-josephi* H. Pascual, the new lupin species described here, is not related to any other lupin species in the Iberian Peninsula (3). It is also very different from the other species known in Europe and Africa (2).

Insert

Botanical description

Plants of *L. mariae-josephi* are erect and are approximately 50 cm high. The stems, petioles and backs of the leaves are covered with hairs (1.5 mm). Flowers (approximately 15 mm long) are of a more or less intense red colour. They are grouped in racemes (5–10 cm) with scattered flowers as in *L. albus* and *L. angustifolius.* Plants of *L. mariae-josephi* have a hairy calyx and a corolla similar to other species of the *Lupinus* genus. The pods (50 x 20 mm long) contain 3–4 seeds (8 x 6 x 4 mm). The seeds are ellipsoidal, slightly kidney-shaped, with a rough surface characterised by uniform pyramid-shaped brown granules.

The most distinctive feature of the newly discovered lupin species is its uniformly granulated seeds. The plants were 30 cm high when cultivated in 2003. Plants of 50 cm were observed in their natural habitat (Ramón Jorge, pers. comm.). For a complete botanical description see Insert 1.

A new lupin species discovered

In 2001, during a visit to the Experimental Agricultural Institute of Carcaixent (Valencia), some seeds of a lupin species that could not be identified were discovered. These were part of a gene bank of local horticultural varieties. The seeds had been collected in 1976 on a small calcareous hill near Carcaixent by an agricultural producer, Ramón Jorge Perpiña. At that time the plants were covering an area of 400 m^2 on a group of south facing natural limestone terraces. Ramón Jorge Perpiña had collected the seeds in order to use them as attractants for partridges; he had observed that the birds sought refuge among those plants. He had also observed that the plants were growing in pure stands; no other species were present in the surroundings. In the end he did not use the seeds but donated them to the Agricultural Institute in Carcaixent. In 2001, Joseph Roselló, a senior scientist at the Institute, gave the seeds to Higinio Pascual and colleagues for evaluation.

(Photo A. Ruano, INIA, Madrid, Spain)

***Lupinus mariae-josephi* at the flowering stage.**

Germination of the seeds

A few seeds of the unknown species were planted in 2002 at the Agricultural Research Institute of Madrid (IMIA). Only 10% of the seeds germinated after mechanical scarification and the others disintegrated when wetted. The seedlings showed abundant disease symptoms. Only a few plants set seed but enough material was eventually obtained to establish that they belonged to a new species, and voucher specimens for the Royal Botanical Garden of Madrid were prepared. A few seeds were sown in a calcareous soil at the Institute for Plant Genetic Resources in Madrid. Five plants were obtained, which flowered and set seed. In the coming months, the few remaining seeds will be sown with care in the glasshouses and experimental fields of different institutes across Spain. Seeds will be multiplied and further research will be conducted.

A new genetic resource

The new lupin species was found in a calcareous area, and when grown in the past few years, it has always performed better in alkaline soils. Hence, the cultivation of the genus *Lupinus* could potentially be extended to the East of the Iberian Peninsula (typically calcareous soils) and to other Mediterranean countries with similar soil types. Some universities have already expressed interest in the DNA of the new species.

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*IMIA (Institute for Agricultural and Food Research and Technology of Madrid) and High Technical School of Agronomic Engineering, Polytechnic University of Madrid, Madrid, Spain. (cesarpascual@terra.es)

**Biosystems Department, Risø National Laboratory, Roskilde, Denmark.

***Agricultural Sciences Department, The Royal Veterinary and Agricultural University Taastrup, Denmark.

(Photo A. Ruano, INIA, Madrid, Spain)

Pods of *Lupinus mariae-josephi*.

The EU-funded LIFE-Nature project for protecting and recovering endangered plant species, led by Dr Laguna in Valencia, has not succeeded in multiplying the new lupin species *in vitro.*

The species was thought to be extinct for a number of years due to the establishment of a quarry in the surroundings of the site where it was first found. However, thanks to the efforts of the botanists of the above mentioned EU project, a new population has just been discovered, which opens up new possibilities for the utilisation of this species. ■

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[1] This article is based on the paper published in the Spanish journal *Annals of the Botanical Garden of Madrid* **61**, 69–72 (www.rjb.csic.es)

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(1) Castroviejo, S. and Pascual, H. (1999). In: Flora Ibérica **7** (1), 251–260 (Eds S. Talavera *et al.*). Real Jardín Botánico (Consejo Superior de Investigaciones Científicas) Madrid.

(2) Gladstones, J. S. (1974). Technical Bulletin, Department of Agriculture, Western Australia. **26**, 1–48.

(3) Pascual, H. (1986). In: comun. INIA, Ser. Prod. Veg. **67**, 1–90. Instituto Nacional de Investigación Agraria y Alimentaria, Madrid.

PhD theses

Mouse models ot peanut allergy: contribution of oral and nasal sentitization to allergic reactions to peanut and cross-reactivity with food and environmental antigens

by Romy FISCHER*

Food-allergic patients can develop adverse reactions to members of the same and even unrelated botanical families. IgE and Th2-type responses play an important role in allergic reactions although it is now clear that these reactions involve other cellular and molecular interactions. We investigated the role played by the mucosal sites of initial priming to peanut (*Arachis hypogaea*) on subsequent immune responses to peanut and reactivity to airway antigen challenge. For this purpose, we analysed antibody responses to peanut immunisation, as well as cytokine and airway responses to nasal antigen challenge in mice orally or nasally sensitised to peanut in the presence of cholera toxin. Oral peanut sensitisation induced higher levels of IgE but lower IgG responses than nasal immunisation. Mice sensitised both orally and nasally to peanut experienced airway hyper-reactivity upon nasal peanut challenge. However, orally sensitised mice exhibited higher levels of lung eosinophilia and IL-4 in response to peanut challenge. In contrast, higher levels of lung MAC-1^+ cells and inflammatory cytokines were seen in nasally sensitised mice. Finally, nasal but not oral sensitisation promoted lung inflammatory responses to unrelated antigens. These findings suggest that the initial route of sensitisation influences the responses of peanut allergic individuals to airborne antigens and allergens. ■

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*PhD thesis November 2005, Institut National Agronomique Paris-Grignon, Paris, France in collaboration with the Department of Microbiology, The University of Alabama, Birmingham, USA. (fischer@inapg.inra.fr)

Ex ante assessment of varietal innovations in winter pea (*Pisum sativum* L.): modelling approach at the plot and farm scales*

Evaluation ex ante *d'innovations variétales en pois d'hiver (*Pisum sativum *L.) : approche par modélisation au niveau de la parcelle et de l'exploitation agricole*

by Aurélie VOCANSON

The aim of this work was to develop a methodology to assess the agronomic and environmental potential of some new winter pea cultivars before marketing, and to determine the characteristics they should combine to guarantee these advantages.

There were three stages to the work. First, four experiments (two years and two sites) were carried out to determine the effects of soil structure, sowing period and cultivar on growth (aerial and root) of a pea crop. Secondly, the results obtained were compared with other databases and used to compare and assess a dynamic pea crop model which predicts yield, grain protein content, the proportion of nitrogen derived from fixation, the nitrogen balance and the water consumption at the plot scale. Thirdly, this model was used to assess different potential candidate cultivars. In this last stage, the model was coupled with two main models. The first one was a model of work organisation at the farm scale to determine the possible sowing periods for pea cultivars, considering the problems associated with task competition in autumn. The second one was a model simulating soil structure evolution according to the soil water content to determine the risk of soil compaction under pea and the consequences on the yield.

This work increased the knowledge on root system development for different sowing and soil structure conditions. A crop model for spring and winter cultivars and sowing period, that takes into account the variability of nitrogen availability and soil structure, is usable. Finally, the combined use of different models showed that the results of the assessments of potential cultivars were different depending on whether constraints at the farm scale were taken into account or not. The work helps to alert breeders to cultivars that present agronomic and environmental potential on farm. ■

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*PhD thesis March 2006, Institut National Agronomique Paris-Grignon, France. (vocanson@grignon.inra.fr)

Agro-economic relevance of grain legumes in soil tillage systems

Intérêts agro-économiques des légumineuses à graines dans les systèmes agraires à labour

by Franz-Ferdinand GRÖBLINGHOFF*, Norbert LÜTKE-ENTRUP and Marco SCHNEIDER

Farmers are challenged by stagnating or decreasing market prices for arable crops and increasing production costs due to rising prices for fertiliser and fuel. If marketing the harvested products is already optimised, the production costs need to be examined. The direct costs of arable farming (seed, fertiliser, plant protection, grain drying/storage, hail insurance, calculated interest) are usually already optimised: in successful and less successful farms the levels of direct costs hardly vary. However, great differences between farms are found for machinery and labour costs, which normally represent more than half of the total production costs. Machinery and labour costs include wages for hired labour, the calculated wage of the owner of the farm (based on the farmer paying a manager to do the same work for him), contractor charges, machine rental as well as fixed and variable costs of owned machines. A reduction of machinery and labour costs is possible by minimising tillage intensity, but to do without ploughing in rotations with a high proportion of winter cereals can provoke many problems, for example, an increase in specific diseases and grass weeds.

Grain legumes can reduce tillage intensity

If cereal-rich rotations are diversified with grain legumes, it becomes feasible to consistently reduce machinery and labour costs and to ease phytosanitary problems. The crucial factor is the alternating of cereals and break crops, taking advantage of the precedent crop effect. The resulting savings in production costs usually more than compensate for the lower output of spring grain legumes, when introducing faba beans, peas or lupins into the cropping system.

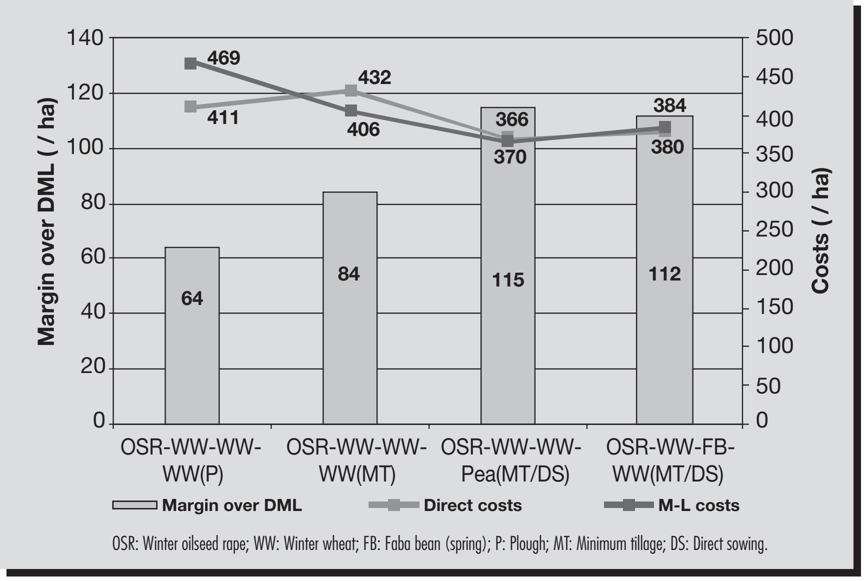
This was shown over several years in field trails performed at four locations: Soest in Northrhine-Westphalia (West), Munich in Bavaria (South), Braunschweig in Lower Saxony (North-West) and Guelzow in Mecklenburg-Western Pomerania (North-East). To compare the profitability of rotations and tillage systems, the margin over direct costs, machinery and labour costs (DML costs) was taken into consideration. The results of the cost analyses for Soest and Guelzow are shown.

Reduced tillage cuts labour and machinery costs

Although the loamy soils in Soest are characterised by high yields of wheat following wheat (average yields in 2003–05 were 9.71 t/ha with minimum tillage, and 9.88 t/ha with ploughing) the margin over DML costs was higher for the diversified rotations.

In the cereal-rich rotation winter oilseed rape/winter wheat/winter wheat/winter wheat (75% cereals) the margin over DML costs (€64/ha) was €20/ha higher with minimum tillage compared with ploughing (Figure 1). Diversified rotations with peas or faba beans managed with minimum tillage and direct drilling reached a margin over DML costs which was up to €51/ha higher than the margin of the rotation with 75% cereals and ploughing.

In the light soils of Mecklenburg-Western Pomerania high costs and low yields of wheat after wheat (average yields in 2003–05 were 7.02 t/ha for minimum tillage and 6.61 t/ha with ploughing) resulted in significant losses in the rotation winter oilseed rape/winter wheat/winter wheat/winter wheat and ploughing (–€137/ha) (Figure 2). In contrast, the diversified rotations winter oilseed rape/winter wheat/winter wheat/(catch-crop) blue lupin and winter oilseed



OSR: Winter oilseed rape; WW: Winter wheat; FB: Faba bean (spring); P: Plough; MT: Minimum tillage; DS: Direct sowing.

Figure 1. Margin over DML costs, direct costs and machinery and labour costs of different tillage systems and crop rotations on a 300-ha model farm (Soest, Northrhine-Westphalia, 2003–2005).

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*Fachhochschule Südwestfalen (FH SWF), Soest, Germany. (groeblinghoff@fh-swf.de) rape/winter wheat/(catch-crop) blue lupin/winter wheat performed better by up to €169/ha and even reached a level at which DML costs were recovered.

The changing political and business environment requires cost management in arable farming and all production costs have to be questioned. Minimum tillage systems in combination with diversified crop rotations including grain legumes can effectively reduce machinery and labour costs. Therefore diversified rotations alternating cereals and break crops are more profitable than cereal-rich rotations. It is certain, that if the standard feed outlets for peas, faba beans and lupins could be developed and added-value markets established, the competitiveness of grain legume rotations could be improved further. Specific crop rotations suitable for different farms, depend on the location, the farmers' priorities and the markets. ■

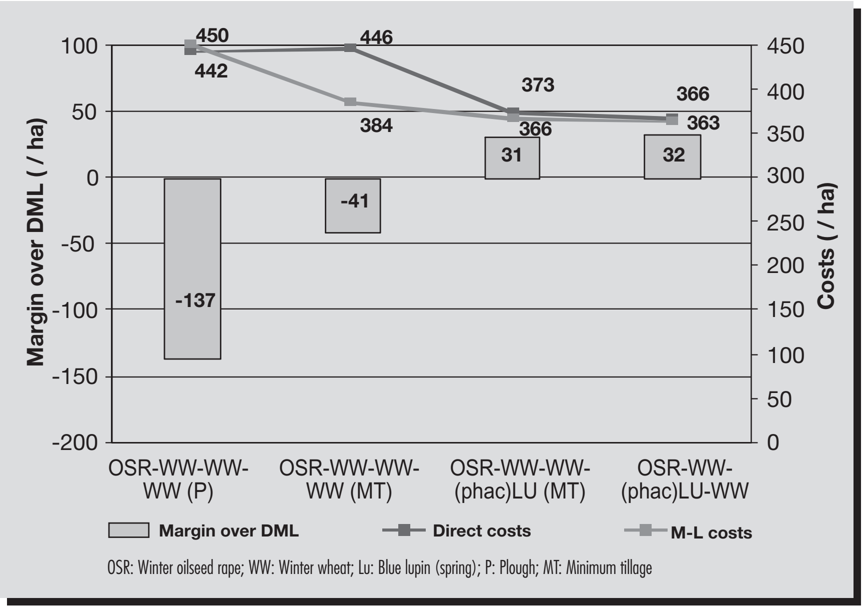
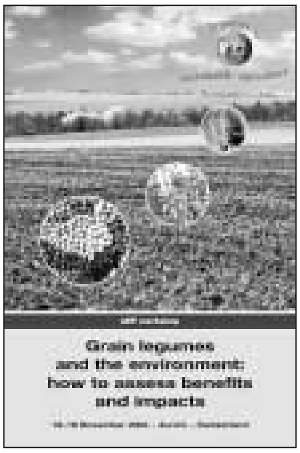


Figure 2. Margin over DML costs, direct costs and machinery and labour costs of different tillage systems and crop rotations on a 600-ha model farm (Mecklenburg-Western Pomerania, 2003–2005).

NEW BOOKS



Grain legumes and the environment: how to assess benefits and impacts

International workshop on the methodology for environmental assessment of grain legumes, 18–19 November 2004, Agroscope FAL Reckenholz, Zurich, Switzerland

March 2006, 226 pages, 160 x 240 mm
AEP, Paris, France (Ed. and publisher)
ISBN 2-9509491-8-5

To determine the environmental impact of increasing the production and use of grain legumes in Europe, specific methods of measurement are required, some of which are not currently available. It was in this context that the international scientific workshop was organised, supported by the EU Concerted Action known as GL-Pro (European Extension Network for the Development of Grain Legume Production in the EU).

These workshop proceedings include the peer-reviewed papers presented in the four themed sessions: methodology for environmental assessment of grain legumes: state of the art; grain legumes in crop rotations; nitrogen cycle of grain legume crops; and grain legumes in animal feed. They also include an introductory paper, syntheses of the sessions, the material from the posters and the major conclusions and outlook. The names and addresses of the 48 participants of the workshop provide the beginnings of an inter-disciplinary expert network of scientists working on environmental aspects of grain legumes.

€40 (€30 for AEP members and GL-Pro contractors)
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EVENTS

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IX ESA Congress
Warsaw, Poland
Web (under construction): www.esagr.org/

October 25–27, 2006
Faba bean 2006
International workshop on faba bean breeding and agronomy
Córdoba, Spain
Email: anam.torres.romero@juntadeandalucia.es
Web: www.grainlegumes.com

October 26–27, 2006
CIAA Congress 2006: Food for life, meeting consumers' needs
Brussels, Belgium
Web: http://www.ciaacongress.be

January 21–26, 2007
15th International Congress on Nitrogen Fixation & 12th International Conference of the African Association for Biological Nitrogen Fixation
Cape Town, South Africa
Email: aecon.e@mweb.co.za

November 12–16, 2007
6th AEP Conference and Final GLIP meeting
Lisbon, Portugal
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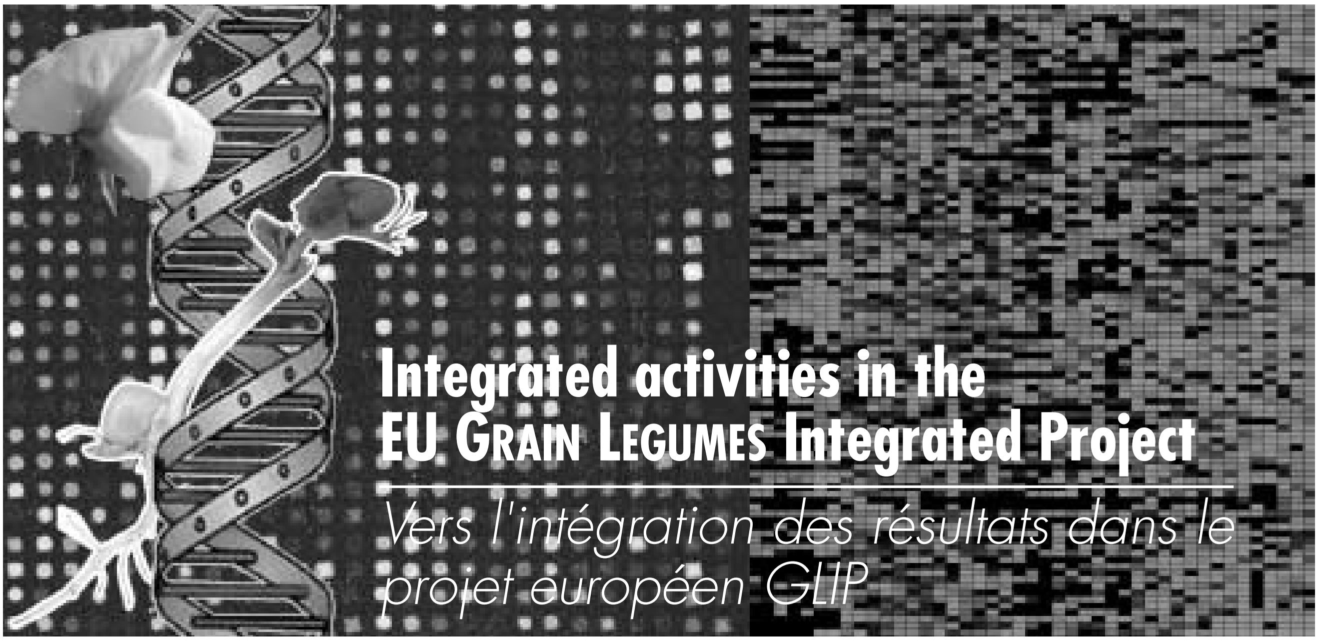
SPECIAL REPORT


(Photo Bielefeld University, JIC, UNIP, University of Wageningen)

Integrated activities in the EU GRAIN LEGUMES Integrated Project

Vers l'intégration des résultats dans le projet européen GLIP

Pea seedling, pea flower, DNA molecule, images of a micro-array and analyses of clusters.

How do we aggregate specific items of scientific information from different disciplines or levels of analysis? How do we accelerate their exploitation and enrichment if not by combining them and facilitating their access to other expert areas?

As highlighted by our special report, these are some of the key questions arising from large scale multidisciplinary projects such as the EU GRAIN LEGUMES Integrated Project[1], where there is a need to deal with the complexity of biological systems and the increased specialisation of scientific research.

The comparative genetics and genomics approaches enable the integration of knowledge obtained for model legume species with that of the legume species of agronomic interest. Gene expression profiling (transcriptomics) and the analysis of elaborated proteins (proteomics) facilitate a comparison of information on plant reactions in different conditions. Bioinformatics will combine a large quantity of heterogeneous data generated by high-throughput genomic techniques into easy-to-use interfaces in order to facilitate their inter-linkage and their exploitation by physiologists, geneticists and other users. Combining expertise from eco-physiology, genetics and genomics through integrative biology is the major on-going challenge to accompany efficient strategies to breed improved cultivars.

An integrated system approach is also required for reaching an economic and environmental assessment of agricultural systems, as summarised briefly in this report and developed in our previous special report. The air-classification process illustrates integration of scientific results with a view to industrial application.

An additional step in the challenge will be the integration of current knowledge with the requirements of the different stakeholders: the GL-TTP[2] now established will contribute to this through the exploitation of GLIP and other results, especially for breeding purposes. ■

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[1] *GRAIN LEGUMES Integrated Project: New Strategies to Improve Grain Legumes for Food and Feed (EU Reference contract FOOD-CT-2004-506223) 10 February 2004 – 09 February 2008. http://www.eugrainlegumes.org/*

[2] *Grain Legumes Technology Transfer Platform: http://www.grainlegumes.com/gl-ttp*

Comment agréger les connaissances spécifiques acquises dans différentes disciplines scientifiques et à différents niveaux d'analyse? Comment accélérer leur valorisation et leur enrichissement si ce n'est en facilitant leur accès par d'autres domaines d'expertise?

Comme souligné par notre dossier spécial, ces questions émergent des projets multidisciplinaires d'envergure tels que le projet européen GRAIN LEGUMES[1], questions essentielles pour pouvoir embrasser la complexité des systèmes biologiques alors que s'accentue la spécialisation des recherches scientifiques.

La génétique-génomique comparative permet l'intégration des connaissances acquise sur une espèce modèle de légumineuses avec celles concernant les espèces d'intérêt agronomique. L'analyse de l'expression des gènes (transcriptomique) et des protéines produites (protéomique) facilitent la comparaison des réactions de l'organisme à des conditions différentes. La bioinformatique va permettre l'intégration d'une quantité importante de données hétérogènes issues de techniques à haut débit de la génomique, afin de faciliter leur mise en liaison et leur exploitation par les physiologistes, généticiens et autres utilisateurs. Combiner les expertises de l'écophysiologie, de la génétique et de la génomique à travers une biologie des systèmes constitue l'étape clé, en cours d'élaboration, pour accompagner efficacement des stratégies d'amélioration des variétés culturales.

Une approche systémique intégrative est également nécessaire pour une évaluation économique et environnementale des systèmes de production agricoles, comme résumé ici brièvement et et développé dans le dossier précédent. Le fractionnement par densité des particules illustre l'intégration de résultats scientifiques en vue d'une application industrielle.

Une des prochaines étapes du défi sera l'intégration des connaissances actuelles en regard des besoins des différents acteurs économiques : la GL-TTP[2] maintenant mise en place va y contribuer en exploitant les résultats de GLIP et autres projets, notamment pour des objectifs d'amélioration des plantes. ■

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[1] *GRAIN LEGUMES Integrated Project: New Strategies to Improve Grain Legumes for Food and Feed (EU Reference contract FOOD-CT-2004-506223) 10 February 2004 – 09 February 2008. http://www.eugrainlegumes.org/*

[2] *Grain Legumes Technology Transfer Platform: http://www.grainlegumes.com/gl-ttp*

Integration efforts in the European GRAIN LEGUMES Project

Efforts d'intégration dans le projet européen « GRAIN LEGUMES »

by Jean DÉNARIÉ*

The European FP6 Grain Legumes Integrated Project (GLIP) is extremely large and associates 54 participants (institutions) working in quite distinct and complementary domains. Research activities are grouped in eight modules associated with four objectives (see Insert). This interdisciplinarity is essential to achieve the ambitious goals of the project, paving the way for a better use of grain legumes in Europe, but the coordination and integration of such a large and diverse project is a real challenge for all participants and for persons in charge of the scientific management.

Some of the challenges are similar to the three classical objectives of integrative biology (see Figure 1):

(i) how to make sense of the enormous amount of data that are generated by high throughput analyses?

(ii) how to integrate data obtained at a certain level of organisation of living organisms to understand higher levels of organisation?

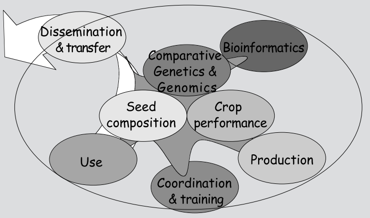
(iii) how to assess the generality of findings obtained in a model system, through comparative biology, in similar but different organisms such as crops.

Other challenges are even more complex than those of integrative biology and concern the interdisciplinary analysis of very complex systems involved in feed technology, crop management and environment conservation. Fortunately progress in information technology makes possible the use of new tools (bioinformatics and modelling) that allow handling of these complex problems.

For the second GLIP annual meeting in Montpellier we have selected a series of presentations to illustrate representative integrative efforts. To be sure to address very diverse problems, these presentations were selected to cover the six research modules of the project. First, a series of three presentations summarised the development of specific tools that facilitate research coordination and integration, for gene expression studies, the comparison of model and crop genomes, and the use of web services to integrate heterogeneous databases.

Other presentations described interdisciplinary approaches, including diverse levels of analysis ranging from molecular, cellular and whole plants to crop systems, and concerning key biological features of legumes, such as nitrogen nutrition and seed formation, including modelling of whole plant functioning for genetic dissection of seed nutritional value, systems approaches to environmental and economic evaluation of grain legumes, and processing seeds for feed and food for a fast transfer into the market.

These presentations were well appreciated by the audience of these plenary sessions and for this reason a selection of written versions based on the oral presentations has been assembled to form a special report in this issue of *Grain Legumes* magazine. ■



Objectives and modules (M) of GLIP

www.eugrainlegumes.org

Objective 1
The impact of grain legumes in animal feed and human food

M1: Grain legumes in feed
M2: Economic and environmental impact

Objective 2
The factors affecting grain legume seed quality, supply and use

M3: Seed composition and quality
M4: Crop functioning and seed quality

Objective 3
Genomic and post-genomic tools needed to improve and sustain grain legume seed quality and supply

M5: Genetic and genomic tools
M6: Bioinformatics

Objective 4
Coordination and integration of grain legume research to provide training in emerging technological approaches, to disseminate the results, and transfer technology to industry

M7: Coordination and training
M8: Dissemination and transfer (Including the technology transfer platform, GLIP-TTP)

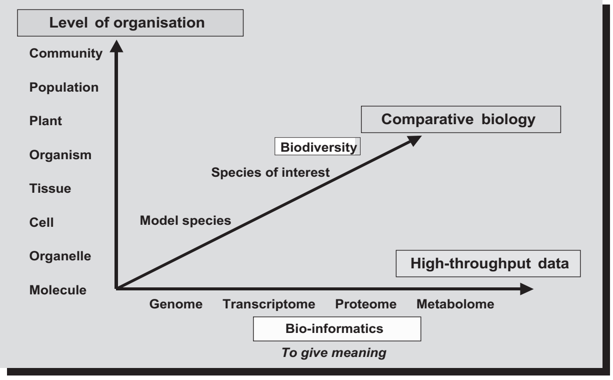


Figure 1. The three main axes of research in integrative biology.
(Source: 'Rapport INRA sur la Biologie Intégrative Végétale', INRA report coordinated by André Charrier)

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*Laboratoire des Interactions Plantes-Microorganismes (LIPM), CNRS-INRA, Castanet-Tolosan, France.
(denarie@toulouse.inra,fr)

Integration of gene expression profiling in European projects on legumes

Integration des profils d'expressions de gènes dans les projets européens sur les légumineuses

by Helge KÜSTER* and Michael DONDRUP*

Within the framework of different genomics projects focusing on the model legume *Medicago truncatula,* a range of expression profiling tools has been generated during the past six years, and these tools have in part been developed within the GRAIN LEGUMES Integrated Project (GLIP).

Construction of microarray tools

Initially, a 2.5k cDNA macroarray representing transcript sequences from arbuscular mycorrhizal roots (5) and a 6k macroarray from root interactions (Mt6k-RIT, (2)) were constructed. The Mt6k-RIT clone collection as well as a 6k unigene clone set of *M. truncatula* (6) were subsequently used for printing microarrays that were predominantly used to study different stages of root nodule development. Relying on a collection of cDNAs from developing flowers and pods, the Mt6k-RIT tool was extended to an Mt8k microarray (3).

During the 1st International Conference on Legume Genomics and Genetics in 2002, the *Medicago* community decided to commission the synthesis of a 16k 70mer oligonucleotide collection representing all TCs from the TIGR *M. truncatula* Gene Index version 5 through the Operon company (http://www.operon.com/arrays/omad.php). This collection of probes was recently extended by 384 probes targeted against transcription factors and other regulators. Within the framework of the EU project GRAIN LEGUMES (http://www.eugrainlegumes.org/) and a German network on arbuscular mycorrhiza (MolMyk, http://www.genetik.uni-bielefeld.de/MolMyk/), these tools are referred to as Mt16kOLI1 (4) and Mt16kOLI1Plus, respectively. Based on the average gene density in the *M. truncatula* genome, it can be estimated that about 35%–40% of all *M. truncatul*a genes are represented on Mt16kOLI1Plus microarrays.

As for other species, the *M. truncatula* field has in the meantime moved from the community- and project-driven construction of cDNA-macroarrays, cDNA-microarrays, and 70mer oligonucleotide microarrays to commercial Affymetrix chips, with a 51k *Medicago* GeneChip being available since the end of 2005.

In the case of pea (*Pisum sativum*), a 70mer oligonucleotide microarray designated Ps6kOLI1 was developed within GLIP. In contrast to the Mt16kOLI1Plus microarray that is based on a collection of cDNAs from a range of different tissues, the pea array was designed primarily to identify genes relevant for seed formation. For this reason, Ps6kOLI1 microarrays were based on probes targeted against ~5200 EST clusters assembled predominantly from cotyledon and seed coat ESTs. Although it has been demonstrated in the meantime that Mt16kOLI1Plus microarrays are suitable for recording expression profiles using hybridisation targets from related grain and forage legumes, the existence of large gene families calls for caution in the interpretation of cross-species hybridisation data. Thus, the existence of a genuine pea microarray tool is of importance for questions targeted at the analysis of transcription profiles in developing pea seeds.

Web-based expression profiling software

The final ambition of GLIP is to deliver an integrated database that stores all high-throughput expression data obtained in the course of the project, together with relevant information on the conditions profiled and the experimental protocols used to obtain transcriptome profiles. Whereas Mt16kOLI1Plus and Ps6kOLI1 microarrays are printed exclusively at a central facility at the Institute for Genome Research of Bielefeld University, hybridisation experiments are also performed in local facilities of different GLIP groups scattered across Europe, and including collaborators from Australia. It is thus evident that the goal of data integration can only be achieved by the development of web-based software tools. These tools had to fulfil two requirements: (1) the ability to upload raw data from microarray scanners, data from image processing software, and the descriptions of experimental conditions into a central data repository and (2) the possibility to combine these data sets to compare the expression profiles obtained in different GLIP laboratories.

The two software tools developed (Figure 1) were designated ArrayLIMS (for storing data on experimental conditions and for storing raw data) and EMMA (for data evaluation and data mining (1)). Either software can be accessed using standard web browsers, eliminating the need for local software installation and facilitating a constant central upgrade as well as an easy integration of novel analysis pipelines into the system. Since the ArrayLIMS/EMMA software is also used in other legume genomics projects, a cross-project integration of expression

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*Institute for Genome Research, International NRW Graduate School in Bioinformatics and Genome Research, Center for Biotechnology (CeBiTec), Universität Bielefeld, Germany.
(helge.kuester@genetik.uni-bielefeld.de)

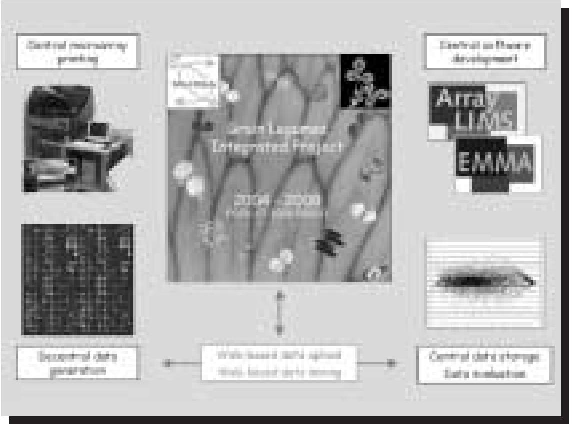

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Figure 1. Integration of microarray-based transcriptome profiling in European projects on legumes.

The web-based upload of expression data to a central data repository facilitates a collection of expression data obtained in different local facilities and is a prerequisite for data mining approaches targeted at a cross-comparison of expression profiles.

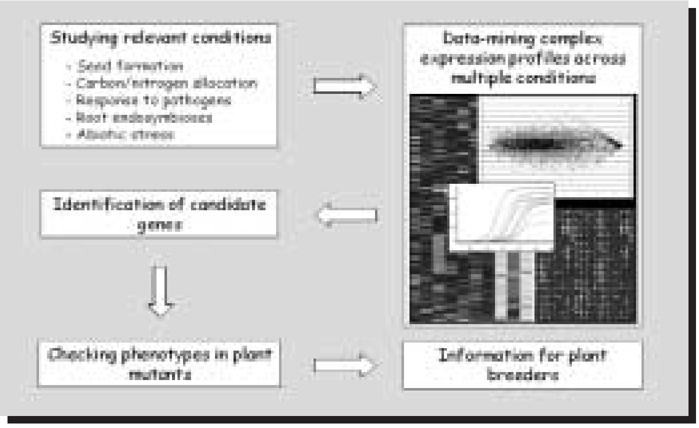

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Figure 2. Advanced data mining strategies facilitate the identification of candidate genes for legume breeding.

Integrated expression databases allow the data-mining of complex expression profiles across multiple conditions to identify candidate genes. These can subsequently be tested functionally in plant mutants, for example, generated by TILLING or retrotransposon mutagenesis. Ultimately, phenotypic information can be transfered to plant breeders.

data obtained from Mt16kOLI1Plus and Ps6kOLI1 microarrays depends only on the willingness of the different projects to exchange expression data.

To facilitate the submission of high-throughput expression data to public databases, for example, ArrayExpress (http://www.ebi.ac.uk/arrayexpress), and to allow an exchange with other projects working in the field of legume genomics, the EMMA software has been designed to comply to the MAGE-ML (MicroArray and Gene Expression Markup Language) standard. This MAGE-compatibility – together with the use of common 16k probe sets in the *M. truncatula* community – lays the foundation for an integration of expression data obtained in GLIP with expression data, for example, collected in the United States transcriptomics projects funded by the National Science Foundation (NSF).

Data-mining strategies to query complex expression profiles

An essential feature of the ArrayLIMS/EMMA software is a password management system that allows the fine-tuning of different levels of access to expression data. In GLIP, we have employed an open access policy that allows members of the GLIP consortium to query all expression data stored in the central data repository. This philosophy of data accessibility is a prerequisite for the application of the advanced data mining strategies implemented in the current release of EMMA. Whereas global data mining approaches require the setup, configuration and detailed analysis of new groups of microarray hybridisations that were imported from the ArrayLIMS system, focused data mining strategies allow targeted questions to be solved quickly. In the most simple case, these can relate to the retrieval of expression information for a gene of interest in specific (or all) conditions profiled in GLIP, whereas more advanced cases require the building of a data mining query that returns the expression information for all genes annotated, for example, as transcription factor or as protein kinase in all the different conditions studied in the project. Such data mining queries can be performed in a matter of minutes, and the resulting data sets can be exported to any spreadsheet software for further analysis.

In the case of *M. truncatula,* ~250 microarray hybridisations covering 43 conditions of legume biology have so far been performed in GLIP. These conditions cover the development of seeds, the development of root nodules and arbuscular mycorrhiza, and the response of resistant and susceptible cultivars to different pathogens, for example, the root pathogens *Aphanomyces euteiches* and *Orobanche crenata* as well as leaf pathogens such as *Phoma medicaginis, Erisyphe pisi* and blue-green aphids. It can be expected that by the end of GLIP, about 600 microarray hybridisations will be entered into the database, covering up to 200 conditions of legume biology, including the profiling of plant mutants and transgenic lines. Since the ultimate goal of the GLIP is to improve legume breeding by identifying target genes (Figure 2), only an integrated approach that allows a combination and cross-referencing of all available expression data is likely to succeed.

Whereas the generation of expression profiles from a sufficient amount of starting material has become a routine technology in many laboratories, obtaining transcriptional snapshots from individual cells or groups of cells is still a technical challenge, since the amount of total RNA available is only in the nanogram range. Nevertheless, in particular the transcriptome profiling of pathogenic or symbiotic interactions suffers considerably from the use of pooled tissue samples. Since several protocols for target amplification have been developed in recent years, these techniques will become increasingly important in future expression profiling experiments. ■

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(2) El Yahyaoui, F. *et al.* (2004). Plant Physiol. **136**, 3159–3176.

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Comparative genetics and genomics of legumes: efforts for inter-specific integration

Génétique et génomique comparatives des légumineuses : des efforts d'intégration inter-spécifique

by T. H. Noel Ellis*

The story of how legume genomes relate to each other has been tracked by previous reports in *Grain Legumes*, notably in Issues 38 and 41. It is now very clear that the genomes of legume crops align simply with those species for which extensive genome sequence is available (6, 2, 14). What this means is that genome sequence from *Medicago truncatula*, *Lotus japonicus* or soyabean can provide useful genetic tools for legume crop species generally. The genetic maps of different legumes can be related to each other relatively easily, but this begs the question of the extent to which related traits in different species are controlled by allelic variation in the same genes.

Same traits, different species

We should certainly give due credit to the great geneticist N. I. Vavilov for his recognition of 'homologous variation' in related species (12), and we can take heart that one of his exemplars was homologous variation on seed characters in *Vicia* and lentil (confusingly called *Evum lens* L. but helpfully Чечевйца[1]). It is clear that homologous variation exists, but to what extent is it governed by allelic variation in homologous (orthologous) genes? This question in relation to legumes has been reviewed recently in two contexts: flower and seed development (4, 3) and it seems as though the issue is complex.

Same traits same or different genes?

Genetic variation for some traits is conferred by orthologous genes, but for others this is not necessarily so. For example seed weight QTL apparently co-locate in legume species as different as *Pisum* and *Vigna* (11). In contrast the orthologous genes *Stp*, and *Pfo* appear to have different roles outside the flower in pea and *Lotus japonicus* (9, 13). A classical experiment in genetics was Punnet's cross between two white flowered sweet peas (*Lathyrus odoratus*) where the F1 had purple flowers, a similar experiment can be done in pea in a cross between *a* and *a2* mutants (8). So duplicate genes, where these represent functional rather than structural redundancy, should be expected to confuse the issue of inter-specific comparisons of gene function.

Mining variation

In practice what this means is that model systems are good at providing information on gene function, and when sufficiently closely related they can provide information on gene order. Thus genetic maps anchored to genomic sequence can tell us about the potential for different genetic intervals to confer interesting phenotypic traits. However, we must rely on diverse germplasm to determine whether useful allelic variation for this potential is available, for example, in *Pisum*. In turn this means we need to understand the genetic and phenotypic variation in germplasm collections. Collaborative efforts at large-scale germplasm genotyping are underway. These efforts should reduce the amount of effort that is needed for phenotypic characterisation of germplasm by directing attention to contrasting genotypes, but whether this works in practice depends on the extent of linkage disequilibrium (LD) within these collections. This information is just beginning to emerge for *Pisum* (1, 5) together with the establishment of relevant bioinformatic tools (7).

A note of caution is needed here, preliminary evidence (unpublished) suggests that LD can be found, but it is associated with population structure rather than genetic linkage. This means that the chance of finding useful marker – trait associations in wide germplasm screens is low, but it does suggest that markers can be used to identify appropriate subsets of germplasm in which this type of study can be performed.

Candidate genes

The approach based on structural genomics and comparative genetic maps tells us that there is a problem of scale for the systematic application of markers for the identification of traits. We need a method to reduce the number of allele by phenotype comparisons that have to be made. Genotyping germplasm collections can tell us how these populations are structured, but we need to match this with a way of limiting the number of genes for which we need to survey genetic variation. This approach has, rather too grandly, been called 'the candidate gene' approach.

Fortunately there are several approaches for the identification of candidate genes. The most obvious is mutant analysis: mutants that have been characterised in model systems can provide obvious candidates if we understand the genetics of the trait in question.

A second approach is to identify genes that respond to changes associated with the trait, and transcriptome analysis has emerged as a popular approach. Here we can take information from transcriptome analysis in model systems, although some

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*John Innes Centre, Norwich, UK.
(noel.ellis@bbsrc.ac.uk)

transcriptome analysis tools are being developed for pea (3, 10).

Can variation be exhausted?

So far I have discussed how genetics can identify useful extant allelic variation, but such variation can also be generated. The most widely discussed method of generating novel variation is the generation of transgenics. While this approach has not had much impact on 'grain legumes', it has had a major impact for soyabean. This has of course created a furore in the EU and the commercialisation of transgenic grain legumes seems unlikely in the near future, but we should not underestimate the potential of this approach either for cultivars or for testing ideas about allelic variation.

A second approach, TILLING (10), has become popular especially for genetic analysis in model systems. In this approach candidate genes are examined directly: a mutant population is screened for new alleles in a chosen gene. Where this gene is associated with a trait in a model system, it may be possible to identify appropriate alleles in a target (crop) species, thus bypassing the need for extensive germplasm screens.

Forward and reverse genetics

In this article I have tried to illustrate both the potential and the difficulties in exploiting genomic tools for grain legume crops, as illustrated by pea. There is a contrast between 'forward' and 'reverse' genetic approaches. In the 'forward' approach the objective is to find desirable existing variation, while in the 'reverse' approach the objective is to create variation in selected genes.

The real contrast between the two approaches is the age of the allelic variation being examined. We know that in pea polymorphism exists that is at least two million years old (5), and that the number of combinations of existing alleles is vastly in excess of the number of germplasm lines. Germplasm thus provides a selected set of allelic combinations: this is both its strength and its weakness. Reverse genetics on the other hand provides (very many) single differences between new and extant alleles, the strength of this approach is its comprehensiveness, but its weakness is that the new alleles do not correspond to phenotypes that have stood the test of time.

These approaches are not mutually exclusive, and together seem to provide tools for understanding and manipulating biological processes that impact on crop performance. ■

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[1] We are often told that the benefit of the binomial nomenclature system is that it is universal, while vernacular names are hard to relate. *Evum lens* however is no longer valid and is ambiguous relating either to *Vicia hirsuta* or *Lens culinaris,* on the other hand lentil in Russian is unambiguous!

[2] Two genes are orthologues if they are the precise counterparts of each other in different genomes: they share a single progenitor gene in the most recent common ancestor. Their function could be a clue to identifying them. Orthologues are one type of homologous genes (i.e. genes equivalent by descent), the second type being paralogues, i.e. genes related by descent but found together in the same genome.

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Insert

In addition to the presentations developed in this special report, the open plenary session of GLIP Montpellier – 2006 included the following examples of the integration of knowledge.

Whole plant response to local limitation of N acquisition

Marc Lepetit (UMR INRA-AgroM-CNRS-UM2, Montpellier France) presented a multidisciplinary approach combining molecular physiology and ecophysiological modelling. This approach was conducted in close collaboration with the group of Christophe Salon (INRA URLEG, Dijon France) in order to characterise carbon/nitrogen fluxes in legumes and their changes within plants in response to heterogenous N provision. Various N sources (including NO_3^-, NH_4^+, and atmospheric dinitrogen) were compared. By integrating knowledge arising from *Arabidopsis,* the two French groups were able to establish a general model concerning the control of nitrogen acquisition in *Medicago truncatula,* involving both local signals from the N sources and systemic control exerted by products of N assimilation and C fixation. Among the N sources tested, the groups found that NO_3^- uptake has a unique ability to compensate rapidly (within four days) for a local N limitation applied to one part of the root system by increasing the N uptake capacity in the other part. Orthologous genes[2] of *Arabidopsis* NO_3^- transporters involved in short-term adaptative responses in *Medicago* have been identified. The absence of a compensating response in the case of NH_4^+ and N_2 is probably explained by a limitation of the N acquisition capacity of the roots and results in a limitation of plant growth when the local root environment is unfavourable to NH_4^+ or N_2 acquisition (water limitation, for example). In the case of N_2 fixation, the plant overcame this problem by a long-term response (observed within 14 days) that involved the increase of nodule biomass. Transcriptomic approaches to investigate both common and specific pathways involved in these controls are currently being conducted. It is expected that important functional and structural targets that limit adaptation of N acquisition to a fluctuating environment will be identified.

Modelling pea seed nitrogen content

Judith Burstin (INRA URLEG, Dijon, France) presented how eco-physiological approaches can be used to explore the genetic basis of the pea seed nutritional value, especially the N content. Three relevant physiological modules have been defined, (i) efficiency of N nutrition by optimising complementarity of assimilation and fixation, (ii) remobilisation of nitrogen from vegetative parts to seeds (the most important N pathway during seed filling), and (iii) seed morphogenesis. In each module the involved genes and QTLs are searched for, using expression studies, and mapping studies. The forthcoming investigations will be to confirm QTLs by varying the environment and population, to identify positional candidate genes using synteny between model and crop species, and to use reverse genetics for validation.

Bioinformatics integration of heterogeneous data: the PlaNet approach as a model for plant and legume genomics

Intégration bioinformatique de données hétérogènes : l'approche PlaNet comme modèle pour la génomique des plantes et des légumineuses

by Rebecca ERNST* and Klaus MAYER*

Probably every biologist trying to make use of plant genome data is familiar with the problem of data retrieval from online databases and their use in analysis tools: most of the databases are distributed, they require different inputs and formats. Complex data and analytical queries require considerable knowledge, and often data transformations are required. Within the framework of a recent EC funded project, the PlaNet project (Plant Network) aimed to overcome these problems by integrating important European plant databases and analysis tools and enabling central access to these resources.

The decentralised PlaNet approach

Some of the most important plant research centres in Europe contributed and participated within the project. At the start of the project the only plant genome sequenced and available was *Arabidopsis thaliana.* In addition a wide range of genome centric resources and analyses were available for *Arabidopsis*. Consequently in the first phase the resources integrated into PlaNet were focused on this small model plant. When additional genomic data became available the PlaNet project integrated these resources whenever possible, for example, the genome data and annotation for maize, *Medicago* and rice that were made available through the plant databases at MIPS.

In contrast to other approaches PlaNet does not use a data warehouse solution where all data are stored in one big database. We decided to make use of a distributed approach where the datasets remain distributed and can be accessed remotely. The advantages of this approach are obvious: the dataset is always up-to-date as data are retrieved from the local datasets without use of precomputed data and generated at the moment the query is submitted ('on the fly'), data remain with the specialists annotating them, new datasets can be added easily and the system setup is low maintenance. However for a user interacting with, and using the virtual rather than centralised system the look and feel is similar.

This 'virtual' database holds all kinds of data and tools such as: (*Arabidopsis*) sequences and annotations, stocks, insertions, protein–protein interactions (PPIs), literature, gene ontology (GO), Interpro accessions, expression data, mutants and phenotypes, synonyms, expressed sequence tags (ESTs), BLAST (Basic Local Alignment Search Tool) against *Arabidopsis* proteins, transmembrane prediction, sequence and annotation data for *Medicago*, maize and rice. Integration, even for small datasets, is one of the major advantages of the distributed approach. Thus data generated by the GLIP project can be made accessible to the community as soon as they are made publicly available from a remote site. To make data accessible a web service needs to be set up by the data provider. Web services are systems similar to web pages. However unlike a web page, which is mainly developed for human interaction, web services are designed to support machine–machine interactions. From the technical side web services exchange XML that is usually transported via HTTP.

PLANET
A NETWORK OF EUROPEAN
PLANT DATABASES

BioMoby and web services

The technology used for PlaNet has been based on web services but uses a special standard for biological web services called BioMoby (http://biomoby.org). There are several differences to standard web services. The most important difference is that BioMoby uses a central 'registry' comparable to yellow pages. Service providers register their service and the input and output objects on which the service operates. Requests to the registry will list all BioMoby web services which can be used. An additional difference is that BioMoby makes use of ontologies, hierarchically structured object models which add semantics; the ontologies are also part of the registry. In contrast to standard web services this makes the system user friendly and 'intelligent'. For example,

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*GSF Research Center for Environment and Health, Neuherberg, Germany.
(kmayer@gsf.de)

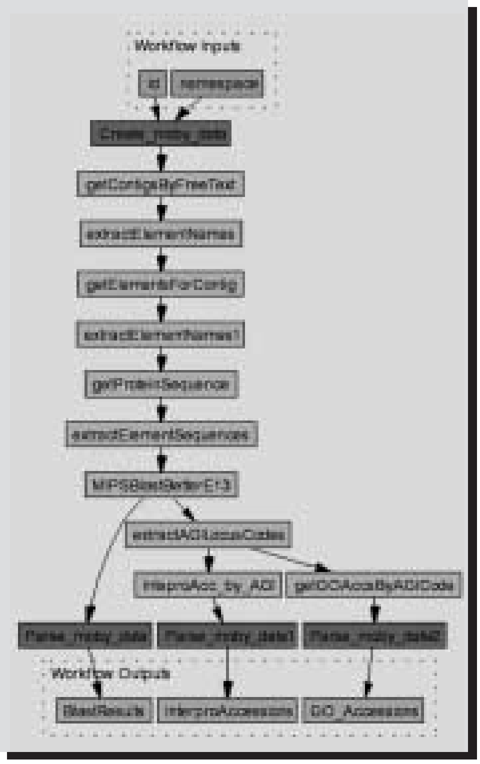
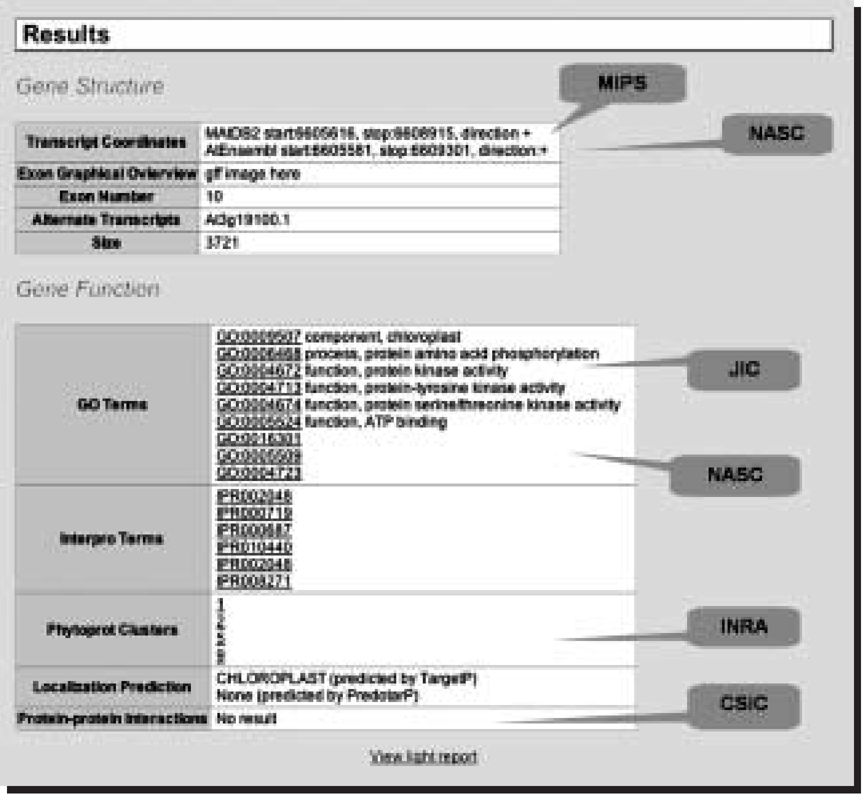


Figure 1. A Taverna workflow example to retrieve BLAST similarity data, Interpro domain data and GO functional classification for selected gene identifiers.

if a user wants to find a biological service he will not end up with the list of 130 services that are registered in PlaNet but will only receive a list of those services which, depending on the input data given, are of relevance.

PlaNet offers several different opportunities to make use of the integrated data depending on the problem that the researcher/user is aiming to solve. A common scenario is that a researcher sets out to retrieve all available information for a particular gene of interest. For this purpose a generic gene report tool (BioFloWeb) has been developed within the PlaNet project at INRA. Using BioFloWeb a researcher enters the identifier of interest and a comprehensive, configurable gene report containing the data collected (via BioMoby and 'on the fly') is returned (Figure 1). The implementation of this gene report has been done for *Arabidopsis* and will be adapted for *Medicago* as soon as data become available.


Results

Gene Structure

Transcript Coordinates	MAtDB2 start:8605616, stop:8608915, direction + AtEnsembl start:8605581, stop:8609301, direction +
Exon Graphical Overview	gif image here
Exon Number	10
Alternate Transcripts	At3g19100.1
Size	3721

Gene Function

GO Terms	GO:0009507 component, chloroplast GO:0006468 process, protein amino acid phosphorylation GO:0004672 function, protein kinase activity GO:0004713 function, protein-tyrosine kinase activity GO:0004674 function, protein serine/threonine kinase activity GO:0005524 function, ATP binding GO:0016301 GO:0005509 GO:0004723
Interpro Terms	IPR002048 IPR000719 IPR000687 IPR010440 IPR002048 IPR008271
Phytoprot Clusters	1 [illegible]
Localization Prediction	CHLOROPLAST (predicted by TargetP) None (predicted by PredotarP)
Protein-protein Interactions	No result

View light report

Figure 2. Results output of the query undertaken with the Taverna workflow depicted in Figure 1.

Web services have tremendous advantages when it comes to high-throughput data analyses. One example would be the use of a comparative genomics approach to annotate a *Medicago* contiguous stretch of sequence (contig) based on similarity. Consequently the researcher would aim to retrieve all protein sequences related to this contig, BLAST them against a database of *Arabidopsis* proteins and finally retrieve the GO accessions and Interpro accessions for these genes. These sequential analysis steps ('workflow') would take a considerable amount of time by a manual approach. Using PlaNet BioMOBY services *Medicago* contigs are defined as input and GO- and Interpro Accessions as outputs. Sequential selection of the required steps from a list of 'services' complements the approach. In this example the following steps are required (simplified): retrieve the *Medicago* contig for the contig ID, get the elements for the contig, get the protein sequence for the element, BLAST the protein sequence against *Arabidopsis* proteins, extract the *Arabidopsis* Genome Initiative (AGI) codes, retrieve the GO accessions for the extracted AGI codes, retrieve the Interpro accessions for extracted AGI codes.

Taverna driven workflow composition

Researchers can make use of Taverna (taverna.sf.net) to help them pipeline web services. Taverna is a workflow composition tool allowing for the definition of inputs and outputs and the creation of connecting workflows. Using Taverna it becomes possible to set up complex workflows that would be time consuming if the information had to be retrieved through web pages (Figure 2). Once a workflow has been built in Taverna it can be saved and executed whenever needed. That way it can be enormously useful even for small workflows executed regularly (for example, a weekly matching of Genbank-accessions to *Medicago* gene identifiers by taking the NCGI-gi, BLAST it against *Medicago* proteins and output the AGI-code of the best BLAST hit). ■

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[1] PlaNet are: GSF (MIPS) Neuherberg, VIB Ghent, NASC Nottingham, JIC Norwich, PRI Wageningen, CSIC Madrid and INRA Evry. Planet has been funded by the EC (QLRI-CT-2001-00006). More info available at: http://www.eu-plant-genome.net

SPECIAL REPORT
INTEGRATED ACTIVITIES IN GLIP

Unravelling metabolic and transcriptional control of legume seed development

Contrôle métabolique et transcriptionnel du développement des graines de légumineuses

by Karine GALLARDO*, Judith BURSTIN* and Richard THOMPSON*

Protein content and quality are important breeding objectives for grain legumes. Genomics tools have recently been applied to dissect the networks of gene expression that unfold during seed development of the annual barrel medic, *Medicago truncatula,* for which extensive genomic resources are available. This species produces protein-rich seeds and is characterised by a process of seed development very similar to that of other legumes, the only notable difference being an endosperm layer that remains at seed maturity (4). Moreover, this species being phylogenetically related to the major legume crops (3), such as pea, make it a suitable model to study seed biology, to identify key genes regulating seed composition, and to transfer information to legume crops.

Endosperm and seed coat contribute to storage protein synthesis

During seed filling, the young seed coat supports accumulation of storage proteins in the filial tissues by importing organic nutrients from the phloem, mainly sugars and amino acids (10). These nutrients are stored transiently within the seed coat, further metabolised and supplied to the filial organ by a passive, facilitated membrane-transport process (Figure 1). In legume species, the growing embryo has high sink strength at the onset of seed filling which promotes assimilate uptake from the surrounding tissues. An *in vitro* strategy to investigate embryo response to nitrogen has been developed (6). With an exogenous nitrogen supply, seed storage protein synthesis is comparable to that observed *in planta* as revealed by two-dimensional gel electrophoretic profiles of entire seeds or isolated embryos. In the absence of added nitrogen, seeds and isolated embryos responded differently; with intact seeds there was a remobilisation of endogenous nitrogen during the initial stages of embryo development from tissues surrounding the embryo, thereby ensuring initial storage protein accumulation, whereas isolated embryos were unable to synthesise *de novo* storage proteins. This phase of dependence involves initially the integument, and subsequently remobilisation of temporary stores in the endosperm (Figure 1). Recently, it has also been demonstrated in *Arabidopsis* that the maternal control of integument cell elongation and the zygotic control of endosperm growth are coordinated to determine seed size (7).

Kinetics of storage protein synthesis and related metabolic processes

A set of more than 80 proteins expressed at specific stages during seed filling were identified by mass spectrometry (5). This study revealed the early abundance of proteins related to cell division, for example, annexin, which decrease prior to the accumulation of the major storage proteins. These appear sequentially, in the order: vicilins (14 DAP) – legumins (16 DAP) – convicilins (18 DAP). Other proteins

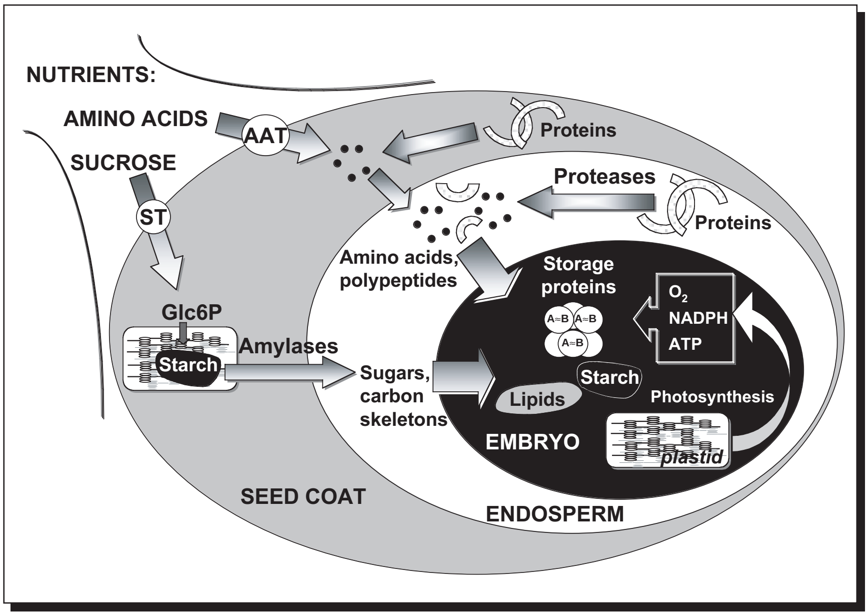

Figure 1. Role of intermediary stores in developing seeds of legumes.

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*URLEG-INRA, Domaine d'Epoisses, 21110 Bretenières, France. (gallardo@epoisses.inra.fr; burstin@epoisses.inra.fr; thompson@epoisses.inra.fr) putatively involved in protein deposition (molecular chaperones such as disulphide isomerase, a binding protein homologue), or cell expansion (for example, reversibly glycosylated polypeptide), are co-expressed. Several anti-nutritional factors, such as lipoxygenases, and components of the precursor-accumulating vesicles (PV100), whose maturation releases a trypsin inhibitor, also accumulate during this phase. At around 16 days after pollination, a temporary accumulation of photosynthetic enzymes (oxygen-evolving enhancer, chlorophyll a/b binding) and proteins involved in carbon metabolism (sucrose synthase, starch synthase) is observed. The latter enzymes may relate to the transitory accumulation of starch in mid-maturation grains (Figure 1, (4)). Finally, the differential patterns of appearance of enzymes involved in methionine metabolism provide new information about the metabolic control of seed development. Consistent with the requirement of methionine for the initiation of polypeptide chains, the met-forming enzyme methionine synthetase is expressed early in seed development. The methionine-consuming enzyme *S*-adenosylmethionine synthetase was found to decrease during seed filling, whereas gene-encoding enzymes involved in pathways of methionine recycling are expressed during this process, including homocysteine *S*-methyltransferase. This differential expression may ensure free methionine for storage protein synthesis at these stages. Finally, 1-aminocyclopropane-1-carboxylate oxidase, which is involved in the metabolic route from *S*-adenosylmethionine to ethylene, is detected late in seed development, consistent with its role in the ripening process.

Regulatory factors expressed in specific seed tissue types

More recently, the proteomic analysis has been extended (264 spot identifications) and related to >4600 EST sequences also expressed during seed development (collaboration with C. Firnhaber and H. Küster from the University of Bielefeld; Gallardo *et al.,* in preparation). This technique has allowed us to profile the expression of a much larger set of genes, and to compare transcript and protein profiles. The latter comparison revealed a transcriptional control for many genes, with exceptions being mainly proteins processed post-translationally or turned over rapidly. Probably the most striking feature of the new dataset is the extent of specialisation of the component seed tissues, which applies equally to genes encoding structural proteins, enzymes, and putative regulatory factors. Analysis of expression ratios between the different seed tissues of *M. truncatula* have highlighted distinct gene products in the filial organ and in the surrounding tissues at the switch towards storage functions (Gallardo *et al.* in preparation). As the quantification of low abundance transcripts encoding regulatory factors using microarray hybridisations is less sensitive than quantitative RT-PCR measurement, we have utilised the latter approach to profile the expression of more than 700 transcription factors in the developing seed in collaboration with M. Udvardi's group from the Max-Planck-Institut at Golm (9). The factors identified correspond in sequence type to those reported from *Arabidopsis* and from other model plant species, that is, the regulation of seed development in legumes appears to be largely based on regulatory proteins homologous to those reported in *Arabidopsis*. Again, many of these sequences are restricted in their expression to one of the main seed cell-types. The availability of comprehensive mutant collections in *M. truncatula* (TILLING, Tnt1 insertion mutants, Fast Neutron deletions) should now enable us to assign functions to those factors showing interesting expression patterns.

Transfer to *Pisum sativum* and functional validation

A composite functional map built in pea was connected to that of *M. truncatula* to allow the transfer of the knowledge (1). In agreement with Choi *et al.* (3), a high level of conservation of gene order and linkage group between the genomes of *M. truncatula* and *P. sativum* was observed. This should facilitate the transfer of information collected in the model plant to the pea crop. QTLs that affect seed size and protein content have been mapped (2, 8) and loci that contribute to the accumulation of proteins determining nutritional value are being identified through the 'Protein Quantity Loci' (PQL) methodology. The comparison of the location of the orthologous pea genes, after mapping, with QTL/PQL positions will identify those genes potentially involved in the determinism of these characters. The function of these genes can be demonstrated by inspecting phenotypes of the corresponding pea mutants isolated from a TILLING resource in the cultivar Caméor (collaboration with A. Bendahmane, URGV-Evry) and allelic variation examined in a collection of pea ecotypes showing contrasted protein content and composition (Centre de Ressources Biologiques, INRA Dijon). The alleles of interest (and eventually point mutant lines derived from the pea TILLING resource) would be of direct use in pea breeding to improve the seed quality characters. ■

Acknowledgement. This research was supported by the FP6 EU project GRAIN LEGUMES (FOOD-CT-2004-506223). Genetic mapping in pea (1, 2, 8) was supported by Genoplante Projects GOP PEAA and GOP PEAC.

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Air-classification of grain legumes for feed and food

Fractionnement sur lit fluidisé des légumineuses à graines pour l'alimentation humaine et animale

by Katrin HASENKOPF* and Florian WILD*

With a protein content of 20%–45%, grain legumes are among the plant materials that are highest in protein. Therefore, they are valuable ingredients for feed and food and can often replace animal protein. For some applications, however, ingredients with higher protein contents are necessary. One example is fish feed for carnivorous species, that has to contain up to 50% protein and 30% fat. The proteins are provided mainly by fish meal produced by wild fish, but fish meal is an expensive material and it takes up to 5 kg wild fish to produce 1 kg farmed fish like salmon (3). To make aquaculture more sustainable, fish meal needs to be replaced, at least in part, by plant proteins.

By including grain legume meals in diets, a high percentage of other components, mainly starch and fibre, is also added. This reduces the performance in aquaculture, and so the inclusion rates for legume meal in fish diets are limited.

The problem can be reduced by using protein concentrates that usually consist of about 65% protein, and isolates which have a protein content in excess of 90%. These products are usually produced by wet processes. In general, drying costs are the biggest share of the processing costs and so protein products are relatively expensive.

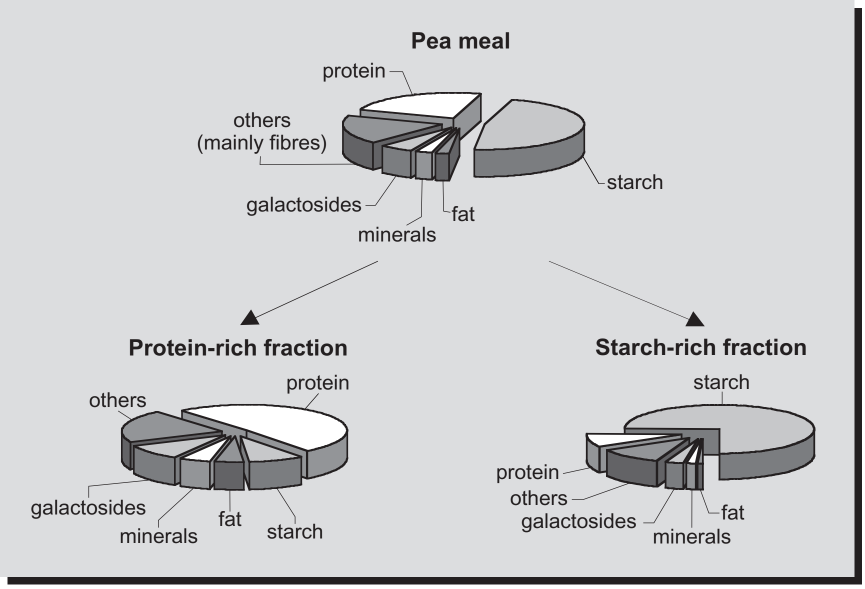

Figure 1. Impact of air-classification on the composition of pea meal.

Dry separation increases protein

The aim of our studies within the Grain Legumes Integrated Project was to examine the possibility of using air-classification, a dry separation technique, to increase the protein content of pea and faba bean meals (1, 2). Samples were produced from pea (*Pisum sativum* L.) cv. Attika and from faba beans (*Vicia faba* L.) cv. Divine and Disco. The composition of the protein-enriched products (protein concentrates) and their digestibility in Atlantic salmon were analysed.

By air-classification, the protein content of these legume meals could be increased from 20% to 55% in pea and from 30% to 65% in faba bean, whereas the starch content was decreased in both materials to about 6%. The concentrations of fat and minerals were about doubled to 4% and 6%, respectively. The amount of fibre was increased slightly compared with the untreated meal. A closer look at the products also revealed that α-galactosides, phytic acid and trypsin inhibitors were accumulated in the protein-enriched fraction.

Protein enrichment to 60%

The enrichment of protein could be increased even more by changing the settings of the process. The protein content of the resulting pea meal fraction could thereby reach more than 60% with a yield of 25%.

The products were tested in digestibility trials with Atlantic salmon. Meal and protein concentrates of pea and the two faba bean varieties were included in the diets and the protein digestibility of the ingredients was determined. The protein concentrates showed a higher partial protein apparent digestibility (ADC) than the meals in these trials, although the protein contents in the diets were at the same level. The ADC of the protein concentrates from pea were 20% higher than for the meal, the ADC of the faba bean varieties Divine and Disco were 10% and 2% higher, respectively. The tested diets showed a similar performance to the conventionally composed control diet.

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*Fraunhofer IVV, Freising, Germany.
(katrin.hasenkopf@ivv.fraunhofer.de)

In addition to the protein-enriched product, a starch-enriched fraction was obtained by air classification. This product comprised of 75% starch, whereas the concentrations of the other components were reduced.

Relatively low costs

Air-classification is a suitable method for producing protein concentrates from pea and faba bean at relatively low costs. The protein content can be more than doubled by this process, whereas the starch content is reduced at the same time. With these concentrates, it is possible to increase the inclusion levels of legume proteins in fish feed to about 20% and, as a consequence, less fish protein is required. The increased level of α-galactosides, phytic acid and trypsin inhibitors – substances that are often regarded as antinutritive – had no negative effect on Atlantic salmon.

Protein enriched legume meals can be used directly as feed ingredients but also as starting material for producing protein isolates in wet processes. When starting with protein-enriched meals, less material has to be put through the wet process and dried afterwards. Therefore, combined processes containing dry and wet operations can make the production of these products more economic.

Many applications

These protein isolates can be used for many applications in food, like substitutes for egg and milk protein and as a raw material for meat analogues. The starch fraction obtained by air-classification can be used for a wide range of applications – as raw material in starch-rich foodstuff like pasta, as a functional ingredient replacing starch isolates, and for technical applications like surgical bandages and the production of ethanol.

Because of the wide variety of applications and the relatively low costs of the process, air classification is an interesting technique for producing grain legumes ingredients for feed and food. ■

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Systems approaches to environmental and economic evaluation of grain legumes

Approches systémiques pour l'évaluation environnementale et économique des légumineuses à graines

by Thomas Nemecek*

When assessing the sustainability of the production and the use of grain legumes, researchers face a number of challenges: (i) the globalised economy leads to a highly complex network of trade relationships, (ii) due to rapid information exchange by electronic means, the production systems and their interactions are changing rapidly, (iii) we are dealing with numerous decision makers, for example, authorities, managers in the private sector or consumers with diverging decision criteria, and (iv) we have to reach different goals (economic, social, environmental), often leading to conflicts.

A lot of knowledge is already available, but there is a need to integrate this knowledge in order to develop a general, holistic view, which requires a system approach as a framework. We should consider whole systems, not only single elements. We have to combine different tools and models in order to create added value. The gaps between different disciplines must be bridged with respect to different cultures, terminologies and approaches.

To achieve an integrated view

In the project GLIP we aim to combine different models, tools and approaches in order to achieve an integrated view of the potential and benefits of grain legume production and use. An example of such a system approach has recently been published (1). These results (from the concerted action GL-Pro) show that introducing grain legumes in European crop rotations leads in most cases to economically sustainable and environmentally sound systems. In GLIP the work is extended to the use of grain legumes as feed (for pig, poultry and dairy cows) and in human nutrition. The first results indicate that grain legumes form an interesting alternative to imported soyabean meal and are under-exploited in Europe.

Our first experiences underline the importance of considering whole systems and not just isolated elements. Therefore, crop rotations should be studied instead of single crops, feed formulas instead of single raw materials, animal husbandry systems instead of animal feed, and full meals instead of single ingredients.
We need to develop a global view and not be too reductionistic. The question is: "How can the system be sustainable in the long term?" and not "How can we maximise the profit in the next quarter?" Considerable knowledge and many tools are already available. Now we have to combine the knowledge and tools that exist and network people in order to develop really sustainable systems.
We are convinced that grain legumes will be a key element in this respect.

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*Agroscope Reckenholz-Taenikon Research Station ART, Zurich, Switzerland.
(thomas.nemecek@art.admin.ch)

(1) Nemecek T. and GL-Pro partners (2006). Environmental impact of grain legumes in regional crop rotations. Grain Legumes 45, 20–22.

UFOP promotes the cultivation of native grain legumes

L'UFOP veut promouvoir la production domestique des légumineuses à graines

by Manuela SPECHT*

At present less than 2% of the arable area in Germany is sown with grain legumes, mainly field peas, lupins and faba beans (Table 1). This is a small percentage compared with other European countries (Spain 6.5%, UK 6% or France 4%). Moreover, since 2002 the grain legume area in Germany has decreased steadily. In 2005 the area was 168,700 ha, 23% less than in 2001 when it was 219,000 ha.

While the grain legume area is decreasing, the area of winter wheat is increasing. In the last two years its share of the arable area has increased by 8% to 3.15 million ha. Farmers in Germany have reacted to the recent economic situation in agriculture, which was further aggravated by de-coupling, by restricting their crop rotations and growing more crops with higher margins.

The previous subsidies have not been sufficient to stop the negative trend in grain legume production, and the additional bonus of €55.57/ha, which is only paid for a maximum surface of 1.6 million ha as stipulated in EU-25, has not yet produced a sufficient incentive for the cultivation of protein crops. Given the knowledge that grain legumes have indisputable advantages in crop rotations and also constitute high quality fodder for livestock, UFOP has endorsed their cultivation (see Insert) and is also promoting projects aimed at expanding the cultivation of faba beans, field peas and sweet lupin species in Germany. The targets and results of these UFOP projects can be explained in greater detail by means of two selected examples.

New systems of soil management

In this project managed by the Department of Agriculture of the University of Applied Sciences of Southern Westphalia (FH SWF), between July 2001 and November 2005 at four locations, a wheat-dominated rotation managed with plough or through mulching was compared with a rotation established without ploughing and extended by grain legumes. The principle of alternating between cereals and break crops as well as the utilisation of precedent crop effects could be applied consistently by arranging the tillage systems in extended crop rotations.

By abandoning ploughing, there was an immediate reduction of up to 15% in the machinery and labour costs of the wheat-dominated rotation. Additionally, the

Federal state	**Grain legumes**								
	Total		among those . . .						
			Field pea		Faba bean		Lupin		
	1000 ha	% of arable land	1000 ha	% of arable land	1000 ha	% of arable land	1000 ha	% of arable land	Arable land (1000 ha)
Baden-Württemberg	6.1	0.7	4.5	0.5	0.9	0.1	0.2	0.0	830.2
Bavaria	17.4	0.8	13.7	0.6	2.3	0.1	0.7	0.0	2131.4
Brandenburg	38.3	3.7	16.9	1.6	0.1	0.0	21.0	2.0	1046.9
Hesse	6.1	1.3	4.4	0.9	1.3	0.3			486.8
Mecklenburg Western Pomerania	12.2	1.1	5.4	0.5	0.3	0.0	6.4	0.6	1079.9
Lower Saxony	6.5	0.3	3.4	0.2	1.5	0.1	1.3	0.1	1860.8
Northrhine-Westphalia	5.4	0.5	1.8	0.2	2.8	0.3	0.2	0.0	1089.5
Rhineland Palatinate	2.7	0.7	2.1	0.5	0.1	0.0	0.3	0.1	393.7
Saarland	0.3	0.8	0.2	0.5	0.0	0.0	0.1	0.3	37.6
Saxony	19.3	2.7	15.8	2.2	1.7	0.2	1.6	0.2	719.7
Saxony-Anhalt	32.7	3.3	24.7	2.5	0.9	0.1	6.0	0.6	998.2
Schleswig-Holstein	2.5	0.4	0.9	0.1	1.1	0.2	0.3	0.0	651.0
Thuringia	19.2	3.1	16.3	2.7	2.5	0.4	0.4	0.1	615.0
Germany total[1]	168.7	1.4	110.3	0.9	15.7	0.1	38.6	0.3	11949.4

[1] including city states Bremen, Hamburg, Berlin

Source: Statistisches Bundesamt

Table 1. Grain legume area in Germany 2005 (absolute and % of arable land).

Insert

Policy to promote native grain legumes in Germany

(extracted from the UFOP Board of Directors meeting, Berlin 5 September 2005)

On the occasion of its meeting on 5 September 2005, the UFOP Boards of Directors called for more financial incentives for the cultivation of native grain legumes in order to:

- reduce dependence on imported protein supplies,
- increase bio-diversity by using a larger range of crop plants,
- integrate new crops into rotations to reduce production intensity and, in particular, as a substitute for expensive stubble wheat,
- retain and increase the output of tillage systems in German agriculture by mulching and direct sowing methods,
- reduce the problems of pesticide resistance in the case of some diseases and grass weeds associated with cereal-dominated rotations.

The special significance of grain legumes in crop production, processing and use has to be appreciated fully by farmers and end users. The advantages of grain legumes are under exploited and under utilised.

A comprehensive support programme is required with varied measures:

– to promote breeding,
– to promote cultivation,
– to promote processing and marketing.

In crop rotations grain legumes have undisputable advantages but the area under cultivation is still decreasing primarily because of the low producer prices for grain legumes that do not adequately represent their value.

Farmers' incomes must not drop any further and so financial incentives will be a prerequisite to make the cultivation of grain legumes attractive to farmers. The native grain legumes, faba beans, field peas and sweet lupins, can meet the needs of society and the environment, but need improved production characteristics.

The diversification of crop rotations would have positive effects on the environment and should be carried out with plant species, that

– supply local vegetable protein and reduce the large deficit between consumption and production,
– favour the environment by decreasing the use of mineral nitrogen,
– ensure sustained crop yields and soil viability,
– reduce production intensity in the cropping system by diversifying the crop rotation.

The current decreasing trend in the cultivation area of grain legumes will coincide with an increased use of follow-up seeds for economic reasons. This will inevitably lead to a reduction in the intensity of breeding these crop plants. This will have consequences for environment-friendly agriculture that is dependent on biological nitrogen fixation by legume species.

At present, there is only one breeding programme for peas, faba beans and sweet lupins in Germany. Two other breeding programmes for field peas and sweet lupins were discontinued at the beginning of 2005 and the existing programme is threatened because of the decreasing area of cultivation As breeding programmes are planned over very long periods of time, and a discontinuation cannot be revised at short notice, know-how and job opportunities in Germany are already under threat.

diversification of the rotation with native grain legumes reduced the machinery and labour costs even further. These economies were produced by husbandry-related as well as process-related effects. By extending the break in cultivation, the straw could rot without any deeper digging-in process which contributed to an inexpensive solution of the straw problem. Infection cycles were interrupted during the change between cereals and break crops. As a result of the new system, the mechanisation required for a diversified crop rotation could be reduced by levelling out work peaks. The machine capital employed was used more efficiently during the course of the year.

In growing systems, in particular, the ploughless cultivation systems on the basis of crop rotations expanded by grain legumes permit the cultivation of an additional area without machine investments or additional labour.

Successful cultivation and marketing systems

Although the cultivation of native grain legumes is decreasing in general in Germany, there are some regions with either agricultural operations and/or mixed feed manufacturers where broad beans, field peas and sweet lupin species are cultivated or processed successfully. The successful strategies involving grain legumes which are employed in these regions are not known in detail and are not being extended to other regions.

This is the context for the current project of the Federal Agricultural Research Centre FAL of Brunswick, which will run from May 2006 to November 2008, and is designed to analyse the regionally successful developments involving native grain legumes to identify the success factors and to derive strategies for an expansion of the cultivation of grain legumes. In this process, the entire value chain will be included from cultivation to feeding.

The active supervision of the project is being carried out by a UFOP study group entitled "Körnerleguminosen" ("Grain Legumes"). This approach involves close cooperation between the regional offices for consultation integrated in the UFOP Division "Protein-Bearing Plants" as well as in the Technical Commission "Economy and Market" and the farmers growing native grain legumes.

The experiences gained during the EU GL-Pro project and in other projects promoted by UFOP in the field of grain legumes will be included in the current project.

In addition to the actual project work, it is planned to use targeted PR (public relations) campaigns to communicate the strategies identified in the project to be successful for grain legumes. The aim is to improve the cultivation and marketing situation for native grain legumes by improving their image. Regions with successful cultivation and marketing/processing strategies and a certain cultivation density of different species will be used as model regions for other areas, where grain legume cultivation is still less significant.

For further information on grain legumes in Germany, please visit www.ufop.de. ■

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*UFOP (Union zur Förderung von Oel- und Proteinpflanzen e.V.), Berlin, Federal Republic of Germany. (m.specht@bauernverband.net)

UK pulses at the crossroads

Les protéagineux anglais à la croisée des chemins

by Geoffrey GENT*

Overall pulse output in the UK has increased slightly during the new millennium, but this has been achieved through an expansion in the area of faba beans compensating for a reduction in the area of peas (Figure 1). With peas, a reduction in the area from 100,000 ha in 2001 to less than 50,000 ha for 2006 emphasises the need for new thinking on varietal characteristics. Beans, in contrast suit most UK farmers through their flexibility and ease of integration in arable farming systems. Interest continues in navy beans, with field scale trials in the South and East of England, but lupins have again failed to build on the interest generated by seedsmen in the early 2000s.

Pea varieties need specific agronomic attributes

Peas have the major strength of being suitable for a large number of markets, some of which give price premiums of up to twice the value of crops for animal feed use. Their agronomic weaknesses are that harvesting can clash with cereals, some crops still lodge despite significant plant breeding progress in this area and crop establishment can be difficult in wet springs. These negative points have become more important in recent years with the drive to simpler and cheaper crop production. So, pea breeding based on the concept of "same again, but with higher yield" will not work for UK growers. Improvements in earliness to avoid the clash with cereals, improved standing ability, improved determinacy to minimise the adverse effect of wet weather at flowering and enhanced colour stability will have greater commercial usefulness. These agronomic attributes need to be linked with the suitability of produce for premium markets. Human consumption or speciality animal feed usage generates additional income that is essential for the economic competitiveness of the pea crop.

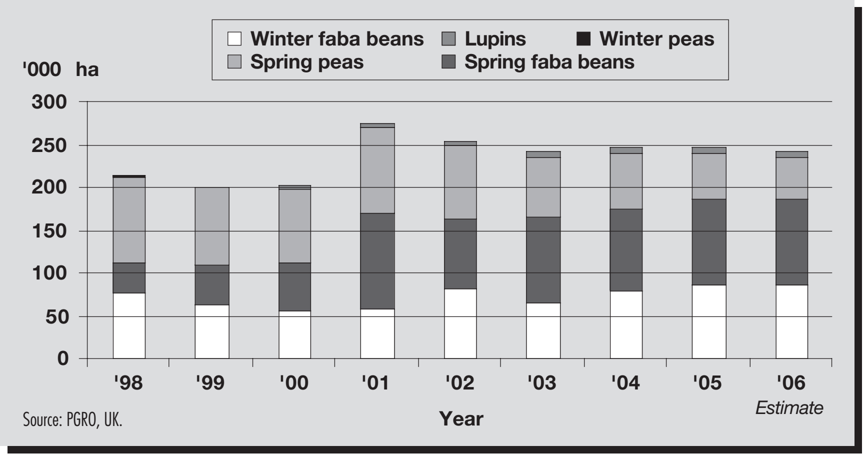
Additionally, the similarity of the characteristics of the major varieties Nitouche, Venture and Cooper has added to this problem. Greater varietal diversity would allow growers to select ones that suit their needs for timeliness, plant height and disease resistance. The newly recommended maple pea Rose and small blue Hawaii add to the diversity of type for UK growers, while the very early small blue Zero4 could be an even bigger asset through its very early maturity.

New faba beans offer major advances

In the UK, faba beans can be established in either the autumn or spring. Different varieties are used with different agronomy recommendations, but both types have prospered recently. Agronomically, faba beans have the major advantage that they mature after cereals, so allowing additional crop area to be harvested by each combine. They are also easy to harvest, being either determinate and erect, (Spring types), or tall and intertwined with pods clear of the ground (Winter types). Both types include varieties that are suitable for human consumption in the Middle East. Spring beans have the basic limitation that they are vulnerable to drought during their flowering period and if winter beans produce excessive vegetative growth they can be vulnerable to foliar diseases.

Breeding faba beans is a complex matter through their low seed multiplication and cross pollinating ability. Despite this, the winter variety Wizard and the spring variety Fuego offer major advances. Wizard has the agronomic advantage of a more compact plant, together with produce that can be suitable for human consumption. Fuego provides a 20% yield improvement over Victor, the first of the 'modern' Spring bean varieties or a 10% improvement over most other commercial varieties. Again, this is linked with human consumption quality.

UK bean production is now around 700,000 tonnes per annum with the crop established in all the major arable cropping areas up to central Scotland. New uses are being considered with perhaps the most significant being for the farmed salmon in Scotland and Scandinavia. Beans are also being developed as snack products, but currently over half the UK production is used for animal feed. Here, growers have to accept prices that allow the beans to compete economically with other sources of vegetable protein. ■



Source: PGRO, UK.

Figure 1. UK pulse area, 1998–2006.

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*Processors and Growers Research Organisation, Peterborough, UK. (geoffrey@pgro.org)

GRAIN LEGUMES

The magazine of the European Association for Grain Legume Research

Le magazine de l'Association Européenne de Recherche sur les Protéagineux

AEP
12, avenue George V, 75008 Paris, France
Tel: +33 1 40 69 49 09 · Fax: +33 1 47 23 58 72
http://www.grainlegumes.com · Email: aep@prolea.com
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COVER PHOTO:
Photocomposition of a pea flower, a chick, fluorescent pea chromosomes, a robot for hybridisation, a fluorescent image of a microarray and grain legume seeds; background: faded pea petal (Bielefeld University, JIC, UNIP, University of Wageningen)

PHOTO DE COUVERTURE :
Montage photographique: fleur de pois, poussin, chromosomes fluorescents de pois, robot pour hybridisation, image fluorescente de puce à ADN, graines de légumineuses, fond voilé de pétale de pois (Bielefeld University, JIC, UNIP, University of Wageningen)

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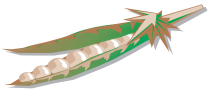

AEP

European Association for Grain Legume Research
Association Européenne de recherche sur les Protéagineux

12 Avenue George V – 75008 Paris – France
Tel: +33 1 40 69 49 09 • Fax: +33 1 47 23 58 72
Email: aep@prolea.com • http://www.grainlegumes.com

The AEP is an associative network of persons with interests in grain legume research (peas, faba beans, lupins, chickpeas, lentils, dry beans, etc.) to favour the exchange of information and multidisciplinary collaborations (Conferences, publications, workshops, joint projects). It aims both to strengthen the research works and to enhance the application of research into the integrated chain of grain legumes.

UNIP

French Interprofessional Organisation of Protein Crops
Union Nationale Interprofessionnelle des plantes riches en Protéines

12 Avenue George V – 75008 Paris – France
Tel: +33 1 40 69 49 14 • Fax: +33 1 47 23 58 72
Email: unip@prolea.com • http://www.prolea.com/unip

The UNIP is the representative organisation of all the French professional branches of the economic integrated chain of grain legumes. It provides information about pulse production, utilisation, and the market and it coordinates research works related to grain legumes in France, especially peas, faba beans and lupins for animal feeding.

Processors and Growers Research Organisation

Research Station – Thornhaugh
PE8 6HJ Peterborough – United Kingdom
Tel: +44 1780 78 25 85 • Fax: +44 1780 78 39 93
Email: info@pgro.co.uk • http://www.pgro.co.uk

The PGRO provides technical support for producers and users of all types of peas and beans. Advice is based on data from trials sited from Scotland to the South West of England and passed to growers and processors through technical bulletins and articles in the farming press.

APPO

Belgian Association for Oilseeds and Protein Crops
Association pour la promotion des protéagineux et des oléagineux

Faculté universitaire des sciences agronomiques
Passage des déportés, 2 – 530 Gembloux – Belgium
Tel: +32 81 62 21 37 • Fax: +32 81 62 24 07 • Email: appo@fsagx.ac.be

The APPO is the representative organisation of Belgian growers of oilseeds and protein crops, especially rapeseed, peas and faba beans. The main tasks are experimentation, giving advice to producers, providing technical and economic information through meetings and mailings and encouraging non-food uses of vegetable oil.

Technical Institute for Cereals and Forage

Arvalis – Institut du végétal

3 rue Joseph et Marie Hackin – 75116 PARIS
Tel: 33 (0)1 44 31 10 00 • Fax: 33 (0)1 44 31 10 10
Email: infos@arvalisinstitutduvegetal.fr • http://www.arvalisinstitutduvegetal.fr

Run and financed by French farmers, Arvalis-Institut du végétal carries out and disseminates applied research on the production, storage and utilisation of cereals, grain legumes, potatoes, and forage.

UFOP

Union zu Förderung von Oel- und Proteinpflanzen

Andreas Hermes Haus – Godesberger Allee 142-148 – 53175 Bonn – Germany
Tel: +49 22 88 19 82 27 • Fax: +49 22 88 19 82 03
Email: ufop@bauernverband.net • http: //www.ufop.de

UFOP is the representative organisation for German producers of oil and protein crops. It encourages professional communication, supports the dissemination of technical information on these crops and also supports research programmes to improve their production and use.

CRA-W

Animal Production and Nutrition Department
Rue de Liroux 8 – 5030 Gembloux (Belgique)
Tel: +32 81 62 67 70 • Fax: +32 81 61 58 68
Email: prodanim@cra.wallonie.be • http://cra.wallonie.be

A broad research topic of the Animal Production and Nutrition Department deals with the utilisation of lupin and pea seeds in animal feeding (ruminant, monogastric and poultry) in terms of nutritional value, environmental benefits, protein utilisation and economic aspects. The research is also concerned with the development of legume silages, seed treatments prior to feeding and seed processing for non-food uses.

Pulse Canada

1212–220 Portage Avenue – Winnipeg
Manitoba – Canada R3C 0A5
Tel: +306 651 0858 • Fax: +306 668 5557
Email: office@pulsecanada.com • http://www.pulsecanada.com

Pulse Canada is a national industry association. This organisation represents provincial pulse grower groups from Alberta, Saskatchewan, Manitoba, Ontario and the pulse trade from across Canada who are members of the Canadian Special Crops Association. Pulse crops include peas, lentils, beans and chickpeas.

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