



Federal Centre for Breeding Research on Cultivated Plants

Annual Report 2006

Dresden-Pillnitz
Groß Lüsewitz
Quedlinburg
Siebeldingen



Bundesministerium für
Ernährung, Landwirtschaft
und Verbraucherschutz

The Internet address of the Federal Centre for Breeding Research on Cultivated Plants is

www.bafz.de

Here you find up-to-date information about BAZ activities, a survey of the organizational units and a complete list of the staff's e-mail addresses.

The Annual Report of the Federal Centre for Breeding Research on Cultivated Plants (BAZ) is self-published.

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Preface



Dear Sir or Madam,
Dear reader,

Almost daily plant genetics and plant breeding produce large quantities of data, which can only be handled and analysed with the help of powerful information systems. Long ago biodiversity informatics developed into a key technology to the success of any plant genetic and breeding activity. In addition, the rapid developments in the area of web technologies allow an appropriate and diverse use of once captured data in response to stakeholder interests.

Taking present and future requirements of breeding research into account, the BAZ has intensified its efforts of creating information systems on the base of cutting-edge technologies of software development in the reporting year. In the field of specialized software development we took a big step forward when completing the pilot version of a web-based lab information management system (LIMS) for molecular data. A next, but considerably more complex project that is high on our agenda in this field is the development of a national information system on the characterization and evaluation of plant genetic resources data. This information system will, among others, basically enhance the working base for the two National Gene Banks the BAZ is in charge of: Fruit and Grapevine. It is particularly in this field that our Federal Centre is given special responsibility on national and international level.

The present report informs the reader about the comprehensive scientific activities of BAZ staff in the year 2006. More detailed information is available on our website www.bafz.de.

The German version of the Annual Report was published in booklet form, but is available on CD as well.

I hope you will enjoy reading the report. However, comments and proposals for improvement are again welcome.

Thomas Kühne

I. The Federal Centre for Breeding Research on Cultivated Plants in the year 2006

Tasks of BAZ

The Federal Centre for Breeding Research on Cultivated Plants (BAZ) was founded on January 1, 1992, upon a recommendation of the German Science Council (Wissenschaftsrat). Since then, it has developed into a major centre of national and international renown for breeding research. The head office and management of BAZ are located in Quedlinburg.

As an institution responsible to the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV), BAZ makes a significant contribution to policy advice, in which its major assignment is in the field of all aspects of the conservation and sustainable use of plant genetic resources for food and agriculture (PGRFA), on the one hand, and the complex field of breeding research and breeding of cultivated crops in Germany, on the other hand. The necessary prerequisites are provided by the acknowledged expertise of BAZ in the genetics and breeding of agricultural and horticultural crops, including fruit and grapevine, as well as by the close and multifaceted relations with scientific institutions and breeders in Germany and abroad. Research conducted at BAZ contributes directly to fulfilling the international obligation of the Federal Republic of Germany in the field of plant genetic resources. It is designed to counteract the genetic erosion of our crops and essentially supports the continuous improvement of their genetic basis to meet the current and the predictable challenges of the agrarian and consumer policies.

Breeding research done by BAZ is at the beginning of the chain of economic value added in agricultural production and is therefore pre-competitive. Breeding research is a long-term, method-extensive and interdisciplinary task. Variety and sustainability in present and future agriculture are highly dependent on our ability to preserve, enlarge and use the

genetic diversity of cultivated plants. It is and remains the aim of all breeding research to create the scientific conditions for the development of high-quality plants characterized by high and stable yields, improved disease and pest resistance, stress tolerance, and high nutrient use efficiency, plants that are fit for new fields of application and better adapted to processing. In this context, attention has also to be given to the general conditions that are continuously changing in consequence of the technological progress, on the one hand, and the climate change, on the other hand. However, the progressing warming in Central Europe will, without a doubt, fundamentally change the abiotic as well as biotic stress factors of high-performance plants within the next years and decades. To respond to this challenge, research activities in this field have to be intensified.

All in all, research pursued by the BAZ makes a contribution to approach the urgent and future problems in agriculture. Paying due regard to the provision of services of general interests, breeding research at BAZ addresses key issues such as

- Safeguarding the genetically based yield stability of crops under changing technological and climatic conditions of production,
- Enhancing the environmental compatibility and sustainability of agricultural production by adapted crops,
- Investigating the genetic potential of cultivated plants as to diversifying the value creation in agricultural production,
- Preserving the diversity of cultivated plants in the German agricultural landscape,
- Investigating the suitability and the characters of cultivated plants with a view to their application as food, fodder, raw material and energy resource,

- Improving the selection for rare and valuable genetic trait variants,
- Screening plant genetic resources for their genetic diversity and their usage potential to breed well adapted cultivated plants,
- Pre-breeding programmes and transfer of knowledge to promote a vast sector of medium-sized plant-breeding companies in Germany.

Research priorities

1. Improvement of crop resistance to pathogens and pests

In terms of an environmentally friendly agriculture and a consumer health protection, breeding research shall increase the genetically-based resistance to crop diseases and pests and, thereby, contribute to minimizing the use of plant protective agents. BAZ projects concentrate on economically important crop species. However, attention is also given to minor crops that are usually neglected by private breeders and that are a difficult object of chemical plant protection because of a lack of listed agents or special quality requirements (e.g. medicinal and aromatic plants). Nevertheless, they are an important factor in the agricultural production and, moreover, they increase the biological diversity in a multi-functional cultivated landscape.

2. Improvement of crop resistance to abiotic stress

The broad range of climatic and site-specific conditions of cultivation requires ecologically well adapted species and cultivars. With a view to the obvious climate change, but also due to higher demands on the environmental compatibility of agricultural production, more attention is given to plants characterized by high energy and nutrient efficiency as well as tolerance to cold. This is of special relevance to alternative, thermophile crops or new winter crops and in the case of late frost resistance of fruit.

3. Improvement of product quality

Product quality is the result of an interdependent functioning of genotype, environment and man's action. Breeding research creates essential prerequisites for the development of specially designed varieties that are the basis of all creation of value in agriculture and ensuing processes. This includes plant raw materials and so-called energy crops whose optimized or completely new properties allow special applications

and a gradual replacement of fossil fuels; however, it also includes food and fodder plants exhibiting, for example, a nutritionally more favourable composition.

4. Enlargement of the diversity in agricultural ecosystems

The enlargement of the range of crop species and cultivars and the consideration of so far scarcely investigated crops is a strategic aim with relevance to both plant cultivation and economy. By expanding narrow crop rotations, it is also an important contribution to an environmentally sound agriculture. A purposeful and continual development of cultivated plants provides alternative solutions to global problems like the finiteness of resources (e.g. water, nutrients, and fossil fuels) or the CO₂ balance. Evaluating the potential of species that are not yet established in agricultural production and finding suitable genetic resources is a necessity that entails a special need for research in this field.

5. Development of strategies for a sustainable use of plant genetic resources

Measures to increase the diversity of species and intraspecific forms in agricultural production help to implement international and all-European strategies. The BAZ activities are an essential contribution to the realisation of the National Expert Programme for the Conservation and Sustainable Use of Genetic Resources of Agricultural and Horticultural Crops, a programme realized in close collaboration with other federal or Länder research institutions. On behalf of the Federal Ministry, the BAZ maintains the collections of plant genetic resources of apple, sweet and sour cherry, plum, strawberry, and grapevine. The establishment of a decentralized national gene bank under the direction of the BAZ Institute of Fruit Breeding in Dresden-Pillnitz is in progress. The central, crop-specific databases run by BAZ serve the co-ordination of national activities with those on European level.

6. Breeding research and breeding of top and soft fruit species and grapevine

On behalf of the Federal Ministry, the BAZ is engaged in the breeding of top and soft fruit as well as grapevine varieties that have to meet the standards of the different cultivation technologies. Fruit breeding includes the breeding of scions and rootstocks, grapevine breeding the breeding of grapevine scions. The BAZ is an active member in national and international organisations and boards for fruit, grapevine and wine.

Organisational structure of BAZ

According to the BAZ statute, the above-mentioned priorities in BAZ research are carried out by the following scientific institutes and working groups.

These are the Institutes of

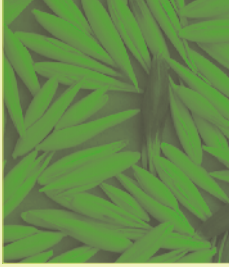
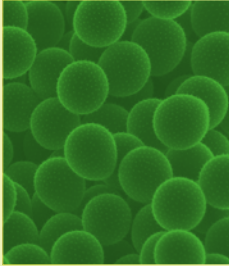
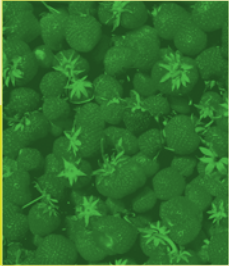
- Fruit Breeding (Dresden-Pillnitz)
- Agricultural Crops (Groß Lüsewitz)
- Abiotic Stress Tolerance (Groß Lüsewitz)
- Horticultural Crops (Quedlinburg)
- Epidemiology and Resistance Resources (Quedlinburg)
- Plant Analysis (Quedlinburg)
- Resistance Research and Pathogen Diagnostics (Quedlinburg)
- Grapevine Breeding Geilweilerhof (Siebeldingen)

and the working group

- Research and Coordination Centre for Plant Genetic Resources (Quedlinburg).

The work in the institutes is supported by research service units such as the data processing group, libraries, field and greenhouse units as well as by the administration department of BAZ.

II. Reports



BAZ Management

The most outstanding and visible result in the year under review was the completion of the third phase of construction for the new BAZ complex on the Moorberg site in Quedlinburg. With the new laboratory and office building a building project that had started on 25 September 2003 was finalized within the agreed budget and timeframe. It is quite natural that this success has many mothers and fathers. On behalf of the BAZ staff I would like to thank everyone participating in the planning and realization of the building project for their contribution to this excellent work. In a period of a bit more than 3 years, one of the biggest structural engineering investments of the Federal government in the New Laender was realized. To finance the project the Federal government invested 50 Mio euros and had a completely new research complex built, adjacent to the trial field of the BAZ in Quedlinburg and in immediate neighbourhood to a research greenhouse (completed in 2005) with 108 individually adjustable cubicles and 32 modern climatic chambers and a central utility unit. The new building provides working places for 200 people on a gross storey area of 15,000 square metres. The new ensemble of buildings meets highest standards and considerably improves the working conditions of all staff working on this site. However, this ultra-modern institution



New BAZ complex
on the Moorberg site

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Head

Grit Lautenbach
librarian

Hand-over of the key
at official opening on 30 November 2006



will not only enhance future breeding research on cultivated plants, it also enriches the townscape of Quedlinburg and will give new impetus to the local labour market.

In a festive ceremony on 30 November 2006 attended by many guests, the laboratory and office building was handed over to its users by the Parliamentary State Secretary in the Federal Ministry of Transport, Building and Urban Affairs, Ulrich Kasparick, in the presence of the State Secretary in the Federal Ministry of Food, Agriculture and Consumer Protection, Gert Lindemann, and the State Secretary in the Ministry of Agriculture and Environment of the Land Saxony-Anhalt, Dr. Hermann Onko Aikens.

In 1996, the Federal government had decided a schedule of further concentrating BAZ institutes on the sites of Quedlinburg, Groß Lüsewitz, Dresden-Pillnitz and Siebeldingen. The new building was the precondition to close the site of Aschersleben and the inner-city building of Quedlinburg and to bring together the four institutes onto a single site at Quedlinburg. At the same time, the scientists of the Gene Bank at Braunschweig moved into the new complex as well. In 1995 the former Federal Gene Bank had come from the Federal Agricultural Research Centre to BAZ. In the years that followed, first the accessions and then the data records were transferred to the German central ex-situ gene bank of agricultural and horticultural crops, which is affiliated to the Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) at Gatersleben. On 14 and 15 December 2006, a scientific colloquium marked the official completion of the unification of the two German gene banks. The BAZ continues to be in charge of the German Fruit Gene Bank, a decentral gene bank network maintained

by the Institute of Fruit Breeding (IOZ) in Dresden-Pillnitz, and the *Vitis* Gene Bank in the Institute of Grapevine Breeding Geilweilerhof (IRZ) in Siebeldingen.

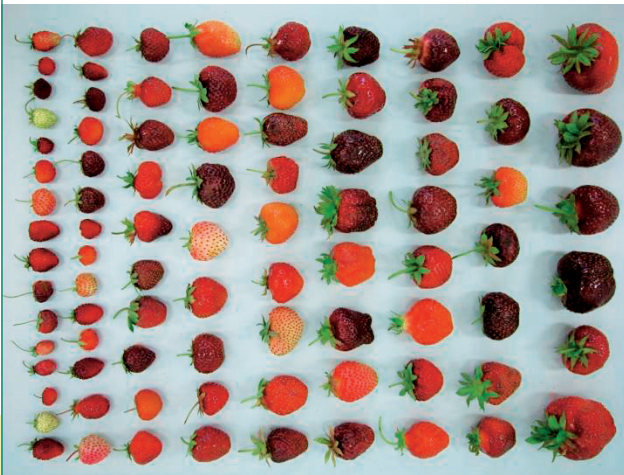
Besides a great many additional activities particularly in connection with the completion of the new building, planning the technical equipment and furnishing of offices and laboratories and, last not least, clearing out the old premises, the BAZ staff continued its research work with great commitment in 2006 as well. With the results presented in this report, they were able to keep up with the successful performance of previous years. The programmatic base of all scientific work is again provided by the BMELV research plan and BAZ makes here a major contribution to the implementation of the following main objectives:

- to promote a sustainable agriculture, forestry and fishery
- to ensure and improve product and processing quality of food and other products
- to protect public health through enhanced food and product safety

High-quality breeding research as it is pursued by BAZ in the areas of emphasis

- evaluation and characterization of plant genetic resources for application in agriculture and nutrition
- understanding the genetic conditions underlying breeding-relevant traits
- improvement of methods applied in breeding research and plant breeding

creates the scientific foundation for giving BMELV an impartial and topical advice on breeding-relevant issues of agricultural policy and consumer protection.



Natural diversity of the genus *Fragaria*



Mildew-infested grapevine

Some of the results of the reporting year shall be already highlighted here:

- In its statutory function as sending or receiving party of plant genetic resources, BAZ has responsibility for continuously compiling and analysing large quantities of quite different information on biological diversity and for making these data available to third parties. Today this task requires high-performance information systems that record data and help interlink fields of expertise and key personnel and upload the information to scientific networks. The access to respective data management systems is nowadays of crucial importance for further scientific progress. Consequently, research institutions need enough qualified personnel for developing, optimizing and continuously updating such systems. Thanks to the allocation of additional funds by BMELV, BAZ could employ a computer scientist for two years who has developed a pilot version of a web-based lab information system (LIMS) for molecular markers in close cooperation with the scientists specialized in this field in the Institute of Agricultural Crops, Groß Lüsewitz. The software is still in its trial phase. It is of relevance to all institutes and will help to make molecular genetic research much more efficient. With LIMS, the BAZ has taken an important step forward in the area of modern data management.
- With regard to the statutory obligations of BAZ, BMELV commissioned the federal centre to evaluate information systems available in Germany for their serviceableness from the perspective of a competent user and to make suggestions for improvement. The analysis revealed considerable deficits and backed the necessity of developing a national information system specialized in the compiling and publishing of

characterization and evaluation data on plant genetic resources. This very comprehensive and demanding task needs to be addressed by breeding research in the next years.

- The Bundesortenamt (Federal Variety Office) granted variety protection for 6 new apple cultivars. Among them, the cv. 'Pisaxa' appears to be a basically improved alternative to 'Boskoop' as regards size, shape and fruit quality. In the storable cv. 'Pivita', the researcher succeeded in further improving the excellent fruit qualities of the popular and commercially widespread cultivar 'Pinova'. In addition, the newly bred variety can do without fruit thinning and is therefore of great interest to commercial fruit growers.
- BAZ scientists tried a novel strategy in aroma analysis by combining gas chromatography coupled with a headspace-solid phase microextraction unit for automated sample preparation, on the one hand, with a chemometric software of pattern recognition, on the other hand. The method was applied in strawberry breeding and, after crosses with wild species, produced breeding strains that are characterized by new aroma patterns and whose aroma contents sometimes exceed the presently cultivated varieties by factor 5.
- As part of a research program focussing on the improvement of the natural resistance of carrots to phytopathogenic fungi and insects, a method was developed to efficiently characterize the epicuticular wax layer of leaves. By means of Fourier-Transform-Infrared-Spectrometer, genotype-specific fingerprints for characteristic wax components can be made and used in selection. The method has far-reaching significance since such wax layers are natural protection barriers in a number of cultivated plants.

- In grapevine, scientists succeeded for the first time in pyramiding two resistance loci to mildew in cross progenies by means of specific molecular markers. In addition, they developed a molecular marker with outstanding significance to early diagnosis as it allows the assessment of fruit coloration in grapevine already 3 to 5 years prior to the first bearing of grapes.
- Taking findings on the rice genome into account, a comparative study in rye could identify for the first time exactly the genome segment that codes for increased resistance to ergot.
- For the first time, a resistance source to anthracnosis could be detected in the lupin gene pool, which is of huge importance for improved target-oriented breeding of sweet-blue lupin.
- In 77 accessions, the evaluation of barley genebank material revealed resistance to the new pathotype of the *Barley mild mosaic virus* that is able to break *rym5* resistance; 37 of the 77 accessions exhibited resistance to all currently known pathogens causing yellow mosaic virosis of barley.
- In a number of isolates presenting the currently most damaging virus in potato growing, *Potato virus Y*, a reliable correlation between the RNA sequence and the specific trait of inducing tuber necrosis was found for the first time.
- BAZ responsibilities include the International Database for Beta which has been purposefully further developed in recent years. Since 2006, it has been offering a visualisation of single populations and their quality traits on European maps. Surveys of that kind have great relevance to preserving commercially important populations in different regions.

Working jointly with colleagues at FAL and BBA¹, the “Research programme to ensure the protection of GM-free and GM-based agriculture and of biodiversity” – initiated in 2005 by BMELV – has been successfully continued with field trials at the Groß Lüsewitz site of BAZ as well as in the test fields of FAL and BBA.

In the period reviewed, BAZ again hosted several scientific events, e.g.

- EUCARPIA Rye Meeting (27–30 June)
- Symposium on the fundamentals in hybrid breeding of medicinal and aromatic plants (23 August)
- Workshops on the sensory assessment of asparagus (01–02 March and 07–08 March)

One of the highlights in public relation work is traditionally the International Green Week in Berlin. In the year of the Football World Cup, “Fair play in all fields” was the motto of the Federal ministry’s special exhibition and BAZ participated with topics focussing on the genetic improvement of lawn

¹ Federal Agricultural Research Centre (FAL) and Federal Biological Research Centre (BBA)



Organic cultivation of blue lupins at Groß Lüsewitz



Apple Day at Dresden-Pillnitz



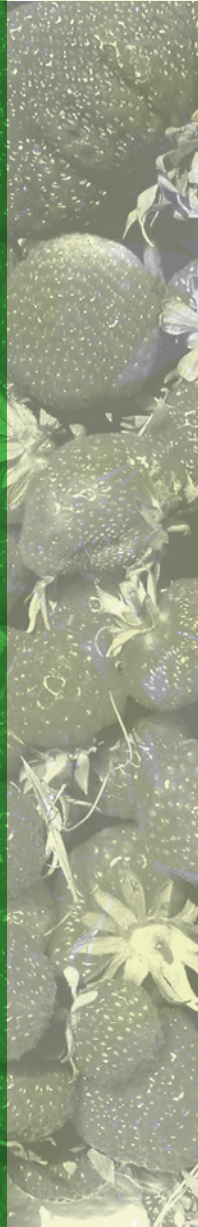
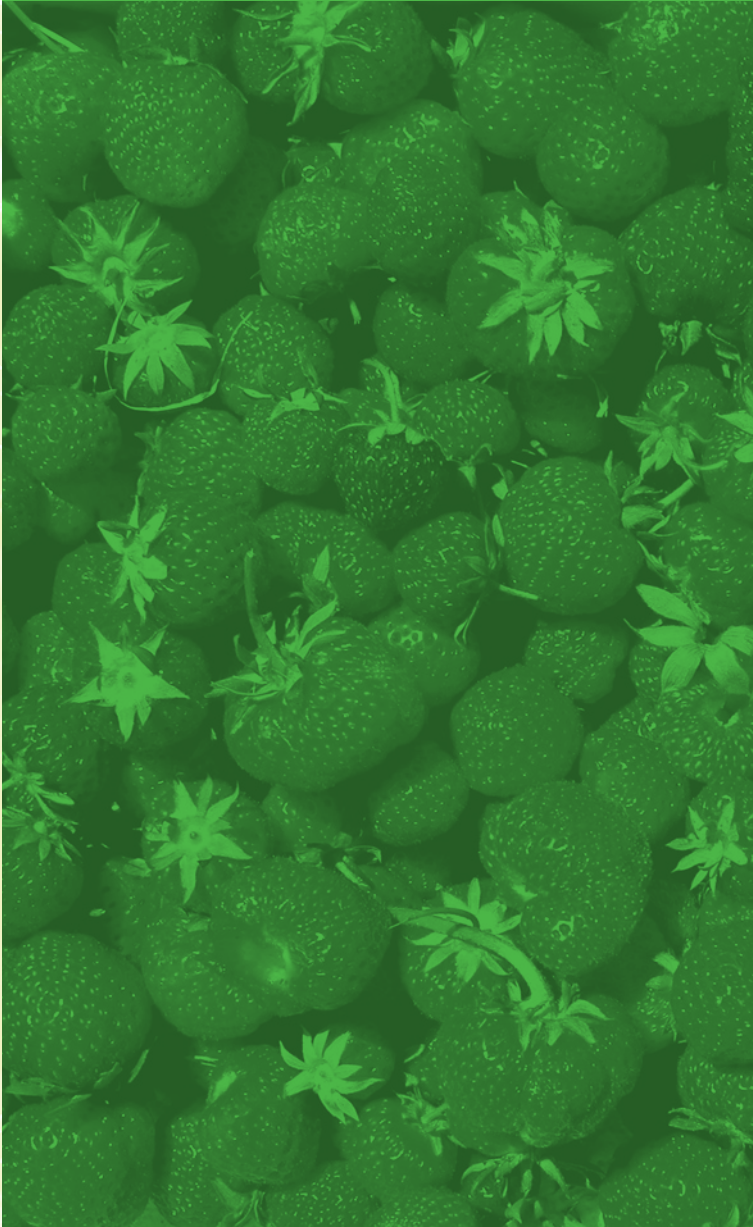
Biology lab assistants taking their final exams

grasses, the genetic diversity of vegetables and presented new fruit cultivars. Furthermore, BAZ contributed with an exhibit of its own as well as with a series of popular scientific lectures to Saxony-Anhalt's Regional Garden Show in Wernigerode. In July, the Institute of Grapevine Breeding organized the 3rd Regent Forum in Siebeldingen. This event always meets great attention among professional user communities and the general public and is meanwhile a kind of tradition. In the Institute of Fruit Breeding Dresden-Pillnitz, the 2nd Apple Day was again a great success. As in previous years, BAZ welcomed many visitors on the "Girls' Day". This special campaign as well as the visits and internships of school and university students in the BAZ institutes are organized by our staff to allow the young generation to gain insight into the activities of the federal research centre and, at the best, to fill as many young people as possible with enthusiasm for the future-oriented science of breeding research and plant breeding.

Although the personnel situation is rather tense, BAZ could manage to hold its high rate of the previous years in the field of vocational training. Altogether 38 young people have been trained in 5 occupations that require apprenticeships, as well as in biotechnology, as part of their technical college education.

Lab assistant (biology)	23
Agriculturist	2
Cellarman	1
Winegrower	5
Assistant in office communication	5
Graduate in biotechnology (Dipl.-Ing.)	2
Total	38

BAZ seeks to retain a proportion of at least 10 % apprentices among the total staff also in the years to come.



Institute
of
Fruit Breeding

Dresden-Pillnitz

Institute of Fruit Breeding

Research at the Institute of Fruit Breeding is carried out in accordance with the Research Program of the Federal Ministry of Consumer Protection, Food and Agriculture (BMELV). The scientific results will contribute to the main goals of this BMELV program in the field of consumer's health protection, healthy nutrition and sustainable agriculture. Research is focused mainly on collection, conservation and evaluation of fruit genetic resources and on the development of top and soft fruit cultivars and rootstocks for a sustainable and environmentally friendly fruit production in both integrated and organic crop management systems. Resistance breeding to minimize the application of chemical pesticides and the improvement of fruit quality for consumers and processing industries are the main topics in fruit breeding. Furthermore, the development of breeding methods is another important field of the Institute's scientific program which provides an improvement in the efficiency in selection, the evaluation of resistance to biotic and abiotic factors in breeding material and the nutritional value of fruit.

The Institute is taking part in two international research projects of the European Union (HiDRAS and SMADIA) and in two COST-actions (EUROBERRY und POMEFRUITHEALTH). The Institute of Fruit Breeding continues its long tradition of being a reliable partner for collaborations with universities and academies of the city of Dresden and the state Saxony. In 2006, 29 students and pupils received a practical training in different working groups of the institute. Four students were coached during their work for the diploma thesis. Two students specialized in biotechnics successfully finished their education at the institute's lab and defended their thesis. Since 2006 the institute realizes the education for two lab technicians. In 2006, the „2. Pillnitzer Apfeltag“ (Apple Day) themed “The Apple – yesterday, today and tomorrow” was organized (Fig. 1). A broad program was organized and various interested guests were welcomed from Saxony and beyond.

Following, the areas of important research progress in 2006 are highlighted:

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Scientists

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Dr. agr. Andreas Peil
agricultural engineer

Dr. agr. Mirko Schuster
agricultural engineer

Anastassija Boudichevskaia
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agricultural engineer (project contract since 01.05.2006)

Silke Lesemann
agricultural engineer (project contract since 31.01.2006)

Stefanie Reim
agricultural engineer (project contract since 31.12.2006)

Matthias Vitten
agricultural engineer (project contract since 31.03.2007)

Conny Hättasch
biologist (project contract since 01.09.2006)

Fruit genetic resources

Besides the Institute of Fruit Breeding, other federal and state institutions are responsible in maintaining fruit species and cultivars in Germany. But also non-governmental organisations are active in preservation of old fruit cultivars. At present, there is no coordination of these collections and conservation activities. Because of the lack in coordination, the maintenance system is very cost-intensive and bears the risk of losing irrecoverable genetic material.

To secure the long term and efficient utilization of fruit genetic resources in Germany and to ensure the availability of germplasm for research, breeding and fruit production as well as landscaping needs, a **German Fruit Genebank** will be established. It consists of a national network to maintain fruit genetic resources. The network is decentralized so that federal, state and non-governmental institutions can contribute. On behalf of the Federal Ministry of Food, Agriculture and Consumer Protection, the Institute of Fruit Breeding is the central coordinator of the national genebank network. In cooperation with the Information and Coordination Centre for Biological Diversity the Institute of Fruit Breeding generated a concept for the establishment of such a network (Fig. 2). The development and subsequent realization of a decentralized network of fruit genetic resources in Germany will make a fundamental contribution towards the 'National Programme for Conservation and Sustainable Utilization of Genetic Resources of Agricultural and Horticultural Crops' in Germany.



Fig. 1: 2nd Apple Day 2006 – exposition of 150 old apple cultivars

International Tasks

- Representation
- Material Transfer Agreements
- Coordination of international databases for Plant Genetic Resources (PGR)

ECP/WG
Malus/Pyrus and
Prunus

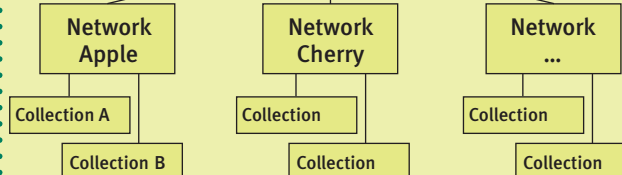
Documentation

Collection of material

German Fruit Genebank

National Information and Coordination Centre for Biological Diversity
IBV Bonn

Coordination Centre of the German Fruit Genebank
IOZ, Dreden Pillnitz



National Tasks

- National Programme for Conservation and Sustainable Utilization of Genetic Resources of Agricultural and Horticultural Crops
- National inventory of PGRDEU

Coordination of networks

Collection of material
Maintenance, evaluation, documentation and utilization of material (MTA)

Fig. 2: Decentralized network for maintenance of fruit genetic resources in the frame of the 'German Fruit Genebank'

The results of the project 'Acquisition and documentation of fruit genetic resources in Germany, which was realized in the field of studies on biological diversity founded by the Federal Agency for Agriculture and Food in 2005, are the basis for the further establishment of the **German Fruit Genebank**. This project was performed by the Humboldt-University Berlin, Faculty of Agriculture and Horticulture (*ex situ*) and the State Office for Environment Brandenburg (*in situ*). The project was finished successfully and provided a documentation of 316 *in situ* locations and 94 *ex situ* collections in which 6,128 cultivars were acquired.

At the Fruit Genebank Dresden-Pillnitz in 2006, evaluation was mainly focused on the *Malus sieversii* collection. The *Malus sieversii* collection of the institute (*Malus sieversii* is the main progenitor of the domesticated apple) consists of 35 single populations from 10 areas where seeds were

collected by US expeditions to the centre of apple origin in Kazakhstan. 113 seedlings were investigated regarding their alleles of the self-incompatibility-loci. Eleven known S-alleles could be detected. Detailed experiments could reveal further unknown S-alleles. Within 994 seedlings, 60 % up to now were bearing fruit for the first time. A comprehensive evaluation using 12 different fruit descriptors showed a vast diversity regarding colour, fruit shape and size of the fruit (Fig. 3). Variability in fruit diameter from 2 to 6,5 cm were detected. These wild apples are comparable to the cultivated apples concerning fruit size. The same conclusion could be drawn for the five investigated inner parameters of the fruit; fruit with strong bitter substances were found but also very tasty fruit. On the basis of all evaluation data regarding resistance, frost tolerance, fruit quality and molecular markers, 112 genotypes were selected to establish a *Malus sieversii* core collection.



Fig. 3: Fruit diversity of the wild species *Malus sieversii*

Breeding of new fruit cultivars

Breeding of new cultivars is focused on **apple**, **sour** and **sweet cherry**, and **strawberry**. Breeding starts with the generation of genetic variability by crossing definite parents to combine the desired traits into a new selection. The breeder has to evaluate and to select seedlings of the progenies carrying the desired traits. Breeding and breeding research are realized in cooperation with colleagues of the BAZ, State institutions and international organisations.

■ Apple

The main focus in apple breeding is the pyramiding of resistance genes to the fungal pathogens scab (*Venturia inaequalis*) and powdery mildew (*Podosphaera leucotricha*), and to the fire blight bacterium (*Erwinia amylovora*). In 2006 specific crosses were performed to combine the scab resistance genes *Vf* and *Vr*, and the powdery mildew resistance genes *PI1* and *PI2* in a breeding selection. Screening of the pyramided resistance genes is no longer feasible using the greenhouse inoculation of the seedlings with the pathogens, but requires the application of molecular markers. Utilization of molecular assisted selection allows the evaluation of seedlings for desired traits. Thereby, the number of seeds can be increased because only progenies which carry the combined resistance genes will be grafted into the orchard to evaluate inner and outer fruit quality. Apple breeding is aimed at an excellent inner and outer fruit quality in combination with pyramided resistance genes to allow sustainable and biological production. Beside this, research was also focused on the determination of self-incompatibility alleles in the Pillnitz apple cultivars and on the improvement of a genetic map for the fire blight resistant wild species accession *M. x robusta* 5 in cooperation with the ARC Seibersdorf, Austria. In 2006 plant breeder's rights were released for the six new Pillnitz apple cultivars 'Pilana', 'Pikosa', 'Pisaxa', 'Pivita', 'Recolor' and 'Rekarda' (Fig. 4 and 5).

■ Sour cherry

The improvement of fruit and processing characteristics, tolerance to biotic stress and a high yield capacity are the main aims of sour cherry breeding. A pool for selection of new sour cherry cultivars was built based on the best trees of progenies. As a result of 40 years of continuous sour cherry breeding in Germany, the cultivar 'Rubellit' was selected. 'Rubellit' achieved plant breeder's rights in 2006 (Fig. 6). Now, together with 'Achat' and 'Jade', there are three sour cherry cultivars available for German fruit production. The rights for propagation of 'Achat' and 'Jade' were assigned to the Artus Group. In addition to the main breeding activities research in sour cherry was focused on determination of



Fig. 4: 'Pivita' – a new cultivar of the Institute of Fruit Breeding, plant breeder's rights were released in 2006 (Picture: H.G. Levin, BLE)

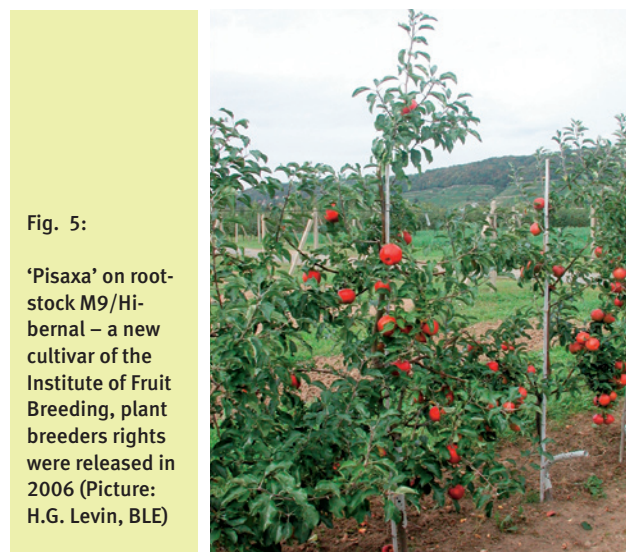


Fig. 5:

'Pisaxa' on root-stock M9/Hibernal – a new cultivar of the Institute of Fruit Breeding, plant breeder's rights were released in 2006 (Picture: H.G. Levin, BLE)

fertility in sour cherries, performed in cooperation with East Malling Research, United Kingdom and on development of a serological assay for the fungus *Monilinia laxa*, performed in cooperation with the Institute of Resistance Research and Pathogen Diagnostic of the BAZ in Quedlinburg.

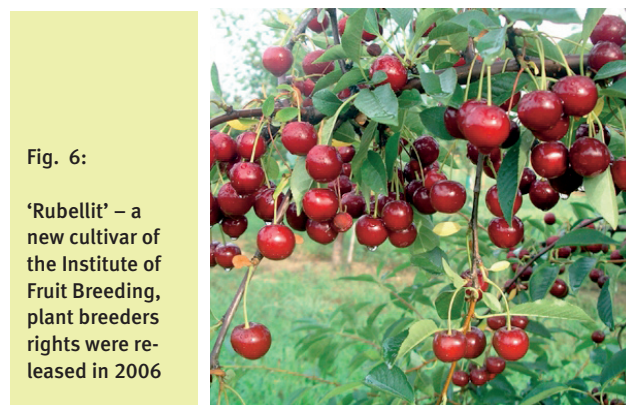


Fig. 6:

'Rubellit' – a new cultivar of the Institute of Fruit Breeding, plant breeder's rights were released in 2006



Fig. 7:

Fruits of an advanced selection from the sweet cherry breeding program



Fig. 8: Cross combination of *Fragaria xanassa* cv. „Mieze Schindler“ with *Potentilla palustris* resulted in healthy and vigorous plants with a high everbearing potential.

■ Sweet cherry

Breeding in sweet cherry is aimed at the improvement of fruit traits, self fertility, resistance to biotic pathogens and a prolonged ripening time altogether with a high yield capacity. In 2006, a large number of breeding selections was evaluated for the first time, since sweet cherry breeding was interrupted for a long time due to restructuring. Some advanced breeding selections with excellent fruit characteristics will be evaluated for their suitability of production under different environmental conditions at different locations in Germany (Fig. 7). Research was also carried out to determine self-incompatibility alleles of sweet cherry cultivars and to evaluate resistance to the pathogen *Blumeriella jaapii* in sweet cherry cultivars, wild species and progenies of crosses using different species.

■ Strawberry

In the field of strawberry breeding five C-selections were found that are now available for trials at different locations in Germany. Improved fruit characteristics and resistance traits of these breeding selections offer the potential to compete against existing cultivars in self picking production. Beside breeding performed at the octoploid level of strawberry cultivars, interspecific crosses with wild species aimed at increasing the gene pool which could be utilized in breeding were successfully carried out. An intergeneric cross with *Potentilla palustris* was performed resulting in resistant and strongly everbearing F_1 -hybrids (Fig. 8). Screening of Asian strawberry species for resistance to *Verticillium* was started. The provocation field for *Verticillium* which was

established in 2003, is available now and field resistance of strawberry cultivars to *Verticillium* can be determined.

■ Quality analysis in breeding material

Sensorial and analytical studies on fruit quality assist the selection of breeding material and cultivars. In apple breeding, the positive features of the scab resistant selection E6 16,43 have been confirmed. It is characterized by high content of flavour substances, favourable texture, attractive appearance, and suitability for long time storage. In comparison with several new cultivars coming from abroad, the selection was very competitive. In order to improve the dietary value of apples, the content of vitamin C was determined in apple cultivars. Cultivars with high values have to be combined to increase the content of the vitamin. In sweet and sour cherry, evaluations of fruit quality traits have been continued to improve the efficiency in selecting parents for crossbreeding. The youngest sour cherry cultivars bred in Pillnitz, 'Jade' and 'Achat', proved to be superior to 'Schattenmorelle' in the content of soluble solids and the colour intensity important for taste and fruit processing, respectively. Because of the increasing importance of processed sour cherries for healthy nutrition, preliminary qualitative and quantitative analyses of anthocyanidines in cultivars and in a crossbreeding population were carried out in cooperation with the Institute of Plant Analysis in Quedlinburg. Efforts in the field of fruit quality in strawberry were concentrated on the evaluation of a progeny of the parental cultivars 'Mieze Schindler' × 'Elsanta' to obtain information on the inheritance of important fruit traits.

Biotechnological approach in breeding

■ Molecular methods

Molecular breeding in cultivated apple is aimed at the identification of new fungal resistance genes in the genus *Malus*, on their genetic analysis and localization in the apple genome, and on the characterization of new pathogen races. Based on results of these investigations, diagnostic DNA markers for resistance genes are developed which can be applied to marker assisted selection and molecular breeding. Genetic and molecular research is also aimed at fruit quality traits with the goal to more effectively select apple genotypes combining durable resistance and high fruit quality. The apple wild species *Malus sieversii* from Central Asia has been considered to be a very valuable genetic resource for resistance as well as for fruit quality traits. Scab resistant *M. sieversii* genotypes of different geographic origin were crossed with scab susceptible apple cultivars to generate seven progenies with a total of about 700 individuals. In some of these progenies simply inherited (monogenic) resistance has been found based on scab tests in the greenhouse. These genes are especially important for practical resistance breeding in apple because they are acting against scab race 7 which is able to overcome the *Vf* resistance from *M. floribunda*. *Vf* resistance was used in the past within most apple breeding programs worldwide. Microsatellite markers are presently applied in a genome-wide scan approach to localize the resistance genes on the apple linkage maps. In addition, it was investigated if some of the newly identified scab resistance genes are really new genes or genetic variants of genes within the already well known *Vf* resistance gene cluster located on apple linkage group (LG) 1. The same question has yet to be answered for a scab resistance gene from the Russian apple cultivar ‘Antonowka’ which could be mapped in the vicinity of the *Vf* locus on LG 1. Regarding the second important fungal pathogen apple powdery mildew, a major resistance gene (called *Plbf*) has been identified in two apple progenies derived from a *M. baccata* accession. An easy-to-use SCAR marker that has been developed from an AFLP fragment identified by bulked-segregant analysis can now be used for marker assisted selection. Mildew research was also focused on the generation and analysis of multi-resistant apple genotypes suitable as basis material for breeding durable mildew resistant apple cultivars. Individuals with combinations of the mildew resistance genes *Pl1* and *Pl2* were crossed with the ‘Mildew Immune Seedling’ (MIS, resistance gene *Plmis*) and the threefold - resistant individuals were successfully selected by DNA markers. The major part of the research on fruit quality traits was performed within the European project HiDRAS which is based on a pedigree-

based QTL-analysis strategy. The final aim is to identify genetic loci and allelic series controlling the most important parameters of fruit quality. Traits considered in the project are: fruit size, taste, fruit firmness, juiciness, acidity, sugar content, vitamin content, flesh texture, storability and shelf-life. The molecular data production was completed in 2006. The Institute of Fruit Breeding was in charge of producing about a third (28 out of 83) of the SSR data needed for the pedigree-based QTL mapping procedure. In total, about 100.000 validated molecular data points were released to the HIDRAS database. In addition, conventional QTL mapping was realized for flavour components and other fruit parameters in a single apple progeny (Discovery x Prima) for which a saturated genetic linkage map has been constructed previously. A series of biochemical substances involved in the phenomenon apple fruit flavour was analysed by SPME-GC in collaboration with the Institute for Plant Analyses of the BAZ in Quedlinburg and some very interesting genomic regions carrying several important QTLs were detected, i. e. on the linkage groups LG 3, LG 9, and LG 15 (Fig. 9).

■ Genetic engineering

One of the most important problems for fruit tree breeding is the long generation time. This developmental process from the juvenile to the adult stage can encompass a number of years. Thereby traditional breeding cycles are time consuming and expensive. Besides, many genes of economical im-

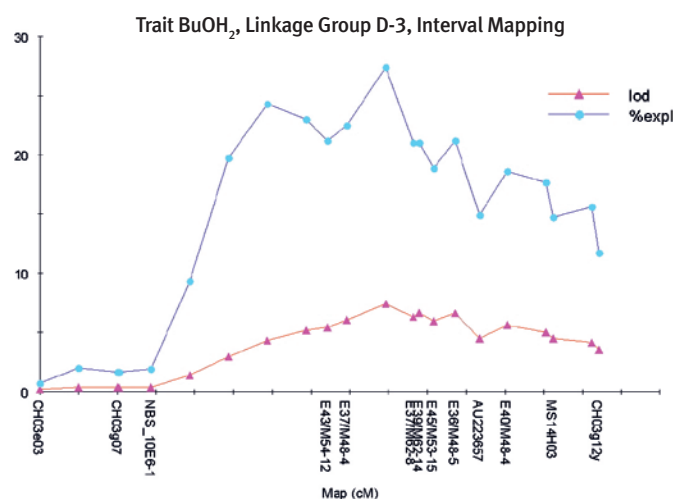


Fig. 9: QTL analysis of apple flavour – QTL identified for the aroma component butanol (BuOH) on linkage group D-3. The course of the LOD curve (in red) over the linkage group (marker names on the X-axis with genetic distances in cM) indicates a major QTL which explains more than 25 % of the total phenotypic variance.

portance occur frequently in apple wild species with small fruit size and low fruit quality. Numerous backcrosses are necessary to eliminate all negative traits of the wild species. To realize backcross breeding programs within a manageable time-frame, shortened juvenility and precocious flowering are important breeding goals.

Little is known about the factors controlling the transition from the juvenile to the adult stage in fruit trees. On this account, we have started with the isolation of native apple genes which are involved in the floral meristem transition. The expression patterns of these genes were subsequently studied in different tissues. Based on the obtained results, individual genes were selected to generate transgenic apple trees. The transgenic plants will be used to study the real function of the transferred genes. Individually selected genes were integrated into existing linkage maps to study the genomic organization of flowering genes in apple.

In 2006, we started with transformation of strawberry. We established an efficient transformation protocol based on kanamycin selection and were able to develop transgenic plants. At present, we are working on the establishment of new selection strategies based on native selectable marker genes as well as on site specific recombination of traditionally used marker genes like *nptII*.

■ Biosafety Research

The project on biosafety research in apple which was supported by the Saxon State named "Studies on putative dissemination of transgenes in apple" was successfully completed this year. Part of the results was summarized and published in the journal 'Environmental Biosafety Research'. The second

part of the project has still to be summarized for publication. The studies on systemic acquired gene silencing in apple are part of a research project funded by the Federal Ministry of Education and Research (BMBF). Therefore, different transgenic apple lines were developed to block the expression of individual genes involved in the anthocyanin biosynthetic pathway of apple using an approach based on RNA interference (RNAi). Thereby, the mRNA of these genes will be degraded to short interfering RNA (siRNA) molecules. These siRNA's are able to bind new mRNA molecules and initiate their decomposition. Individual plants of each line will be used as rootstocks and grafted with scions of a red coloured accession of an apple wild species in spring 2007. The biosynthesis of red coloured pigments will be prevented in the case of an existing transport of siRNA molecules from the transgenic rootstock to the scion and the plants will become green. A successful systemic transport of siRNA's would be of particular importance for the use of biotechnological methods in apple breeding. In this way it would be possible to modify different apple cultivars by grafting onto to the same transgenic rootstock. An additional advantage of this system is that the distribution of the foreign genes is prevented because the generative part of the plant is not genetically modified.



Institute
of
Agricultural Crops

Groß Lüsewitz

Institute of Agricultural Crops

■ Tasks

The Institute of Agricultural Crops (ILK) is charged with characterizing plant genetic resources for food and agriculture (PGRFA) with regard to their genetic potentials for adapting crop plants to changing land uses, specialization of production and agro-ecological conditions. To fulfill this task, the institute applies the current repertoire of approaches and methods in plant-breeding research. Our work, which can be coined with the term *Genetic Enhancement*, is directed to broadening the genetic bases of selected crops in respect to plant health, quality aspects and renewable resources, the latter of which includes the use of plants for raw materials as well as for energy production. Another focus of ILK's research is on neglected or novel crop plants which offer interesting perspectives for Germany's agriculture but require further agronomic adaptation via breeding. Enriching genetic diversity and broadening the spectra of crop species and their purposes of use provide the prerequisites for maintaining agrobiodiversity and enhancing versatility of agricultural production. Results of our research are meant to support federal policies in warranting agricultural production which is environmentally friendly, sustainable and meets the consumers' demands.

To meet the above-mentioned tasks the institute is organized in three work groups, namely 'Classical Breeding Methods', 'Molecular Breeding Methods' and 'Biotechnology'. With their specific expertise these work groups take joint action to approach crop-specific problems from various sides. Pursuing these problems also requires scientific exchange with university and extramural research institutions, genebanks and commercial plant breeders. Besides its original breeding research the institute advises the BMELV with regard to areas related to breeding, e.g., to coexistence in the farming of genetically engineered and conventional crop species. In the period under review, the spectra of crop species considered by ILK comprised rye, barley, triticale, oat, ryegrass, narrow-leaved lupin, oilseed rape as well as other Brassicaceae, and potato. In addition, maize was included in the frame of a large-scale coexistence field trial.

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Beckmann, Katrin
Master of Science (project from 01.10.2006)



Fig. 1 Participants of the 8th International EUCARPIA Symposium on Rye Breeding and Genetics, 28-30 June 2006 in Rostock/Groß Lüsewitz

■ Groß Lüsewitz – a location for plant-breeding research on agricultural crop plants

The coastal region in the northeast of Germany has always been a prime location for plant breeding and research. At the Groß Lüsewitz location a rare combination of favorable factors is available, providing ideal conditions for meaningful breeding research with regard to both conventional and organic agriculture. The northeastern coastal region of Germany is considered to represent Europe's best 'healthy region' for potato growing, with a low incidence of those aphid species effective as potato-virus vectors. The near-coastal climate also provides excellent conditions for disease-resistance breeding, because natural infection pressure is high, continuous and reliable with regard to most of the important crop pathogens, including potato late blight as well as *Fusarium*, leaf rust, scald and powdery mildew in cereals. Besides field trials, resistance tests in semi-open systems, i.e., artificial inoculation of plants in the field or greenhouse, are successful in four of five years and yield meaningful results in most cases due to the high air-humidity. This is an essential for efficient and directed research on 'genetic plant protection' approaches in agricultural crops.

The Groß Lüsewitz trial-field area is of diluvial origin, with a soil-classification score of 47 (German scoring system), making it representative in agronomical respect for the North German Plain and West Poland, as well as for a large fraction of arable farm land in the New Lander of Germany.

Sites of this type are light with a tendency to pre-summer drought and are grown with crop plants such as oilseed rape, rye, barley, potato, and narrow-leafed lupin.

Breeding research of BAZ institutes in Groß Lüsewitz profits from the close cooperation with the Gatersleben Genebank external locations nearby, namely in Groß Lüsewitz (potato) and Malchow/Isle of Poel (oil and forage plants). Networking with other research institutions in the Groß Lüsewitz region was enhanced in the past. For instance, in 2006 the two BAZ institutes at this location were actively involved in two innovation symposia on *Biopolymers from Cereal Flours for Paper Industry* and *Extraction of Biofunctional Food Ingredients from Lupin Seeds*, respectively, which were funded by the Federal Ministry of Education and Research (BMBF) and organized by the Agrobiotechnicum Groß Lüsewitz. Also in 2006 first steps were done together with the Agrobiotechnicum towards setting up a centre of competence for bio-functional food ingredients, with an initial focus on narrow-leafed lupin while open also to other oil and protein crops. Breeding research done at the Groß Lüsewitz location is situated between basic research and breeding practice and is recognized at a national and international scale. In the period under review, e.g., our location had the honour to host the 8th International EUCARPIA Symposium on Rye Breeding and Genetics, 28-30 June, with 80 scientists and breeders from 11 European countries and from Australia (Fig. 1).

Official Functions

■ Distinguishing hybrids of oilseed rape within the scope of DUS testing

In the period under survey we completed our studies on oilseed hybrids which started in 2005 in support of the Bundessortenamt (BSA, German Federal Plant Variety Rights Office). This effort aimed at elucidating technical feasibility to distinguish hybrids (including so-called half-sib hybrids) by means of molecular markers. Specifically, the effort was meant to flank a current EU project of some national offices of the Community Plant Variety Office (CPVO) on the use of molecular markers to optimize reference collections. Since cultivar differentiation with morphological criteria becomes increasingly difficult the applicability of microsatellite (SSR) markers was to be determined in this effort. To this end, 96 samples of oilseed-rape hybrids and their parent lines were examined at ILK and a private breeders' laboratory with PCR primers drawn from public resources, e.g., UK Cropnet database (<http://ukcrop.net/perl/ace/search/BrassicaDB>) and ASTRA database (<http://hornbill.csp.la-trobe.edu.au/>). Hybrids and their parent lines proved to be quite similar even at the molecular level. Thus, a panel of SSR markers was necessary to make clearcut distinctions. In some cases hybrids were identified whose SSR marker alleles were not consistent with those of the parent lines. The results elaborated at ILK are part of a final report of the Bundessortenamt, Division of DUS (distinctness, uniformity, and stability) Test.

■ Coexistence in maize growing

In 2006 the large-scale coexistence field trial in maize was continued for the second year. This field trial was designed by three research centres in the scope of the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV), namely, the Federal Centre for Breeding Research on Culti-

vated Plants (BAZ), the Federal Biological Research Centre (BBA), and the Federal Agricultural Research Centre (FAL). The field trial was meant to address open questions related to the coexistence of genetically engineered and conventional maize growing and to formulate rules of good agricultural practice in maize growing under the agronomical conditions in Germany. As in the year before, the BAZ part of this effort was performed at the Groß Lüsewitz research location. A 9.8 ha field trial was laid out including 3.5 ha Bt-maize (MON810) as a pollen donor, 4.5 ha conventional maize as recipient as well as 1.8 ha of clover/grass mixture as barrier crop. The field trial was sown on 28 April; flowering of donor and recipient was recorded in August and single cobs were manually collected on 16 October. Estimation of outcrossing was accomplished by accredited laboratories. The field trial shall be repeated in 2007 to collect sufficient data with regard to environmental influence on outcrossing.

■ Training and Education

Our BAZ location is actively engaged in the training of professionals, students and schoolchildren. In 2006 a total of 16 internal and external trainees for the profession of Biological Laboratory Assistant passed the two institutes at Groß Lüsewitz (Fig. 2). Due to the acreage planted, the diversity of crops considered and the comprehensiveness of the agricultural education curricula, the trial-field facility at Groß Lüsewitz is the only one among BAZ research locations where trainees for the farmer profession may be educated. In 2006 three trainees of terms 1-3 were educated in this facility (Fig. 3). Furthermore, 12 students of biology from the universities of Rostock and Greifswald as well as from Sweden had a traineeship or accomplished their experimental work for bachelor degree. An educational activity of growing importance is focussed on schoolchildren of all education levels. These efforts aim at promoting a better understanding of the complexity and the impact agriculture



Fig. 2 Trainees for the profession of Biological Laboratory Assistant get familiar with crossing techniques in cereals



Fig. 3 a,b Trainees for the farmer profession at potato harvest (left-hand side) and on the 145 HP tractor (right-hand side)



Fig. 4 a-d From the left to the right: Pupils' Day at the Groß Lüsewitz location in the greenhouse and lab; schoolgirls Maria Hentschel and Anja Ewert from the secondary school in Sanitz doing research at ILK in the frame of the CreateMV development programme; student of biology Manuela Rimke from the University of Greifswald working on her diploma thesis in the ILK molecular marker lab

and plant breeding have in modern societies. In the period under review, two projects on breeding research in lupins were launched at the ILK under the patronage of the CreateMV initiative, involving pupils at the grammar school of the town of Sanitz (Fig. 4).

Breeding Research

■ Rye (*Secale cereale* L.)

Plant genetic resources for healthy rye

Due to the excellent infection conditions in our trial field in 2006 our efforts to unlock plant genetic resources for disease resistance from a "world collection" of rye accessions (Fig. 5) could be continued successfully. With regard to resistance to leaf rust (*Puccinia recondita*) effectiveness in the adult-plant stage of a resistance gene with the preliminary designation *Pr-t* was demonstrated in growth-chamber tests. There was a tight correlation (0.81) between the *Pr-t* resistance test scorings in the seedling vs. adult-plant stage. To-date, 13 of a total of 15 *Pr* genes identified at ILK proved to be effective

in the adult plant. The set-up of a standard set of near-isogenic lines (NIL) each carrying a defined *Pr* gene was also continued. At present, NIL are available for resistance genes *Pr1*, *Pr2*, *Pr3*, *Pr4*, *Pr5*, *Pr-d*, *Pr-e*, and *Pr-f*. These NIL are suited as differential lines and shall serve as gene resources for proceeding studies, e.g., on the effectiveness of *Pr*-gene combinations. As a first step NIL were crossed with each other in 2006 to produce most of the possible two-gene combinations as well as all of the four-gene combinations of resistance genes *Pr1-Pr5*.

Further efforts of the work group of 'Classical Breeding Methods' were directed to resistance against leaf blotch (*Rhynchosporium secalis*). In the period under survey, 40 F3 progenies each with 15 individuals were tested in the field for their resistance upon artificial inoculation with three isolates (Fig. 6). The F3 progenies had been generated by crossing of a susceptible with a resistant inbred line from the Groß Lüsewitz gene pool. Genetic analysis of F3 progeny demonstrated that resistance was governed by a single dominant gene and thereby corroborated the F2 data of the previous year. After a final genetic analysis in 2007 this resistance gene shall be mapped with the aid of molecular markers.



◀◀◀ Fig. 5
Characterizing plant genetic resources in the outbreeder rye encompasses elaborate crossing programmes

Fig. 6 ▶▶▶
Field testing of rye for resistance to *Rhynchosporium* leaf blotch after artificial inoculation. Left-hand side, resistant plant; right-hand side, susceptible plant showing symptoms of infestation



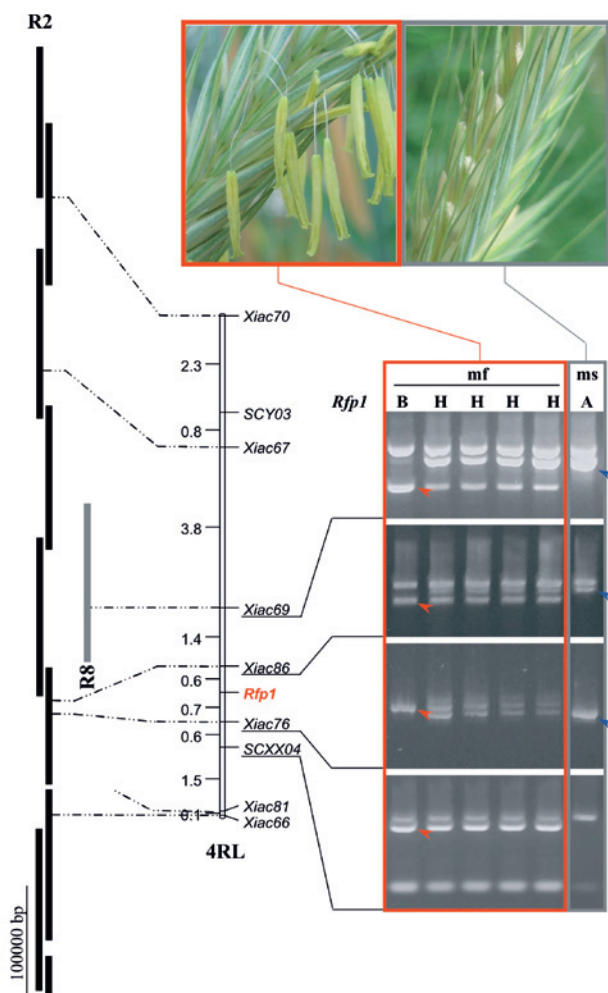


Fig. 7

Development of molecular markers for the restorer gene *Rfp1* on rye chromosome 4RL via comparative genetics. Sub-genomic regions of rice chromosomes R2 and R8 (left) which are of common origin with rye chromosome 4RL served as a starting point. Novel markers are tightly linked with *Rfp1* (middle). Marker analysis in the lab (right-hand, from above) displays codominant alleles (red and blue arrows) of the novel STS markers *Xiac69*, *Xiac86*, and *Xiac76* as well as the single dominant allele of an older RAPD marker (arrows). Codominant STS markers allow for the identification of male fertile (mf) vs. sterile (ms) plants as well as of genotypes homozygous (B) or heterozygous (H) for the *Rfp1* restorer gene.

Fighting ergot via precision breeding

Rye as an outbreeding species widens its spikelets during flowering time, which in turn renders this species particularly susceptible for the ergot fungus, *Claviceps purpurea*. Infestation with ergot became increasingly important with the advent of novel, high-performing hybrid varieties which also proved to be highly susceptible to *C. purpurea* due to reduced pollen shedding under unfavorable weather conditions. Hybrid breeding in rye is based on cytoplasmic male sterility (CMS), with the Pampa (P) cytoplasm being the predominant type. Dominant restorer genes, *Rfp1* and *Rfp2*, have been identified in exotic rye accessions which lead to improved restoration of male fertility (pollen shedding) in the P cytoplasm and, thus, reduce the risk of infection by *C. purpurea*. Addressing these restorer genes in a sufficiently ac-

curate way has, however, been hampered by lack of molecular markers which (i) are tightly linked to the *Rfp* genes, (ii) flank these genes and (iii) are codominantly inherited. This and the fact that there is linkage drag around *Rfp* genes involving unfavorable genes for plant height constitute drawbacks for the breeder in using the restorer genes. For this reason we started an effort to develop codominant molecular markers for *Rfp1*. To this end we systematically compared the *Rfp1*-bearing genomic region in rye with its orthologous counterpart in rice. The rice genome serves a model for the grass species and has completely been sequenced. Based on the rice-genomic DNA-sequence information, we identified short DNA segments, amongst them the sequence-tagged sites (STS) *Xiac76* and *Xiac86*, which map close to *Rfp1* in rye. Two F2 families segregating with *Rfp1* alleles (restoring vs. non-restoring) were scored for anther size and pollen shedding. Linkage analysis comprising 155 plants allowed us to map *Rfp1* within a 1.3 cM interval, the latter of which is defined by the novel markers *Xiac76* and *Xiac86* (Fig. 7). Both STS markers are codominant and allow, thus, to distinguish homozygous and heterozygous states of *Rfp1*. When the two flanking markers are considered as a single selection criterion there remains a low chance of 0.000043 for recombination between the target gene and the markers. To conclude, these markers allow to identify and select *Rfp1* genotypes with a high precision which had not been feasible before.

■ Barley (*Hordeum vulgare* L.)

Unlocking genetic diversity with SMART Breeding

When enriching the genetic base of cultivated barley with regard to virus and fungus resistance the breeder, meanwhile, may use both the primary and secondary gene pools. The secondary gene pool consists of a single wild barley species, *H. bulbosum*, and constitutes a rich genetic resource for resistance breeding (cv. Annual Report 2005). In the period under survey, we conducted studies on to what extent 'SMART Breeding' approaches can be used to generate barley with genetically novel and multiple disease resistance. In a marker-assisted approach we introgressed different chromosomal segments from *H. bulbosum* into a common barley genetic background. The chromosomal segments introgressed were previously shown to confer resistance to barley yellow mosaic virus (resistance gene *Rym14^{Hb}* introgressed on chromosome 6HS) and *Rhynchosporium* leaf blotch (gene *Rrs16^{Hb}* introgressed on chromosome 4HS), respectively. Parents homozygous for either resistance were crossed to produce double-heterozygous resistant offspring. The latter was selfed to produce segregants homozygous both for the *Rym14^{Hb}* and *Rrs16^{Hb}* molecular markers. These plants will be tested for their resistance in 2007.

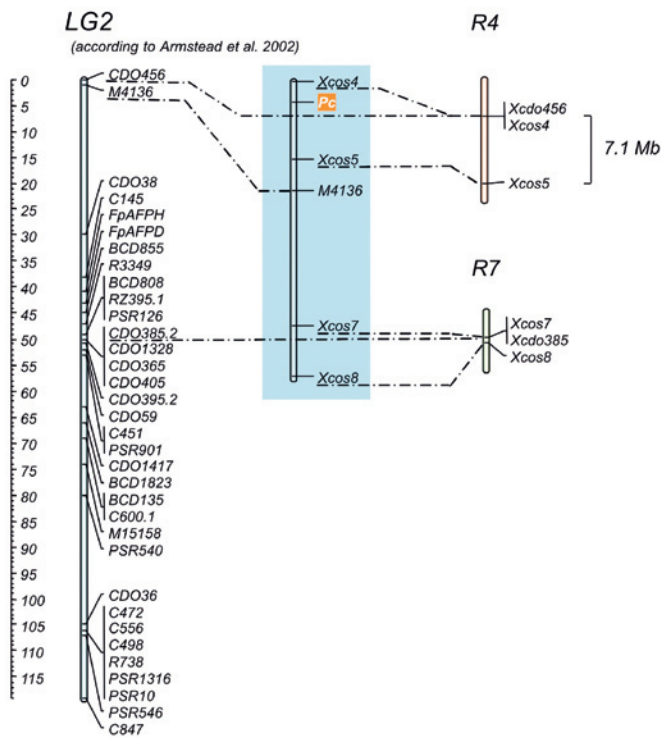


Fig. 8

Comparative approach for the mapping of a crown-rust resistance gene, *Pc*, in Italian ryegrass. On the left, molecular marker map of linkage group (LG) 2 according to Armstead et al. 2002; on the right, parts of rice chromosomes R4 and R7 which are of common origin with *Lolium* LG2 served a starting point for marker development in *L. multiflorum*; middle, genetic map of *Pc*

■ Ryegrasses (*Lolium perenne* L. and *L. multiflorum* L.)

Healthy forage grasses for high-quality dairy and meat production

Grasses on pasture grounds provide the basis for high-quality dairy and meat production. Of Germany's farmland, nearly one third (5.2 million ha) is permanent grassland. With intensive grazing the fast-growing and high-yielding *Lolium* and *Festuca* species constitute the dominating grassland plants. A major disease of these grass species is crown rust caused by the fungus *Puccinia coronata* ssp., the latter of which has evolved specialized subspecies on these grasses. Infestation with crown rust may result in considerable yield losses in green matter as well as reduction in pasture quality. Crown-rust infection decreases water-soluble carbohydrates and digestibility of the dry matter. The distribution of the crown-rust disease has, meanwhile, reached northern areas of Europe which before had been deemed devoid of this disease.

Identification of resistance genes against crown rust

Part of ILK's research activity is dedicated to searching for genetic resources of crown-rust resistance among ryegrass accessions. As a result, dominant resistance genes against *P.*

coronata ssp. *lolii* have been identified in *L. multiflorum* and *L. perenne*. One of these genes (*Pc*) was genetically mapped in Italian ryegrass using four backcross families with a total of 274 individuals. Using bulked segregant analysis, linkage was detected between *Pc* and microsatellite marker M4136 the latter of which is located on linkage group (LG) 2. Additional PCR markers in the vicinity of M4136 were then derived via comparative mapping based on rice-genomic data. Using these markers a 57 cM interval was defined which encompasses the *Pc* gene flanked by the markers COS4 and COS5 (Fig. 8). The genetic map position of *Pc* suggests that this gene is different from either of three QTLs for crown-rust resistance which had been mapped by others before on LG 2 in *L. perenne*.

■ Potato (*Solanum tuberosum* L. ssp. *tuberosum*)

From a wild species to cultivated potato with durable resistance to late blight

Due to increasing demands of environmental and consumer policies with regard to agricultural production methods there is growing importance of resistance breeding which at least in part, may substitute for chemical plant protection measures. In potato growing, late blight caused by *Phytophthora infestans* is in the focus of chemical plant protection. For this reason, durable resistance to this disease is a major concern in our breeding research on potato. To our current knowledge durability of late-blight resistance requires exploitation of the quantitative and polygenic type of resistance. Resistance resources of this type of resistance have been drawn from the IPK potato genebank in Groß Lüsewitz. The long-term prebreeding of adapted germplasm at ILK constitutes the link between non-adapted genebank accessions and commercial cultivar breeding of potato. Figures 9 and 10 give an impression of the extent of adaptation which has to be accomplished in the prebreeding process. A major goal of prebreeding in potato is to combine polygenes for late-blight resistance with polygenes for early maturity and quality traits.

At the tetraploid level our progress to combine late-blight resistance with middle-early to early maturity as well as good table or processing quality or high starch contents demonstrates that durable resistance can be combined with other important traits via conventional prebreeding strategies. There also was progress with regard to the combination of resistance to late blight, *Globodera pallida*, starch contents and maturity type. Of the 51 tetraploid inheritors of *Phytophthora* resistance, 20 are suited for the breeding of table potatoes, 9 for processing potatoes and 9 for starch potatoes. In addition, 10 prebreeding clones display high virus resistance. Besides tetraploid potato clones, 18 dihaploid clones were selected with good processing quality following storage at 4° C. These clones may contribute to efforts to reduce acrylamide

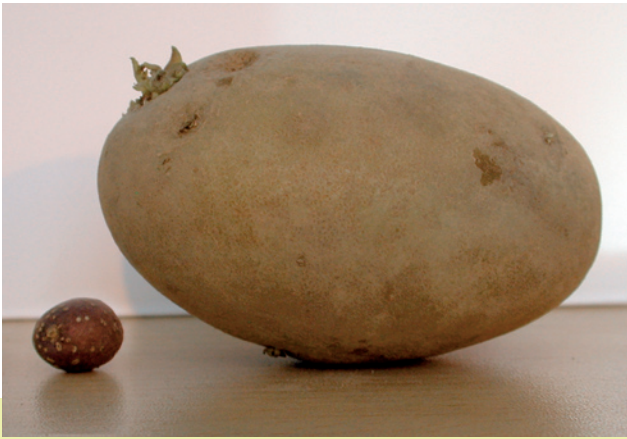


Fig. 9 Wild species as a resistance donor (on the left) and cultivated potato as a recipient in a size comparison



Fig. 10 Clone from the Groß Lüsewitz potato germplasm with good table quality and durable late-blight resistance

formation during potato processing. We expect that the potato germplasm developed so far in Groß Lüsewitz is suited to breed cultivars which require up to one third less fungicide treatment. Besides commercial breeding programmes, the Groß Lüsewitz potato clones have been entered as experimental materials in the research projects of other groups, e.g. in plant-genome programmes such as GABI or in projects directed to the mapping of QTLs for late-blight resistance.

tance of narrow-leafed lupin in Germany breeding research activity on this crop plant has remained weak in this country. For this reason, we started a research programme at the Groß Lüsewitz location where there are optimal growing conditions for narrow-leafed lupin. The programme was launched in 2004 in cooperation with Saatzucht Steinach, Bornhof, the only one variety breeder of narrow-leafed lupin left in Germany.

Neglected/Novel Crop Plants

■ Narrow-leafed lupin (*Lupinus angustifolius* L.)

A versatile protein crop plant

Due to its richness in protein, N fixation, tap-root formation and environmental robustness, narrow-leafed lupin offers interesting perspectives for food and feed usage, plant cultivation, as well as agroecology. In Germany, the crop area of narrow-leafed lupin of approx. 33000 ha is restricted to the lighter, dryer and less calcareous soils in the east and northeast where narrow-leafed lupin can unfold its strengths relative to other protein plants most easily. The protein of narrow-leafed lupin is suitable for human nutrition. Since narrow-leafed lupin is a relatively recent crop plant it still displays non-domesticated behaviour such as pod dropping and seed shedding which limits its attractiveness to the grower. In addition, incomplete tolerance to anthracnose as well as sensitivity to soil-pH values of >5.8 limit the growing area in Germany. Due to the presently limited impor-

Lupins which are resistant to anthracnose? Promising perspectives via breeding research

In the period under review the German cvs. 'Bora' and 'Borweta' were tested for their anthracnose resistance using a novel resistance test which we adopted by courtesy of the Department of Agriculture, Western Australia (cv. Annual Report 2005). The two cultivars had been reported in the literature as being resistant. Under the revised test conditions, however, plants of these cultivars reacted susceptible to *Colletotrichum lupini* and did not differ in this respect from the susceptible standards 'Borlu' and 'Bolivio'. Yet another cultivar which had not been tested before and also turned out to be susceptible is 'Vitabor'. As a conclusion from our findings, there is no anthracnose resistance available at present among the narrow-leafed lupin cultivars grown in Germany.

At ILK we introduced *Lanr1*, which is the only one resistance gene identified so far, from the Australian cv. 'Tanjil' into German lupin germplasm in a marker-assisted approach. The goal was to check whether *Lanr1* is also effective in the genetic background of germplasm adapted to local growth conditions. Of 89 crosses we selected 40 lines with homozy-

gosity for the *Lanr1* molecular selection marker. Resistance tests with some of these lines proved effectiveness of *Lanr1* in different genetic backgrounds. This opens up the promising perspective that antracnose resistance can be made available in the near future for narrow-leaved lupin growing in Germany.

Domestication and genetic enhancement – prerequisites for future success

To study feasibility of improving agronomic traits not yet completely domesticated (e.g., pod dropping and seed shedding) we started a mutagenesis programme. For mutagenesis, 40000 seeds of cv. ‘Boruta’ were treated with ethylmethanesulfonate (EMS) and 20000 M2 progeny were collected. This genetic material is now available for *SMART-Breeding* approaches such as TILLING.

Sweet narrow-leaved lupin as a crop has a very narrow genetic basis. It is, thus, of interest to study trait variation including additional lupin species and to estimate their value for broadening the genetic base of narrow-leaved lupin via interspecific crossing or somatic hybridization. Our *Lupinus* collection evaluated in 2006 comprised 138 accessions of 31 species, among them 11 Old-World species (Fig. 11) the latter of which encompassed accessions of *L. angustifolius* (N=31), *L. atlanticus* (18), *L. cosentinii* (20), *L. digitatus* (4), and *L. pilosus* (17). Of the New-World species, *L. mutabilis* was represented with five accessions and the remaining species with 1–2 accessions each. Trait evaluation was done following the Lupin Descriptors of IPGRI. A photographic record was launched which provides data on seed traits, growth habit, flower and pod traits and which is supplemented on a current basis.

In June 2006, colleagues from the Centre for Legumes in Mediterranean Agriculture (CLIMA), University of Western Australia, visited our location for exchange of experience in the breeding research on narrow-leaved lupin (Fig. 12).

False flax (*Camelina sativa*) as an oil crop

False flax (Fig. 13) is among the neglected crop plants in Germany. This crop belongs to the family of Brassicaceae and thrives on light soils, is not vulnerable to many diseases and does not outcross to oilseed rape. The seed of false flax is relatively small (TKM < 2 g) and contains up to 40 % linolenic acid (C18:3) and 20–25 % eicosenic acid (C20:1). There were some efforts in the past to exploit this crop as a renewable resource for raw materials. These efforts, though, have been obstructed by the suboptimal fatty-acid composition, the small seed size as well as difficulties in valorizing the press cake. If unfavorable seed traits and composition could be improved via plant breeding false flax may become interesting as a vegetable oil resource which because of existing crossing barriers to oilseed rape



Fig. 11 a-c

Flowers and pods of the lupin New-World species *Lupinus stiversii* and *L. mutabilis*, respectively, as well as the Old-World species *L. hispanicus* (from the top to the bottom)



Fig. 12 Dr. Julia Wilson from CLIMA (on the right) and Dr. Karin Sonntag are viewing the interspecific crossing programme in lupin at ILK

(as the predominating oil plant), would offer a potential for the production of specific oil qualities. Since a number of agronomic and quality traits will have to be improved in false flax a mutagenesis programme was started in 2006. To-date, a limited number of 746 M2 lines was generated which will be subjected to evaluation in seed traits and fatty-acid composition.

■ *Cuphea* species (*Cuphea spec.*) as oil crops

Appealing oil characteristics ...

The genus *Cuphea* encompasses more than 40 annual and perennial herbaceous species which are endemic in Central America. Seeds are small (TKM 0.4-2.8 g) and contain 28-33 % oil the latter of which is rich in saturated medium-chain fatty acids (MCFAs) of between 8 and 14 C atoms in length. Depending on the *Cuphea* species certain MCFAs may reach a proportion of more than 80 % in the seed oil. MCFA-rich (lauric) vegetable oils are utilized as renewable raw materials mainly in oleochemistry, where palm kernel oil and coconut oil constitute the prevailing MCFAs. In Germany, 300000 tons of these oils are processed annually. Genes responsible for MCFA accumulation in the seed have been transferred from *Cuphea spec.* into oilseed rape via genetic engineering. Besides this there are efforts to domesticate wild *Cuphea* species via conventional breeding approaches and introduce these species as novel oil crops in agricultural

production. In the United States, the first *Cuphea* cultivars have been registered. There also were efforts some 20 years ago in Germany to domesticate *Cuphea spec.* but these have been discontinued meanwhile.

...yet much to do towards domestication

In 2006 we did an initial screening on a work collection of 147 *Cuphea* accessions from the Germplasm Resources Information Network (GRIN) at the USDA. Because of the seed dormancy prevailing among *Cuphea spec.* all accessions were tested in winter 2005/2006 for germination capacity. Thirty-one accessions were found not to be germinable; 28, 65 and 23 accessions had germination rates of 5-20 %, 25-70 % and >70 %, respectively. For the field screening 67 accessions from 24 species were selected. Plant development under field conditions was fast and the first plants started flowering on 29 June. The growth habit varied between "creeping" and "upright". Most of the accessions tested were rich in flowers (Fig. 14) and were visited by large numbers of insects. Nearly all of the accessions displayed more or less pronounced trichome coverage of stems, leaves or flowers. Trichomes were extremely sticky in some of the species, thus capable to capture small insects such as blossom rape beetles and aphids (Fig. 15). Trait evaluation of the accessions followed the descriptor list of the USDA. Special focus was laid onto traits which may hamper agricultural use most severely. These were

- the dense coverage of stem, leaf and hypanthium with sticky trichomes which may impair harvest (Fig. 16),
- tendency of seed shedding up to total seed loss (Fig. 17),
- non-determined growth which prevents uniform ripening of the seed.

A number of accessions displayed advantageous characteristics. For instance, in *C. glutinosa* which is a small-seeded species there were accessions with minor incidence of seed shedding and less coverage with trichomes which were non-sticky. *C. lutea* also hardly showed seed shedding and was characterized by numerous yet non-sticky trichomes. Accessions of *C. lanceolata* the latter of which is a relatively large-seeded species, displayed rich flowering and high seed production, however, seed shedding is relatively intense and stems and flowers are very sticky. Accessions displaying non-determined growth were not found.

■ Sorghum (*Sorghum bicolor*) and sudan grass (*S. sudanense*) as biomass crops

Grasses of the genus *Sorghum* can tolerate drought much better than maize. For this reason sorghum may be an interesting crop rotation component in biomass production under dry



Fig. 13 False flax (*Camelina sativa*)



Fig. 14 Multiple flower formation in *Cuphea koehneana*



Fig. 15 *Cuphea koehneana* with sticky trichomes on stem and leaf

Fig. 16 *Cuphea wrightii* with trichomes on flowers and stem



Fig. 17 *Cuphea lanceolata* with hypanthium torn open (left) and seed shedded (right)



growth conditions. When sown in May as an intercrop, sorghum allows for the preceding growing of rye for greenmatter harvest. With sowing sorghum in June total plants silage of cereals is feasible. Combining sorghum and rye, the latter of which has the most rapid early growth among the cereals grown in Germany, would allow for an optimal exploitation of farmland in biomass production. Using sorghum in this way requires that sufficient dry-mass yields can be achieved with this crop under specific growing regimes. In the period under review we started a field trial with sorghum (*S. bicolor*) and a number of *S. bicolor* x *S. sudanense* as well as *S. bicolor* x *S. bicolor* hybrids. A total of 16 sorghum and sudan grass accessions and their hybrids were involved in the Groß Lüsewitz field trial. Despite pronounced summer heat and

drought at the Groß Lüsewitz field location – with a total of 10 mm precipitation during the first 40 days after sowing – there were some sorghum genotypes which produced approx. 150 dt dry mass per hectare within the growing period of 107 days (end of June till beginning of October). Thus, sorghum grown as second crop after rye may yield almost as high as silage maize and there is considerable total dry mass yield potential when combining rye and sorghum as biomass crops in German agriculture. One of the bicolor x bicolor hybrids tested outyielded the sudan grass standard cultivar by 66 % with regard to dry matter yield. The Groß Lüsewitz 2006 field trial which met public interest (Fig. 18) was part of a larger cooperation of German plant breeders and public research.

Conclusions and Prospects

The phenotypic and genetic characterization of plant genetic resources for food and agriculture (PGRFA) and the investigation of neglected or novel crop species requires dedicated, long-termed research. Research on agro-biodiversity gains increasing public relevance under the impacts of a changing climate and fading biotic and abiotic resources in agriculture. Following the predefinitions of the national BMELV programmes ‘Plant Genetic Resources’ and ‘Reducing Chemical Plant Protection’ the prevailing research topics of ILK are directed to maintain and broaden agro-biodiversity with regard to genetic and crop-species diversity. The importance and necessity of our research are confirmed by the report on ‘Alternative Crop Plants and Production Methods’ from November 2006 by the Committee for Education, Research and Technology Assessment of the German Bundestag. Present issues of plant breeding as well as ongoing long-term developments will define our research focus for the years to come. Research topics where

ILK will develop increased activity in the future comprise plant-breeding issues in the context of climate change, especially with regard to “novel” pathogens. Furthermore, the increasing role of diversified use of crop plants, of biomass and bioenergy production in agriculture as well as of coexistence issues in various field crops will have to be considered by us. In taking up such current topics, we will not lose sight of the basic issues of plant-breeding research which continue to be important in the future. Characterizing and mining the tremendous genetic wealth hidden in PGRFA is only at the beginning. The systematic screening of genetic diversity in PGRFA and the association of genetic information with the phenotype (i.e., trait expression) via novel strategies which integrate classical and modern biotechnological approaches such as molecular markers and genomics is one of the publicly most important and scientifically most fascinating tasks of plant breeding research.

Fig. 18 a-c The Groß Lüsewitz sorghum biomass field trial in 2006. From the left to the right: Plants on 25 August; harvest of the overground biomass on 12 October with a NDR television team as onlookers; chaff surveying by the trial field manager





Institute
of
Abiotic
Stress Tolerance

Groß Lüsewitz

Institute of Abiotic Stress Tolerance

The objective of the Institute of Abiotic Stress Tolerance is to characterize and to diminish effects of abiotic stress factors on the performance of crop plants, especially with respect to yield, quality of raw materials, nutrient efficiency and disposition to diseases. Investigations are performed under explicit consideration of genetic resources. This is of special importance in view of the prognosticated climate changes with complex consequences for an economic and at the same time environmentally friendly agriculture. Investigations aim at promoting a competitive and multifunctional agriculture, which allows the production of highly nutritious, healthy and safe food and animal feed as well as raw materials for a broad range of industrial applications. For this purpose the development and adaptation of suitable methods, the evaluation of genetic resources and the long-term observation of indicator assortments (cereals, potatoes, legumes, oilseed crops) under varying environmental conditions are essential. The investigations promote the sustainability of agriculture by improving their competitiveness under both conventional and organic conditions.

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Abiotic Stress

Plants are permanently exposed to environmental stress situations, which impair their development and cause yield and quality losses. In order to minimize these effects, it is essential to increase the tolerance to abiotic stress factors. Prerequisite is a detailed understanding of causes and impacts of the induced damage. In this respect important research work comprises the evaluation of genetic resources, the establishment of indicator assortments, the identification of selection markers, the analysis of the genetic determination of abiotic stress tolerances and the development of tolerant germplasm.

■ Molecular characterization of genetic resources of potato concerning abiotic stress tolerance and associated traits

Drought stress like other stress factors induces diverse changes in the metabolism of plants. Its impact depends on the time, duration and intensity of the stress phases. Among others, plants respond to drought stress with the accumulation of different substances in the leaves, which may be used as indicators for drought tolerance.

At the Institute of Abiotic Stress Tolerance the evaluation of such specific drought induced traits is performed under controlled conditions (rain-out-shelter, *in vitro* culture) (Fig. 1). Among these are the accumulation of free proline and soluble sugars as well as changes in the concentration of nitrogen fractions and the osmolality of the cellular sap. The identification of relevant indicators is the prerequisite for association studies in a large range of potato genetic resources. The selection of promising genotypes was performed on the basis of literature and gene bank data, which, however, have to be balanced and verified by different evaluation methods.

At the same time, different candidate genes were chosen from sequence databases. These sequences will be PCR analysed in selected genotypes for their association to drought tolerance or its respective indicators.

■ Improvement of drought tolerance in faba beans (*Vicia faba* L.) / Investigations into proline accumulation

Climate prognoses predict more and severe drought stress periods during summer months for the next decades in the German area. This is especially problematic for crops, which respond sensitively to drought stress even today.

Breeding of better adapted genotypes is one important method to prevent possible yield losses and yield instability. Complex characters, such as abiotic stress tolerances, are difficult to select for. Therefore, indirect selection criteria are of great interest as they not only allow the evaluation of genetic resources but also the combination of different tolerance mechanisms in terms of pyramidation.

The accumulation of free proline belongs to the physiological characters which are seen in a positive relation to drought tolerance of plants, even if the mode of action of proline within the plant cell is not yet completely understood.

We were able to demonstrate that there is considerable variability regarding proline accumulation under osmotic stress conditions in faba beans. Basing on this variability it was possible to select inbred lines with low and high proline accumulation, respectively, which concomitantly differed in yield stability under drought stress.

Changes in physiological characters, being also investigated (relative leaf water deficit, membrane stability, effective quantum yield of photo system II measured by chlorophyll fluorescence), indicate fundamental differences between the selected lines regarding their response to drought stress. This data confirmed the improved drought tolerance of



Fig. 1: Evaluation of potato genetic resources for drought tolerance



the inbred lines with the higher proline accumulation. Summarized it could be shown that proline accumulation is related to complex changes in the drought stress response of plants and suitable as indirect, physiological marker for the selection of drought tolerant faba beans.

Nutrient efficiency

The release of nitrogen from fertilizers applied to areas used by agriculture accounts for an evidently negative impact on ecosystems. Therefore there is increasing demand for cultivars with optimized nitrogen efficiency. Four different components are differentiated in respect of nitrogen utilization of plants: (1) absorption, (2) assimilation, (3) translocation, and (4) remobilization. The ability for efficient nutrient uptake and utilisation differs between plant species due to specific morphological and physiological characteristics. Furthermore, genetically based differences have been demonstrated within one species. This indicates the feasibility of increasing the nutrient efficiency by plant breeding.

■ Investigation of nitrogen efficiency in *Solanum tuberosum*

In regard to agricultural crop production worldwide potato ranks fourth after wheat, rice and maize. In Europe potato culture comprises an area of approximately 8.39 million ha per year. A research project was started in 2006 which

aims at the establishment of methods which will allow the development of potato genotypes with increased nitrogen efficiency. Special emphasis will be placed on (1) characterization of genetic resources in regard to different components of nutrient uptake and utilization, (2) investigation of effects of nitrogen deficiency on development and physiology of different genotypes, (3) genetic analysis of nitrogen efficiency as well as (4) development of appropriate screening and selection procedures. For characterization and identification of potato genotypes with differing efficiency potentials various cultivars are grown in field, greenhouse and *in vitro* trials with graduated nitrogen supply. Following traits are evaluated considering the development under nitrogen deficiency as compared to that under ample supply: vegetative development, chlorophyll content, protein content of leaves, yield (field and greenhouse); vegetative development, chlorophyll content, protein content of shoots, fresh weight of shoots and roots, dry weight of shoots and roots, root architecture as well as removal of nitrogen from the nutrient solution (*in vitro*). Preliminary results display genotype specific differences in some performance features under nitrogen deficient conditions. For example, a differing diminuation of the chlorophyll content of leaves was determined with a chlorophyll meter (SPAD-502) in the greenhouse trial (Fig. 2). Similarly *in vitro* experiments revealed genotype specific differences in regard to shoot and root development upon reduction of nitrogen to 1/8 of the concentration in the Murashige and Skoog culture medium (Fig. 3).

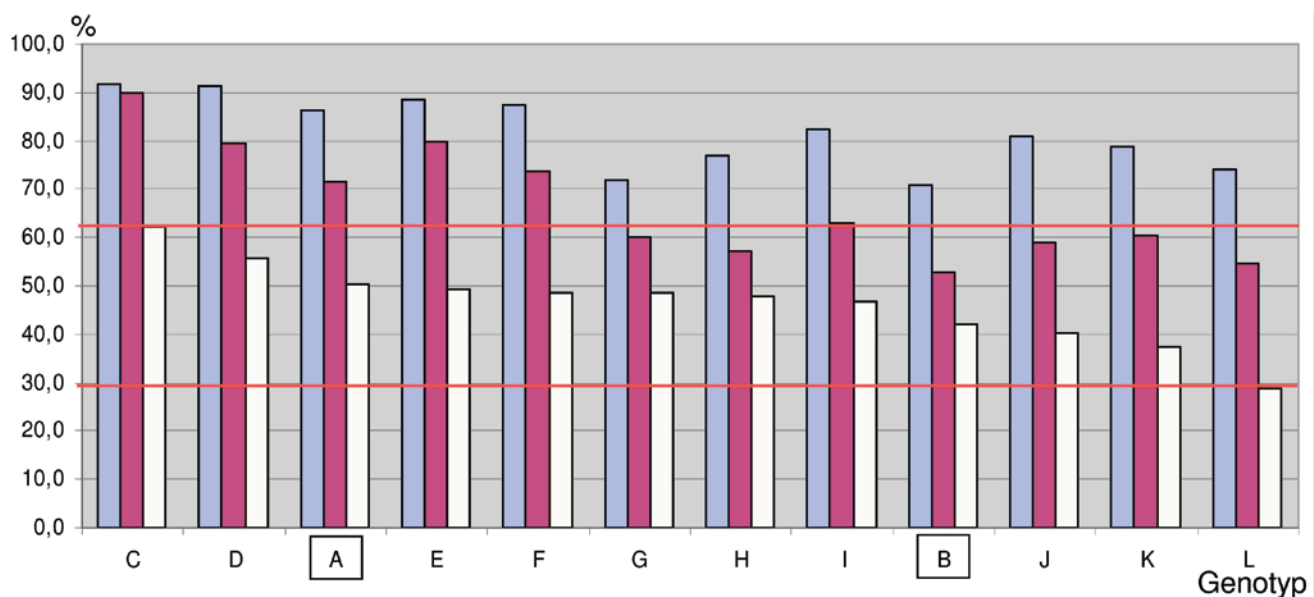


Fig. 2: Leaf chlorophyll content of different genotypes (A – L) after eight weeks of culture in the greenhouse under different nitrogen regimes (1/2 N, 1/4 N, 1/8 N) (values are presented as percentage of those obtained with maximum nitrogen fertilization)

Organic farming

Since 2000, part of the experimental field at the research station in Groß Lüsewitz has been cultivated under organic management, providing without further transitional period the basis for research projects in stress tolerance, nutrient efficiency and quality. The conversion to organic farming with a 6-year crop rotation allows direct comparative investigations with regard to yield and quality stability obtained with different farming systems in the same environment.

■ Lupins (*Lupinus sp.*) as raw material for production of organic feed and food

Sweet lupins are very important protein sources, suitable for organic farming, due to their higher protein yield in comparison with other legumes such as field beans and peas. Lupins may contribute to solving problems related to the use of organic feeding stuffs in animal nutrition and, furthermore, gain more importance as an alternative protein source in food industry.

For two years, cultivars and breeding material of sweet lupins have been cultivated organically at three locations (two in Mecklenburg-Western-Pomerania and one in Low Bavaria) and protein quality, fatty acids and contents of antinutritive substances such as oligosaccharides, non-starch polysaccharides as well as alkaloids were analysed (Fig. 4).

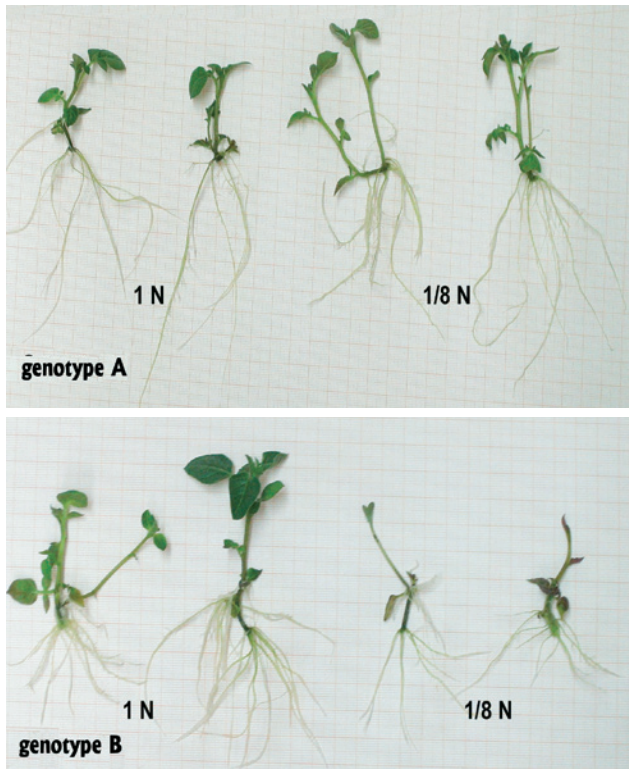


Fig. 3: Genotype specific development of shoots and roots of *in vitro* plantlets upon reduction of nitrogen supply to 1/8 of the concentration in the Murashige and Skoog culture medium

Fig. 4: Organic cultivation and harvest of blue lupins



Blue lupins can be used in organic farming without limitation. They showed a low sensitivity to diseases and ripened early as well as uniformly at all three locations. However, the yellow and white lupins grown at the locations in Mecklenburg-Western Pomerania (MP) did not reach maturity within the vegetation period. When valuing lupins as feeding stuff in organic farming, not only differences in yield but also in components and therefore in feeding quality have to be regarded – especially when plants were grown at different locations. In case of blue lupins differences between locations in yield and quality were so high that in comparison genotypic differences could be neglected. The obvious regional distinctions between Low Bavaria (LB) and MP were probably caused by different soil properties, e.g. a higher pH value at LB. The very low raw protein contents of blue lupins grown at LB were counterbalanced by enhanced contents of fat and non-starch polysaccharides. Starch could not be detected or only in traces (< 1%) in all lupins investigated.

Furthermore, due to the low content of sulphurous amino acids the protein quality is poor and problematic with regard to feeding of monogasters. With significantly higher contents of sulphurous amino acids the protein quality proved to be better in lupins grown at LB, however, the protein content was too low. The alkaloid content of blue lupins was dependent on the location as well (LB<MP). Only a few varieties exceeded the critical value of 0.05% for use in feeding. Interestingly, all new breeding lines revealed lower alkaloid contents than the actual cultivars. Blue lupins have a desired spectrum of fatty acids for human nutrition because of the high proportion of single and polyunsaturated fatty acids.

Altogether, the analyses have shown that lupins can contribute to fodder supply in organic farming and represent a usable potential for a healthy human nutrition. The quality can be improved by breeding strategies as well as by selection of appropriate locations for cultivation.

In early breeding stages only small quantities of plant material are available. At the Institute of Abiotic Stress Tolerance methods for a fast and non-destructive analysis of raw protein were developed. Using NIR-techniques the prediction of raw protein contents in meal and even single seeds of lupins is possible.

Quality

The demands of consumers and producers on the quality of food and feed increase continuously. Additionally, industrial raw materials with specific properties are required. Therefore, customized plants with an adapted composition

of components for most different uses are requested. At the same time these plants should be more tolerant to abiotic stress factors thus ensuring stable yield and quality. For the investigation of such characteristics efficient breeding relevant methods are of special importance.

■ Evaluation of gene bank material in oilseed rape for the production of protein-rich and high-quality feed and for simultaneous use of the oil in food and non-food area

Rapeseed (*Brassica napus* L.), a member of the family *Cruciferae*, is the most important oil-producing plant in Europe. In 2005, five million tons were produced on an acreage of 1.34 million ha in Germany as the leading producer in the European Union (Source: Statistisches Bundesamt, Germany). Rapeseed oil is used in the food-area as high quality cholesterol-free edible oil for cooking and baking or as renewable raw material for biodiesel, biodegradable lubricants and hydraulic oils, surfactants, dyestuffs and varnishes, cosmetics, plasticiser or pesticides.

The improvement of crop yield and oil content remains the most important objective in breeding. In addition, the competitive position of rapeseed may be improved by commercialization of the protein-rich residues derived from the oil production process as a valuable plant-derived animal feed.

The evaluation of genetic resources with respect to value determining components is focussed on the enhancement of oil and protein content, contrary to the desired reduction of crude fibre and antinutritive compounds such as tannins, glucosinolates, phytic acid or sinapine.

A large assortment of 00-rapeseed types (low in erucic acid and glucosinolates) and ++-rapeseed types (high in erucic acid and glucosinolates) was analysed for seed quality. A significant negative correlation between oil and raw protein content of rapeseed was found. The highest differences for both rapeseed types were detected in oil contents. The progress of breeding over the last years is reflected by the fact that mainly the oil content was enhanced, while the protein remained relatively unchanged (Fig. 5).

Further strategies in improvement of rapeseed aim at the development of large-seeded cultivars by increasing the thousand kernel weight as well as at a reduction of the seed coat thickness. The lower coat content of yellow seeded rape types was found to be coincident with an enhanced proportion of oil and protein. However, the use of colour measurements for estimation of the coat thickness is not yet possible due to the heterogeneity of seed colour in rape varieties. Hence, methods based on single kernel analyses have to be developed for future selection.

Detailed analyses of some selected samples were aimed at the evaluation of defatted rapeseed meal for utilisation for



Fig. 5: Investigation of oil- and protein-quality of rapeseed

feed purposes. Relatively high contents of sucrose beside stachyose and raffinose were found in the water-soluble carbohydrate fraction of rapeseed. The seed coat and the cell walls mainly consist of nonstarch polysaccharides (NSP), so-called hemicelluloses which are composed of pentoses, hexoses and uronic acids. From the sum of the monosaccharides measured after acid hydrolysis the content of the NSP could be calculated and conclusions to the structure could be made. The residue still remaining after the acid hydrolysis was denoted by Klason lignin.

The amino acid contents of defatted rapeseed meal were determined after hydrolysis of the samples.

The amino acid composition of the protein, in particular the composition of the essential amino acids, can be regarded as ideal for the animal nutrition. Compared with many plant raw materials higher quantities of the sulphurous amino acids methionine and cysteine are contained. The results of the single plants analyses are the basis for selection of progenies with higher oil and protein content. From that new genotypes are to be developed for the production of protein-rich and high-quality feeding stuffs which can be used parallel for the production of oil.

■ Coloured potatoes and their special features with respect to resistance and quality

For many years growing interest in old coloured potato varieties containing anthocyanin colour pigments can be observed on potato markets worldwide. This is promoted by the attractive colour of tubers, which meets the trend to use speciality potatoes mainly in gourmet restaurants. Furthermore, with increasing health awareness of the consumers, there is considerable interest in anthocyanins

accumulated in coloured tubers because of their putative health benefits as dietary antioxidants. Anthocyanins, belonging to the group of bioactive plant polyphenols, are efficient radical scavenging compounds. Furthermore, they were shown to reduce the risk of several degenerative diseases such as atherosclerosis, cardiovascular diseases, cancer and diabetes. In addition, anthocyanins are of interest in the food sector as natural colour pigments due to increasing public concern about synthetic dyes, which are known for their allergy triggering potential. For all these reasons old coloured potato varieties are increasingly included in current breeding programmes. Recently, we could demonstrate that an integration of such coloured potato cultivars is no risk with respect to tuber soft rot diseases caused by *Pectobacterium carotovorum* (formerly *Erwinia carotovora*). The results clearly demonstrated that anthocyanins in association with total soluble phenols such as chlorogenic acid, known for their antimicrobial activity, contributed crucially to resistance expression in tuber tissue of coloured potato cultivars. Besides the presence of anthocyanins in tuber tissue the old coloured potato cultivars revealed on average significantly increased contents of total soluble phenols in comparison to white or yellow-fleshed cultivars. Similarly elevated amounts of soluble phenols could be detected in tuber tissue of seven purple-fleshed breeding clones (NORIKA, Groß Lüsewitz), derived from crossings with coloured potato cultivars. In this respect it was important to note that extracts prepared from tuber tissue of these coloured clones revealed a significantly increased antioxidative capacity, measured as ascorbic acid equivalent. A high correlation of the antioxidative capacity to the amount of total soluble phenols determined in tuber tissue could be demonstrated. These results indicate that



Fig. 6:

Coloured and white/yellow fleshed potatoes

consumption of coloured potatoes rich in anthocyanins and soluble phenols may enhance the uptake of radical scavenging compounds in human diet. Integration of coloured potatoes in breeding programmes as well as in potato commerce is desirable, because of their positive potentials with regard to quality and resistance of tubers as well as to their nutritional value. In addition, producers might profit from a multicoloured and thus more interesting potato market (Fig. 6). Further work is focussed on elucidation of the role of anthocyanins, especially with respect to resistance expression in tuber tissue.

Due to the good adaptability in geographical extension the production of potatoes is marginally restricted. Even in Asiatic countries such as China or Korea potatoes belong to the main crops in addition to rice and corn. Increasingly local varieties are being developed in such countries. A scientist from the National Highland Agricultural Research Institute of Korea spent two months at the Institute of Abiotic Stress Tolerance. She was particularly interested in analytical methods for value determining ingredients in potatoes and especially for starch quality (Fig. 7).

Outlook

The future competitiveness of agriculture will depend on an efficient breeding research on cultivated crops to a high degree. Thereby, fundamentals are developed for improving the potential of agricultural plants being used as food, feed, industrial raw material and energy supplier. Modern breeding strategies will increasingly facilitate the adaptation of useful plants to regional cultivation conditions as well as to current needs of man and beast and will contribute to enhance the sustainability of agriculture. In this context, the research activities of the Institute of Abiotic Stress Tolerance are focussed on characterization and development of genotypes with increased tolerance to abiotic stress factors in order to promote breeding of new varieties with optimal suitability for an environmentally sound production cultivation under changing climatic conditions. The variability of genetic resources of potatoes, grains and legumes is investigated with



Fig. 7: Visit of a Korean scientist of the National Highland Agricultural Research Institute



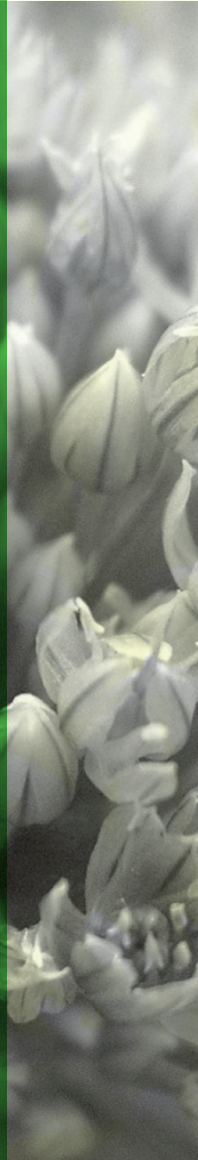
Fig. 8:

Excursion to Groß Lüsewitz during EUCARPIA conference 2006

regard to drought, heat, cold and salt tolerance as well as the potential of adaptation to marginal locations. The effect of these stress factors on yield, quality, nutrient efficiency and disposition to diseases is analysed in different time scales: spontaneously appearing short term weather events as well as longer and more intensive stress periods due to the predicted climate change. The feasibility of identifying morphological, physiological, biochemical and molecular markers for abiotic stress tolerance was demonstrated. Prerequisite for such investigations are appropriate analytical techniques comprising spectroscopy, chromatography and a wide range of biochemical methods. During the last years corresponding analytical procedures were established and will currently be expanded to molecular techniques.

Additionally, special emphasis is laid on the development of breeding relevant non-destructive methods for evaluation of single plants and single kernels. In this way the institute contributes to the elucidation of the biological mechanisms of stress tolerance and provides methods for an efficient adaptation of plant material to modified environmental conditions by breeding.

Now and in future, this scientific work is based on an intensive co-operation within the Federal Centre for Breeding Research on Cultivated Plants as well as with other research facilities in responsibility of the BMELV and, in addition, with German and international gene banks, universities, research centres and commercial breeding companies (Fig. 8).



Institute
of
Horticultural Crops

Quedlinburg

Institute of Horticultural Crops

The history of plant breeding in Germany is closely connected with the town of Quedlinburg. In the middle of the 19th century, Quedlinburg was the home of many gardeners as well as plant breeding companies. In 1947, an Institute of Plant Breeding was founded, which concentrated on both basic research and applied research. The research results of this Institute found their practical application in the breeding of 144 vegetables and 149 ornamental varieties of 14 ornamental plant species. The Institute of Horticultural Crops originated from the merger of two BAZ institutes founded in 1992, the Institute for Breeding of Vegetables, Medicinal and Aromatic Plants and the Institute for Breeding Methods in Vegetables. Modern society demands healthy and tasty agricultural and horticultural food produced by sustainable farming systems that respect nature. For this reason, breeding research carried out by the institute is aimed at providing the conditions for an economically efficient plant breeding and an ecologically balanced horticulture. Special emphasis is given to the resistance to pathogens, a better product quality for the consumer and the utilization of new genetic resources. The main objectives of the institute encompass the generation of new resistance donors, the development and adaptation of novel technologies and breeding strategies for a genetic improvement of horticultural crops. At present, the main focus is in vegetable on the groups of vegetable cabbage (*Brassica*) and related species (*Raphanus*) as well as carrot (*Daucus*), in medicinal and aromatic plants on caraway (*Carum carvi*), fennel (*Foeniculum vulgare*), thyme (*Thymus vulgaris*) and summer savory (*Satureja hortensis*), as well as in ornamental plants on the genera *Pelargonium* and *Hydrangea*. The methodical area of expertise of the Institute in cytology and cytogenetics is the basis for their sovereign duties of providing assistance to the Bundessortenamt (Federal Office for Plant Varieties) with the determination of the ploidy level.

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Sovereign Duties

In current breeding material being submitted for registration of breeders' rights by the "Bundessortenamt", the DNA content was determined by flow cytometry of prepared cell nuclei from leaves for the first time. The studies encompassed in *Beta* beets 40 sugar beets and 8 fodder beet as well as 31 strains of red fescue (*Festuca rubra*) and 2 strains of bent grass (*Agrostis*). During the measurements, which included at least 38 plants per line, it was shown that mainly differences in the preparations in one investigation cycle can provide shifts in the DNA-content. In extreme cases this has the differentiation of ploidy levels without standards impossible. Therefore, it was inevitable to use appropriate standards for each probe for measurement to compare in histograms the relation of test variety and standard. The appropriate standard for *Beta vulgaris* was radish (*Raphanus sativus*) because the DNA amount of the diploid cell nuclei (2C) of radish with 1.31 pg lies under the diploid level of sugar beet with 1.63 pg (Fig. 1). The polyploid nuclei known to be present in plant leaf materials, designated as 4C and 8C, were generally lower in number than their somatic basic level (2C). An exception is visible amongst others in leaves of *Beta* beets in which the 2C peak is lower than that of 4C depending on the development stages of the leaves (Fig. 1 and 3). The overlay of measurements from single plants illustrates the elongation of one as diploid detected sugar-beet line (Fig. 2). A differentiation without overlapping between the *Raphanus* standard and the analysed line of sugar-beet is visible for all single plants in the histogram. The differences between the diploid and triploid levels of sugar-beet are shown in relation to the diploid standard of *Raphanus sativus* in an overlay of Figure 3. The measurement of DNA in red fescue (*Festuca rubra*) should be given an assured determination between the hexaploid and octoploid level. Here was the suitable standard *Pisum sativum*, which lies with a DNA amount of 9.07 pg (2C) significantly under the hexaploid level of 13.68 pg (2C) in red fescue (Fig. 4). The peaks of 6x- and 8x-red fescue, despite their relative adjacency, showed significant differences of around 55 scale values in their means and consequentially a DNA amount difference of 2.97 pg.

Vegetables

The conscious promotion of health by an appropriate, balanced diet has become an important social request. Vegetable thereby possesses a special importance due to its high vitamin, mineral and dietary fibre content. At the start of a consumer-oriented horticultural production chain, plants are necessary that ensure product quality and, above all, sufficient resistance. This makes it possible to renounce the large-scale use of agro-chemicals and equally provides for an improved protection of consumers and environment.

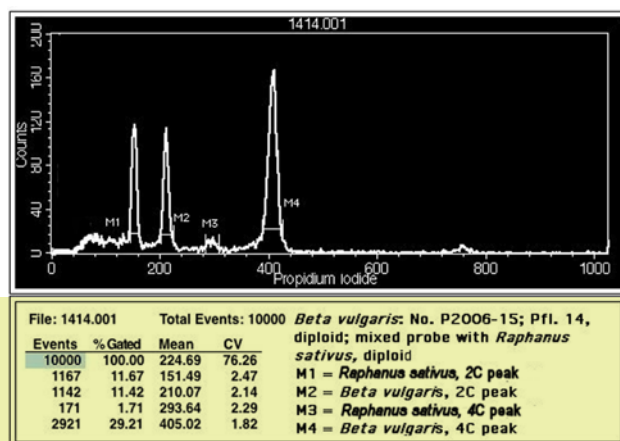


Fig. 1: Histogram of the composite sample of one diploid plant of sugar-beet and the diploid standard of *Raphanus sativus*.

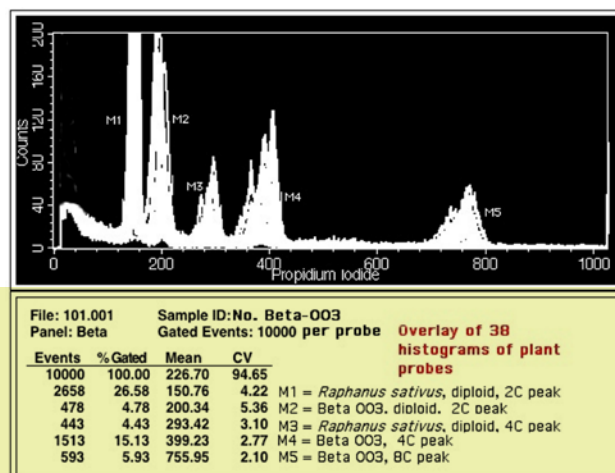


Fig. 2: Overlay of histograms of 38 single plants of the sugar-beet line no. 2006-003 prepared in mixed probes with *Raphanus sativus*.

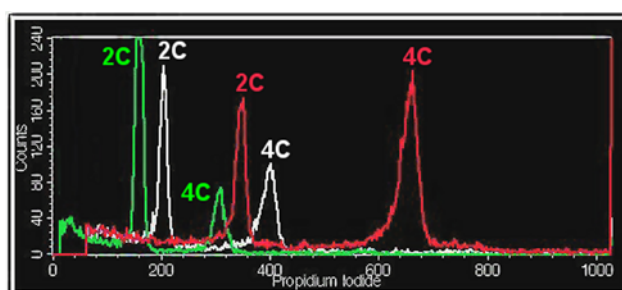


Fig. 3: Histogram of a diploid (white) and triploid (red) sugar-beet as well as with the diploid standard of *Raphanus sativus* (green).

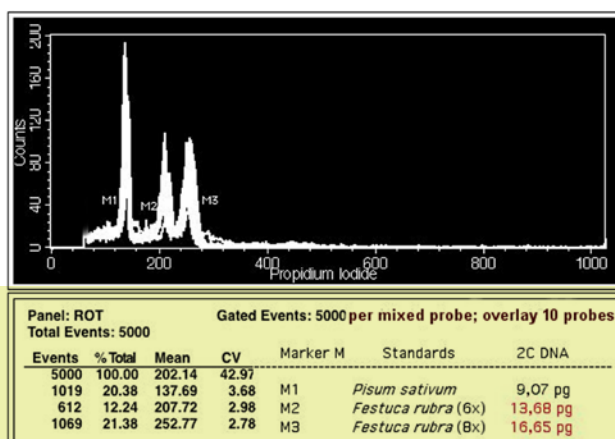


Fig. 4: Overlay of histograms from 10 single measurements of mixed probes with standards of *Pisum sativum* and hexaploid as well as octoploid *Festuca rubra*.

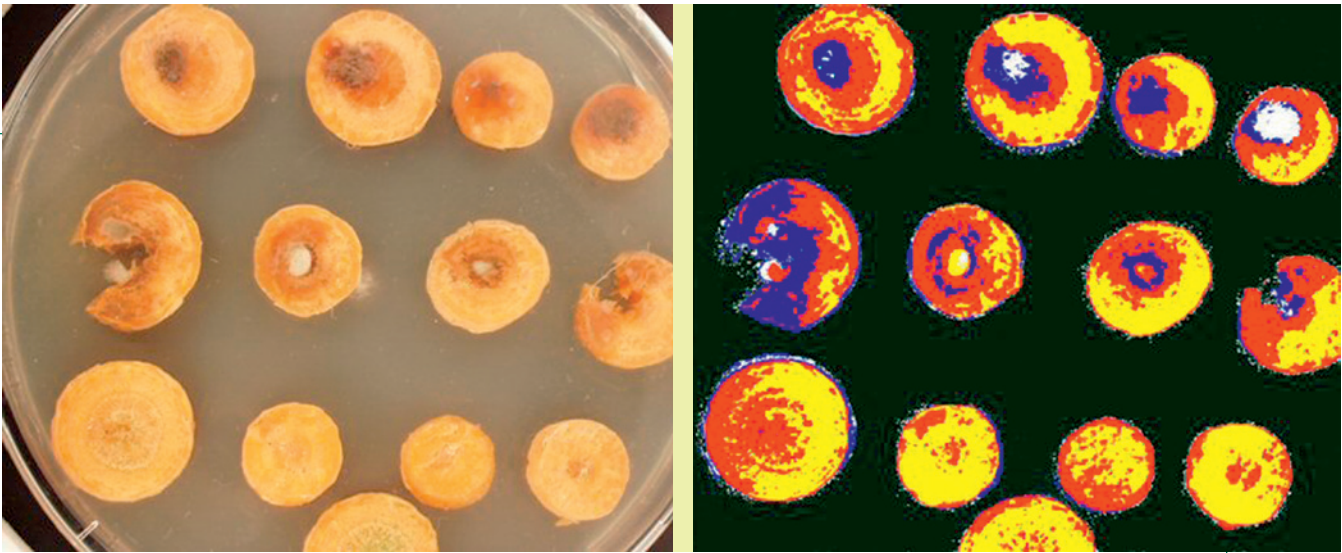


Fig. 5: In vitro assay with root segments for evaluation of carrot resistance to fungal pathogens. First line: *Alternaria radicina*; second line: *Botrytis cinerea*; third line: *Mycocentrospora acerina*. Left: Original. Right: Differentiation of tissue through false colours (red and yellow: healthy tissue; blue: macerated tissue and white: mycelium).

■ Carrot (*Daucus carota*)

Resistance strategies for reduction of plant protective agents

In cultivation of carrots the fungal pathogens *Alternaria radicina*, *Botrytis cinerea* and *Mycocentrospora acerina* are important pathogens causing distinct rot symptoms. These pathogens attack different parts of the carrot plants like roots or leaves at different growth stages. Hence, yield loss and quality reduction could occur during the field growing season or during storage. Establishment of resistance to these fungal pathogens in carrot is an effective way to control these diseases to get stable yield as well as high quality of carrots. Moreover, the application of fungicides could also be reduced. Investigations were started to develop a method for screening carrot accessions to *Alternaria*, *Botrytis* und

Mycocentrospora. A laboratory assay with root segments was established for evaluating carrots (Fig. 5). More than 30 carrot accessions, culture forms and their wild and primitive relatives were screened in this root segment assay. The response of the accessions to fungi was evaluated by symptom scoring (percentage of rotted tissue). First step of a computer imaging analysis was started recently. Most of the tested carrots showed a high level of susceptibility to fungal pathogens *Alternaria*, *Botrytis* and *Mycocentrospora*. In contrast, in several accessions roots were only damaged slightly by one or more tested fungi (Fig. 6). The resistance characteristics inside genotypes generate the prerequisite for a promising selection of single plants. The developed screening method could also be used for evaluating current carrot cultivars or different gene bank material.

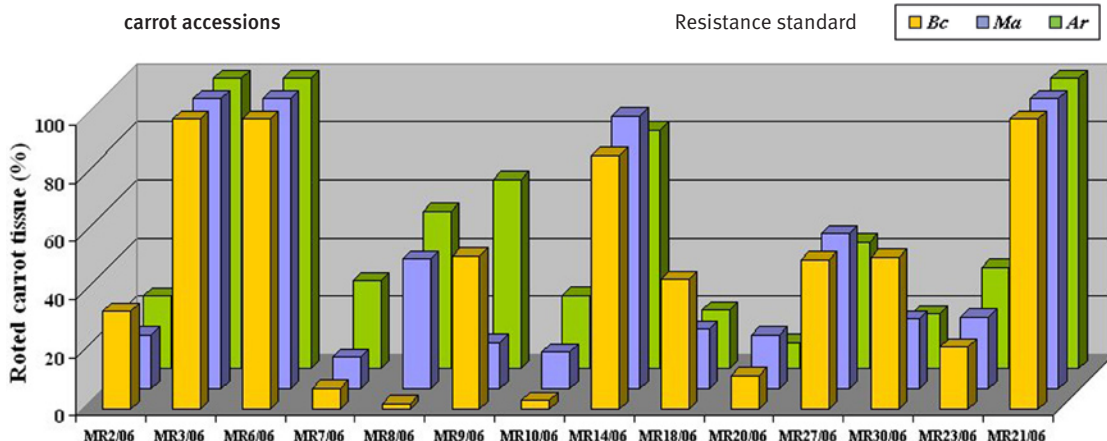


Fig. 6: Evaluation of resistance to fungal pathogens in selected carrot accessions. First line: *Botrytis cinerea*; second line: *Mycocentrospora acerina*; third line: *Alternaria radicina*.

Epicuticular wax layer makes abiotic stress tolerance possible

Some wild relatives of the carrot are adapted to arid, dry and radiation prominent locations by specific construction of the epidermis, cuticle and epicuticular wax layer. Furthermore, epidermis, cuticle and wax layer are a primary barrier against biotic influences like phytopathogenic fungi and insects. If it is possible to establish methods to transfer these characters from the wild forms into new varieties, carrot production in Europe will be possible also under a changed climate. A selection method was developed in cooperation with the Institute for Plant Analysis making an effective characterization of the epicuticular wax layer possible. By means of Fourier-Transform-Infrared-Spectrometer, genotype specific fingerprints can be made for characteristic wax components (Fig.7). Plants which show the typical leaf traits of the wild relatives could be selected in descendants of different crosses of wild and culture carrots meanwhile. A number of unwanted root traits of the wild relatives are still present in these plants, though, so that further backcrosses are necessary to be able to select carrot specific root traits in return again.

Vegetable Brassicas (*Brassica oleracea*)

As is the case of all vegetables the quality is the crucial factor. Besides quality, criteria like typical appearance and uniformity of the products the importance of factors like no rests of pesticides, taste and especially healthy effects of special components is growing. The goal of the work of the last years was to present options for sustainable use of plant genetic resources. Besides the using of resistances from vegetable brassicas (*B. oleracea*) the work was especially focused on new resistances from related species of the tertiary gene pool. For this reason fusions of somatic protoplasts of different species with *B. oleracea* were carried out in the last years. Black mustard (*B. nigra*), Ethiopian mustard (*B. carinata*), Indian mustard (*B. juncea*) and radish (*Raphanus sativus*) were of special interest. For all combinations sexual progenies were produced. They are resistant to the following pathogens: Turnip mosaic virus (TuMV), clubroot (*Plasmodiophora brassicae*), leaf spot (*Xanthomonas campestris* pv. *campestris*). The most substantial population as to genotype number and number of generations results from combination of *B. oleracea* and *B. nigra*. For this population, the intention was to transfer the resistance to black rot, caused by *X. c.* pv. *Campestris*, and to clubroot, caused by *P. brassicae*, into the C-genome of *B. oleracea* by introgressions. The B-genome chromosomes of *B. nigra* have to be eliminated by intensive backcrossing with *B. oleracea* when bastards passed meiosis sufficient times by producing new generations. All the embryos resulting from backcrossing and self pollination were cultured *in vitro* by embryo rescue technique. Table 1 shows the number

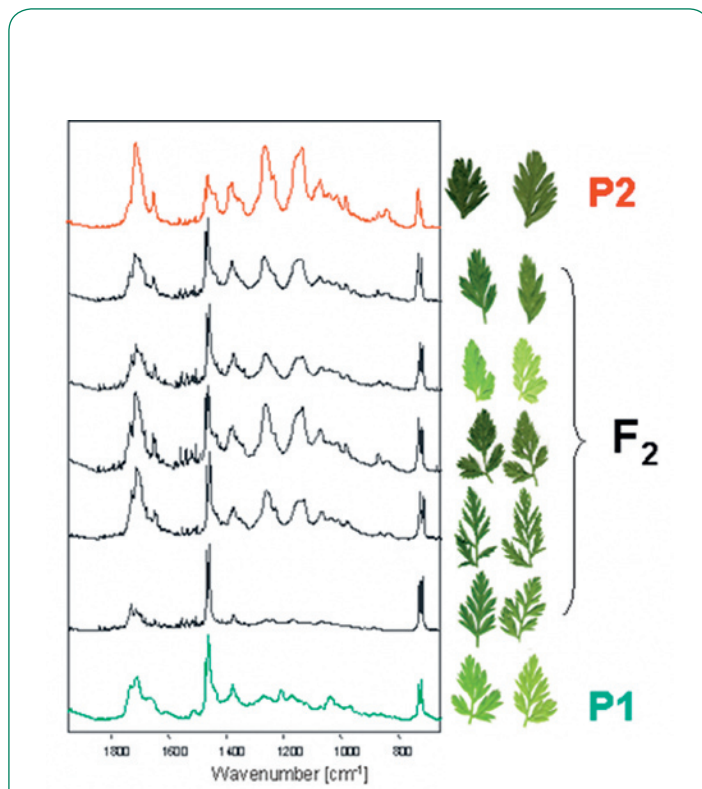


Fig. 7: FT-Infrared spectra of the epicuticular waxes and leaf segments of F_2 single plants obtained from a cross between carrot (P1) and a wild relative (P2).

of produced bastard plants and for each plant the number of self pollination (F) and backcrossing (BC) steps in the pedigree. All parents of these plants were resistant to *X. c.* pv. *campestris*.

Table 1: Population structure of interspecific bastards from *Brassica oleracea* (+) *B. nigra* produced in 2006

Number of parent plants	Progeny number	Pedigree of progeny
7	22	$F_{11}BC_1$
22	70	$F_{10}BC_2$
20	61	F_9BC_3
14	38	F_8BC_4
10	16	F_7BC_5
3	9	F_6BC_6
1	0	F_5BC_7
1	9	$F_{10}BC_1$
4	14	F_9BC_2
1	0	F_8BC_3
3	11	F_7BC_3
86	250	total

■ Leek (*Allium ampeloprasum*)

Leek (*Allium ampeloprasum*) belongs with onion, chives and garlic to the edible *Alliums*, which have been used for their typical flavour and broad medical-therapeutic effect since ancient times. In 2004 Germany produced 70,353 t of leek on an area of 2,218 ha. In addition to the growth on small fields by gardeners, the cultivation is also possible on a large scale with mechanical harvest and processing using adapted leek varieties. Today's varieties, open-pollinating varieties as well as F₁ hybrids, have been developed by selection of germplasm from land races. Crosses within and between varieties are the only source of variation. Therefore, the low genetic variability will restrict future advances in improvement for resistance and homogeneity. New possibilities for extension of variation in leek result from interspecific crosses with other *Allium* vegetable species. Hybrid plants of leek with onion (*Allium cepa*), chives (*Allium schoenoprasum*, Fig. 8) and bunching onion (*Allium fistulosum*) were produced and characterized for the first time. Some of these new plants are characterized by good vigour. Hybrids between bunching onion and leek showed resistance traits of the former parent which were not present in leek. Backcrosses to leek were successful for onion-leek hybrids but not yet with bunching onion-leek hybrids.

Medicinal and Aromatic Plants

Medicinal and aromatic plant products have many side effects due to special substances being generated in the secondary metabolism. While agricultural main crops, vegetables and fruits provide energy rich substances, vitamins, dietary fiber, and mineral compounds, medicinal and aromatic plants are

appreciated for their constitutional effects as herbal remedy or as condiment to make our food tasty and more digestible and, last but not least, for their odor. Due to their biological effects, some of these plants can be used as source for natural plant protection products. As natural products, goods from medicinal and aromatic plants are highly appreciated by the population, which results in the noticeable growth of this market. The crop spectrum investigated in the BAZ covers also medicinal and aromatic plants because of their importance and popularity. Research focuses on evaluation of the natural variability of important traits but also on testing methods for generation of new variability; both is done to explore the scope for breeding high yielding new cultivars resistant to pests and diseases and with high content of desired compounds but also low content of harmful substances. This information is needed by the decision makers of the Federal Ministry of Food, Agriculture and Consumer Protection for elaboration of development programs of this special branch of plant production.

■ Caraway (*Carum carvi*)

Caraway fruits are preferably used as spice. But they are also listed in the European Pharmacopoeia as herbal medicinal product. In Central Europe, a biennial caraway form prevails, growing also in the wild in meadows (Fig. 9). In the first year, biennial caraway produces only a leaf rosette, flowers develop in May of the second year and the ripe fruits can be gathered in July. An annual caraway form is endemic in the Mediterranean. It can be harvested already in September in the first year when sown in April. Therefore, annual caraway provides advantages in comparison with biennial cultivars from the economic point of view, but the quality of hitherto available annual cultivars was unsatisfying due to their low

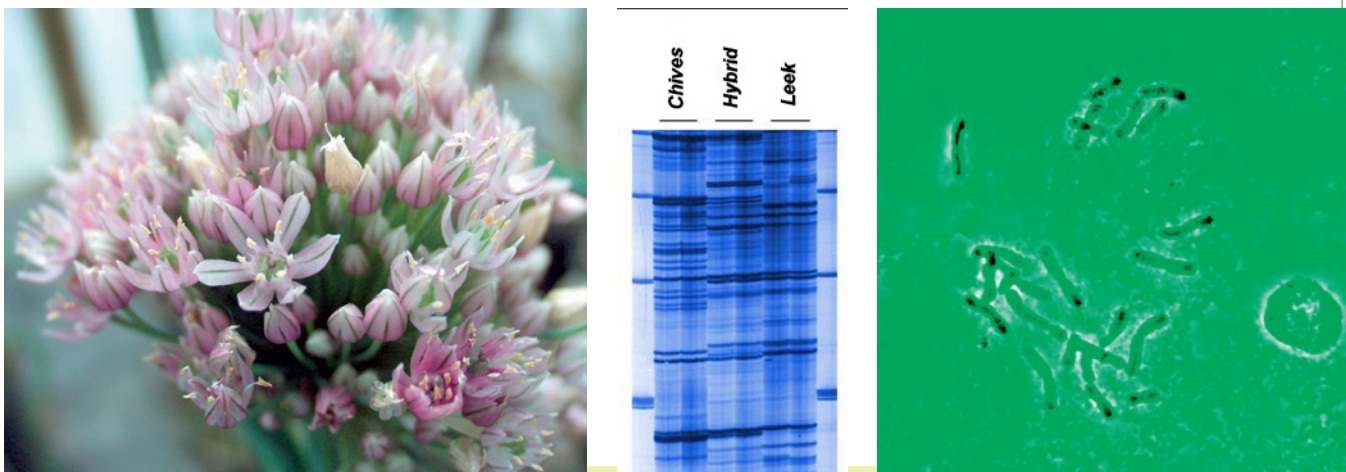


Fig. 8: *Allium* hybrid between chives and leek. Left: flower; middle: hybrid detection; right: Chromosomes.



Fig. 9: Caraway in the natural habitat.



Fig. 10: Diversity of inbred lines of annual caraway.



Fig 11: Fennel umbel infested by fennel blight.

essential oil content. The current research project aims at the investigation of natural variability and at generation of new trait combinations by classical breeding methods. The evaluation of different accessions revealed that primarily only biennial caraway has high essential oil content. The following approaches aimed at the generation of annual caraway populations with improved variability of important traits and with aspired trait combinations: a) repeated long term selection in one annual caraway population to improve its essential oil content, b) crossing of biennial and annual caraway forms with subsequent selection of aspired genotypes, c) repeated cycles of inbreeding and selection, and d) exploitation of good combination ability of suitable parental lines for generation of high performance progenies which can be used as synthetic varieties. Recurrent selection resulted in significant improvement of the essential oil content from lower than 3 to more than 5%. It corresponds to or exceeds the essential oil content of biennial cultivars. The improved populations could be used for the development of the first German annual caraway variety and have been already widely introduced in practice. Selection, crossing with subsequent selection and inbreeding (Fig. 10) proved to be suitable as methods to improve variability and combination of aspired traits. The performance tests of progenies arising from different parental lines with high combination ability will be continued in the following years.

■ Fennel (*Foeniculum vulgare*)

The so called bitter fennel is used as remedy. The current research focuses on testing methods for the generation of genotypes excelling by good agronomic characteristics, high content of important constituents and resistance to plant diseases (Fig.11). At the outset, 200 different accessions were collected and evaluated to explore the natural variability of important characteristics. Recurrent selection with progeny testing and combination of trait expressions by crossing stood the test to improve the expression of aspired characteristics

in high performance accessions. Cultivation of the new strains in the neighbourhood of a special genotype highly susceptible to fennel blight as spreader proved to be suitable for testing the disease resistance of the new strains in the experimental field (Fig. 12). The generated genotypes were primarily evaluated for the following traits: low growth height, no shedding of the fruits, early maturity, small shaped fruits - necessary for tea bag filling machines, resistance to fennel blight, quality determining constituents - at least 4 % essential oil in the fruits with more than 60 % trans-anethole and more than 15 % fenchone. Particular attention has to be paid to the estragole content of the essential oil which has been classified by the Scientific Committee on Food of the European Commission as risky substance. The investigations show the existence of high natural variability of important traits and the feasibility of combination of aspired traits in crossing progenies initially distributed on different parents.



Fig 12: Infection of fennel strains with fennel blight by a highly susceptible spreader (right) in a resistance test in the field.

Fig. 13:

Experimental cultivation of thyme.



Fig. 14:

Anther with normal and degenerated pollen grains.

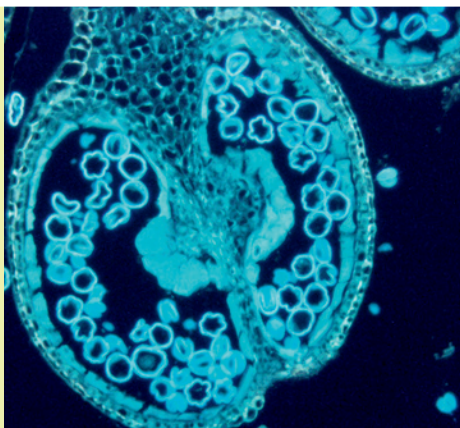


Fig. 15:

Different savory types.



Fig. 16:

Evaluation of selected strains in the experimental field.



■ Thyme (*Thymus vulgaris*)

Thyme is an evergreen semi shrub endemic in Central and South Europe whose leaves and flowers are also used as spice but primarily as remedy. The active principles with antimicrobial and antioxidative properties are the phenols thymol and carvacrol, which are contained in the essential oil. Currently in Germany, cultivated thyme variety 'Deutscher Winter' is very heterogeneous but the industry requires a homogeneous raw material with high content of important constituents (Fig. 13). The research project aims at the detailed investigation of the reproductive biology to exploit its specifics for breeding homogeneous varieties with high content of important constituents. Thyme is a gynodioecious species, which means the coexistence of hermaphroditic plants (flowers with pistils and stamens) and male sterile plants without stamens. By directed selection of particular suitable hermaphroditic and male sterile plants as parents, the breeder can produce seeds of high performance and, above all, thoroughly uniform varieties. The needed directed pollination is facilitated by the use of thorough male sterile lines as maternal parent. The investigation of the flower biology revealed that there are numerous medium forms between male fertile and thorough male sterile plants not suitable as parental lines for a hybrid variety (Fig. 14). A set of traits has been defined for unambiguous identification of the reproductive type which enables the breeder to select the most suitable forms for hybrid variety development with high reliability.

■ Summer savory (*Satureja hortensis*)

The essential oil of Summer savory contains carvacrol with antioxidative and antimicrobial properties. Carvacrol scavenges harmful free radicals in the metabolism of man and animals and inhibits the development of microorganisms injurious to health. Therefore, carvacrol containing essential oils are an alternative to antibiotic performance-improving additives to animal feed which have been prohibited in the EU since 2006. In collaboration with companies, the institute has accomplished a joint research project of the InnoRegio-Initiative of the Federal Ministry of Education and Research which aimed at the development of initial genetic material for summer savory cultivars excelling by high yield and high essential oil content with improved carvacrol content. The natural variability of the important characteristics has been investigated by evaluation of 58 accessions cultivated in summer and in autumn as well (Fig. 15). The investigations covered besides agronomic properties among others the following traits: precocity, yield and content of essential oil and carvacrol content of the essential oil. Investigations on the influence of the ontogenetic stage showed that savory bears the highest essential oil yield and an appropriate level of carvacrol content when it is harvested shortly before full flowering. Three cycles

of recurrent selection resulted in the generation of genetic material with an essential oil content of more than 3% in dry herb and a carvacrol content in the essential oil higher than 60%. The best populations (Fig. 16) were passed on to the company involved in the project for breeding special varieties particularly qualified for cost-efficient production of carvacrol containing essential oils from summer savory.

Ornamental Plants

Within the plant types classified as horticultural crops the ornamental plants by far represent the largest group of cultivated plants. However, just for Europe approximately 400 species are of economic importance, which can be assigned to approximately 250 genera and cover up to 100 different plant families. Ornamental plants are important genetic resources and with their native relatives an essential component of our ecological system.

■ Pelargonium

The genetics of Pelargoniums

The Pelargoniums represent a recent example for the development of cultivated plants from wild species (Fig. 17). Similar as for other important cultivated plants, interspecific hybridizations were starting points of the development. The horticultural Pelargoniums arose at Europe about two centuries ago after hybridizations between some of the about 280 botanical wild species endemic in Southern Africa. It is not known precisely how many and which species have contributed to the modern Pelargoniums as well as which way the sterility occurring in primary species hybrids was overcome. Methods of molecular biology and cytogenetics allow a view into the genetical structure of plants and thus make possible conclusions to the history of domestication. With the production of experimental hybrids and their analysis, the evolution of Pelargoniums should be investigated and new genetic resources should be opened for breeding. The most important group of cultivated Pelargoniums, the Zonal Pelargoniums, were bred presumably from a few species of section *Ciconium*. Within this group there are both diploid and tetraploid genotypes (Fig. 18). The different chromosomal constitution has effects on fertility and inheritance. Knowledge of chromosome numbers of cultivated and wild Pelargoniums is also important to judge the chances of interesting cross combinations. The determination of chromosome number is not sufficient to discriminate related *Pelargonium* species of the section *Ciconium*, because most of the species in this section have the same chromosome number $2n=18$. Therefore, two gene-specific DNA probes were used to recognize differences in chromosomal structure. The analysis included wild species which were assumed to be parents of the cultivated Pelargoniums (Fig. 19).



Fig. 17: Wild *Pelargonium* species (*Pelargonium oblongatum*).

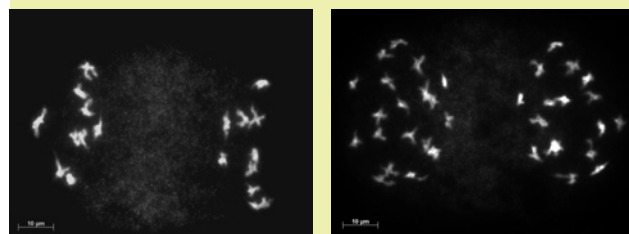


Fig. 18: Different ploidy levels of Pelargoniums (Anaphase I of meiosis). Left: diploid; right: tetraploid.

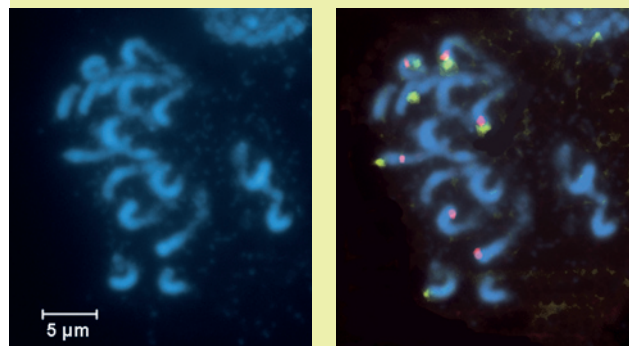


Fig. 19: Characterization of karyotypes in *Pelargonium* by fluorescence in situ hybridization (FISH) with gene-specific probes. The somatic metaphase chromosomes of *Pelargonium peltatum* ($2n=18$) show six chromosomes hybridizing with 5S-rDNA (yellow) and 18/25S-rDNA (red). Four chromosomes have signals for both sequences.

The four species investigated, *P. zonale*, *P. inquinans*, *P. acetosum* and *P. peltatum*, had uniformly six chromosomes with a signal for probe 5S-rDNA (Tab. 2). The species were distinguishable by number of chromosomes hybridizing for 18/25S-rDNA and especially for chromosomes showing double labelling. *P. peltatum* was most different in its chromosomal structure from the other species.

Tab. 2: Chromosomes with signal expression after fluorescence in situ hybridization with 5S- and 18/25S-rDNA in four diploid wild *Pelargonium* species from section *Ciconium*

	5S-rDNA	18/25S-rDNA	Double labelling
<i>P. zonale</i>	6	4	0
<i>P. inquinans</i>	6	★	★
<i>P. acetosum</i>	6	4	2
<i>P. peltatum</i>	6	6	4

★ not investigated

The evolutionary relationship of the different chromosomal types which were detected remains to be explored. It should be interesting to produce hybrids between such species having clear differences in the chromosomal structure such as *P. peltatum* x *P. zonale* and *P. peltatum* x *P. acetosum*, and to compare them to cultivated Pelargoniums. Therefore, a hybridization program for production of sexual interspecific hybrids was started. The following wild species were included as parents: *P. acetosum*, *P. zonale*, *P. inquinans*, *P. peltatum*, *P. frutetorum*, *P. articulatum*, *P. quinquelobatum*, *P. aridum* and *P. reniforme*. Seeds from harvested hybrid fruits were sown *in vitro* to obtain a maximal rate of germination (Fig. 20).

New genetic variation in Pelargoniums

For a lot of crop plants, related wild species are used as a gene pool for the resistance breeding programs. Some of the scented-leaved pelargonium and hybrid groups as well as wild species have resistances against a lot of pathogens. However, sexual incompatibility between different *Pelargonium* species prevents improvement by crossing. Somatic hybridization may be an achievable alternative to

overcome these difficulties. An *in vitro* culture system for different *Pelargonium* species has been established. From this collection, *Pelargonium* x *hortorum* 'Antik', 'Perlkette' and the scented-leaf pelargonium 'Concolor Lace' were used in order to improve protoplast isolation as well as culture techniques. Until now, mesophyll protoplasts (Fig. 21) from micro-propagated plants especially of the cultivar 'Concolor Lace' have been successfully isolated, grown into colonies and regenerated in plants. Another source of protoplasts are suspension cultures. Currently, suspension cultures from eight different *Pelargonium* genotypes have been developed. After protoplast release all genotypes gave calli, three ('Atomic Snowflake', *P. x fragans*, 'Pink Capitatum') regenerated in plants (Fig. 22). First attempts of protoplast fusion will be discussed.

■ Azalea (*Rhododendron simsii*)

Azaleas are important in German production of flowering potted plants. They originate from China, Taiwan and Japan. For more than 150 years azaleas have been bred in Germany, which is why there are huge amounts of varieties. Important characteristics of a variety are flowering time, flower colour, flower filling and longevity of flowers as well as the habit. In addition to horticultural characteristics resistances against diseases, particularly fungal infections, play an important role in successful growing. Against the background of political requirements for the saving of plant protection agents the latter has gained substantially in importance recently. More than 1000 wild species within different sections belong to the genus *Rhododendron*. Such immense gene pool gives the opportunity to find suitable crossing partners with desirable characteristics like resistances to improve cultivated azaleas. At first close relatives to azaleas are evaluated with focus

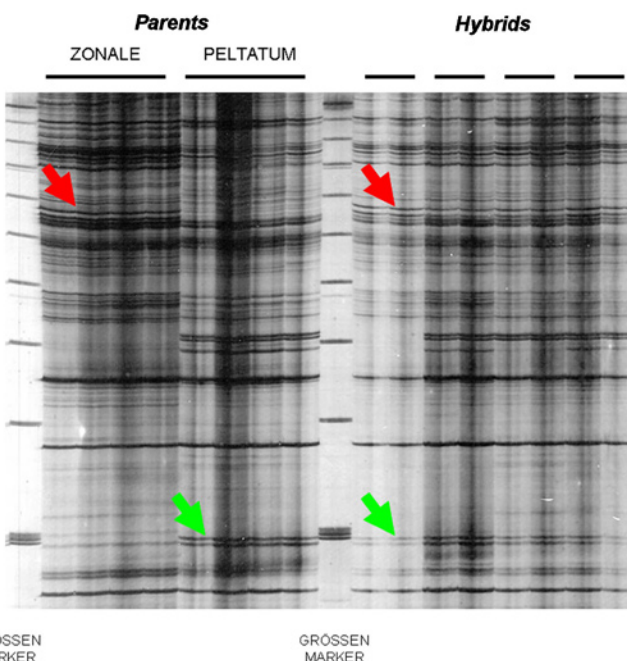


Fig. 20: Molecular detection of hybrids in *Pelargonium* (left); interspecific hybrid (right middle) and parental species.



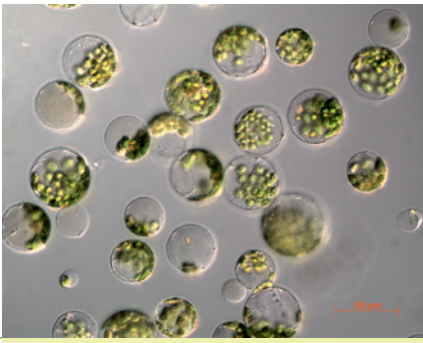


Fig. 21: Mesophyll protoplasts of *Pelargonium*.

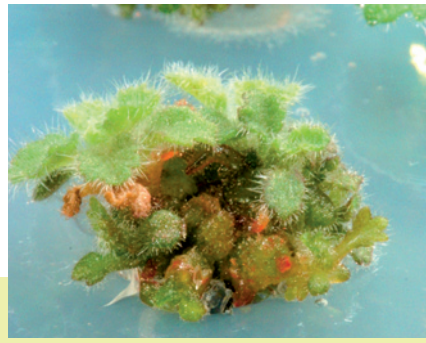


Fig. 22: Plant regeneration from callus tissue.



Fig. 23: Seedlings of the cross 'Violacea' x 'Haerensiana' after *in vitro* sowing.

on resistance against fungal infections and their crossing ability with azaleas. Biotechnological, cytogenetic and molecular genetic methods are adapted to azalea focussing on the acceleration of the breeding process. In 2006 first crossings were made and the sowing of immature seeds *in vitro* was tested. Moreover, the fertility and the long-time storage of pollen were proved. Long-time storage of pollen allows crossings independently of the flowering time of the male elder. Vegetative plant material was established *in vitro* to use it in later experiments like polyploidization. The investigation of ploidy levels will start in spring 2007 using flow cytometry. This method allows the throughput of a high amount of probes.

■ Hydrangea

Hydrangeas, naturally occurring in Eastern Asia and America, were first introduced to Europe at the beginning of the 18th century. With its decorative inflorescences of sterile and fertile flowers, hydrangeas are still popular garden shrubs as well as potted plants (Fig. 25). Because of their great diversity of species and cultivars breeders have access to a large pool of characteristics interesting for development of new cultivars,

e.g. colour of the inflorescence, plant habit or disease resistance. This project supported by the German Federation of Industrial Research Associations „Otto von Guericke“ (Arbeitsgemeinschaft industrieller Forschungsvereinigungen „Otto von Guericke“ e.V.) (AiF) since 2005 is occupied with the development of breeding methods for *Hydrangea macrophylla*. The close cooperation with the firm Synergy Breeding GmbH und Co KG Billerbeck and the University of Applied Science Weihenstephan could be continued successfully in 2006. The Institute of Horticultural Crops mainly focuses on ploidy, induction of mutation and DNA-marker-techniques for *Hydrangea*. Currently, there exists only a limited number of publications concerning ploidy and chromosome number of hydrangeas but some diploid and triploid cultivars are known. In the previous year the flowcytometric measurement of DNA of hydrangea was established. Now, chromosomes from enzymatically digested cells of root tips from one cultivar were counted using light microscopy for obtaining a standard for flowcytometry. Afterwards, ploidy levels of cultivars of *Hydrangea macrophylla*, provided by Synergy Breeding, could be determined comparing the reference cultivar with the

Fig. 24: *Rhododendron simsii* 'Roi Leopold' pollen tube growth on media for controlling the pollen fertility.

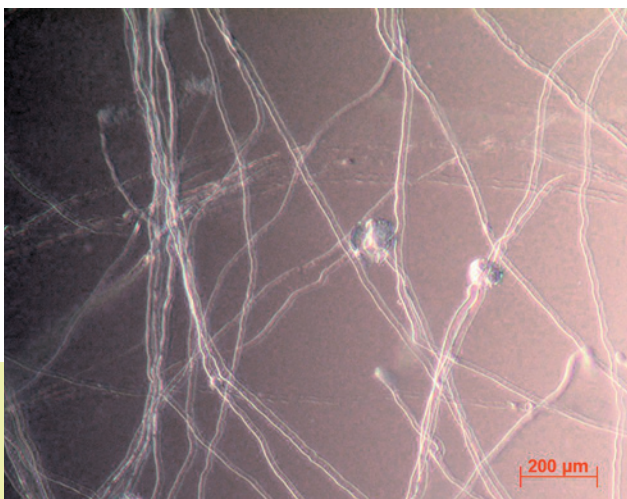


Fig. 25: Example for a cultivar of *Hydrangea macrophylla*: 'Adria'.



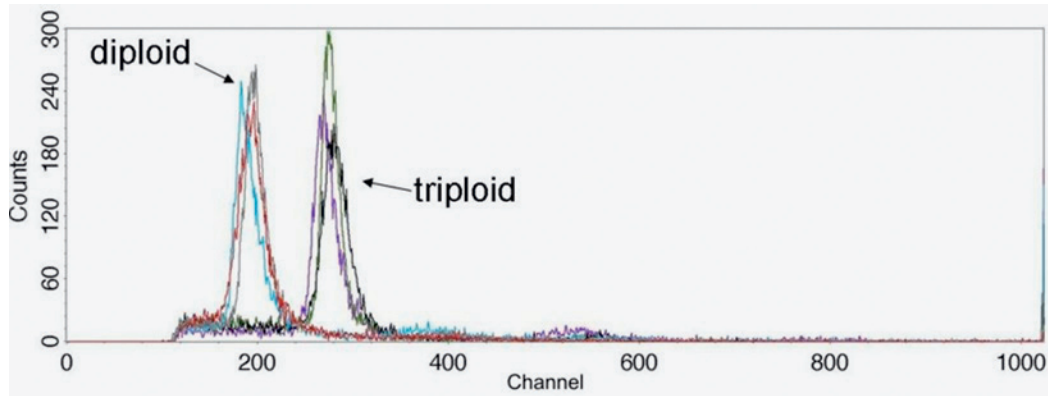


Fig. 26:

Histogram of fluorescence intensity of PI stained nuclei showing 6 cultivars of *H. macrophylla* ($2n=36$).

known ploidy (Fig. 26). Determination of chromosome numbers of further species is still in progress and should be finished in the following period. The results are important for understanding the phylogenetic background as well as crop improvement and conservation. Polyploidisation experiments are a promising tool for creation of new interesting characteristics of ornamental plants. For this reason, one diploid and a triploid cultivar were chosen to test the polyploidisation possibilities of *Hydrangea macrophylla*. For analyses of genetic distances between species and cultivars the RAPD-technique was applied. For getting more serious data AFLP-analyses were started with a first screening of primer combinations. Again mutation induction by using X-rays was applied on unrooted *in vivo* cuttings which were cultivated and evaluated at Synergy Breeding afterwards. Similarly, to this attempt *in vitro* cuttings and *in vitro* leaf explants were also irradiated with different doses of X-rays.

Perspective

Against the background of structural reorganisation of the departmental research, part plant, of the BMELV, the institute continues its sovereign functions of providing assistance to the Bundessortenamt (Federal Office for Plant Varieties) with the determination of the ploidy level. Within the scope of political decisions new research projects orientate towards the given innovation fields of the ministry and the aspired governmental precaution/provisions. As known from current research activities, there will be a special need for concepts that are tailored to utilize plant genetic resources for generating resistance against biotic pests and abiotic stress in vegetables, aromatic and medicinal plants.



Institute
of Epidemiology
and Resistance
Resources

Quedlinburg

Institute of Epidemiology and Resistance Resources

Resistance has to be considered as the most environment and consumer friendly way of plant protection. Due to protection of natural resources (soil, water, biodiversity) and reducing the risk of yield losses, resistance is an essential prerequisite for a sustainable plant production. With respect to soil-borne pathogens – e.g. viruses – which cannot be combated by chemical measures, only the availability of resistant cultivars does ensure wide and economic crop rotations. For broadening the genetic base and improving resistance of crop plants the evaluation and genetic analyses of plant genetic resources is the starting point. Therefore, research of the Institute of Epidemiology and Resistance Resources (IER) aims at improving resistance of crop plants by analysing virulence of pathogens of agronomic importance (fungi, viruses, bacteria, insects) and evaluating plant genetic resources for resistance. Based on results of genetic analyses of resistance, strategies for an efficient use of qualitative and quantitative resistances including molecular techniques are developed in order to broaden the genetic base of resistance and to create durable resistances. Results of these studies are the basis for a long term improvement of the resistance level of plants of agricultural or horticultural importance, respectively. Research carried out at the IER contributes to the “National programme for the conservation and sustainable use of genetic resources of agricultural and horticultural crops” with respect to “enhance the exploitation of diversity present in genetic resources by characterisation, evaluation, documentation and breeding” as well as to the protection of consumers and natural resources. According to the different pathogens the institute is sub-divided into the following research groups “Viruses and Invertebrate Pests”, “Fungi”, “Bacteria” and “Molecular Markers”. Respective pathogens are hosted at the Institute of Epidemiology and Resistance Resources in several collections.

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*0,5 release for tasks on BMELV and BAZ staff councils

Viruses and invertebrate pests

For many years soil-borne viruses of barley, i.e. *Barley mild mosaic virus* (BaMMV) and *Barley yellow mosaic virus* (BaYMV) have been in the focus of interest. These viruses which have been detected in Germany for the first time in 1978 are of special importance due to a constant spread and high yield losses frequently observed in susceptible winter barley crop. A new strain of BaMMV being able to overcome *rym5* which was detected for the first time in 2003/2004 has been also found in 2005/2006 and within a project funded by the AIF aiming at the “Identification of barley germplasm resistant to BaMMV-SIL and the new resistance breaking German BaMMV strain as well as the identification of markers closely linked to *rym13*” 77 barley accession were identified being resistant against this new strain and out of these 37 are also resistant to BaMMV, BaYMV and BaYMV-2. First genetic analyses give hint that the resistance against this new strain of the barley accession ‘Taihoku A’ which is resistant to all strains known in Europe is also encoded by a single recessive gene. Based on these phenotypic data molecular markers are developed at the moment at the University of Giessen (Prof. Dr. Wolfgang Friedt). Based on the evaluation of genetic resources and the analysis of the genetics of resistance these results contribute to preserve winter barley cultivation in the growing area of infested fields. With respect to broadening the genetic base of resistance against these viruses, many different alleles were detected at the *Rym4/Rym5* locus at the IPK Gatersleben (Prof. Dr. Andreas Graner/Dr. Nils Stein) which at the moment are analysed at the Institute of Epidemiology and Resistance Resources for their effectiveness against the different strains of BaMMV and BaYMV.

In France, *Soil-borne cereal mosaic virus* (SBCMV) is already an important pathogen in wheat (*Triticum aestivum*) and is expected to become important in Germany as well. Therefore, data on the genetics of resistance against this pathogen are of special importance to facilitate efficient breeding of resistant cultivars as a prerequisite for ensuring winter wheat cultivation, which is of special economic importance for most farmers and cannot be replaced by other crops. In the frame of the EU-CRAFT Project “Structural and functional analysis of virus resistance in wheat (WHEATPROTECT)” it was shown that resistance is inherited in a monogenic manner and by the analysis of several DH-line populations this gene was located on chromosome 5DL and closely linked SSR and AFLP markers have been developed (Fig. 1). This is of special importance as in Germany up to now no fields facilitating reliable selection are known. In order to identify additional genes involved in this translocation resistance against SBCMV, expression profiling has been carried out in collaboration with the IPK (Prof. Dr. Andreas Graner) using the 10.000 unigene barley array. In these

analyses 15 genes differentially expressed in susceptible and resistant genotypes were identified in roots (7), hypocotyl (4) and leaves (4). These genes are at the moment mapped in respective DH-populations.

Besides resistance to soil-borne viruses being a precondition for growing these crops in the increasing area of infested field thereby affecting the development of rural areas and the maintenance of wide crop rotations, resistance to insect transmitted viruses has a strong impact on consumer protection and biodiversity. Epidemiological studies have shown that in 2006 *Barley yellow dwarf virus* (BYDV) and *Wheat dwarf virus* (WDV) were present in wheat and barley at the same frequencies. However, in comparison to 2004/2005 WDV was detected more frequently (Fig. 2). Based on efficient screening methods in the field developed in the last years, barley and wheat accessions were tested for resistance to WDV, but all accessions turned out to be susceptible. Therefore, in barley future work will concentrate on the cultivar ‘Post’ which was identified to be tolerant to WDV in several screenings (see below, Fig. 2). Furthermore, with respect to WDV first results give hint that besides a wheat and a barley strain an oat specific strain of WDV has been detected, as this strain could be re-transmitted to oats but not to wheat and barley.

In the expanding acreage grown with rape seed the aphid transmitted *Turnip yellows virus* (TuYV) has become a serious pathogen which is investigated at the Institute of Epidemiology and Resistance Resources for several years now. In two years field trials (2004/2005, 2005/2006) – assuming a threshold for resistance of $E_{405} = 0.1$ in December – a monogenic mode of inheritance for resistance was

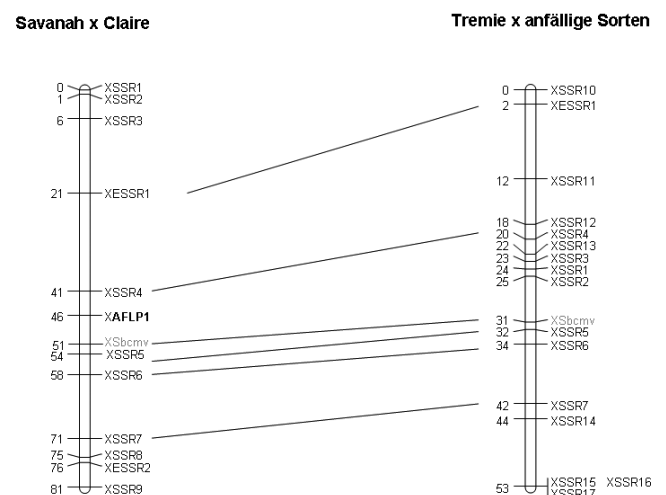


Fig. 1: Mapping of SBCMV resistance on wheat chromosome 5DL in two DH populations of *Triticum aestivum*

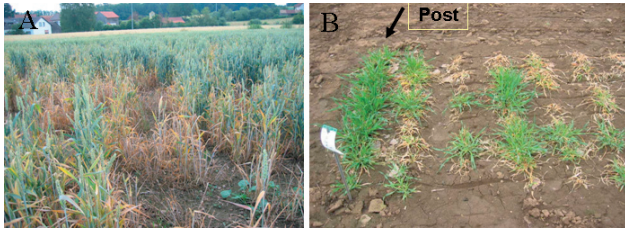


Fig. 2: A: Symptoms of *Wheat dwarf virus* (WDV) in a wheat field in the growing period 2005/2006. B: WDV tolerant barley accession 'Post' in comparison to non tolerant genetic resources

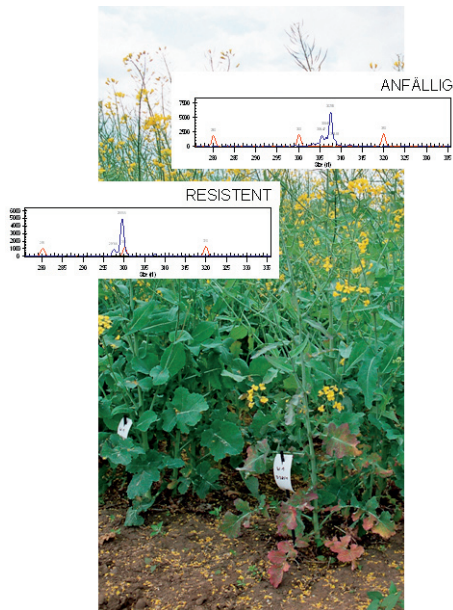


Fig. 3: Development of molecular markers for TuYV resistance in rape seed. On resistant plants (left) a fragment of 299 bp and on susceptible plants (right) of 307 bp is generated by a closely linked SSR

detected after artificial inoculation of DH-lines using virus bearing aphids. However, within the set of susceptible lines a broad variation of the virus titre was observed. Repeating these ELISA measurements from April to June resulted in a continuous rise of the virus titre, i.e. at a threshold of $E_{405}=0.1$ more plants turned out to be susceptible. However, plants classified as resistant in December never reached the virus titre of those plants already susceptible in December. Based on these phenotypic data marker development using bulked segregant analysis was started and closely linked SSR and AFLP markers have been developed (Fig. 3). The availability of markers for this disease is of special importance because the inoculation method using virus bearing aphids which is needed for reliable selection cannot be integrated into an applied breeding scheme, efficiently. Additionally, it turned out in growth chamber experiments

that the rate of infection depends on the acquisition and inoculation time as well as on temperature and genotype. Furthermore, results of field trials give hint that yield reductions caused by TuYV cannot be compensated by higher nitrogen fertilization.

Besides virus transmission, aphids can cause direct plant damages in cereals, e.g. *Rhopalosiphum padi*, *Sitobion avenae* (Fig. 4) and *Metopolophium dirhodum*. In extensive evaluation schemes up to now 493 gene bank accessions of barley and 1936 of wheat have been tested for resistance. In field trials statistically significant differences were observed and in additional growth chamber experiments it turned out that the propagation rates of the different aphid species on a single host genotype are not correlated leading to the conclusion that differences in the level of tolerance are species specific. On average genotypes of *Triticum monococcum*, *Triticum dicoccon* and *Triticum spelta* were less severely damaged than *T. aestivum*.

The research projects mentioned above dealing with soil-borne viruses are the basis to ensure winter barley and winter wheat production in the growing area of infested field thereby contributing to preserving wide rotations and opening new perspectives to agriculture in rural areas. Results of the studies on insect transmitted viruses may be the basis for enhancing the level of resistance against these viruses thereby contributing to the aims of minimizing insecticide sprayings to protect consumers and natural resources.

Fungal and bacterial diseases

Concerning fungal diseases studies, focus on the evaluation and genetic analyses of barley concerning resistance against *Puccinia hordei* and *Pyrenophora teres* as well as on wheat with respect to *Puccinia triticina*, *Pseudocercospora herpotrichoides*, *Ustilago tritici* and *Pyrenophora tritici-repentis*. These studies also include yearly collections of isolates and analyses of virulence, e.g. concerning rusts. Respective isolates are included in official trials for cultivar release as well as in trials for the evaluation of genetic resources and these pathogens are hosted at the Institute of Epidemiology and Resistance Resources in several collections. In a close collaboration with the All Russian Institute of Plant Protection (Dr. Elena Gulyaeva) differences in virulence and their frequencies were observed for *Puccinia triticina* between Russia and Germany but also between German and especially Russian wheat growing areas. Also in close collaboration with the above mentioned institute (Prof. Dr. Olga Afanasenko) it turned out that resistance of barley to *Pyrenophora teres* f. *teres* follows a gene for gene model.



Fig. 4: *Sitobion avenae* on wheat

Within the “German network for the evaluation of cereals for disease resistance (Eva II)”, co-ordinated by the Institute of Epidemiology and Resistance Resources and carried out in collaboration with private cereal breeding companies and ZADI, genetic resources of wheat and barley were evaluated for resistance at up to 20 locations in the growing period 2005/2006. Therefore, also funding had expired already, this programme still considerably contributes to the evaluation and use of genetic resources for improving resistance to fungal and viral pathogens in cereals. Detailed information can be gained at <http://www.genres.de/eva>.

In extensive screening programmes several accessions of diploid *Triticum monococcum* – being one of the ancestors of modern wheat – highly resistant to *Blumeria graminis*, *Puccinia triticina* and *Pyrenophora tritici-repentis* were identified and based on F₂-analyses of crosses between resistant and susceptible *T. monococcum* lines, it turned out that different dominant and recessive genes are involved in pre-haustorial resistance to *P. triticina* – which is race un-specific and does not lead to necrosis or chlorosis. Based on these phenotypic data QTL analyses to determine genomic regions involved in this trait are actually carried out to facilitate a marker based transfer to *T. aestivum* in the future. Besides this, first results on the resistance of *T. monococcum* to Fusarium Head Blight (FHB) obtained within the joint Canadian German Project “Reducing Fusarium Toxins in Wheat through Genomics-Guided Strategies” revealed significant differences regarding susceptibility (Fig. 5).

Besides foliar diseases, soilborne fungi, e.g. *Oculimacula yallundae* (syn. *Tapesia yallundae*, anamorph *Pseudocercospora herpotrichoides* var. *herpotrichoides*) and *O. aciformis* (syn. *T. aciformis*, anamorph: *P. herpotrichoides* var. *aciformis*) have gained evident importance due to an increasing portion of cereals in crop rotations. After an efficient inoculation procedure was established in 2005 a reliable Real-Time-PCR assay has been developed for the differentiation and quantification of *O. yallundae* and *O. aciformis* (Fig. 6). As can be seen in Figure 6 no cross reaction with other pathogenic

fungi on wheat can be detected up to a content of 10⁻¹³g DNA, so that now a specific assay for the detection of *O. yallundae* and *O. aciformis* and the determination of the level of resistance is available. Based on this assay molecular markers will be developed for different resistance genes effective against *Oculimacula* ssp.

Within the frame of the programme to promote eco-farming, studies are carried out on the “Analyses of wheat for resistance to smut (*Ustilago tritici* f. sp. *tritici*) for developing genotypes suited for eco-farming systems”. In order to speed up the detection of resistance or susceptibility to this pathogen (Fig. 7), respectively, an ELISA antiserum detecting purified fungal antigens in a PTA-ELISA has been developed in collaboration with the Institute of Resistance and Pathogen Diagnostics (Dr. Frank Rabenstein). A direct ELISA is actually under development.

Due to the assumed global warming bacterial diseases which cannot be combated by chemical measures may become of increasing importance. In the frame of a long-term project ended in 2006 clear differences between cultivars with respect to susceptibility to *N. galligena* were detected and the cultivar ‘Ahra’ turned out to be resistant. Today and in the future *Erwinia amylovora*, the causal agent of fire blight, will be a pathogen of major importance. Besides the analyses of virulence of different isolates collected all over Germany, genetic analysis of resistance was carried out in collaboration with the Institute of Fruit Breeding (Dr. Andreas Peil). Two *Malus* populations comprising 150 seedlings each were artificially inoculated with *E. amylovora* (10 scions per seedling). As can be seen in Figure 8, a large genetic variation was observed. These phenotypic data will now be the basis for developing molecular markers at the Institute of Fruit Breeding.

In cabbage (*Brassica* spp.) *Xanthomonas campestris* pv. *campestris* is a pathogen of economic importance which has been studied at the IER for a long time. With the analysis of the race specificity of resistance, research on this pathogen in cabbage ended in 2006. In these studies it turned out, that



Fig. 5: Different levels of resistance to *Fusarium culmorum* in *Triticum monococcum* after artificial infection

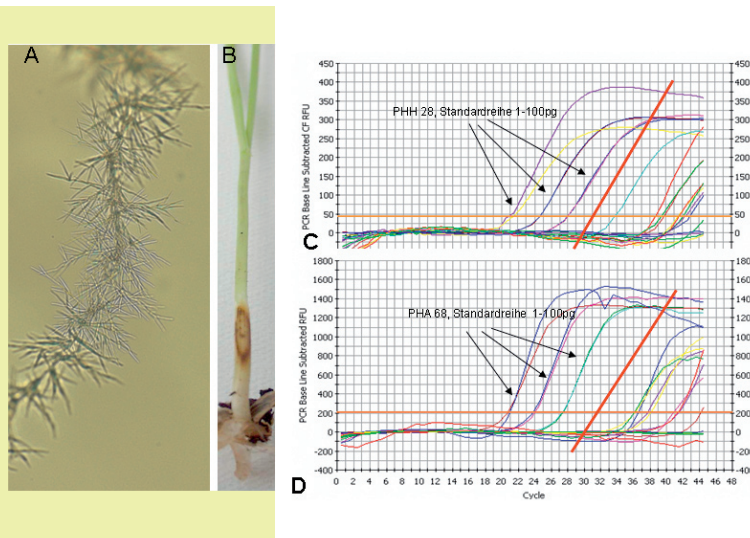


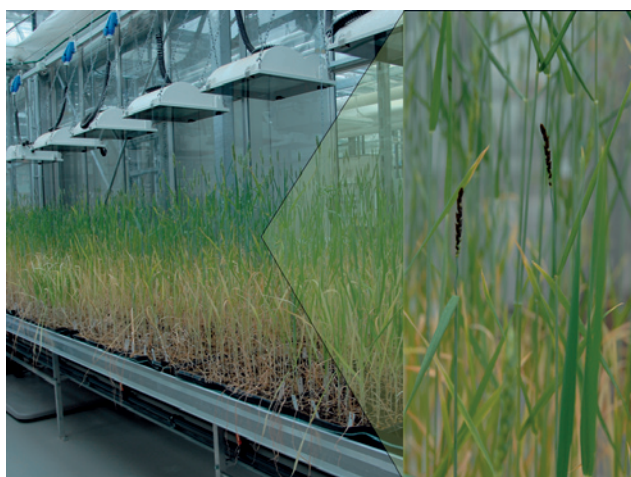
Fig. 6:
A: Sporulation of the *Oculimacula acufiformis* isolate G02 on SNA-Medium

B: Eyespot on a susceptible wheat plant 8 weeks after artificial inoculation

Quantitative and specific detection of *Oculimacula yallundae* (C) and *O. acufiformis* (D). Cross reactions with different pathogens (*Rhizoctonia cerealis*, *Microdochium nivale* var. *nivale*, *Drechslera sorokiniana*, *Fusarium avenaceum*, *Fusarium acuminatum*, *Fusarium graminearum*, *Fusarium oxysporum*, *Fusarium poae*, *Fusarium crookwellense*, *Alternaria alternata*, *Cladosporium herbarum*, *Septoria nodorum*) appear at a threshold level of 10^{13} g (red line).

racess 1 and 4 are in general most damaging. Therefore, it is recommended to test resistance to these races first and test only those genotypes showing a sufficient level of resistance to these races to the other ones (2,3,5,6). After it was shown in 2005 under greenhouse conditions that rape seed (*Brassica napus*) is a host of *Xanthomonas campestris* pv. *campestris* first yield trials to determine losses caused by this pathogen were carried out (Fig. 9). Under optimum conditions for the pathogen, yield losses were determined on the cultivar 'Express' at about 60%. In the growing period 2006/2007 field trials including 16 cultivars are carried out.

Fig. 7: Screening for resistance to *Ustilago tritici* in the greenhouse. Plants have been infested with *U. tritici* in the field in the growing period 2005/2006.



Future perspectives

In the near future the evaluation of genetic resources for resistance and their genetic and molecular characterisation will be the main focus of the Institute of Epidemiology and Resistance Resources thereby contributing to a sustainable as well as consumer and environment friendly plant production and the tasks mentioned within the "National programme for the conservation and sustainable use of genetic resources of agricultural and horticultural crops".

In this respect, the Spanish core collection of *Triticum spelta* will be analysed for resistance to different pathogens in collaboration with Prof. Jose Luis Molina-Cano, University of Lleida, Spain and within the Canadian German Project "Reducing Fusarium Toxins in Wheat through Genomics-Guided Strategies" additional *T. monococcum* accessions will be analysed for resistance to Fusarium Head Blight. Both projects as well as a project aiming at mapping a Soilborne cereal mosaic virus resistance in *T. monococcum* carried out together with Dr. Kostya Kanyuka (Rothamsted, UK) contribute to broadening the genetic base of resistance in wheat (*Triticum aestivum*). Besides this, in 2007 the project "Mapping and use of new sources of resistance against *Pyrenophora tritici-repentis*" funded by the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV) in the frame of the so-called Innovation Programme will be started. Based on long lasting screening programmes genetics of resistance to *P. tritici-repentis* will be analysed in DH populations and molecular markers will be developed facilitating efficient breeding for resistance. Furthermore, the IER together with French, Austrian and German partners is involved in the EURO TRANS-BIO funded project "Marker assisted wheat improvement: creating semi-dwarf phenotypes with Fusarium head blight resistance", which



Fig. 8: Differences in resistance of apple to *Erwinia amylovora* after artificial inoculation with a defined isolate.



Fig. 9: Greenhouse tests to determine yield losses in the rape seed cultivar 'Express' caused by *Xanthomonas campestris* pv. *campestris* (artificial inoculation)

will start in 2007 and aims at improving FHB resistance. Also, a project on resistance to *Puccinia graminis* in wheat will be started funded by the Catholic Academic Exchange Service. *Puccinia graminis* may become important in Germany if temperatures rise.

In line with the above mentioned focus, in barley the project "Pyramiding of QTL for tolerance to *Barley yellow dwarf virus* (BYDV) and genetic analysis of tolerance to *Wheat dwarf virus* (WDV)" also funded in the frame of the Innovation Programme (BMELV), will be started aiming at the improvement of tolerance to these viruses thereby reducing insecticide sprayings.

Additional focus is put on the implementation of methods of association genetics in the characterisation of genetic resources and the determination and use of genetic diversity. In this respect, the proposal "A genome wide approach to associate genetic diversity to agronomically important traits in barley, GABI-GENOBAR" co-ordinate by the Institute of Epidemiology and Resistance Resources has been submitted in the frame of the German Plant Genome Project (GABI) as well as the proposal "Quantitative, genetical and population genomics of barley domestication" which has been submitted to the German-Israeli-Foundation (GIF) together with Dr. Abraham Korol (University of Haifa, Israel) and Dr. Karl Schmid (IPK, Gatersleben). Besides the projects already mentioned, a stronger implementation of the IER into national and international projects is achieved by the involvement in the management committee of the EU-COST Action "Triticeae genomics for the advancement of essential European crops (TritiGen)"

Due to the relocation of the Institute of Epidemiology and Resistance Resources from Aschersleben to Quedlinburg excellent laboratory and greenhouse facilities are available now facilitating precise phenotypic characterisation of

genetic resources for resistance followed by the molecular characterisation of donors of resistance and the development of markers facilitating an efficient exploitation of these resistances. These structural facilities and the up to date lab equipment together with funding acquired for scientific and technical personnel will foster research on the evaluation, characterisation and use of genetic resources for resistance at the IER in accordance with the aims of the Federal Ministry for Food, Agriculture and Consumer Protection (BMVEL).



Institute
of
Plant Analysis
Quedlinburg

Institute of Plant Analysis

The tasks of the Institute of Plant Analysis (IPA) in Quedlinburg are predominantly focused on quality research of selected agricultural and horticultural crops. Furthermore, its research aims to investigate in detail the interaction between improved resistance to various pathogens and increased expression of specific valuable substances and to better understand the molecular background of the biosynthesis for important secondary metabolites. When performing the individual research studies the IPA closely cooperates with other institutes of the BAZ but also with other national as well as international research organisations. In addition the scientists of the institute are in direct dialogue with breeders, farmers, industry as well as consumer associations. Thus, they make an important contribution to further improve the quality standard of plant products in Europe and to develop specific analytical methods for their objective evaluation. At present the following main tasks exist:

- development of efficient analysis methods for selection of qualitatively improved genotypes in the breeding process
- characterisation of genetic resources with regard to valuable as well as toxicologically relevant plant substances
- investigation of the molecular background regarding the biosynthesis of important secondary metabolites
- determination of sensory quality and analytical determination of flavour substances as well as healthy components
- investigation of changes in plant metabolism induced by plant pest organisms (e. g. increased expression of specific protection products)
- characterisation of quality changes induced by postharvest as well as technological processes

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Roselinde Höfer, Teacher for biology and chemistry
(passive phase of partial retirement)

■ International cooperation with other research organisations

In 2006 a new binational project between the Beijing Vegetable Centre (China) and the IPA (Germany) was initiated aiming to develop and apply methods for quality evaluation of vegetable cultivars, with special regard to *Brassica* species (Figure 1).

In this context the research studies are focused on the determination of plant substances in various cabbage varieties regarding cultivation and processing methods. The background of the project both in China and Germany is strongly related to improving sensory and health properties of vegetables.

Presently, plant substances such as anthocyanins, glucosinolates, saponins and terpenes are of increased interest in context with healthy nutrition (Figure 2).

Therefore, modern cabbage cultivars have to fulfil numerous demands set by the producer, the trade and the consumer. Every new cultivar brought into the market has to compete with the quality standard of existing varieties or should even exceed them in certain properties. The project is mainly focused on sensory properties of fresh cabbage, which attains special importance in processed products (so-called “fresh cut vegetables”).

Accordingly, during a visit of the Chinese colleagues in Quedlinburg a new rapid method for the determination



Fig. 1: Because of its outstanding health value Chinese cabbage (*Brassica rapa* L. ssp. *pekinensis*) belongs to the most prominent staple foods in Asia

Fig. 3: Aroma quality of strawberry clones cultivated in the experimental garden of the „Agricultural Research Organisation“ in Israel was investigated in close cooperation with the IPA

Fig. 2: Maize containing high levels of pigments may be used for the extraction of health-effective anthocyanins



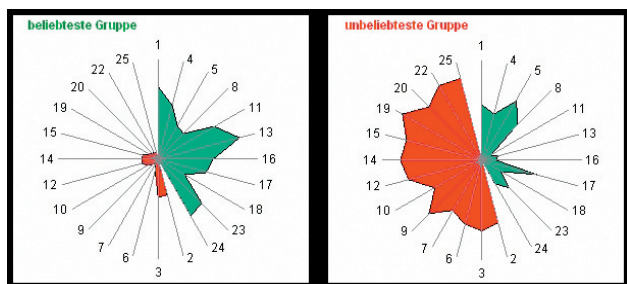


Fig. 4: The analysed 22 carrot varieties obtained from ecological cultivation show significant differences with regard to their sensoric profiles (green: positive descriptors, red: negative descriptors)

of aroma substances in fresh Chinese cabbage has been tested. In future this method will be used to investigate the relationship between health and aroma value of cabbage based on bioactive glucosinolates. On the occasion of a return visit at the Vegetable Research Centre in Beijing the scientific dialogue on this project was continued and new fields for possible cooperation were discussed.

Within the bilateral cooperation with Israel a common workshop entitled “aroma – a key quality attribute in plants” was organised in Bet Dagan. Numerous scientists of the Agricultural Research Organisation (ARO), the Ministry of Science and Technology (MOST), the Hebrew University of Jerusalem, the Ben Gurion University and the Institute of Plant Analysis (IPA) participated in this workshop. Four German Scientists from Quedlinburg, Munich and Rostock attended the meeting. The scientific presentations were supplemented by a visitation of the Israeli institute and two excursions. The programme of the workshop comprised 22 oral presentations and a final panel discussion with representatives of the export industry (Figure 3).

The idea and conception for the realisation of the workshop was based on the activities and results of a bilateral cooperation between IPA and ARO (Institute for Technology & Storage of Agricultural Products, department of Postharvest Science of Fresh Produce). Already at the end of the nineties analytical and sensory methods were developed within a common project for quality research of melons. As a most important result of this cooperation a sensory panel and a sensory test bench were established in the Institute for Technology & Storage of Agricultural Products. In the meantime commonly developed sensory methods are successfully applied also to other cultivated plants such as sweet pepper and strawberry.

The scientific presentations covered topics dealing with problems of cultivation, analytical characterisation of quality, biochemical and molecular background of aroma formation, plant breeding as well as influences of postharvest processes on aroma quality. Especially the topic “biological regulation

of aroma formation” was represented by high-class scientific contributions.

Within another bilateral research project scientists of the Institute of Plant Analysis and the Institute of Horticultural Crops worked together with colleagues of the Department of Genetics, Plant Breeding and Seed Science, University Krakow (Poland) aiming to study the inheritance of certain carrot traits. So far studies on the genetic characterisation of carrot have been performed only by small international groups, so it is not a surprise that because of the limited knowledge regarding heredity transmission currently the considerable potential of this cultivated plant is used only to a moderate extent (e.g. high content of vitamins as well as other secondary metabolites). Based on this bilateral cooperation both partners will apply for further research funds in the near future. At a common workshop in Krakow, organised in December 2005, the results of the research project were discussed and next goals were planned and coordinated. In 2006 main emphasis of the studies was laid on the genetic map of carrot by applying new molecular markers. The genetic map in its present form is the basis to acquire more special knowledge on heredity of individual traits. Carrot lines used in this study are available for interested colleagues. The genetic map, too, can be provided for common research projects.

■ Sensory analysis – an objective tool for plant breeding

The necessity to integrate analytical methods into breeding research and breeding processes is not new. Analytics have been already used to increase the sugar content in sugar beet. In the seventies the content of bitter principles in cucumber was successfully lowered by breeding applying thin layer chromatography and since the eighties first of all gas chromatography has been used for selection of new rape varieties with low erucic acid. In the meantime also human-sensory analysis was developed to an internationally accredited method.

Nevertheless compared to physical-chemical techniques sensory methods are not yet fully integrated in breeding research. That is the reason why consumer’s demand of tasty, healthy and ecologically produced foods is satisfied only in an insufficient way.

Also today, main interest of plant breeders is laid on high yield, low contamination with pesticides, attractive and standardised appearance as well as long shelf life of the individual crop. Merely breeding of cultivated species with a high number of different varieties (e. g. apple and potato) as well as species which have a long tradition regarding aroma quality (e. g. wine) is accompanied by sensory testing. Thus a high flavour diversity and approved sensory quality can be guaranteed. But there are also negative examples; tomato, strawberry, radish, melon,

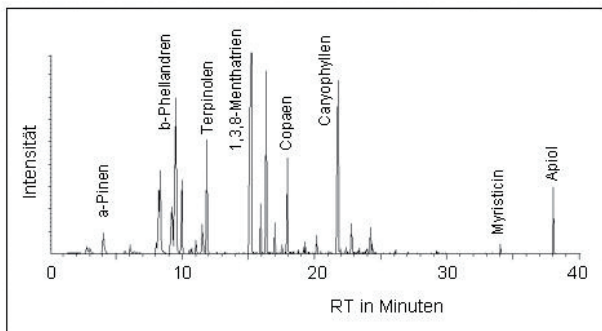


Fig. 5: Total ion chromatogramme (TIC) obtained from a parsley sample. Advantageously, isolation of volatile substances is performed by means of headspace SPME

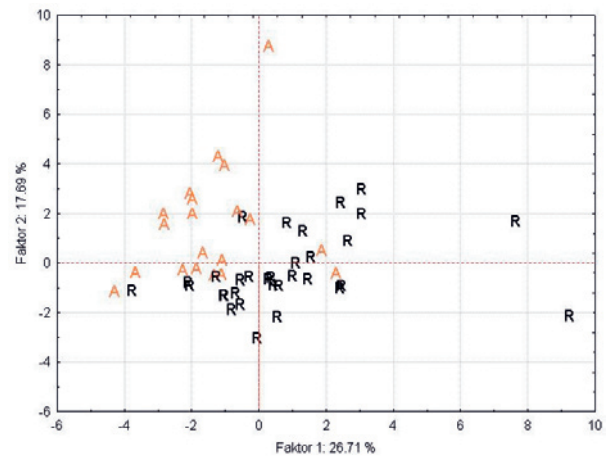


Fig. 6: Based on chemical composition and resistance traits suitable parsley genotypes can be reliably evaluated by Principal Component Analysis

cucumber and several other species have shown a continuous decrease of sensory properties within the past decades. Generally, this process is correlated with a loss of “flavour diversity”. The IPA could already find proofs for this genetic erosion in some selected species. The main reason for this development was and is still today the absence of “sensory standards with long-term availability” as well as the lack of practicable instrumental analysis methods for objective evaluation of aroma and taste. Furthermore, the aim to significantly increase the consumption of fruit and vegetable in order to keep the population well and fit (e. g. the campaign “five a day”) can only be achieved if healthy products offer a high aroma value at the same time. The IPA has access to a continuously trained sensory panel which addresses special tasks and has long standing experience in numerous projects dealing with breeding research. Today the main focus of sensory studies is laid on the description of organoleptic parameters with respect to genetic diversity. In this context the variability of bitterness in asparagus and biodiversity and heredity transmission of strawberry flavour have been investigated in detail. Furthermore, attempts have been performed to study the interrelationship between taste, habitus, chemical composition and *Septoria* resistance. It has been found that sensory and analytical characterisation supply important data to identify off-flavour components as for instance –myrcene and caryophyllene. In this context the scientists of the IPA succeeded to integrate several sensory attributes into the genomic map of carrot. Through this, completely new approaches exist to select new carrot types with increased health potential and approved taste in an efficient way.

■ Terpenes affect flavour quality of parsley

A parsley collection, planted in the experimental garden in Quedlinburg for resistance research, was used to study the sensory properties and variability of chemical composition.

For this a sensory profile for fresh parsley was developed and tested. Additionally, a new effective GC method for determination of terpenoids, which are mainly responsible for the aroma of parsley, was applied. The instrumental analysis method represents a very useful completion of human sensory analysis. The pattern of volatile substances in fresh parsley can be efficiently identified by application of a so-called “virtual electronic nose”. To perform this method, a gas chromatograph, a headspace–solid phase microextraction unit as well as a chemometric software applied for pattern recognition were combined. Advantageously a mass spectrometer was used as GC detector. Figure 5 shows a chromatogramme of a parsley genotype which has been obtained in this manner. Most detected peaks are related to the chemical group of terpenoids; in total 23 components have been quantified. Figure 6 demonstrates the variability of aroma substances occurring in all analysed 52 samples. The individual pattern is characterised by a considerable genetic variability which is also reflected by an extreme variation of sensory quality. The results obtained by Principal Component Analysis, calculated on the basis of different aroma patterns and resistance properties, show a clear separation of resistant and non-resistant parsley genotypes in different clusters. Accordingly it can be assumed that there exists a correlation between terpenoid composition of various parsley types and resistance against fungus attack.

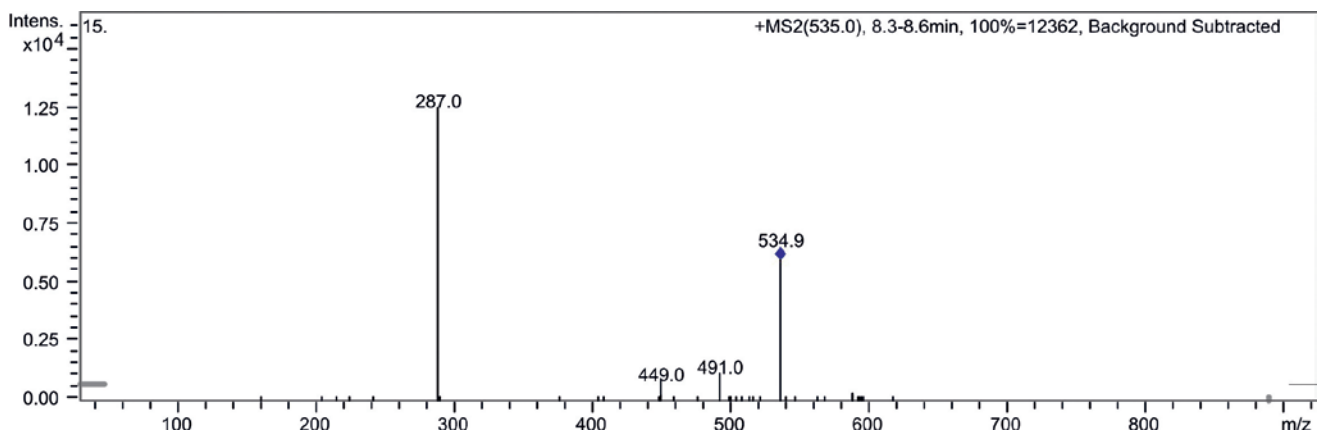
■ Unknown pigments are identified by means of HPLC-MS

Anthocyanins and the related aglycons (anthocyanidins) are widespread in the plant kingdom. They are responsible for the red, purple or blue colour of flowers and fruits. For strawberry the consumer prefers intensively coloured red fruits and they also associate in this context the



Fig. 7:

Usually the molecular structure of unknown plant substances can be properly identified by means of HPLC-MS. The mass signals identified at m/z 535 and 287 can be assigned to the molecule ion and the cyanidin fragment, respectively



individual stage of maturity. Within the identification of plant substances by means of high-performance liquid chromatography/mass spectrometry (HPLC-MS) and the continuous development of an MS library, studies to characterise the anthocyanin composition in wild and cultivated strawberries were performed in cooperation with the Institute of Fruit Breeding in Dresden-Pillnitz. These studies represent a preliminary survey for the chemical characterisation of progenies derived from different crossing experiments. The special advantages for the identification of unknown components by means of HPLC-MS-MS technique without the necessity to use reference substances have been demonstrated. Thus, a pigment occurring in the strawberry cultivar “Alba” (*Fragaria x ananassa*) was identified after HPLC separation of the strawberry extract. The corresponding mass spectrum presented a component with two intensive fragments at m/z 535 and m/z 287 (Figure 7) which indicates that the unknown substance can be classified

as a cyanidin compound substituted with glucose. Further fragment experiments lead to the conclusion that the sugar substituent is esterified with malonic acid ($C_3H_4O_4$). If all pieces of the puzzle, obtained from multidimensional mass spectroscopy data, are put together one can conclude that the unknown plant pigment can be identified as cyanidin malonylglucoside (Figure 8).

■ Already traces of mycotoxins may generate high hazard potential

From ancient times and especially from the late middle ages it is reported that continuously epidemics led to toxications occurring after consumption of rye bread which was prepared from flour contaminated with ergots. Reports are also known from Russia, describing numerous deadly toxications caused by breadstuffs harvested during wintertime which were highly contaminated with fungi

of the genus *Fusarium* and the related toxins. Plant foods are especially susceptible towards fungus deterioration, of which many species have the ability to produce extremely toxic metabolites (so-called mycotoxins). It is assumed that approx. 20% of all plant products are contaminated with mycotoxins. Accordingly there is a special demand for providing an efficient method for rapid quantification of mycotoxins.

Deoxynivalenol (DON), nivalenol (NIV) as well as zeavalenon (ZEA) are mycotoxins occurring in various grain species which are of particular importance. Mycotoxins can be detected in all stages of the food chain and that's the reason why interdisciplinary cooperation between basic research, food safety, consumer protection and animal health is necessary. In order to support breeding methods aimed to lower the mycotoxin content in wheat and other grains, an efficient HPLC-MS method for rapid determination of DON was established (Figure 9). The quantification of mycotoxin was performed on the basis of the isolated fragments m/z 297 ($[M+H]^+$, DON) and m/z 281 ($[M+H]^+$ -DOM) using deoxy-DON (DOM) as internal standard. Furthermore, a NIRS calibration based on HPLC-MS reference data was established. By means of this NIRS method DON contaminations with minimum concentration levels of approx. 15 $\mu\text{l}/\text{kg}$ were successfully analysed without applying any sample clean-up procedures.

■ Chemical compositions of genetic resources are evaluated

The analytical evaluation of secondary metabolites in various medicinal and aromatic plants has been traditionally performed in the IPA on a large scale. Enormous efforts alone were dedicated to analysing numerous wild and cultivated species. In 2006 especially thyme, savory, fennel, caraway, marjoram, chamomile, parsley, coriander, basil, sage, nasturtium and black snakeroot were investigated for their valuable substances. Studies conducted with thyme and savory were financed by third parties. The essential oils of both species contain phenols which are known for their antioxidative and antimicrobial properties. Presently, these compounds are discussed as an alternative for antibiotic feed supplements which have been banned since 2006 by the European Union. Therefore, the aim of running projects is to develop cultivars with high yield and increased oil content by conventional breeding.

For a long time several projects were dealing with fennel and caraway and in this context the main focus was to obtain new annual varieties. In the meantime this aim is more or less reached but now claims regarding resistance and quality of these annual plants have to be satisfied. Because a couple of thousand samples have to be analysed every year, efficient rapid methods have been developed in the IPA to minimize

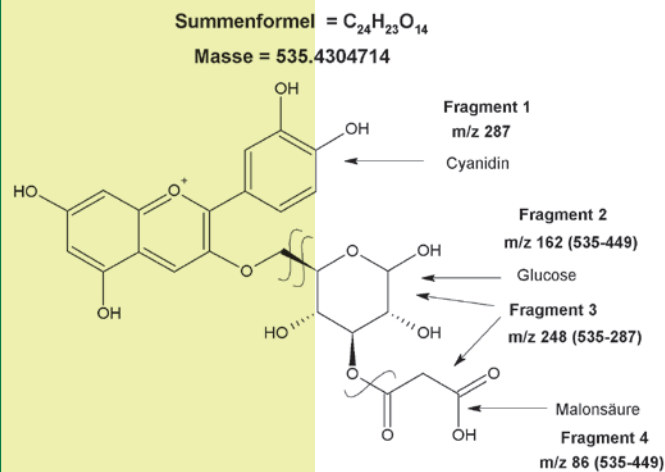


Fig. 8: Further fragmentation of the mass fragments shown in figure 7 forms daughter ions for cyanidin (m/z 287), glucose (m/z 162) and malonic acid (m/z 86). This fragmentation pattern provides important information for the structure analysis of unknown anthocyanin compounds

the efforts in the lab. In this context especially Near-Infrared Spectroscopy has been proved to be a powerful and non-destructive tool which also allows using the analysed seeds and fruits directly for further breeding processes.

Within an "InnoRegio-Initiative" of the BMBF, a project performed in cooperation with partners from small/mid-sized companies that focused on new marjoram types presenting special quality traits has been finished. Another goal was to develop base material to breed new marjoram lines for medicinal applications. From the cooperation with industry partners it turned out that also technological properties such as extraction yield, bulk density or ability

Fig. 9: Mycotoxins generated in wheat can be reliably identified by means of HPLC-MS



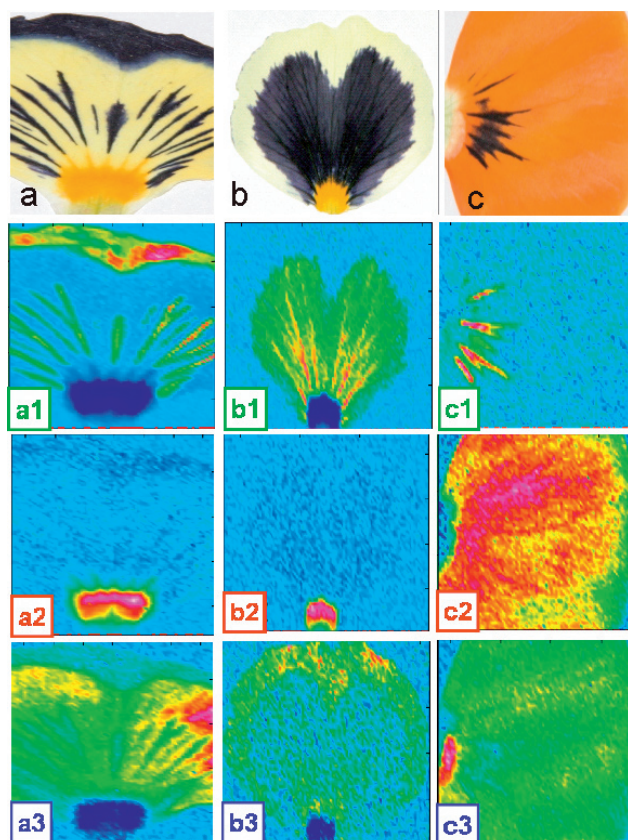


Fig. 10: Based on Raman mapping experiments it is possible to determine simultaneously the spatial distribution of different plant pigments in petals of three *Viola* species.

- a1-a3: integration of anthocyanidin bands in the range between 1225 and 1272 cm^{-1}
- b1-b3: integration of carotenoid bands in the range between 1140 and 1172 cm^{-1}
- c1-c3: integration of flavonol bands in the range between 1550 and 1588 cm^{-1}

of distillation possess an increased significance for plant breeding. Gentle sterilisation processes maintaining more or less the individual quality parameters will also acquire increasing importance in the area of medicinal and spice plants and as a consequence these aspects must be also regarded during the breeding process.

In cooperation with the Institute of Plant Genetics and Crop Plant Research in Gatersleben the morphological, chemical and genetic variability of 457 coriander accessions (*Coriandrum sativum* L.) were investigated. The task of the IPA is to analyse the ex-situ genebank material with regard to valuable substances (essential oil, fatty acids and tocopherols). Then the individual varieties will be discriminated and characterised by means of molecular markers.

In order to characterise different cultivars of medicinal and spice plants precise analytical methods are of particular importance. In this context the IPA has assumed agent analyses to determine the individual value analysis as a

continuous mandatory task for several years.

From time to time the results obtained from these studies are published by the “Bundessortenamt (BSA)”. In 2006 extensive inspections of basil, sage, nasturtium and black snakeroot were provided to the BSA.

Further development of existing analysis methods was focused on tasks of selectively isolating volatile substances from solid phases. It could be proved that hydrophilic alcohols of chamomile such as alpha-bisabololoxide A contribute to a higher extent to the inhalant effect as generally assumed. As a result of this finding it can be expected that new recommendations for optimal chemical composition of tea drugs will be defined. This year first attempts have been done to use the SPME head-space analysis for identification of volatile substances in scented *Pelargonium* species already in the stage of meristem culture.

■ Imaging techniques gain recognition in plant analysis

For the past four years numerous applications for identification and quantification of plant substances by Raman spectroscopy, resulting from a DFG project, were presented.

Contrary to usually applied chromatographic separation techniques such as GC and HPLC, Raman spectroscopy allows to determine simultaneously and non-destructively several chemical components in comparatively short time without any sample preparation. Especially analyses of fresh plant products provide clearly better results in comparison to NIRS measurements, because tissue water generates only signals of low intensity.

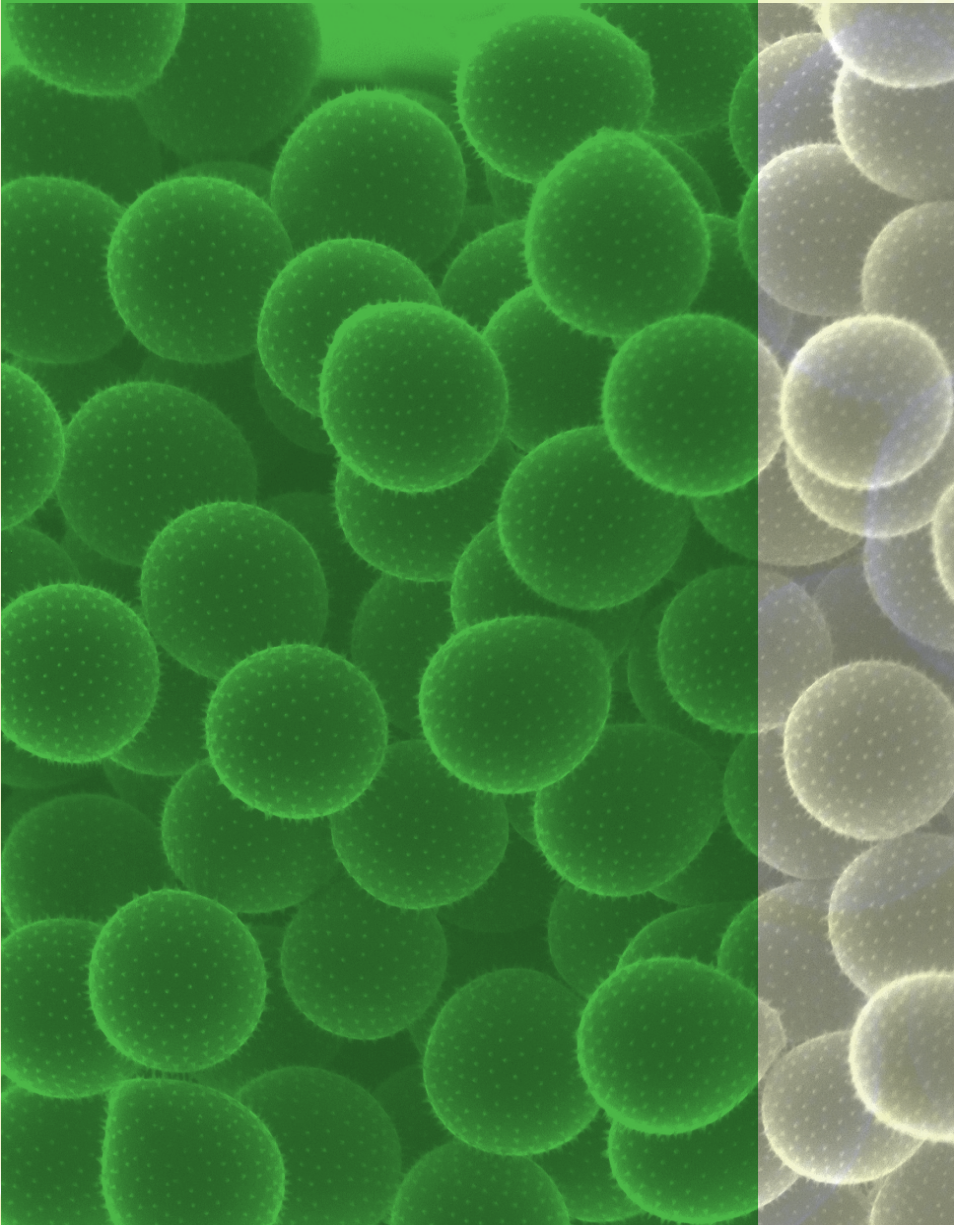
Furthermore, this sophisticated method offers the possibility to measure the chemical composition within cellular dimensions achieving a special resolution between 3 and 100 μm , if a special micro-optics or a light-optical microscope is connected to the Raman spectrometer. Based on individual key bands the distribution of selected plant substances can be illustrated by so-called “Raman maps”. Thereby the concentration of the individual plant components is reflected in miscoloured diagrams. By means of such image techniques, which already have been applied in medicine for several years, different plant pigments of special *Viola* cultivars were detected independently from each other. As can be seen from figure 10 the purple coloured parts of the petals were identified on the basis of the specific anthocyanin Raman signal at 1260 cm^{-1} . Also carotenoids (the analysed *Viola* species contain mainly xanthophylls and violaxanthin) could be successfully detected by suitable marker bands in the wavelength range from 1140 to 1172 cm^{-1} . Finally also the light yellow coloured flavonols could be localised in the plant tissue using the characteristic Raman signal at 1570 cm^{-1} for integration.

Future prospects

Within the next years research activities of the IPA will focus on the analytical characterisation of genetic resources. Results obtained in this context will be available for everybody as suitable databanks. At this the tasks to be fulfilled will be supported by the introduction of a Laboratory Information Management System (LIMS).

Further main activities will be pursued to support future topics such as “effects of climate change on chemical quality”, “safety of plant foods” as well as aspects of “chemical biodiversity” in close cooperation with other research organisations by means of analytical measurements.

Thereby, micro-infrared-imaging as well as micro-Raman-mapping techniques, which have been successfully established in the IPA, will gain more importance in the near future.



Institute
of
Resistance Research
and
Pathogen Diagnostics
Quedlinburg

Institute of Resistance Research and Pathogen Diagnostics

Research in the interest of consumers

Today one can notice an increasing interest of the German population in agriculture in general and in particular in approaches for a sustainable production that help to preserve nature and natural resources. The market for food from organic farming is growing continuously having achieved about 4.5 billion Euros in 2006. Development and application of technologies for a sustainable production represent a central feature of the agricultural policy in Germany. Stepwise further reduction of pest management with agrochemicals and the increase of genetic diversity in crop species and varieties grown in the fields are of outstanding importance.

Consequently, improvement of plant resistance against pathogens and pests by specific resistance breeding based on evaluated genetic resources is becoming more and more important. The main objectives of research at the IRP are investigation of different host-pathogen interactions and elucidation of mechanisms of resistance as well as identification and utilization of novel sources of resistance. Furthermore, a powerful pathogen diagnostics is an indispensable prerequisite for any resistance research. Scientists of IRP are closely collaborating with colleagues at the partner institutes in BAZ to support their breeding research programmes. There are also tight connections and common research projects with external partners in scientific institutions and private breeding companies. The obtained results of research serve to give support and scientific advice to the Federal Ministry of Food, Agriculture and Consumer Protection.

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Natural resistance to diseases – an integral part of modern cultivars

Continuous improvement of resistance of agricultural crops to diseases and pests is an important aspect of a sustainable agriculture. Consequently, it is a research emphasis in the BAZ. Research topics of the IRP result from the request of crop specific institutes. Based on external funds research is done in co-operation with other scientific institutions as well as breeding companies.

■ Potato (*Solanum tuberosum*)

Once it has been one of the most popular German foodstuff. Meanwhile it has lost some of its importance. Specialists expect that potato consumption will undergo a renaissance as it is a healthy staple food which can contribute to defeat hunger in the world.

Unfortunately the potato production is endangered by a large number of diseases. The foliar and tuber late blight disease, caused by *Phytophthora infestans*, plays an important role as well as different viruses.

In co-operation with the Institute of Agricultural Crops Groß Lüsewitz (ILK) new resistance sources will be evaluated in wild potato species. Somatic hybridization of isolated mesophyll protoplasts has been used to overcome the sexual incompatibility between cultivated potato and its wild forms. By backcrossing of somatic hybrids with potato

cultivars, material was developed which is valuable for further breeding. The differentiation of desirable heterologous (hybrids) from homologous fusion products was carried out using microsatellite (SSR) analysis based on polymorphisms among the parental lines and analysing additive patterns of prominent bands expected for heterologous hybrids (Fig. 1, image below, right). Depending on the fusion partner, major differences were obtained concerning the yield of hybrids. For example, in the fusions *S. cardiophyllum* (+) *S. etuberosum* and *S. chacoense* (+) *S. etuberosum* only the fragment pattern of the wild parent *S. etuberosum* but none indicative for hybrids has been detected (Fig. 1, table).

The wild diploid Mexican species *S. pinnatisectum* has a high level of resistance to *P. infestans*. For mapping the resistance gene(s) the generation of a segregating population has been initiated. After crossing a late blight resistant with a susceptible *pnt*-genotype as well as performing the corresponding reciprocal cross, both F₁ populations received have been scored for *Phytophthora*-resistance. Microsatellite analysis of the selected F₁-parents revealed polymorphisms between resistant and susceptible genotypes. Whether the respective markers are linked to the resistance traits will be investigated.

In the near future selected resistant F₁ individuals will be backcrossed to the susceptible *S. pinnatisectum* accession. The BC₁ progenies will be analysed for the inheritance of late blight resistance to develop closely linked resistance markers. These markers will be used for mapping of resistance gene(s) derived from *S. pinnatisectum* and their marker assisted transfer to other potato cultivars. In addition, further BC₁ progenies provided by the ILK based on somatic hybrids 'Delikat' (+) *S. tarnii* and characterized by high levels of resistance to PVY as well as late blight were backcrossed to the susceptible potato cultivar 'Delikat' and integrated into the molecular analysis.

The results of the resistance tests confirmed that both the PVY and late blight resistance derived from *S. tarnii* can be effectively transferred into somatic hybrids and BC₁ progenies.

The named wild species have been proved as excellent donors of resistance both to single and to all known PVY strains. They can be used to develop an extended set of differential hosts for biological differentiation of strains of PVY. Furthermore, they can be used to introduce resistance to most damaging strains of PVY into potato cultivars, mainly to the tuber necrotic strain of this virus (PVY^{NTN}). Attempts to uncover inheritance of susceptibility of potato to PVY-induced tuber necrosis were continued under field conditions in a screenhouse with progenies of resistant x susceptible crossings. Results from both years of testing are contradictory. Thus, we can not yet predict inheritance of this feature.

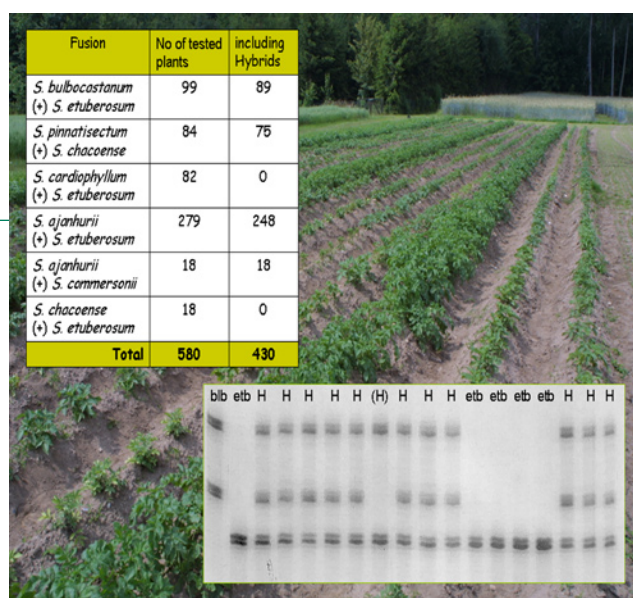


Fig. 1: Identification of true somatic hybrids from mesophyll protoplasts of potato by means of molecular markers. Upper part, left: Number of somatic hybrids among fusions of different *Solanum* species; lower part, right: SSR-analysis of somatic hybrids (H) after fusion of *S. bulbocastanum* (blb) (+) *S. etuberosum* (etb).

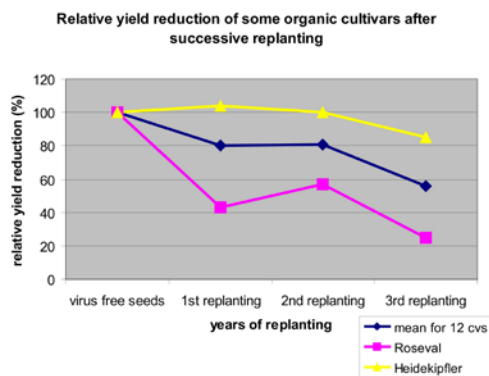


Fig. 2: Yield reduction of different potato cultivars grown under organic conditions after repeated planting.

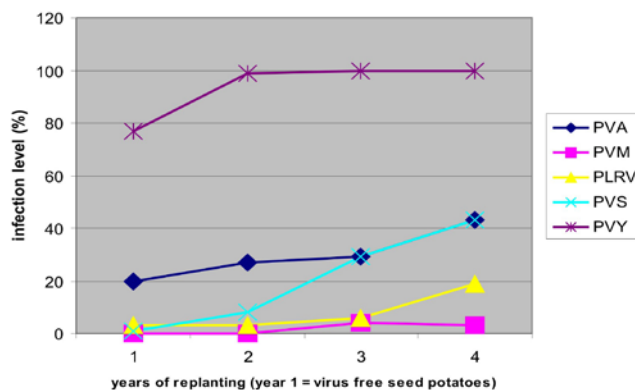


Fig. 3: Level of virus infection of organic potato cultivars after repeated planting.

In the framework of a research project supported by the Federal programme “Organic farming” in co-operation with the Biolandhof Ellenberg we established a collection of more than 100 virus free potato cultivars used in organic farming. Interested potato growers can now receive this material on request. Importance of virus free status was shown in several years’ experiments with selected cultivars. While ‘Heidekipfler’, the new breeding line of Biolandhof Ellenberg, did not reveal marked reduction of yield after repeated replanting, the yield of the cv. ‘Roseval’ was reduced to less than one third of the control (Fig. 2). This was caused by a rising contamination with several viruses (Fig. 3).

Together with the partner it was possible to introduce into breeding material for organic farming resistance to the currently most important potato virus, PVY, as well as to scab (*Streptomyces scabies*) from *Solanum demissum*. Resistance donors were provided by Dr. C. Gebhardt (Max-Planck-Institut für Züchtungsforschung Köln-Vogelsang).

Genetic engineering offers alternatives for the introgression of disease and pest resistance into plants. As main advantage this approach leaves the genetic background of the recipient nearly unchanged after integration of the transgene. This is of particular interest if dealing with tetraploid crops. Concerning possible biosafety consequences of these changes the question arises whether additional information might influence the genetic structure of viruses infecting transgenic plants. A highly variable and consequently well suited research object for these investigations is PVY. During the last year we could identify further recombinant forms of this virus. In the framework of a co-operative research project with BTL-Sagerheide, supported by grants of the Federal Ministry of Education and Research (BMBF), we launched investigations on a possible influence of transgenes in potato plants on recombination frequency of PVY. For this purpose different transgenic lines were inoculated with a mixture of defined O- and N-strains under field conditions in 2006. Virus isolates in harvested tubers are now being analysed for putative genetic diversity, i.e. recombination events.

■ Wheat (*Triticum aestivum*), barley (*Hordeum vulgare*), rye (*Secale cereale*)

In Germany as well as in other European countries wheat, rye and triticale get infected at a growing rate by soil-borne viruses transmitted by *Polymyxa graminis*. These are the furoviruses *Soil-borne cereal mosaic virus* (SBCMV) und *Soil-borne wheat mosaic virus* (SBWMV) as well as the bymovirus *Wheat spindle streak mosaic virus* (WSSMV). As chemical elimination of the vector is not possible and viruses remain infectious inside thick-walled resting spores for many years, development of resistant cultivars and their consequent cultivation is the only chance to defeat the corresponding diseases.

In the frame of investigating the occurrence of soil-borne viruses we determined the appearance of different subspecies of the vector by means of PCR in co-operation with the Catholic University Louvain (Belgium). According to these results *P. graminis* f.sp. *temperata* dominates in barley while wheat is mainly infected by the subspecies *P. tepida*. Next we will have to determine whether these subspecies are specialised in the transfer of specific bymo- and furoviruses. In 2006 a research project, supported by BMBF, dealing with the improvement of virus resistance of rye to SBCMV, SBWMV, and WSSMV was finished. For the first time, in Germany donors of resistance could be identified in nine *S. cereale* and two *S. strictum* accessions among evaluated genetic resources. From these origins 26 full sibling progenies with improved virus resistance were developed by selective pair crosses, which form the basis for future development of resistant rye cultivars.

In wheat material from different gene bank collections, potential donors of resistance to SBCMV and SBWMV were identified. Analysis with molecular markers, performed in co-operation with the RTG 2n company, demonstrated that 10 of the identified sources have probably the same resistance gene as cv. ‘Tremie’. Interestingly, one accession has another so far unknown genetic resistance background.

In the course of our evaluation experiments we noticed that under natural conditions barley became infected by SBWMV but not by SBCMV. Consequently, the further spread of SBWMV also endangers the cultivation of winter barley.

■ Oregano (*Origanum vulgare*)

Consumers have rediscovered spices and for a number of years consumption has been continuously growing. Application of pesticides is restricted when producing medical and spice plants. As a consequence, a high level of disease resistance of these species is desirable to get a good harvest with excellent product quality.

In last years Oregano plantations in Germany suffered from a disease caused by a *Phoma* species. It is characterized by wilted or necrotized shoots covered with black spots (Fig. 4). To ensure an economic production of this herb, genetic resources were screened for useful donors of resistance. In a first step an easy to handle laboratory test was developed. After two years of field experiments we could demonstrate that resistance levels determined with the laboratory method were in consistence with data from field experiments. Based on these findings we were able to screen 43 oregano accessions from the gene bank collection of the IPK Gatersleben for resistance. Among them, 19 accessions revealed reduced disease susceptibility compared to the standard cultivar ‘Vulkan’. Though these results have to be still confirmed they are promising for future activities to improve resistance of oregano to *Phoma* sp.

Modern pathogen diagnostics is indispensable for successful resistance breeding

Diagnostic methods based on the application of antibodies are easy to perform and possess still high importance because of their specificity, sensitivity and practicability. These techniques are completed by molecular methods based on the detection of genomes of pathogens. They require sequence information to be carried out and are more expensive; however, they reveal in general increased sensitivity and specificity. The immunoreagents can be used directly for the development of variants of enzyme-immunoassays or in combination with molecular methods like immuno-capture PCR or PCR-ELISA for the detection of pathogens.

■ Viruses

After having developed appropriate primers for the detection of defined strains of PVY by means of IC-RT-PCR the suitability of these primers in a multiplex detection system was to prove. Because of the specific structure of the PVY genome actually two assays are necessary – one for the basic strains of PVY (N, O and C) and a second for the recombinant strains PVY^{NW} und PVY^{NTN}, since in that case genome fragments in the range of 4 kb have to be amplified. The method allows to distinguish single virus components in a mixed infection (Fig. 5).

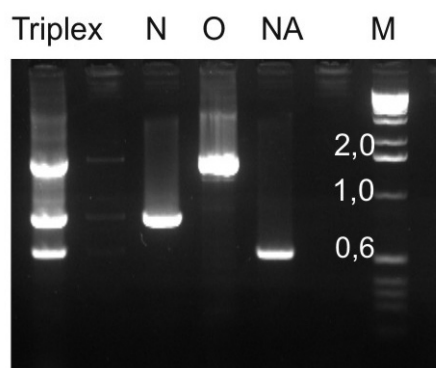
Surprisingly, a New Zealand isolate causing tuber necrosis showed the typical molecular structure of the PVY^N-strain group. Consequently, it differs from all other so far known recombinant PVY^{NTN} strains. These findings further

Fig. 4: Wilted and dead shoots of an oregano plant in the field artificially infected with *Phoma* sp.



Fig. 5: IC-RT-PCR detection of mixed infection of potato with strains of PVY. Triplex: detection of strains in one reaction mixture.

N: detection of N-strain;
 O: detection of O-strain;
 NA: detection of North American N/NTN-strain;
 with specific primers, respectively.
 M: marker (kbp).



exacerbate the problem of a reliable identification of PVY^{NTN} strains in potato farming and quarantine survey.

The results of IC-RT-PCR could be validated by means of monoclonal antibodies (MAb) developed in our institute. By means of MAb 5H3 all strains of PVY can be detected whereas the two MAbs 3E11 and 7C9 specifically recognized PVY^N or PVY^{O/C} serotypes, respectively. The mouse MAbs are used for resistance testing of potato lines in the BAZ as well as for certification of seed potatoes by the BBA¹ in Braunschweig.

Meanwhile, in Germany, asparagus belongs to the most important vegetables and there is a continuously growing demand. It is well known that infection with viruses reduces the yield of the vegetable significantly. Unfortunately, infections are not visible on the plants due to specific leaf morphology. A first analysis of infection levels of plantation in Rhineland-Palatinate and Saxony-Anhalt revealed in some cases rather high infection rates. Obviously, two forms of *Asparagus virus 1* (AV-1) are present, which differ at least in the coding region for the N-terminal part of the coat protein (CP). As a precondition to differentiate both forms of AV-1 the N-terminal part of the CP was expressed in *E. coli*, purified and used for production of antisera. Fig. 6 shows the results of the expression analysis. Besides the elongated AV-1 virions isometric particles were detected in several asparagus samples which were identified as strains of *Cucumber mosaic virus* (CMV). *Asparagus virus 2* was not detected so far.

In a co-operation project with a colleague in Nigeria supported by the DAAD viruses from species of the genus *Cucurbitaceae* have been isolated causing considerable problems in agriculture of the African partner. From *Adenopus breviflorus*, *Cucumis moschata*, *C. sativus* and an undefined *Adenopus* species several virus isolates were gained and designated with the abbreviations AdbreV, CurV, CumV and AdspV. They could be transmitted mechanically as well as by the aphid species *Myzus persicae* and *Aphis gossypii* in a non-persistent manner to diverse host plants. *Macrosiphon euphorbiae* proved to be a further vector for AdspV. Electron microscopical investigations on ultrathin sections of original plants showed, besides the flexible, thread-like particle structure characteristic for potyviruses, also inclusion bodies (Fig. 7). All isolates reacted in PTA-ELISA with potyvirus group-specific antibodies. First results with newly produced polyclonal antisera and sequencing data confirmed that both isolates from *Adenopus* species are closely related to the *Moroccan watermelon mosaic virus* and exhibit only few amino acid sequence differences at the N-terminal part of their

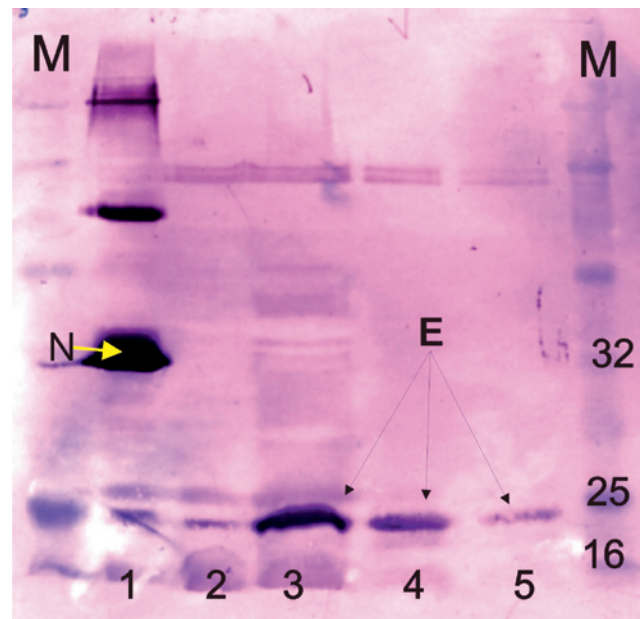
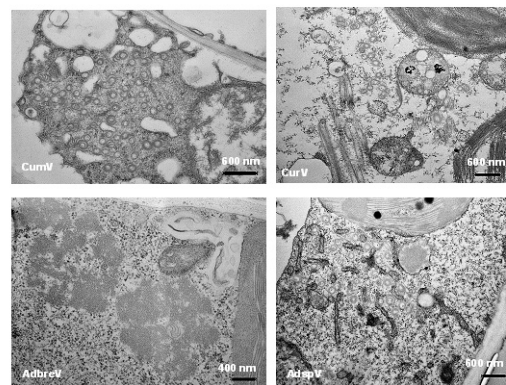


Fig. 6: Detection of the expression of the N-terminal part of the coat protein (CP) of an AV-1 isolate in *E. coli* by Western-blot. M: marker (kDa). 1: infected control; 2: healthy control; N: native CP of the virus; E: expressed fragment of the CP at different levels of purity (3-5). Detection was by polyclonal antibodies to AV-1.

Fig. 7: Potyviral inclusion bodies in form of pinwheels, scrolls and/or tubes in naturally infected plants of *Cucumis sativus* (CumV), *Cucurbita moschata* (CurV) and an *Adenopus*-species (AdspV). Isolate AdbreV did not induce formation of typical inclusion bodies in *A. breviflorus*.



coat proteins. The isolates CurV and CumV could stand for two hitherto unknown potyviruses.

In cooperation with the Institute of Epidemiology and Resistance Resources Quedlinburg and the University of Stuttgart a new genotype of *Wheat dwarf virus* from oat was sequenced and identified as a new member of cereal infecting geminiviruses – Oat dwarf virus. In this context rolling circle amplification proved to be a highly efficient method for amplification and cloning of the complete genome of these viruses. In contrast to PCR no thermal

¹ Federal Biological Research Centre for Agriculture and Forestry (BBA)

cycler is necessary to perform the reaction. Full length clones of the virus will be used to produce infectious clones of the different genotypes of the virus which can be applied for resistance screening.

■ Fungi

In a bilateral project with the Bavarian State Research Center for Agriculture detection methods for smut fungi like *Ustilago nuda*, *Tilletia caries* and *T. controversa* will be developed. The final aim is to build up methods based both on molecular and immunological techniques for the determination and differentiation of fungal species causing smut and bunt diseases mainly on seeds produced under conditions of organic farming. This can contribute to an improvement of the quality of organic seeds as well as to advancement in quarantine certification methods. Beside the PCR-based detection of *T. caries* a polyclonal antiserum (PAs) was produced which enables detection of infection in wheat grains by means of Western blotting. The analysis of total protein extracts revealed a specific reaction in form of a single band, whereas no cross reaction was observed with extracts prepared from *T. controversa* spores. First tests with MAbs and PAs raised to synthetic peptides representing amino acid sequences of heat shock proteins of several *Tilletia* species gave neither in Western blots nor in DAS-ELISA practically usable results.

In frame of co-operation with IER Quedlinburg PAs were produced to hyphae extracts of loose smut (*U. tritici*) reacting specifically with the homologous antigen.

Another project supported by BMBF with the main objective to develop immunological detection methods for *Fusarium* exoantigens in infested grains of cereals was successfully finished. For assessment of *Fusarium* resistance in wheat genotypes the herein developed serological methods were compared in a diploma thesis (Karina Rohrig) with spectroscopical and immunological techniques for the direct estimation of mycotoxin content in grains. This work was carried out in co-operation with Martin-Luther-University Halle and the Institute of Plant Analysis of the BAZ.

Twig blight caused by *Monilia laxa* is still considered to be the most important disease of sour cherry. For this reason, in co-operation with the Institute of Fruit Breeding Dresden-Pillnitz of BAZ (IOZ) new cultivars with improved resistance to this disease will be developed. Results of infection tests with *M. laxa* on “Knip”-trees (two year old trees with one year old crown) of different cultivars of sour cherry confirmed results on resistance level obtained in the open ground. Level of resistance, determined as portion of diseased branches per tree is also reflected by ELISA values obtained for specimens from branches. These results underline that presently available methods are suited to detect different levels of resistance. Use of “Knip”-trees has the limitation that a large number of



Abb. 8: Witches' broom (arrow) at the cv. “Hibernal” induced by an infection with AP.

trees are necessary to obtain valid data. Another disadvantage of these test objects is their high variability in habit. To circumvent these problems and enhance reliability of results we started to test the suitability of detached parts of the trees like blossoms, fruits pedicels and peduncles to determine the level of resistance by visual scoring and serological methods. The experiments have not been finished yet.

■ Phytoplasma

In the last years in Europe an extending spread of apple proliferation (AP, Fig. 8) in fruit plantations is noticed which is characterised by witches' broom, small and badly coloured fruits as well as early autumn colouring of leaves. The disease is caused by phytoplasmas, which are classified as quarantine pathogens. Phytoplasmas are bacteria having a membrane but no cell wall. They are transmitted by phloem feeding insects, mainly psyllids (e.g. *Cacopsylla picta*) and persist only in sieve tubes of infected trees.

The IOZ has taken over a large collection of genetic resources of apple cultivars. Unfortunately, some material proved to be infected by AP. Consequently, intensive attempts have to be undertaken to free the collection from this pathogen as this is a prerequisite to fulfil the tasks of a gene bank.

Apple cultivar 'Hibernal' is used in the gene bank as interstock. To uncover lines of spread of infection we started to test this material as nursery grafted trees for presence of AP. For this purpose nucleic acid extracts were obtained from the bark of twigs and tested by means of PCR utilising specific primers for AP. Phytoplasma was detected in 14 out of 64 samples after budding and in 9 out of 104 samples from bench grafting.

AP can be transmitted by different psyllids. In autumn 2006, 10 knocking tests (E. Schliephake, IER) were performed in the apple tree plantations of IOZ to collect the vector. In these samples, 51 individuals were identified as *C. picta* and 82 as *C. mali* indicating a fairly high population density of these psyllids. Since at least *C. picta* has been described to be an effective vector for AP we are faced with a high risk of spreading apple proliferation from single infected trees to trees in surrounding area.

Future prospects

Research on the development of molecular markers for different valuable traits of potato, including resistance to viruses, will be continued. Based on already generated F₁-populations resistant pedigrees will be selected and backcrossed with susceptible *S. pinnatisectum* accessions. Resulting segregating BC₁ pedigrees form the basis to investigate leaf and stem blight resistance and to develop appropriate molecular markers. In addition, wild potato species will be evaluated for resistance to the soft rot causing *Erwinia* spp. A similar programme for carrot is in preparation.

As we expect a further spread of soil-borne cereal viruses, work on evaluation of sources of resistance will be continued in wheat, triticale and rye. Genes of resistance and their inheritance have to be characterised in already identified sources of virus resistance. As resistance to soil-borne viruses can be based on resistance to their vectors corresponding investigations are in preparation.

Furthermore a method for screening genetic resources of asparagus for resistance to viruses is to be developed. As a first step specific antisera are to be prepared.

Development of serological detection methods for different smut pathogens will be continued which should lead to sensitive, reliable and specific test formats for *T. controversa* and *T. indica*.

In the framework of biosafety research transgenic potato plants from field experiments will be used to investigate recombination events among invading PVY isolates.

As well adopted testing methods for sour cherry are now available we can start evaluation work for resistance to *M. laxa*.

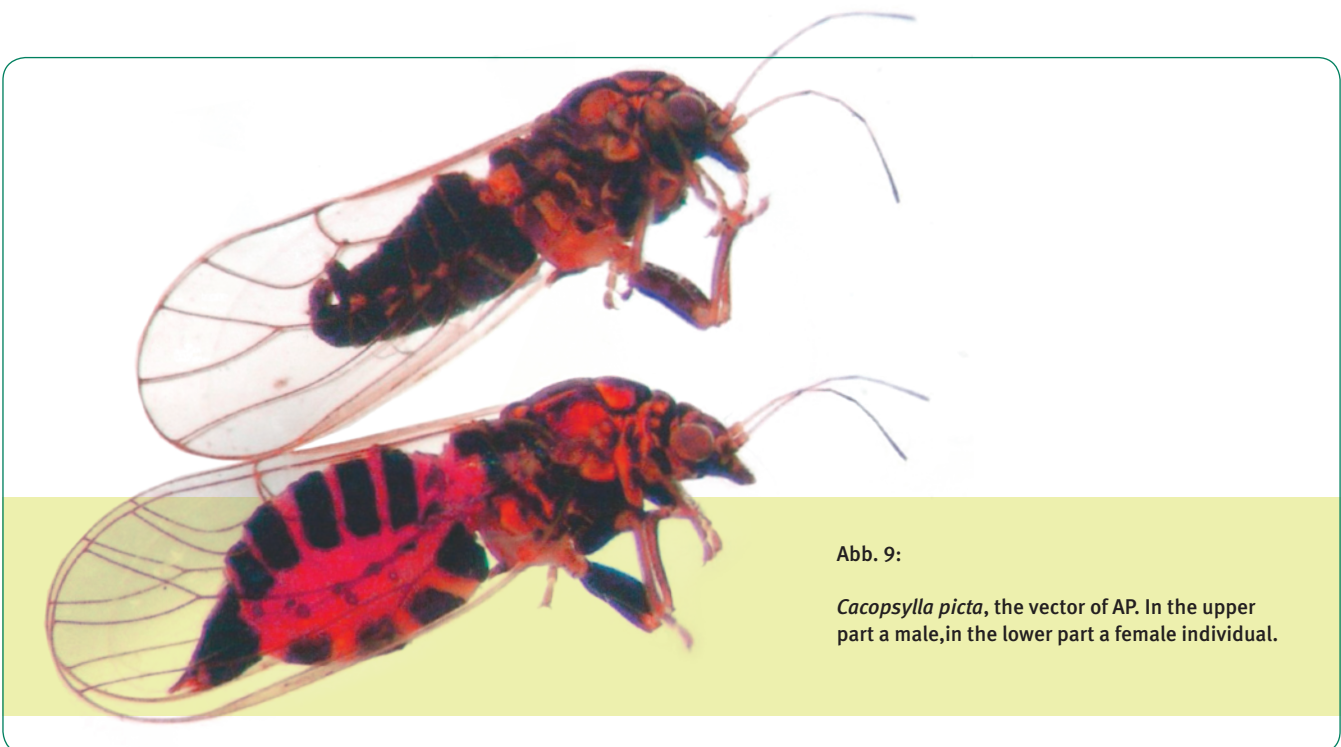
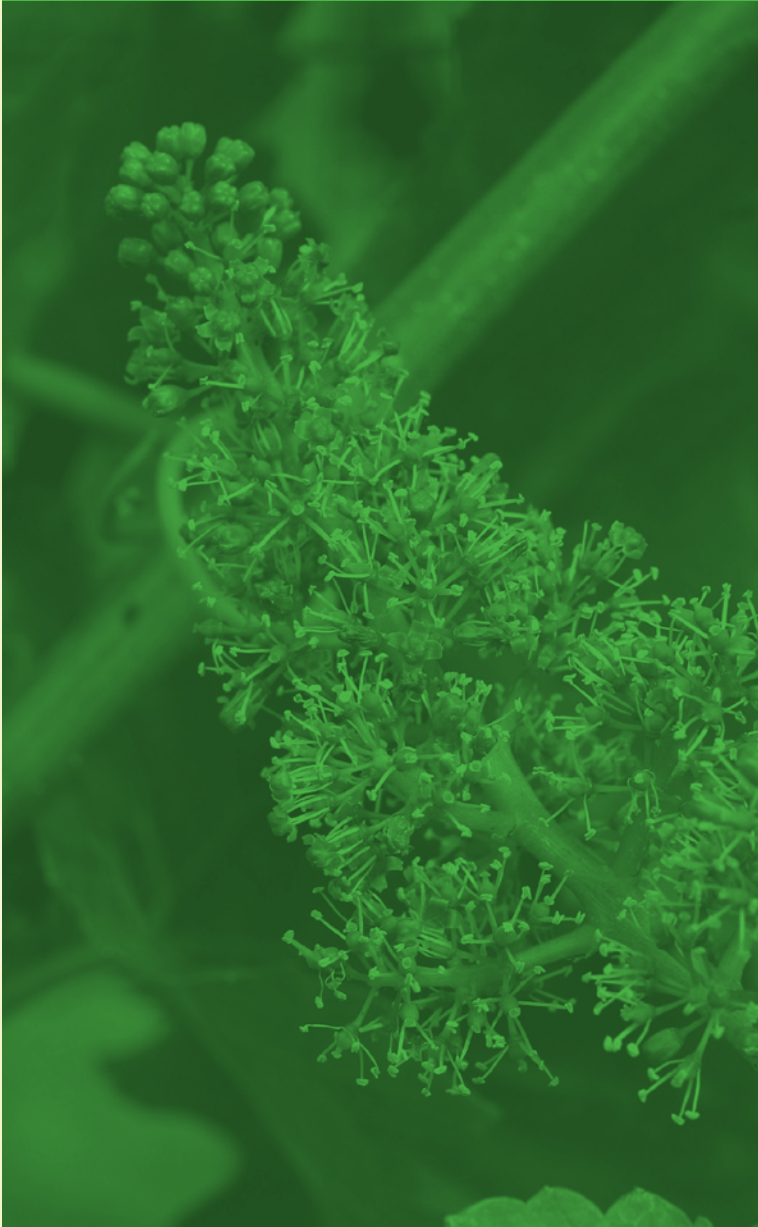


Abb. 9:

Cacopsylla picta, the vector of AP. In the upper part a male, in the lower part a female individual.



Institute
of Grapevine
Breeding
Geilweilerhof

Sieboldingen

Institute of Grapevine Breeding Geilweilerhof

At Geilweilerhof grapevine breeding was started in 1926 when Peter Morio initiated his comprehensive program until 1952. Some of the widespread varieties of today's viticulture, e.g. 'Bacchus' and 'Morio-Muskat', are the results of his breeding efforts. In 1946, Professor Bernhard Husfeld, head of the "Kaiser-Wilhelm-Institute for Grape breeding Research" at Müncheberg, moved to Geilweilerhof and founded the Research Institute for Grapevine Breeding. In 1966, the Federal Ministry of Agriculture became the responsible body for the Institute now called "Federal Research Centre for Grapevine Breeding". Prof. Husfeld continued his activities in breeding phylloxera and Plasmopara resistant varieties with great efforts. His breeding success may be demonstrated by varieties like 'Siegfriedrebe', 'Aris' and 'Pollux'. From 1970 until 1995, Prof. Gerhardt Alleweldt was head of the research centre. He concentrated his breeding activities mainly on fungus diseases putting aside breeding for phylloxera resistance on roots.

Prof. Alleweldt and his team successfully bred new resistant quality grapevines like 'Phoenix' and 'Regent'. For its valuable contribution the Institute for Grapevine Breeding Geilweilerhof received the "Umweltpreis der Stadt Landau" (award for environmental care) in 1996.

In 1991, the institute was merged with the "Federal Research Centre for Horticultural Plant Breeding" in Ahrensburg. In the course of reunification in Germany, the Federal Centre for Breeding Research on Cultivated Plants was created with its head quarter in Quedlinburg. In 1994, the Institute for Grapevine Breeding Geilweilerhof became a member of this Centre.

Regardless of its success grapevine breeding has the task to develop new varieties with high resistance to pest and diseases, to abiotic stress factors (e.g. drought), as well as a highly esteemed wine quality. Grapevine breeding makes continuously use of new scientific findings in particular molecular biological techniques improving breeding efficiency. Therefore, selection methods are being developed for early diagnosis of resistance factors, to parasites, and climatic stress factors as well as aroma- and taste-specific compounds. Additionally, genetical and physical maps of grapevine genomes are developed. The use of gene technology is investigated and genetic resources of grapevine are collected, maintained and evaluated.

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biochemist (PhD student)

Further activities are indexing and abstracting of the word-wide scientific literature which is stored in the literature database VITIS-VEA (<http://vitis-vea.zadi.de>). Furthermore, the international journal “VITIS – Journal of Grapevine Research” (since 1957) and the technical review “Informationsdienst praxisbezogener Literatur im Weinbau” are published. The Institute for Grapevine Breeding also offers positions for apprenticeships for grape growers and wine makers as well as positions for diploma, theses and dissertations.

■ Application of marker-assisted selection (MAS) to pyramid resistance genes in new grapevine cultivars.

The use of molecular markers is becoming more and more important for breeding purposes. This is particularly relevant for polygenic traits such as resistance against the mildews in grapevine. From the breeding point of view it is highly desired to combine as much resistance genes as possible in a new cultivar in order to make resistance as sustainable as possible. Based only on phenotypical evaluation data it is hardly feasible to determine the accumulation of resistance genes in a new breeding line. The use of molecular markers provides a new tool for grapevine breeders and may help to overcome this problem.

The practical application of pyramiding resistance genes by the use of molecular markers was investigated in a progeny derived from the cross of *VHR 3082-1-42* x ‘Regent’. *VHR 3082-1-42* is a cross between *Muscadinia rotundifolia* x *V. vinifera*, backcrossed another four times with *V. vinifera*. It carries a gene which is called *Run1*-gene and which causes resistance to powdery mildew. Furthermore it carries another gene (*Rpv1*-gene) which is related to the resistance against downy mildew. Both genes were introduced from *Muscadinia rotundifolia*. ‘Regent’ is a new cultivar with a high level of resistance against downy and powdery mildew developed at the Institute for Grapevine Breeding Geilweilerhof and released in Germany in 1996 for commercial growing.

119 individuals of the progeny were screened with a molecular marker for the *Run1*-gene and with two markers for the *Rpv1*-gene. They were further screened with several markers which in former investigations have proven to be highly correlated with the downy and powdery mildew resistance of ‘Regent’.

Phenotypical evaluation for downy mildew resistance was done by artificial inoculation of leaf discs (Fig. 1) and for powdery mildew by natural infection in a greenhouse (Fig. 2). Comparison of the phenotypical data with the data revealed by the application of the molecular markers showed a clear correlation between the degree of resistance and the presence of the resistance related alleles. According to the phenotypical data 20 genotypes of the offspring did



Fig. 1: Artificial inoculation with downy mildew in leaf disc assays using few leaf discs per genotype (columns). Levels from left to right, left column: no infestation, right column: strong infestation.



Fig. 2: Natural infection with powdery mildew on premature berries. Left: cluster of a susceptible genotype, right: cluster of a resistant genotype

not show any powdery and downy mildew infection. Based on a marker assisted evaluation out of these 20 genotypes a subset of four genotypes carried all the resistance related alleles for powdery and downy mildew indicating that the resistance genes from both parents are pyramided.

Since marker assisted selection is still labour- and cost-intensive, a combined scheme of phenotypical and genetical selection is proposed. Fig. 3 clarifies the procedure of such a combined selection procedure applied to the investigated population as an example. In the first step the selection of downy mildew resistance can be executed rather easily by artificial inoculation of the seedlings with spores of downy mildew. In a second screening step those seedlings showing no infections are subjected to powdery mildew inoculation. Only the remaining seedlings without infections of downy and powdery mildew are processed for marker assisted selection. In the example demonstrated in Fig. 3 these are 20 seedlings which is around 15% of the initial seedling

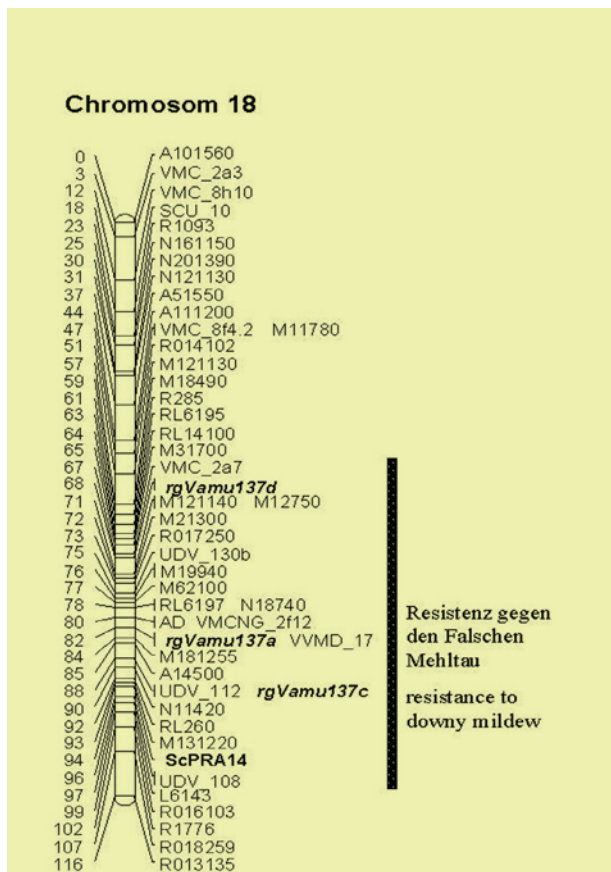


Fig. 3: Presentation of chromosome 18 from the integrated 'Regent' x 'Lemberger' genetic map. The bar to the right indicates the area of resistance to downy mildew. This region contains markers designated *rgVamu* 137a, -c and -d, which are derived from resistance gene analogs. ScPRA14 is a marker especially developed for downy mildew resistance (Akkurt and Zyprian, in prep.).

population. After the following marker assisted selection steps four seedlings can be identified having, as already mentioned, the whole set of powdery and downy mildew related alleles of both parents.

Genetically analysing several segregating populations of grapevine

The research team is genetically analysing several segregating populations of grapevine permitting to follow the segregation of factors promoting resistance to fungal pathogens and other agronomically important traits. Such efforts aim at the localization of resistance factors on the chromosomes of grapevine as a prerequisite to study the underlying genes on molecular level. In addition, small molecular markers from the resistance regions of the genome serve as tools for breeding allowing to follow the introduction and combination of resistance genes from diverse resources in new crosses.

'Regent'

This fungal disease resistant cultivar has already been characterized on genetic level. The progeny of a cross with the susceptible genotype 'Lemberger' has been studied with a variety of molecular markers that were assigned to each of the 2 x 19 chromosomes of both parental grapes. An integrated genetic map has been constructed. This map contains a high number of microsatellite markers enabling to compare mapping data from other crosses as they are well transferable between different grapevine genotypes. An internationally approved nomenclature has been developed based on microsatellite markers. This harmonization allows to validate and integrate results of different crosses and different research teams around the world.

The marker profiles of progeny plants can be studied in conjunction with their inherited traits such as mildew resistances. Employing the genetic map and biostatistic approaches (QTL analysis, quantitative trait loci location) permits the identification of individual chromosomes that carry factors/genes affecting the expression of the trait under investigation. In this way chromosome 15 of 'Regent' has been shown to carry a region with resistance factors to powdery mildew (*Erysiphe necator*, syn. *Uncinula necator*). Resistance to downy mildew (*Plasmopara viticola*) has been found on chromosomes 18 and 5. The biostatistic analysis has recently been refined and is based on five years of resistance evaluations in the field.

Interestingly, the region of downy mildew resistance on chromosome 18 of 'Regent' includes markers derived from resistance gene analogs (Fig. 3). These will be further characterized in the near future to check their functional relevance for resistance. They can be found similarly in other grapevine cultivars and breeding lines that are studied in comparison to 'Regent' (see below).

Besides the investigation of pathogen resistance traits the 'Regent' x 'Lemberger' progeny has also been used to study the inheritance of leaf morphology characteristics and fruit coloration (anthocyanins) as important quality trait.

Based on the powdery mildew resistance identified on chromosome 15, physical mapping of this genomic region has been initiated. Linked molecular markers have been used to identify corresponding BAC clones from a comprehensive library (BACs are artificial bacterial chromosomes serving as vectors and allowing to propagate fragments of grapevine genomic DNA in laboratory strains of *Escherichia coli* bacteria). Marker-positive BAC clones have been sequenced at their ends (and a few almost to completion). This information is used to design new molecular markers to identify the next overlapping BACs in the library (Fig. 4). In this way and consecutive steps a complete set of BAC clones covering the resistance region will be identified. It will contain the contiguous DNA stretch covering that

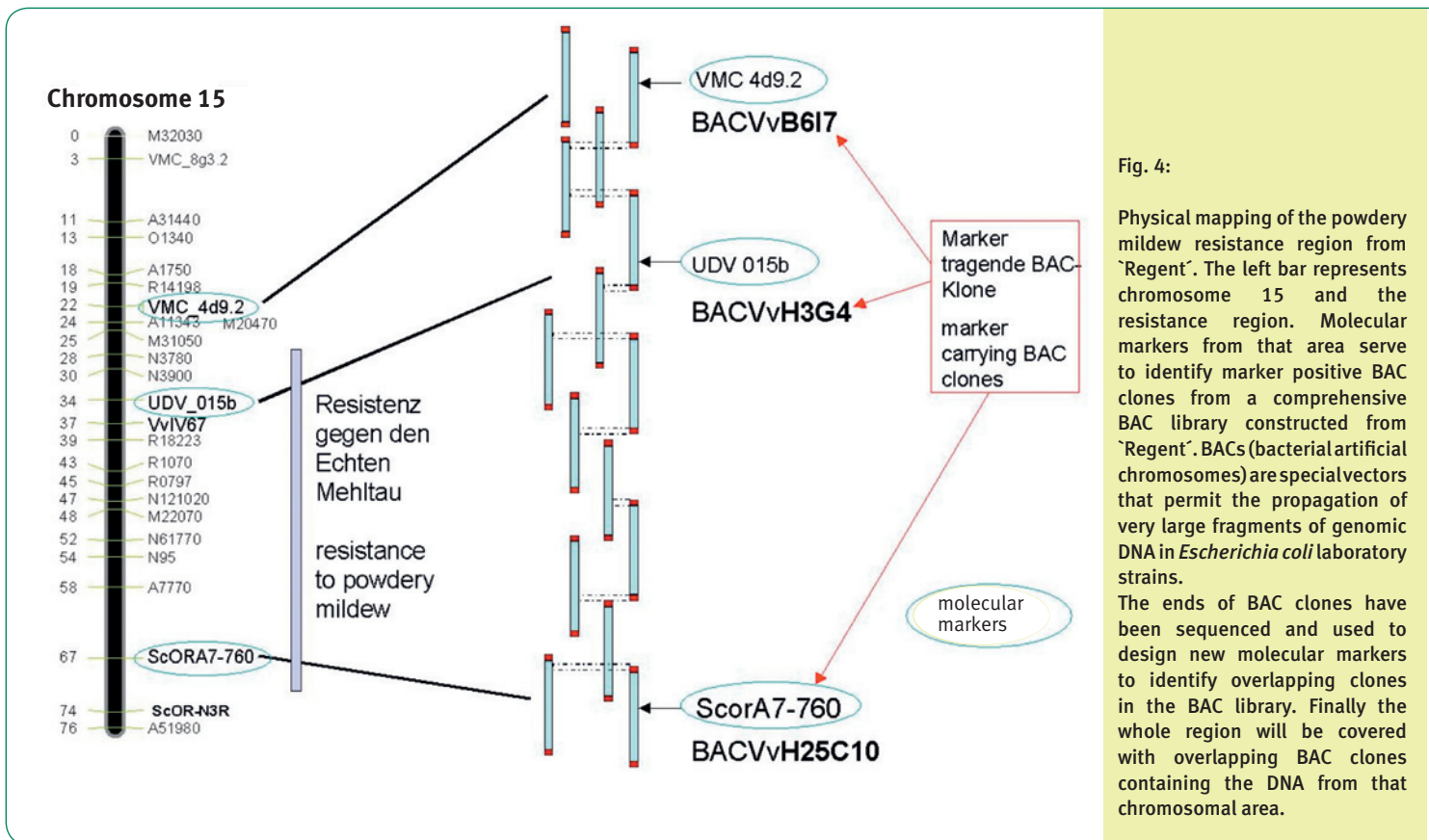


Fig. 4: Physical mapping of the powdery mildew resistance region from 'Regent'. The left bar represents chromosome 15 and the resistance region. Molecular markers from that area serve to identify marker positive BAC clones from a comprehensive BAC library constructed from 'Regent'. BACs (bacterial artificial chromosomes) are special vectors that permit the propagation of very large fragments of genomic DNA in *Escherichia coli* laboratory strains. The ends of BAC clones have been sequenced and used to design new molecular markers to identify overlapping clones in the BAC library. Finally the whole region will be covered with overlapping BAC clones containing the DNA from that chromosomal area.

region for molecular analysis. Its sequence will be analysed by bioinformatics and compared to gene bank data bases to identify putative resistance genes. These efforts also try to exploit the information released through recent grape genome sequencing programs operating in France and Italy. A collaborator has been hosted by IASMA San Michele in the frame of COST action 858 Viticulture (directed by Prof. Serge Delrot, Bordeaux) for four weeks. This exchange and the possibility to utilize data from the almost complete genome sequence of 'Pinot noir' has demonstrated clear differences between 'Regent' and other susceptible *Vitis vinifera* genotypes in the genomic region of resistance. Resistance genes may not only be identified through genetic mapping and map-based cloning, but also through gene expression studies. To this purpose the total mixture of active gene copies (mRNA) from a defined stage after fungal attack is isolated from a resistant and a susceptible grapevine. This mix can be hybridized to high density filters or chips carrying molecular probes of known grapevine genes (14.000 currently represented on commercial chips) to identify the genes activated during the defense response. This experiment has been done in the past with 'Regent' and susceptible 'Chardonnay' challenged with powdery mildew. The results list a set of 100 genes quickly activated in 'Regent' but not activated or to much lesser extent in 'Chardonnay' during powdery mildew attack.

Based on their putative functions, a set of 22 genes has then been selected from the list as candidates to validate their differential activity. This is performed through quantitative real time PCR techniques, a method allowing to determine the relative amounts of gene copies by following their increase as amplification product during polymerase chain reaction (PCR). This technique could be established in the year 2006 in the research team (Fig. 5). A set of 12 genes has already been analysed, a set of further 10 is currently under analysis. An additional set of 12 genes should be investigated during the coming year. Validated candidate genes will be applied as molecular markers for genetic mapping. A co-localisation with the powdery mildew resistance region will support their functional relevance during the defense response.

■ **Localisation of resistance factors in Gf.Ga.47-42 and 'Villard blanc'**

The breeding line Gf.Ga.47-42 and the old French hybrid 'Villard blanc' are both grapevine genotypes with natural resistance to powdery and downy mildew. They have been investigated in comparison to 'Regent'. They were crossed and 141 progeny plants employed to develop a genetic map based on their molecular marker profiles. A previous map has been detailed recently by integration of microsatellite-derived and RGA (resistance gene analogs) markers.

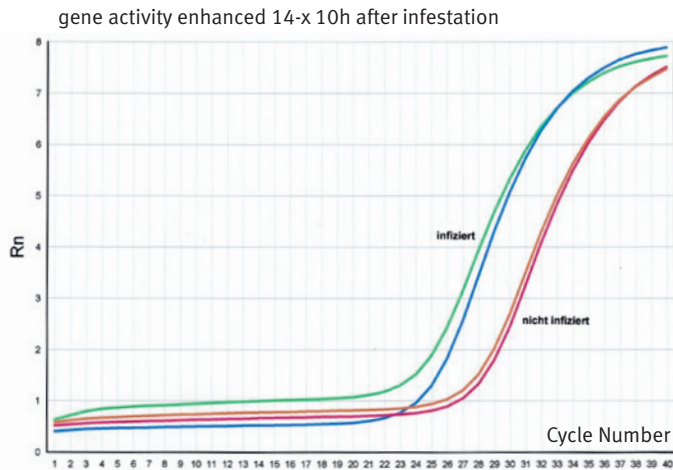


Fig. 5: Presentation of Real-Time PCR. Amplification plot demonstrating the amplification of a resistance gene analog from 'Regent' in real time PCR. Blue/green and light/dark brown give the amplification curves for the two biological replications of 'Regent' inoculated and not inoculated with powdery mildew (*Erysiphe necator*), respectively. Rn is the ratio of fluorescence emission intensity of the reporter dye (SYBR Green) to the fluorescence emission intensity of the reference dye (ROX). Cycle number is the number of DNA synthesis cycles run.

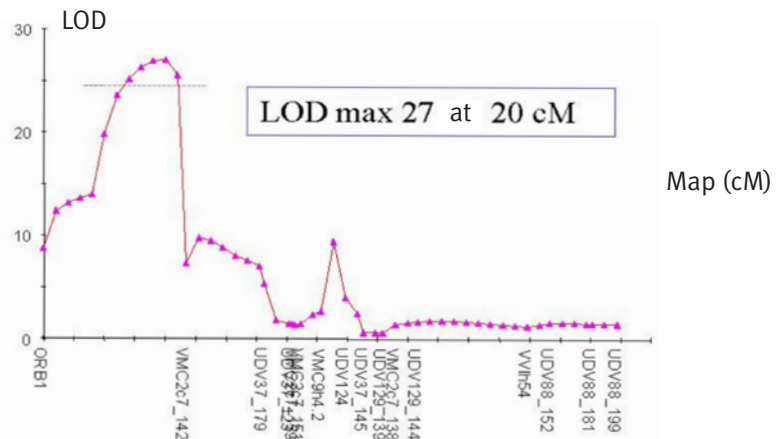


Fig. 6: QTL analysis (MQM mapping) of Phylloxera resistance from 'Börner'. Chromosome 13 from the genetic mapping study is shown on the bottom with the qualitative trait ORB (without Phylloxera infestation) positioned at one end of the chromosome. The chromosome has been scanned for its probability to contain a segregating factor influencing resistance versus the probability not to carry such a resistance factor as expressed in LOD scores (LOD, logarithm of the odds) and shown in the probability curve. The scan shows a highly likely position for an area of resistance extending from position 14 to 23.5 cM located roughly in the same area as the qualitative trait.

Currently, 212 mostly highly informative molecular markers are assigned to the 19 chromosomes with high statistical stringency (formerly used less informative markers have been disregarded in this mapping). The average marker distance is 4.76 cM (centi Morgan, a genetic unit corresponding to 1% of recombination frequency). The chromosomes were numbered according to the international agreement.

The progeny of this cross has been evaluated concerning their resistance to fungal diseases for several years. Data reporting the resistance of individual plants to powdery mildew are available from 1999, 2000, 2003, 2004 and 2005. Resistance to downy mildew has been scored in 1999, 2000, 2003 and 2004. The scores were used for QTL analysis. The unusual climate encountered in 2003 however affected the use of data from this and the following year.

The results indicate the position of resistance factors to downy mildew on chromosome 18 (in agreement with the findings from 'Regent'), but the same or a closely neighbouring region seems to be responsible also for resistance to powdery mildew (contrasting results obtained from 'Regent'). Interestingly, again this region contains a clustering of markers derived from resistance gene analogs. The meaning of this has to be investigated by further characterization of the corresponding marker fragments.

Besides the major region on chromosome 18, several other regions of probably lower significance have been identified. In cooperation with Dr. Sabine Wiedemann-Merdingöglu (INRA Colmar) leaf disc assays have been performed with progeny plants to observe the different levels of infestation after experimental infection with downy mildew. These efforts aim at the development of fast and reliable screening methods for resistance. Checking of their agreement with field data and computation of responsible resistance factors is currently performed.

'Börner'

The rootstock cultivar 'Börner' possesses characteristics of high relevance for breeding: It shows resistance to phylloxera at its roots in addition to powdery and downy mildew resistances. To investigate these characteristics, 'Börner' has been crossed as pollen donor to the completely susceptible breeding line V3125. The progeny of 188 individual plants segregates for the resistance traits allowing to genetically map and analyse the position of resistance traits by QTL analysis. To this purpose, 178 microsatellite markers were employed to construct a first genetic map. Resistance to phylloxera has first been characterized as a simple qualitative trait scoring the absence or presence of phylloxera infestation at the roots

of test plants experimentally infected in the greenhouse. The trait mapped to the terminus of chromosome 13 (Fig. 6). In the year 2006, a more detailed analysis was performed by counting the number of nodosities (tissue swellings caused by the insects) at vegetatively triplicated test plants maintained in the greenhouse. The following QTL analysis indicated again the terminal region of chromosome 13 as chromosomal location of relevant factors (Fig. 6). In order to analyze this region on a molecular level (by map-based cloning) it is necessary to flank it from both sides with molecular markers. Only in this case, the markers can be applied usefully to screen a BAC library from 'Börner' available at the Institute. For this reason, there has been a new effort undertaken to map informative markers and find some flanking the trait from both sides. A set of 151 microsatellite markers was screened for informative segregation in a subset of the progeny. A selected set of 40 highly informative markers is currently being mapped over the complete population of 188 plants.

■ CoreGrapeGene Project

How wild grapevines can improve quality of life

Due to ecological and economical reasons the breeding of fungus resistant high quality grapevines is of major importance in grape breeding. Mildew diseases are the most threatening. A new approach to elucidate the relationship between valued traits and the putatively responsible candidate genes is studied in grapevine through an association study since the year 2005 at the Institute for Grapevine Breeding Geilweilerhof.

In the frame of the trilateral project CoreGrapeGene based on a French-Spanish-German cooperation barely studied grapevines from the worldwide genepool possessing important characteristics were characterized by molecular markers. European grapevine repositories represent valuable genetic resources. There is a need to characterize wild grapevines to exploit them for resistance breeding in combination with best fruit quality as the cultivars of *Vitis vinifera* do not possess any mildew resistances.

North-American e.g. (*V. labrusca*, *V. riparia*) and one Asian *Vitis* wild species (*V. amurensis*) are best suited to improve resistance to mildew pathogens as they show natural resistance. Evaluation data for resistance to mildew have been collected in the Institutes germplasm repository for several years. Based on these phenotypic data, 357 *Vitis* accessions comprising fungus-resistant grapevines were selected and investigated for genetic variability by analyzing genetic variation at 20 simple sequence repeat (SSR) loci. These data will be used to construct a *Vitis* „Core“ set. A „Core“-set comprises of few individuals that represents most of the genetic variability within a species. Within the

genotype set studied at Siebeldingen a very high genetic variability was observed. The resistance donors included in the sample set were investigated by pedigree studies showing 15 different resistance sources combined in 38 different ways.

Based on both the phenotypic and genotypic data a European *Vitis* core set will be selected by maximizing genetic diversity and phenotypic traits and minimizing number of individuals.

Based on the genetic data, a core set of 135 *Vitis* genotypes from the primary *Vitis* genotype set of 357 comprises 99% of the genetic diversity (Fig. 7). For the analysis of mutations a smaller core set based on both genetic as well as phenotypic traits and the putative origins of resistance will be constructed.

Candidate genes for mildew resistance on grapevine were chosen by homology studies with *Arabidopsis thaliana* - the model organism for dicots - and are currently analysed for homologues in grapevine and their sequence variation. Knowledge of the extent of nucleotide diversity in relationship to the expression of resistance traits can subsequently be collected by analysing the distribution of mutations within the 135 individuals "Core"-set. Thus, the first molecularly characterized *Vitis* "Core"-Collection represents a valuable tool with respect to the extended use of the existing *Vitis* gene pool.

■ New programming and further development of the local working database and the Internet database for grapes

Since 1984 the Institute of Grapevine Breeding Geilweilerhof is registering the grapevine cultivars, wild species and new crosses, maintained worldwide in grapevine collections and / or described in literature in a database (*Vitis* International Variety Catalogue (VIVC)). Of over 23.000 registered genotypes passport data are available. Since 2004, in collaboration with the IT-department in Quedlinburg, a complete new database is developed linking characterisation and evaluation data, pictures, herbarium specimen, area of distribution, breeder to the cultivar specific passport data. A concise layout and links facilitate data retrieval, data processing and entry. Results of database queries can be displayed as a list and pedigree construction will be available. In parallel, the database was updated with literature and information from germplasm repositories, e.g. in the scope of an IPGRI coordinated project on conservation and sustainable use of the grape genetic resources in the Caucasus and Northern Black Sea region. From the 1300 autochthonous varieties of those regions, 40% had not yet been registered in the VIVC. Nearly 100% of the grapevine diversity to be found over there are preserved only in Eastern European grapevine repositories. A high percentage of the varieties are female

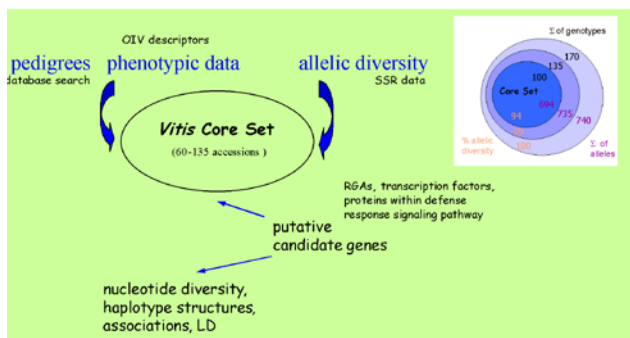


Fig. 7: Construction of a *Vitis* core set based on phenotypic traits and allelic richness. Different core sizes corresponding to their number of observed alleles and allelic richness (740 allele lengths) are shown in a close-up.

and hence may be closely related to the Caucasian wild grape (Fig. 8).

A subset of this database with multiple search options will be published on the internet addressing curators, scientists, breeders, winemakers and wine enthusiasts. The replacement of “*Vitis* International Variety Catalogue” [2] (<http://www.genres.de/idb/vitis>) by this new database is scheduled for 2007.

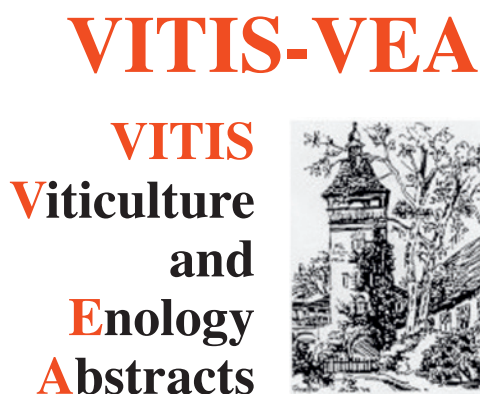
■ Documentation of Viticultural Research

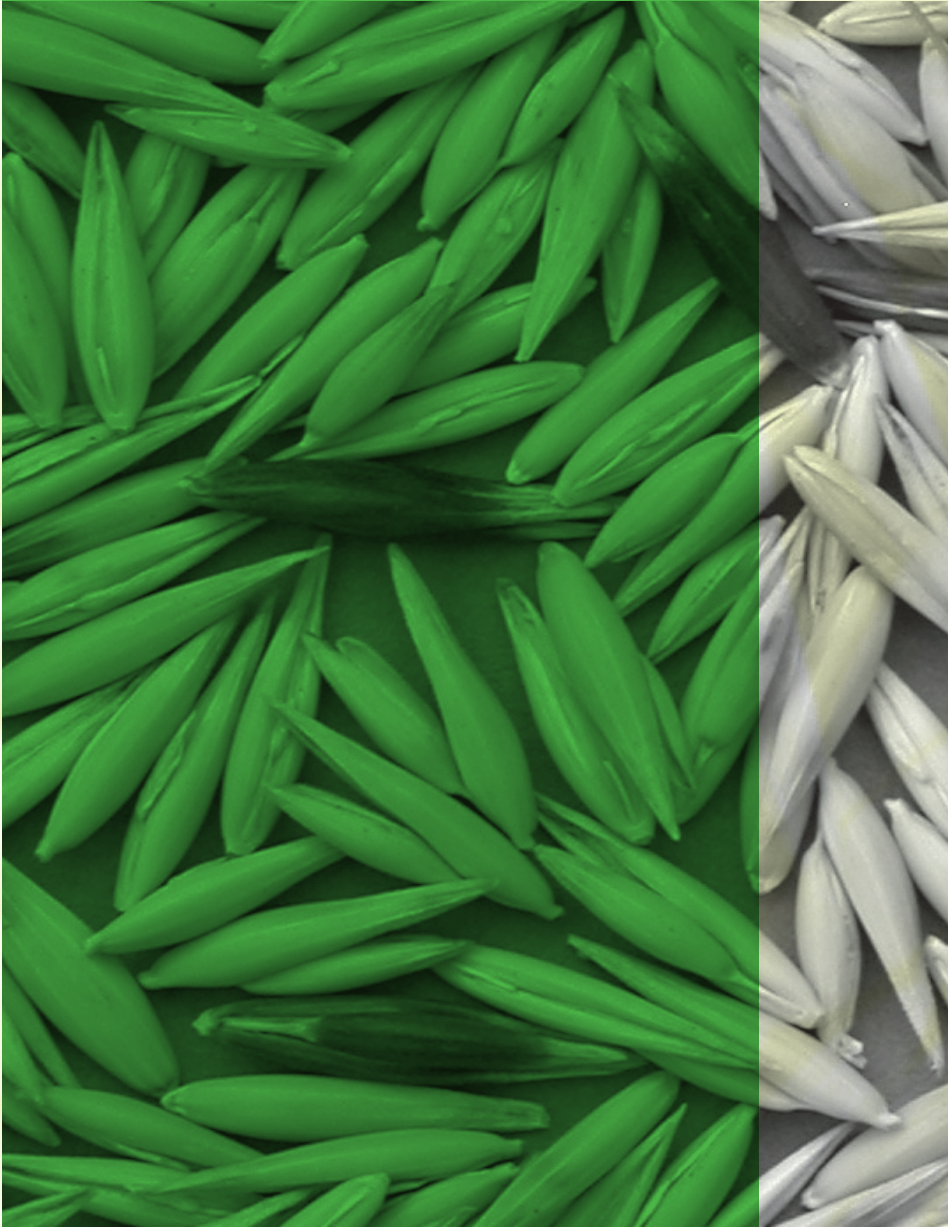
The specialised library of Geilweilerhof Institute is amongst the largest of its kind world wide. Publications in the field of vine and wine add up to the hundreds of periodicals, conference proceedings or individual papers in one of the thousands of international publications per month. The department for Documentation of Viticultural Research has evaluated and archived this knowledge in the fields

of viticulture, oenology, breeding and breeding research for almost 40 years and made it publically accessible. This knowledge database VITIS-VEA [Fig. 9] with at present almost 53,000 accessions is available on the internet at <http://vitis-vea.zadi.de>. The electronic conversion of back-issues of the periodical VITIS – Journal of Grapevine Research, published at Geilweilerhof, has been completed. Full texts as PDF-files of the years 1957–1969 will be uploaded shortly. The whole archive of the journal will therefore be available in a contemporary way on the net. One year after publication of the last issue of a volume, these contents will be appended. Links are provided to full texts of open access journals. In order to save resources, links to abstracts on the internet are provided for publications in border topics of the database like medicine and for works on wine analysis rather than producing own abstracts.

Fig. 8: Male wild grape from Azerbaijan. Photo M. Amanov, Azerbaijan

Fig. 9: Logo of the database VITIS-VEA on its homepage <http://vitis-vea.zadi.de>





Research and
Coordination Centre
for Plant Genetic
Resources

Quedlinburg

Research and Coordination Centre for Plant Genetic Resources

For good reasons, the discussion on plant genetic resources for food and agriculture becomes more important in species protection, as this sector of biodiversity is of essential importance for the food production and for the production of raw materials for industrial purposes. Inter- and intraspecific diversity is a prerequisite for agricultural production well adapted to local conditions. The development of cultivars with specific adaptation to the production conditions of a region as well as to the continuously changing technical and economical framework conditions is not possible without intraspecific diversity. The required genetic diversity is being stored deep-frozen in *ex situ* collections of plant genetic resources, however, above all novel diversity evolves both in the natural habitat of the species and in the traditional, rural agriculture within the centers of diversity. In the highly sophisticated agriculture of Germany based on division of labour the selection fields of commercial plant breeders or in the public breeding research sector can be considered likewise as the natural habitat of domesticated species, where genetic diversity is created and maintained.

Not only wild plant species are threatened by genetic erosion, but also cultivated forms, the production of which was abandoned for diverse reasons in favour of new cultivars. The storage of reproductive plant parts or seed in genebanks is one possibility to maintain threatened plant genetic diversity. A sustainable maintenance of genetic diversity, however, is only possible by the protection of the natural habitats of wild plant species or, with crop plants, by the organisation of a very diverse agricultural production. Merely that way a continuous evolution of plant genetic resources can be guaranteed.

The loss of genetic resources for food and agriculture has not yet been registered by the public as a global problem as are the possible consequences of the global climate change. Notwithstanding the environmental policy has taken a number of important decisions in the past decades and has provided strategies and work programmes aiming at the reduction of the species' loss rate. The Federal Republic of Germany, represented by the Ministry of Food, Agriculture and Consumer Protection (BMELV), is responsible for the development of strategies for the maintenance of genetic resources for food and agriculture as well as for the organisation of adequate legal and regulatory structures

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Management of plant genetic resources

based on scientific knowledge derived from plant genetic science. As concerns the BAZ, operations are based on the International Treaty on Plant Genetic Resources for Food and Agriculture of 29th June 2005 as well as the Convention of Biodiversity dating back to the year 1993. At the national level, plant genetic research in the BAZ is based on the sustainability strategy of the federal government and, above all, on the agrobiodiversity strategy of the BMELV. By prioritising the biodiversity and genetic resources themes in its concept for innovative research BMELV recognises the increasing need for actions and research within its own research sector.

After the abandoning of the plant genetic resources collection of the BAZ, branch office Braunschweig, by the BMELV as well as the relocation of the staff, the working group continues to fulfil its research and coordination tasks in the field of plant genetic resources at Quedlinburg. The group represents the BAZ in the following working groups and advisory boards:

- Advisory board for biodiversity and genetic resources at the BMELV
- Senate working group for biodiversity
- BMELV advisory and coordination committee for genetic resources of agricultural and horticultural crops
- Genebank advisory board of the IPK
- Networks and working groups of the European Program for Plant Genetic Resources Networks (ECPGR)
- Member of the Crop Wild Relative Specialist Group of the IUCN Species Survival Commission

The work of the Research and Coordination Centre of PGR aligns with the need of the BMELV for advice and decision support and encompasses the following fields:

- Management of plant genetic resources *in situ* and on farm
- Organisation the European and international cooperation in this field
- Acquisition and documentation of data on plant genetic resources

■ National

The National Expert Program for the Maintenance and Sustainable Use of Plant Genetic Resources of Agricultural and Horticultural Crops serves the implementation of international agreements at the national level. For that purpose a diversity of individual measures are necessary amongst which is the development of monitoring and management concepts. Genetic diversity in agricultural production systems can be increased or decreased by regulatory interventions of the state. National inventories of plant genetic resources as well as monitoring programmes are required to be able to assess effects of changed legal framework conditions, such as the planned amendment of the seed marketing regulations with the possible acceptance of so-called conservation varieties, on the maintenance and deployment of genetic diversity in agriculture. The establishment of monitoring programmes in the field of biodiversity also arises from the obligation to collaborate constructively with the Organisation for Economic Co-operation and Development (OECD).

The OECD and the European Environment Agency (EEA) currently use the indicator “genetic diversity” (IRENA 25) to map genetic diversity deployed in agriculture. BMELV charged the BAZ and the Information and Coordination Centre for Biodiversity (BLE-IBV) with the assessment of this indicator and with the development of a concept for genetic monitoring in agricultural crops and crop wild relatives. For that purpose literature was reviewed with the following result: IRENA 25 can readily be generated from existing data files and is suited for general reporting purposes. The indicator does not allow quantifiable conclusions on genetic distances between cultivars. Furthermore a qualification of genetic distances between cultivars is possible for very few major cash crops only. Even if IRENA 25 is qualified through genetic information, the indicator would still be no useful instrument for shaping policy as the deployment of cultivars can be governed in a free market economy to a very limited extent only. It is therefore proposed to use the “crop species diversity” as indicator in addition to IRENA 25. The species diversity in crop production can be influenced by the recently launched innovation programme or similar incentive systems more effectively than the choice of cultivars by farmers.

Genetic monitoring in the strict sense requires genetic analysis and should be scheduled particularly where the state can indeed govern safeguarding and sustainable use of plant genetic resources: in genebanks, in plant breeding

research and in species protection. These three public sectors are responsible for the safeguarding of gene pools of crops and their related wild species. The development of an indicator scheme for genetic monitoring in agricultural genetic resources through the plant genetic sector following the scheme for genetic monitoring in forestry has highest priority.



Fig. 1: The ECPGR working group on Beta determines the genetic erosion threat status of a population of *B. procumbens*. As a source of strong resistance genes, among inter alia the resistance to the beet cyst nematode (*Heterodera schachtii*), the wild species is of great significance for sugar beet breeding.

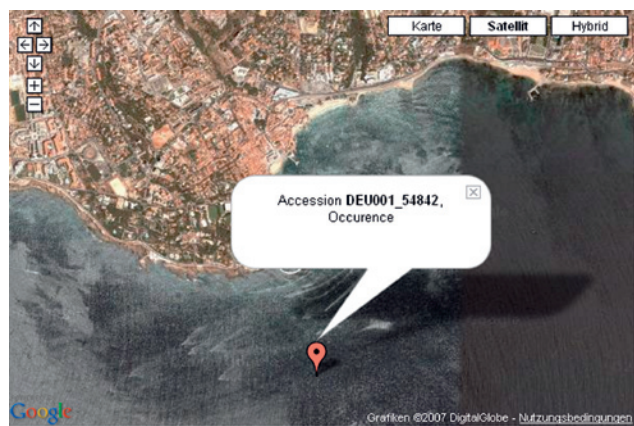


Fig. 2: Specific types of cytoplasmic male sterile forms of *B. vulgaris* subsp. *maritima* are distributed along the cost line „Boca do Inferno“ close to Lisboa. Using the International Data Base for Beta (IDBB) collecting sites can be mapped. In the long run monitoring procedures are to be developed for the management of plant genetic resources allowing conclusions from changes in the landscape features on the integrity of those wild populations known as important genetic resources for breeding.

■ Europe

Since the establishment of the European Programme for Plant Genetic Resources Networks (ECPGR) in the year 1979 German institutions have been collaborating with this pan-european organisation. The programme of the ECPGR is financed by the member states and is governed by a steering committee. Amongst others partner institutions operate approximately 52 central crop specific databases. The ECPGR sustains working groups that are organised in networks. The Research and Coordination Centre of PGR chairs the Sugar, Starch and Fibre Crops Network as well as the *Beta* working group of this network.

A working group meeting from 8-11 March 2006 of the ECPGR *Beta* working group was organised in collaboration of the Botanic Garden of Teneriffa and the ECPGR secretariat. The focus was set on in situ management issues. The management of species and populations in situ requires multidisciplinary approaches and in the case of a genus widely distributed in Europe collaboration of institutions at the national, regional and local level, whereby exchange of data and information between all levels plays a prominent role. The in situ management demands a combination of species, populations and sites related decisions. Hence, cooperation with the nature protection organisations is absolutely needed. The working group addressed the question why, how and where genetic resources of the genus *Beta* should be maintained in situ. The working group

- developed principles for the prioritisation of species
- evaluated at the site descriptors for the assessment of the threat status of populations (Fig. 1)
- discussed the role of the International Data Base for *Beta* (IDBB) and possible legal problems arising from the documentation and publication of national data from in situ management measures in an international database (Fig. 2).

■ International

Responsibilities distributed over numerous institutions hinder measures aiming at the maintenance of plant genetic resources not only in Europe but also at the international level. The ECPGR implemented a case study titled “A European Genebank Integrated System (AEGIS)” in cooperation with the former BAZ Gene Bank. The project aims at the establishment of a coherent European system for plant genetic resources for food and agriculture similar to the US-American National Plant Genetic Resources System (NPGS) of the USDA/ARS. Expertise gained in AEGIS is used by the Global Crop Diversity Trust for the development of global crop specific conservation strategies for species listed on Annex I of the



Fig. 3: Oat – an internationally important species, listed on Annex I of the Treaty.



Fig. 4: Geographic origin of *Beta* – accessions with data on Rizomania resistance were plotted using the WebService Google Map. Green= resistant, red= susceptible.

Treaty. In cooperation with the most important experts in oat genetic resources and many collection curators, the Research and Coordination Centre of PGR currently undertakes an inventory of global collections holdings. The identification of the most important subgroups of genetic diversity of the genus *Avena* in these holdings is an aim of the study. According to fixed criteria the Trust intends to support the maintenance of collections based on the study. The acquisition of information was almost completed in the year 2006 and first results were discussed during an expert meeting at Fargo (USA) in July 2006. The study will be accomplished after a meeting in March 2007 at St. Petersburg and submitted to the Trust in May 2007.

Information management

■ ECPGR databases

Plant genetic resources form a subset of biodiversity. Biodiversity is the product of complex interactions between the three levels: the habitat diversity, the species diversity and the diversity within species. Data on plant genetic resources show a correspondingly complex structure. The European and international crop specific databases are particularly suited to management of information on plant genetic resources, as they can best map the real world in crop specific data models in high resolution. The International Data Base for *Beta* (IDBB) at the Research and Coordination Centre of PGR contains geographic data as well data on the diversity of species within the genus and data on intraspecific diversity, mainly characterisation and evaluation data. During 2006 the IDBB was extended by a Geographic Information System Module. The module allows the visualisation of the geographic structure of trait variation on maps. The extension does not only improve

the service function of the IDBB for external users but also serves the development of data base structures, required to record and provide data on *in situ* management measures.

■ Contribution to data management within the BAZ

During the past six years the Research and Coordination Centre of PGR facilitated proceedings of the BAZ data management working group composed of members of all BAZ institutes. The working group aims at the reduction of deficits in the field of deployment of database technologies within the BAZ. The considerable constitutionally determined short-comings, affecting the efficiency of political advice on the one hand and the cooperation of the BAZ in national and international information networks in the field of biodiversity science on the other hand, are to be removed stepwise. For that purpose the BMELV provided additional funds that were used to elaborate a concept for the development of software technologies as well as for the development of a Laboratory Information and Management System (LIMS) for molecular biology. A report on the central communication platform for data management within the decentrally organised BAZ was already established in the year 2005. Software development tools which were investigated then were considered in a more comprehensive concept outlined in paragraph "Perspective".

The prototype of the LIMS was tested with real data in Groß Lüsewitz in the year 2006, resulting in new or altered specifications of the requirements, and the LIMS was adapted accordingly. The system was planned as a web application. Right from the beginning it was developed towards Java EE5 to allow for future changes in technologies.

Java EE5 was not available as an accomplished component at the start of the project. Therefore the LIMS was constructed based on components shown in Fig. 5, for EJB3 was not

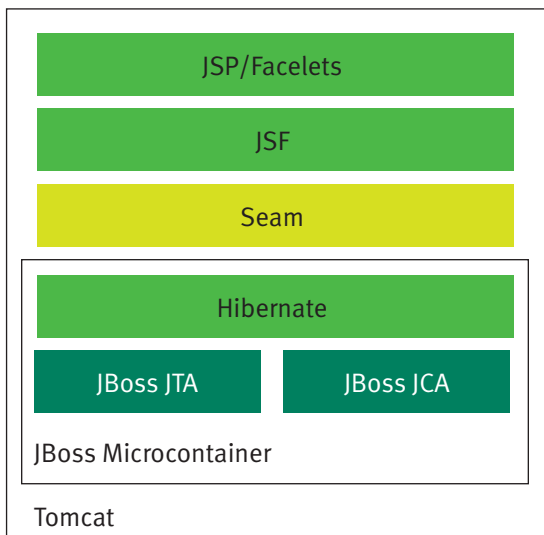


Fig. 5: Components used for the development of the LIMS.

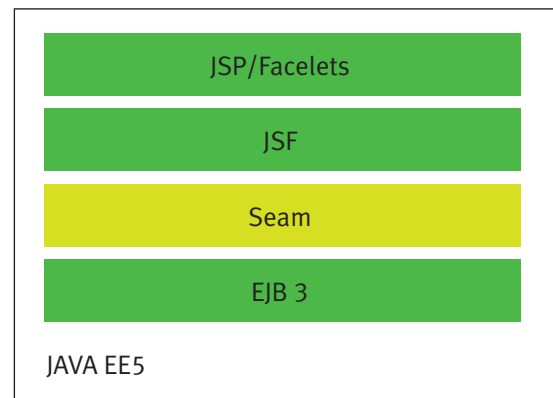


Fig. 6: Components in the JEE5 frame-

yet available then. Components displayed in Fig. 5, however, made a great leap forward in development. As newer versions of the applied components with extended size of functions became available, they could replace the out-dated ones. The investment in time related to the necessary adaptations proved to be very advantageous for the LIMS which from then onward could be better adapted to the users' requirements and it clearly gained stability. The following graphs were taken from the JBoss SEAM documentation.

According to the current state of the art the application could be converted following Fig. 6. This, however, would not help to improve the functionalities. Only the complexity of the application is shifted to other areas, for Hibernate is encapsulated in the JBoss EJB3 container. It is recommended to apply the EJB3 container for the development of new applications in future thereby reducing the complexity of the application structure according to Fig. 6. The familiarisation is reduced as EJB3 needs to be apprehended only once, whereby the Hibernate-interface triggers expenses for each application development.

The current SAGA-Standard Version 3.0 classifies JEE5 as "under observation". As JEE5 entails massive simplifications regarding the deployed technologies and the programming methodologies, it is particularly suited for the development of new applications. In the next SAGA-version JEE5 will at least be classified as "recommended". Moreover, it should be born in mind that Java version 6 is the currently recommended standard and that JEE6 is already being forged. Hence, JEE5 is already to be considered as established standard for new applications.

In the meanwhile sufficient literature is available for the development of applications based on JEE5. The training on the job for JEE5 is far less than the training of J2EE.

Developers knowing J2EE do have a higher threshold level for JEE5 compared to those developers starting without prior knowledge. Popular keywords such as Service Oriented Architecture (SOA) can be implemented with JEE5 without the known administrative overhead of J2EE. The use of further techniques, such as work flow modelling, opens additional productivity sources. Fig. 7 shows how an application flow can be modelled. Graphs used in Fig. 5 to 7 were taken from the JBoss SEAM documentation.

At the end of the project, the LIMS will be on hand in a version allowing a general use in the scope of molecular biological laboratories. Basic modules have been created giving a start for an effective management of molecular data according to the current requirements of the BAZ. The targeted standardisation of molecular biological methods and work flows will be met with the application of the LIMS. A solution has been found for the BAZ, allowing adaptations of the application after the end of the temporarily limited project.

Perspective

In the year 2006, the working group received grants for the coordination of two projects financed by the EU council regulation AGRI GENRES 870/2004. Both projects will shape the work of the Research and Coordination Centre of PGR until the year 2010. The project "An integrated European *In Situ* Management Workplan: Implementing Genetic Reserves and On Farm Concepts" (AEGRO) pursues similar aims as set for the *ex situ* management in AEGIS. AEGRO partners will investigate how *in situ* management projects for plant genetic resources can be tuned and coordinated with nature preservation programmes.

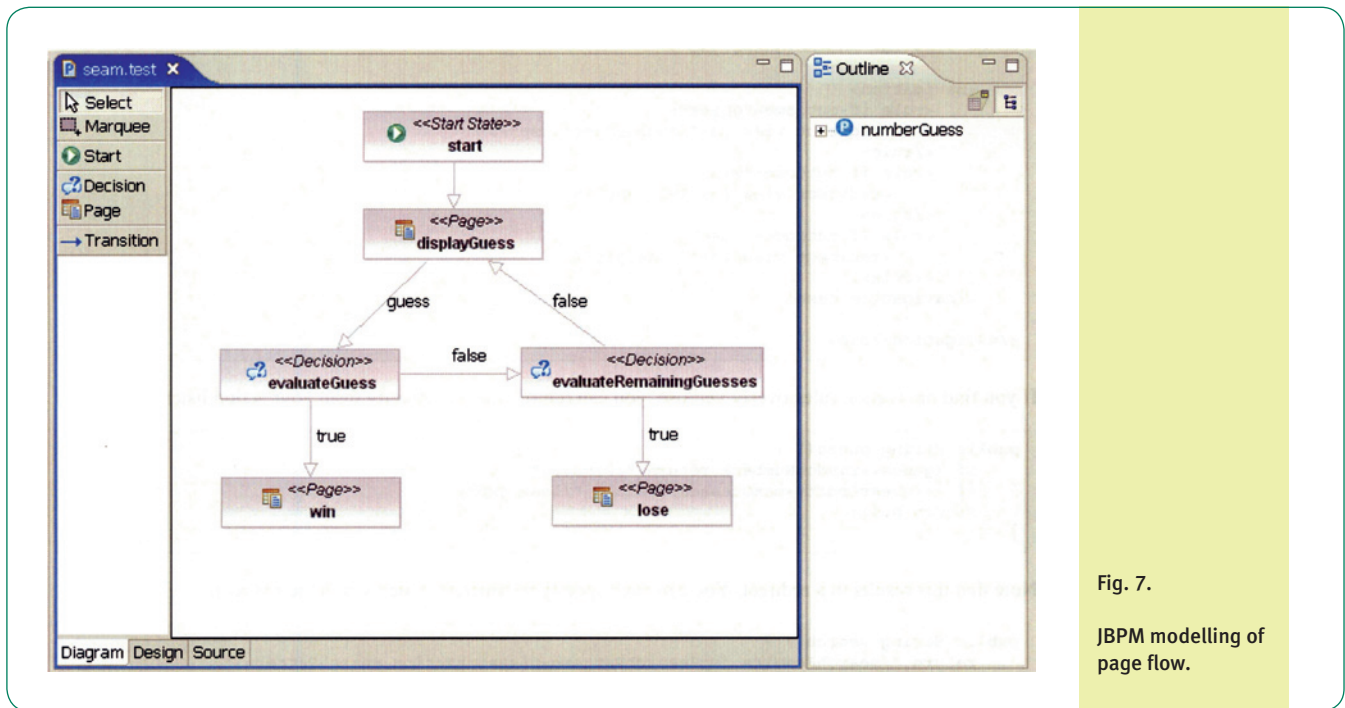


Fig. 7.

JBPM modelling of page flow.

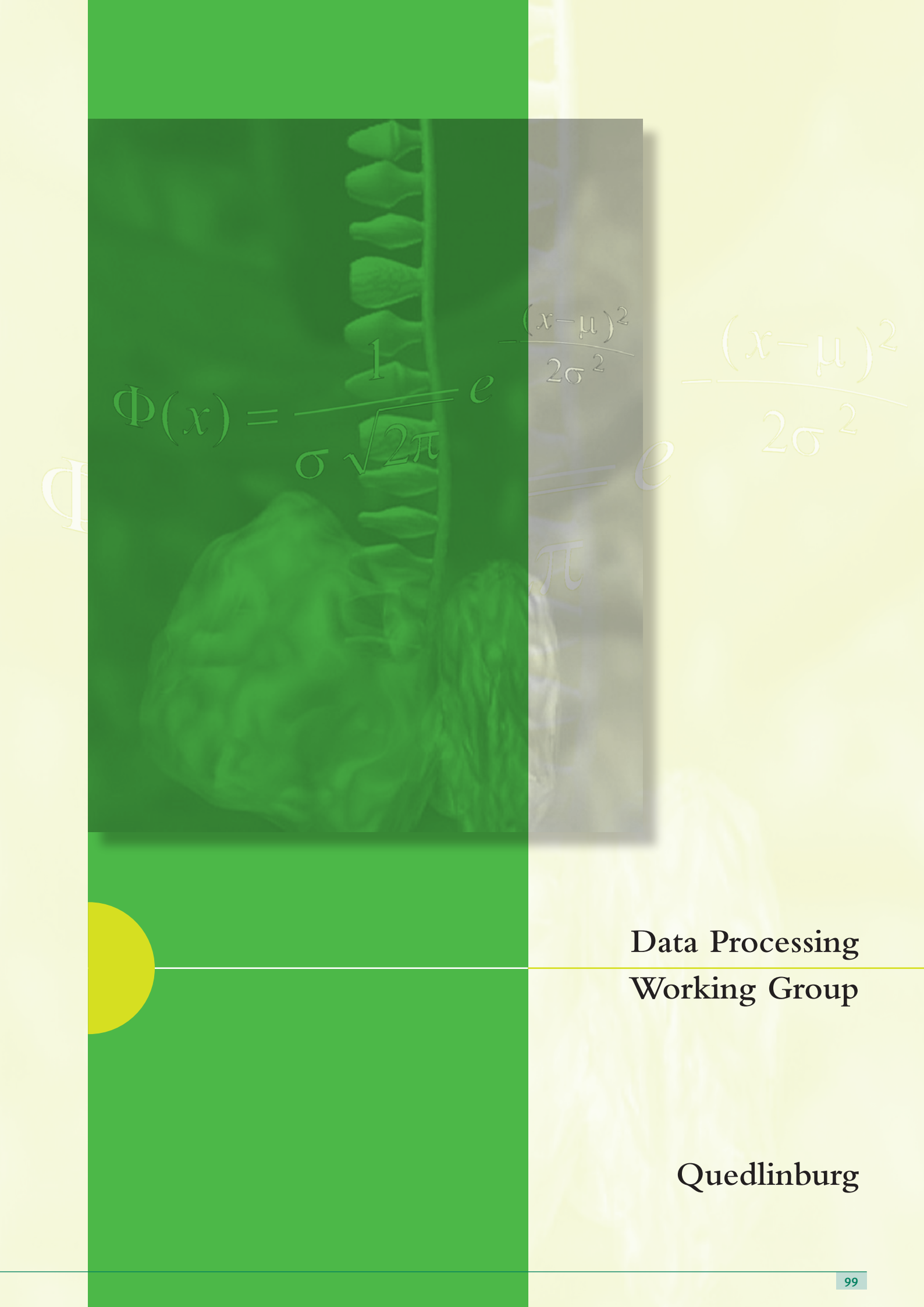
According to chapter 5.1 “*In situ* maintenance, monitoring and development of the national expert programme for plant genetic resources”, answers to these very questions are required by the BMELV as well.

The second project „Oat genetic resources for quality in human consumption“ (AVEQ) serves the characterisation and evaluation of genetic resources of the genus *Avena*. It is a consequent continuation of the EU project GENRES CT99-106. In that project the former BAZ Gene Bank has been responsible for the acquisition and provision of data via the European *Avena* Data Base (EADB). The project fits well in the existing research activities at the Institute of Agricultural Crops of the BAZ being one of the project partners. The BAZ gains further profile with this project and still ongoing works on the Global Oat Conservation Strategy and could qualify on this basis within the framework of the AEGIS process as a European expert centre for genetics and genetic resources of the genus *Avena*.

Article 12 (4) of the „Treaty“ makes arrangements that facilitated access to plant genetic resources is guaranteed within the framework of the Multilateral System (MLS) based on a standardised Material Transfer Agreement (sMTA). The sMTA was passed in June 2006 and is to be applied by the BMELV research sector. The recipient of materials provides the MLS via an information system all non-confidential information arising from research on the material. From this follows an additional obligation for judicious recording, documentation and provision of research data particularly in the plant genetic research sector of the BMELV.

In addition, the Federal Republic of Germany has to pass on all data generated under the regime of the sMTA via a central national interface to the information system of the MLS. Hence, next to scientific reasons arising from the growing

demand in genome research for precise phenotypic data on genetic resources, legal and political obligations are calling for the improvement and extension of suitable information systems. This challenge needs to be addressed by the future Federal Research Institute for Crop Plants, Julius-Kühne-Institute (JKI). The BMELV charged therefore the central IT-group of the BAZ and the Research and Coordination Centre of PGR with the elaboration of a concept for a national information system for characterisation and evaluation data (NICE-D) and the organisation of a workshop on NICE-D in the year 2007 with the participation of institutions that generate and use data on plant genetic resources. The year 2007 will therefore be determined by the start of both EU-projects. Furthermore our tasks and responsibilities as research and coordination centre for plant genetic resources within the JKI need to be clarified.


$$\Phi(x) = \frac{1}{\sigma \sqrt{2\pi}} e^{-\frac{(x-\mu)^2}{2\sigma^2}}$$

Data Processing
Working Group

Quedlinburg

Data Processing Working Group

Tasks of the work group

Participation in research projects of BAZ institutes with main focus on data management and software development as well as biometrics were again the fields of emphasis in the scientific work of the IT-group in 2006.

It is recognised by the scientists of all BAZ institutes that information technology (IT) is an essential key to the success in research. The IT-group in BAZ sees its input in this field as part of its overall responsibility. In addition to operating all networks and systems the IT-group has to work on the following duties.

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■ Data management

In close cooperation with BAZ scientists, the group develops software solutions for the handling of scientific data. As part of a system analysis, it is tried to find a universal and modular method that addresses research issues in response to the user's specific requirements. The IT-group addresses this task from a more overall point of view, independently from the institutes. This approach allows the group to develop a universal system for data management which minimizes redundant data and can be applied for all kinds of reporting, presentation and editing.

The working group „data management“, in which the IT-group is actively involved, is the centre for all such communications in BAZ.

■ Biometrics

This range of duties starts with the organisation of biometrical advanced training and ends with the support in solving biometrical problems faced by scientists in the institutes.

The head of the IT-group is an active member of the biometrics work group, which is affiliated to the Senate of Federal Research Centres.

Because of the soaring need of involvement in the field of „data management“ it is more and more a problem to solve biometric problems with the existing IT-personnel.

■ Bioinformatics – management of biomolecular data

Up to now tasks in this field, in most cases, could not be taken over by the IT-group. But biomolecular data as a special kind of scientific data are handled in many data management projects.

Establishment of biomolecular methods in IT will be a key activity in the near future.

In the reporting period the capacities of the IT-group were heavily tied up by preparation and moving to the new BAZ site in Quedlinburg. Assembling the new and high-grade IT-equipment at the new location made high demands on the personnel. Many systems of new quality were installed with high complexity for adjustment and training.

This investment in the future will be paid off in short time if, as planned in the near future, a national information system for characterisation and evaluation data on plant genetic resources (NICE-D) can be established in Quedlinburg.

Research results

In addition to the maintenance and further development of existing software solutions such as the EVA-System for evaluation data of plant genetic resources (BAZ project

9002) and the Plant Data Storage (BAZ project 9004/1), the main focus was on the development of the documentation system „Vitis International Variety Catalogue“.

■ Individual projects - 9005

Design and implementation of the database „gbvitis“ as well as the client application „gbvitis“ for editing descriptive data were the main task of software development in the IT-group in 2006.

The task is structured into the following subtasks:

1. Design of the data model
2. Implementation of the database and data import
3. Development of a client application to edit data
4. Enhancement of the client application with search modules and integration of evaluation data.
5. Development of an Internet application for database search

Subtasks 1, 2 and 3 are realized. The database was launched to productive system after importing all data. With the contribution of a software developer in Siebeldingen, an online search module has been developed. The final launch is planned in 2007. For this task, a daily adjustment with a slave database in Quedlinburg has been established. This data mirroring is an additional measure of data backup as well.

● Data model

The data model of „gbvitis“ was basically relaunched. The entities (tables) with evaluation data were removed since they turned out to be too specific and inflexible for several experiments in future. A new idea was implemented instead. Therefore the user is now able to create a lot of experimental designs without changing the data model. The new tables introduced are named with the prefix „eva_“ – a synonym for evaluation data. They can be used with other databases in future.

● Implementation of database and data import

Based on the data model the database „gbvitis“ was implemented on a MySQL database server. After checking of all data in the Institute of Grapevine Breeding in Siebeldingen they were imported.

● Development of a client application for data editing

The client application „gbvitis“ is relaunched in version 0.3-12 and works in the productive mode. Therewith the scientists in Siebeldingen are able to edit all passport data of the international Vitis variety catalogue. For special editing of the Siebeldingen assortment a separate module was created (see Fig. 2).

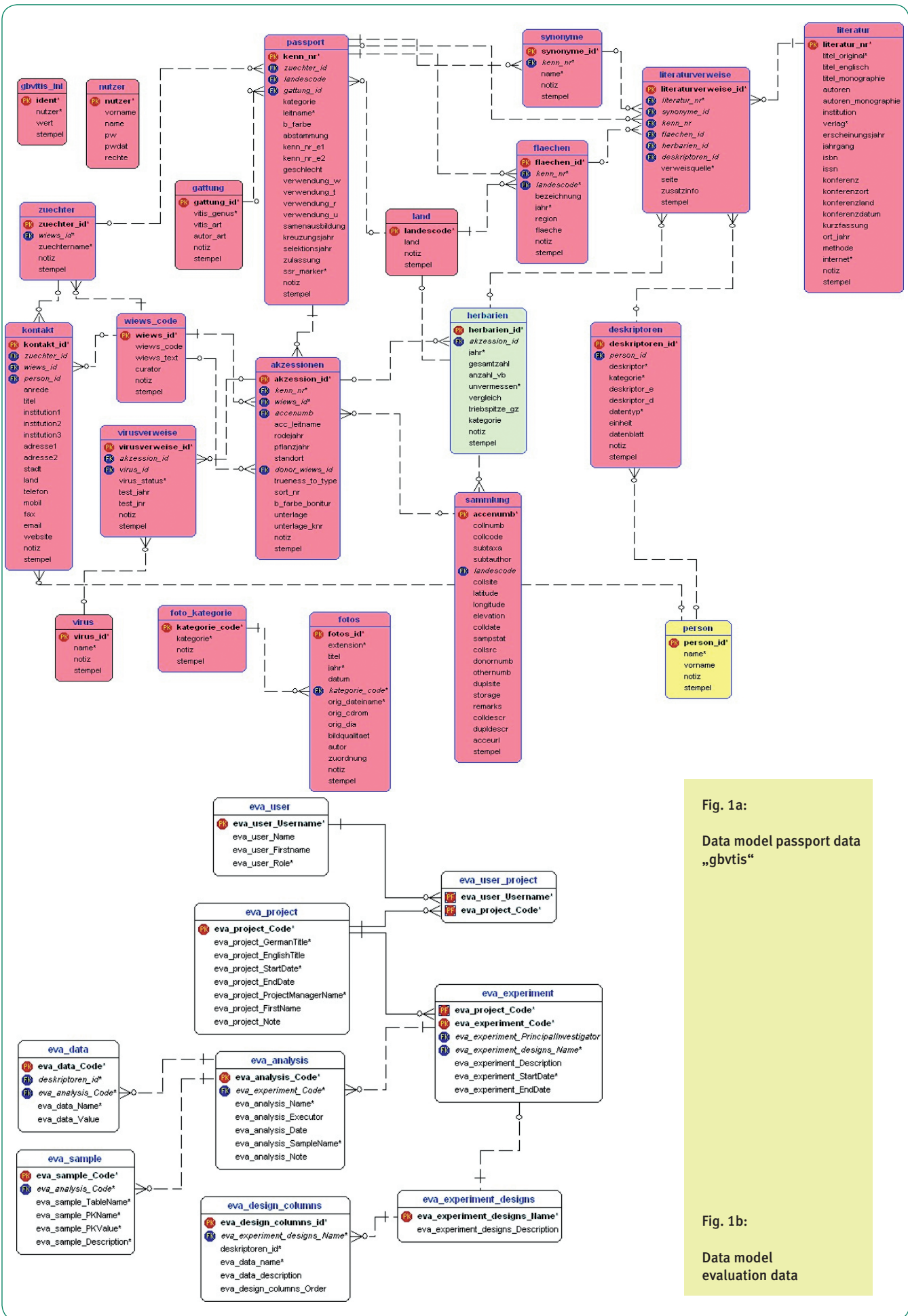


Fig. 1a:
Data model passport data
„gbvtis“

Fig. 1b:
Data model
evaluation data

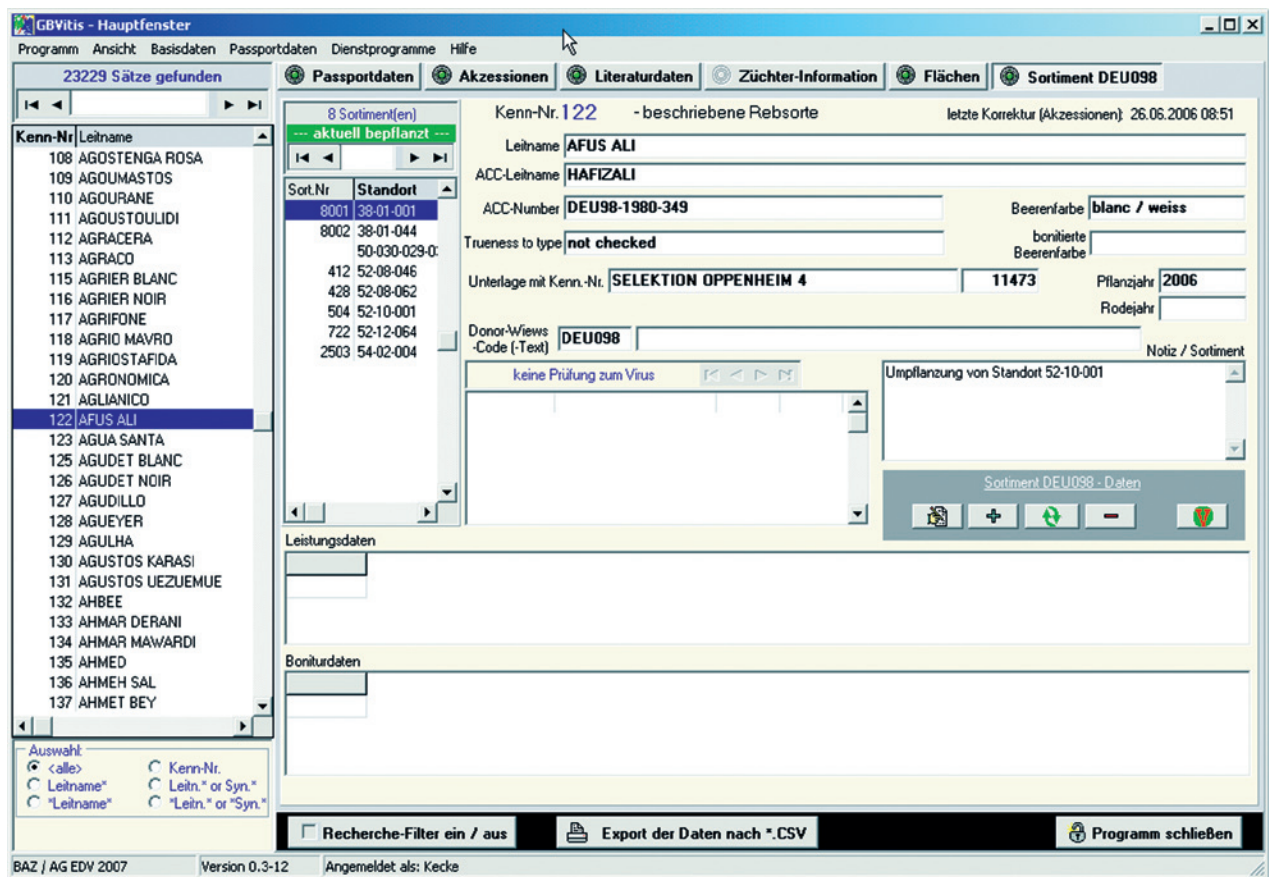


Fig. 2: Client application „gbvitis“ - assortment DEU098

Development of an Internet application for data investigation

The development of an Internet browser application for data investigation in the catalogue has been based on PHP. Here the user has access to some biomolecular data, too.

Future research objectives

The implementation of a modular documentation system integrating most of the existing solutions will be the main challenge for the IT-group. The next module to be developed is the fruit genebank database in the Institute of Fruit Breeding in Dresden-Pillnitz. The aim is a maximum of reusability of software modules developed before.

The object model of universal handling of evaluation data has to be enhanced to use it for existing solutions like „Vitis International Variety Catalogue“, „Plant Data Storage“ and others. In this context the integration of biomolecular data becomes important.

With the establishment of the „Julius-Kühn Federal Research Institute of Cultivated Plants“ the research objectives of the IT-group will be revised with the aim to have a reliable base for personnel planning in the near future because the current staff capacities are too small to meet all challenges. After having completed the establishment of the planned documentation systems and new development strategies in the near future, the scientific analysis of data with biometrical and other methods will become the key activity of the IT-group's scientific work.

III. Publications

Scientific Publications

■ Institute of Fruit Breeding Dresden

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- SCHUSTER, M.: Stand der Züchtung von Süßkirschen. 16. Obstbautag des Landesverbandes Gartenbau Brandenburg, Landesfachgruppe Obstbau. 31.01.2006, Großbeeren, lecture
- SCHUSTER, M.: Fragen zur Fertilität bei Sauerkirschen. Kolloquium Institut für Pflanzenzüchtung u. Pflanzenschutz, Landwirtschaftliche Fakultät, Martin-Luther-Universität Halle, 24.05.2006, Halle, lecture
- SCHUSTER, M.: Süß- und Sauerkirschzüchtung. Tagung Fachgruppe Obstbau des Bundesverbandes Obst und Gemüse, 23.05.2006, Dresden, lecture
- SCHUSTER, M.: S-Allel-Bestimmung bei Süß- und Sauerkirschen. Tagung AK Steinobst, 05.06.2006, Stade, lecture
- SCHUSTER, M.: Züchtung von Sauerkirschen. Landesgartenschau Sachsen, Juli bis August 2006, Oschatz, poster
- SCHUSTER, M.: Züchtung von Süßkirschen. Landesgartenschau Sachsen, Juli bis August 2006, Oschatz, poster

- SCHUSTER, M.: Stand der Züchtung von Süßkirschen. Kolloquium Kompetenzzentrum Obstbau Bodensee, 19.-20.08.2006, Ravensburg, lecture
- SCHUSTER, M.: Aktueller Stand der Süßkirschen. Bundesarbeitstagung der Fachberater im Obstbau, 01.-03.11.2006, Grünberg, lecture
- SCHUSTER, M.; WOLFRAM, B.: Untersuchungen zur Fertilität bei Sauerkirschen. 8. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
- SCHUSTER, M.; WOLFRAM, B.: Fragen zur Fertilität bei Sauerkirschen, *Prunus cerasus* L. 32. Bundesseminar Steinobst, 28.-30.11.2006, Ahrweiler, lecture
- SCHUSTER, M.; ZAKOSTELECKY, A.: Baumveredelung am Beispiel von Kirschbäumen. Int. Grüne Woche 2006, 13.01.2006, Berlin, poster
- SCHUSTER, M.; ZAKOSTELECKY, A.: Warum müssen wir Obstbäume veredeln? Lange Nacht der Wissenschaften der Stadt Dresden, 30.06.2006, Dresden, poster
- STRISSEL, T.; HALBWIRTH, H.; MILCEVICOVA, R.; PEIL, A.; HANKE, M.-V.; RICHTER, K.; WILHELM, E.; STICH, K.; TREUTTER, D.: Untersuchung des Phenylpropanoidgehaltes von Apfelwildarten und unterschiedlichen schorfanfälligen Sorten. 43. Gartenbauwiss. Tagung, 22.-25.02.2006, Potsdam, poster
- SZANKOWSKI, I.; GESSLER, C.; SANSAVINI, S.; TARTARINI, S.; PATOCCHI, A.; FLACHOWSKY, H.; HANKE, M.-V.; FISCHER, T.; FORKMANN, G.; TREUTTER, D.: Genetic engineering of apple and pear. COST Action 864 "Pome Fruit Health Research in Europe – Current Status 2006", Combined Meeting of Work Groups 1-4, 20.-21.11.2006, Vienna, Austria, poster
- ULRICH, D.; OLBRICHT, K.; ROUDEILLAC, P.: Inheritance of bioactive terpenoid compounds in *Fragaria*. 1st Joint Meeting of WGI and WG4, Genetic bases for bioactive compounds affecting human health in berry fruits, 28.-30.09.2006, Barcelona, Spain, lecture
- VITTEN, M.: Zuchtstammentwicklung Erdbeere zur Fruchtverarbeitung in der Gefriertrocknung. MOLDA AG, 10.07.2006, Dahlenburg, lecture
- VITTEN, M.; OLBRICHT, K.: Untersuchungen zur Vererbung der Frucht-Trockenmasse bei Erdbeeren. 43. Gartenbauliche Tagung der Deut. Gartenbauwiss. Gesellschaft, 22.-25.02.2006, Potsdam, lecture and poster
- VITTEN, M.; OLBRICHT, K.: Investigations of dry matter in fruits of *Fragaria* L., 8. GPZ-Vortragstagung, 14.-16.03.2006, Freising-Weihenstephan, lecture
- VITTEN, M.; OLBRICHT, K.; ULRICH, D.; HOBERG, E.; TIEDKE, F.: Quality traits in freeze dried strawberries. 1st Joint Meeting of WGI and WG4, Genetic bases for bioactive compounds affecting human health in berry fruits, 28.-30.09.2006, Barcelona, Spain, poster
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- BÖHME, H.; RUDLOFF, E.; SCHÖNE, F.; HÜTHER, L.; FLACHOWSKY, G.: Nutritional assessment of genetically modified (GM) rapeseed with a changed fatty acid profile. Ges. für Ernährungsphysiologie: 60. Tagung vom 21.-23.03.2006 Göttingen, poster
- DARSOW, U.: Pre-breeding auf *Phytophthora*-Resistenz der Kartoffel – Ergebnisse eines laufenden Langzeitprojekts und Aussichten für den ökologischen Anbau. Vortrags-tagung, Senatsarbeitsgruppe Ökol. Landbau, „Ressort-forschung für den ökologischen Landbau“ FAL Braun-schweig, 02.03.2006, lecture
- DARSOW, U.: EUCABLIGHT- Ergebnisse des EU-Projekts zur Harmonisierung der Phytophthora-Resistenzprüfungen. Wintertagung der AG Kartoffelzüchtung und Pflanzguterzeugung in der GPZ, Göttingen, 22.-23.11.2006, lecture
- DARSOW, U.: Vorzüchtung (pre-breeding) bei der Kartoffel im ILK Groß Lüsewitz der BAZ. Wintertagung der AG Kartoffelzüchtung und Pflanzguterzeugung in der GPZ, Göttingen, 22.-23.11.2006, lecture
- DARSOW, U.; COLON, L.: Results, decisions and stimulations of the Host resistance meeting at Rostock 2005 for the Eucablight project. Final Eucablight Workshop, 23.-25.01.2006, Rennes, France, lecture
- DARSOW, U.; STRAHWALD, J.: Foliage blight resistance after correction of attack to maturity. Final Eucablight Workshop, 23.-25.01.2006, Rennes, France, lecture
- DARSOW, U.; WEHLING, P.: Pre-breeding in potato to combine quantitative resistance to late blight with earliness and fresh-market or processing-quality traits. Potato Europe 2006, 04.-06.09.2006, Hameln, poster
- DARSOW, U.; WEHLING, P.: From wild species to potatoes resistant to *Phytophthora infestans*. Potato Europe 2006, 04.-06.09.2006, Hameln, poster
- HANSEN, J. G.; HERMANSEN, A.; COLON, L. T.; COOKE, D. E. L.; ANDERSSON, B.; NIELSEN, B. J.; DARSOW, U.; BAKONYI, J.; LASSEN P.; LEES, A. K.: "Eucablight - demonstrating new tools for collating and analysing plant pathology data on a European scale. EFPP 13.-17.08.2006 Copenhagen, Denmark, poster
- HACKAUF, B.; WORTMANN, H.; WEHLING, P.: Addressing genomic regions involved in fertilization control in rye: advances and prospects. EUCARPIA-Int. Symp. on Rye Breeding and Genetics, 28.-30.06.2006, Rostock / Groß Lüsewitz, lecture
- HACKAUF, B.; WORTMANN, H.; WEHLING, P.: Nutzung von genomischen Ressourcen aus Reis und Gerste zur gezielten Markierung von Genen der Befruchtungskontrolle bei Roggen. 57. Pflanzenzüchtertagung, 21.-23.11.2006, Gumpenstein, Austria, lecture

- HERRMANN, M.: Virulenzuntersuchung von verschiedenen Flugbrandrassen bei Hafer (*Avena sativa*). 9. Wissenschaftstagung Ökologischer Landbau, 20.-23.03.2006, Hohenheim, poster
- HERRMANN, M.: Widening the genetic base of triticale via crosses with primary triticale. EUCARPIA-Int. Symp. on Rye Breeding and Genetics, 28.-30.06.2006, Rostock / Groß Lüsewitz, poster
- LELLBACH, H.: Züchtungsforschung an Gräsern. Sommer-tagung der Abt. Futterpflanzen der GFP, 25.-26.04.2006, Malchow/Poel, lecture
- ROUX, S. R.; HACKAUF, B.; RUGE, B.; LINZ, A.; WEHLING, P.: Exploitation and comprehensive characterization of leaf-rust resistance in rye. EUCARPIA-Int. Symp. on Rye Breeding and Genetics, 28.-30.06.2006, Rostock / Groß Lüsewitz, lecture
- RUDLOFF, E.: Freisetzung von transgenem Raps - Ergebnisse zur Verfütterung von MCFA-haltigem Rapschrot. Sommertagung der Abt. Öl- und Eiweißpflanzen der GFP, 07.-08.06.2006, Gatersleben, lecture
- RUGE-WEHLING, B.; SONNTAG, K.; RUDLOFF, E.; KUHLMANN, J.; EICKMEYER, F.; WEHLING, P.: Entwicklung und Einsatz innovativer Züchtungsstrategien zur Erhöhung der Anbaubedeutung der Blauen Süßblupine. Innovationsforum: Gewinnung von biofunktionellen Food Ingredients aus Lupinensaat für die Lebensmittelindustrie. 06-07.12.2006, Rostock-Warnemünde, lecture
- RUGE-WEHLING, B.; KUHLMANN, J.; EICKMEYER, F.; WEHLING, P.: Markergestützte Selektion neuer Resistenzen gegenüber Anthraknose bei der Blauen Süßblupine. 6. Heidelberger Lupinentagung, 26.-27.01.2006, Heidelberg, lecture
- SCHOLZ, M.; RUGE-WEHLING, B.; HABEKUSS, A.; SCHRADER, O.; GROSSE, E.; FLATH, K.; WEHLING, P.: Erschließung des sekundären Genpools der Gerste zur Übertragung von Resistenzen gegen Pathogene. 55. Deut. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, lecture
- SCHUBERT, J.; FOMITCHEVA, V.; SZANGRET-WISNIEWSKA, J.; THIEME, R.: Aufklärung der genetischen Struktur von Stämmen des *Potato virus Y* als Voraussetzung für ihren gezielten Einsatz in der Virusresistenzzüchtung bei Kartoffeln. 8. GPZ-Vortragstagung, 14.-16.03.2006, Freising-Weihenstephan, poster
- SONNTAG, K.: Somatic hybridization between *Lupinus angustifolius* and its wild relatives for plant breeding purposes. NAROSSA 2006, 12th Int. Conf. for Renewable Resources and Plant Biotechnology, 12.-13.06.2006, Magdeburg, lecture and poster
- SONNTAG, K.: In vitro breeding of lupins as protein crops. AGRITEC, Plant Biotechnology Department, 20.06.2006, Sumperk, Czech Republic, lecture
- SONNTAG, K.: In-vitro-Kultur bei Lupinen. Arbeitstreffen in Steinach, 10.11.2006, Steinach, lecture
- SONNTAG, K.: Die Blaue Süßblupine - eine neue Kulturpflanze. Mitgliederversammlung - 20 Jahre ADIVK, Forschungsanstalt Geisenheim, 22.09.2006, Geisenheim, lecture
- SONNTAG, K.; RUDLOFF, E.: Modification of oil and meal composition in doubled haploid lines of *Brassica napus* by UV treatment of isolated microspores. Int. Conf. "Haploid in Higher Plants III", 12.-15.02.2005, Vienna, Austria, poster
- SONNTAG, K.; RUGE-WEHLING, B.; RUDLOFF, E.; WEHLING, P.: Development of somatic hybrids between *Lupinus angustifolius* and its wild relatives to improve their agronomic traits. Narossa, 12th Int. Conf. for Renewable Resources and Plant Biotechnology, 12.-13.06.2006, Magdeburg, poster
- THIEME, R.: Erschließung von Wildkartoffelarten als genetische Ressourcen für eine verbesserte Resistenz gegen Pathogene und Schaderreger in der Kartoffelzüchtungsforschung. Arbeitsmeeting, Institut für Pflanzenschutz in Ackerbau und Grünland, BBA, 29.06.2006, Braunschweig, lecture
- THIEME, R.: Screening of incompatible wild potato species as genetic resources for the improvement of resistance to *Phytophthora* and viruses for potato breeding: introduction of basic material produced by biotechnological methods, and test methods for resistance assessment. University of Veszprem, Georgikon Faculty of Agriculture Keszthely, Regional Potato Research Centre, 30.10.2006, Keszthely, Hungary, lecture
- THIEME, R.: Use of biotechnological methods for the transfer of resistance from wild potato species into cultivated potato. Results and prospects. Northwest Agriculture & Forestry University, College of Horticulture, 11.05.2006, Yangling, Shaanxi, China, lecture
- THIEME, R.: Utilization of the resistance to pathogens and pests in wild species of *Solanum* for breeding research of potatoes. Northwest Agriculture & Forestry University, College of Plant Protection, Dept. of Pathology, 15.05.2006 Yangling, Shaanxi, China, lecture
- THIEME, R.; SCHUBERT, M.; NACHTIGALL, M.; HEIMBACH, U.; THIEME, T.: Virus- und Krautfäulere-sistenz bei Nachkommen der Wildart *Solanum tarnii*. Wiss. Konferenz Pflanzenbiotechnologie, IAPTC&B, Sektionen Österreichs, Deutschlands und der Switzerland, 22.-24.03.2006, Vienna, Austria, poster
- THIEME, R.; THIEME T.: Breeding research for aphid and virus resistance in potatoes. Use of EPG -technique and other test methods to proof resistance to *Potato virus Y*, *Potato leafroll virus*. Northwest Agriculture & Forestry University, College of Plant Protection, Dept. of Entomology, 10.05.2006, Yangling, Shaanxi, China, lecture

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- THIEME R.; THIEME, T.; HEIMBACH, U.; NACHTIGALL, M.; SCHUBERT, J.; SCHLIEPHAKE, E.; RAKOSY-TICAN, L.: Resistenzen gegen Pathogene und Schaderreger in Wildkartoffeln und Übertragung in die Kulturkartoffel durch Einsatz biotechnologischer Methoden. 55. Deut. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, lecture
- WEHLING, P.: Züchtungsforschung zu Qualitätseigenschaften bei Getreide. Innovationsforum „Biopolymere aus Getreidemehl für die papierverarbeitende und -veredelnde Industrie“, 11.10.2006, Rostock, lecture

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- BADANI-DEHMER, A. G.: Landsorten in Bolivien, Eigenversorgung und der Markt als Schlüssel zur Erhaltung. Fachtagung „Ackersegen und wiedergewonnene Vielfalt“; Veranstaltung des KERN-Verbundes mit dem VERN e. V. und dem NABU e. V., 18.-20.08.2006, Blumberger Mühle, Angermünde, lecture
- BALKO, C.: Untersuchungen zur Frosttoleranz und Winterhärte von Ackerbohnen. GFP-Jahrestagung, 08.11.2006, Bonn, lecture
- ENGEL, F.; DOIL, A.; WINKELMANN, T.; GÜRTLER, S.; KLOCKE, E.; SCHUM, A.: Erweiterung der Zuchtmethodik bei Hortensien (*Hydrangea macrophylla*). 13. Innovationstag Mittelstand der Arbeitsgemeinschaft industrieller Forschungsvereinigungen „Otto von Guericke“ e.V. (AIF), 01.06.2006, Berlin, poster
- JANSEN, G.; JÜRGENS, H.-U.; SEDDIG, S.: Qualitätsuntersuchungen von Süßlupinen im Hinblick auf ihre Eignung als Nahrungs- und Futtermittel. Tagung „Gewinnung von biofunktionellen Food Ingredients aus Lupinensaat für die Lebensmittelindustrie“, 06.-07.12.2006, Rostock, lecture
- JANSEN, G.; SEDDIG, S.; JÜRGENS, H.-U.: Untersuchungen zum „Stärkegehalt“ in Blauen Süßlupinen. 8. GPZ-Tagung, 14.-16.03.2006, Freising-Weißenstephan, poster
- LEHMANN, C.; BIELA, C.; TÖPFL, S.; JANSEN, G.; VÖGEL, R.: Ist *Solanum scabrum* (Garden Huckleberry) zur Gewinnung von Lebensmittelfarbe geeignet? 45. Gartenbauwissenschaftliche Tagung, 22.-24.02.2006, Potsdam, poster
- SEDDIG, S.; SCHMIDT, R.; JANSEN, G.: Pre-harvest sprouting – efficient selection possibilities. Int. Symposium on Rye Breeding Genetics, 28.-30.06.2006, Rostock/Groß Lüsewitz, poster
- WEGENER, C.; JANSEN, G.: Farbige Kartoffeln – ein Vergleich mit konventionellen, hellfleischigen Sorten (*Solanum tuberosum* L.) hinsichtlich Qualität und Resistenz. 41. Vortragstagung der DGQ, 20.-21.03.2006, Wädenswil, Switzerland, poster
- WEGENER, C.; JANSEN, G.: Resistance of blue-violet potatoes to *Erwinia* soft rot – a comparison with white yellow-fleshed *Solanum tuberosum* cultivars. Int. Society Plant Pathology: 11th Int. Conf. Plant Pathogenic Bacteria, 09.-14.07.2006, Edinburgh, UK, poster
- WEGENER, C.; JANSEN, G.: Farbige Kartoffeln und ihre Besonderheiten: Eine Betrachtung hinsichtlich Resistenz und Qualität. GFP Jahrestagung, 08.11.2006, Bonn, lecture

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- BARANSKI, R.; KLOCKE, E.: The use of *Agrobacterium rhizogenes* for the effective carrot transformation. 11. Polnische Konferenz für In-vitro-Kultur und Biotechnologie der Pflanzen, 06.-09.09.2006, Universität Szczecinski, Poland, poster
- BARANSKI, R.; KLOCKE, E.: GFP fluorescence in carrot: from protoplasts to flowers. 11. Polnische Konferenz für In-vitro-Kultur und Biotechnologie der Pflanzen, 06.-09.09.2006, Universität Szczecinski, Poland, lecture
- BUDAHN, H.; PETERKA, H.; SCHRADER, O.; ZHANG, S.; LI, J.; MOUSA, M.A.A.; SCHÜTZE, W.; KRÄMER, R.: Potentials of a complete series of disomic rape-radish addition lines. Fa. Rijk Zwaan, De Lier, 05.10.2006, Netherlands, lecture
- DING, Y.; BUDAHN, H.; PETERKA, H.: Define genetic linkage groups with assigned markers of *Raphanus sativus* chromosomes. Int. Horticultural Congr., 13.-19.08.2006, Seoul, South Korea, lecture
- GÜRTLER, S.: Hortensien – Neue züchterische Aspekte für eine alte Kultur. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture
- KLOCKE, E.: Somatische Hybridisierung verschiedener Brassicaceae. Mitgliederversammlung 20 Jahre ADIVK, 21.-22.09.2006, Geisenheim, lecture
- KRÄMER, R.; MARTHE, F.; KLOCKE, E.; RYSCHKA, U.; SCHUMANN, G.; RABENSTEIN, F.; SCHUBERT, J.; EHRIG, F.: *Turnip mosaic virus* im Kohl (*Brassica Oleracea* L.) – Ansätze zur Resistenzverbesserung. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture
- MARTHE, F.: Verbreiterung der genetischen Basis des Kohls (*Brassica oleracea*) für Resistenz gegen *Xanthomonas campestris* pv. *campestris*, *Leptosphaeria maculans*, *Plasmiodiophora brassicae* und Turnip mosaic virus. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture

- MARTHE, F.: Untersuchungen zur Resistenz von *Brassica oleracea* gegen *Xanthomonas campestris* pv. *campestris*. 2. Projektmeeting zwischen Marner GZG Saaten AG und der BAZ, Inst. f. Epidemiologie u. Resistenz und Inst. f. gartenbaul. Kulturen, 21.06.2006, BAZ Quedlinburg, lecture
- MARTHE, F.: Wege zur Verbesserung der Resistenz von Kohl gegen Viruskrankheiten – konventionell und gentechnisch. Hochschule Ahnhalt, Fachbereich Landwirtschaft, Ökotröphologie und Landschaftsentwicklung, 09.11.2006, Bernburg, lecture
- MARTHE, F.; KRÄMER, R.; RICHTER, K.; SCHRA-DER, O.; RYSCHKA, U.: Genetic variation improve-ment of cabbage (*Brassica oleracea*) for new resistances to black rot (*Xanthomonas campestris* pv. *campestris*), black leg (*Leptosphaeria maculans*), clubroot (*Plasmidiophora brassi-cae*) and Turnip mosaic virus (TuMV) from black mustar. 15th Crucifer Genetic Workshop, 02.10.2006, Wagenin-gen, Netherlands, lecture
- MARTHE, F.; KRÄMER, R.; RICHTER, K.; SCHRA-DER, O.; RYSCHKA, U.: Genetic variation improve-ment of cabbage (*Brassica oleracea*). Workshop Brassica Rijk Zwaan, 05.10.2006, Fijnaart, Netherlands, lecture
- MEWES, S.: Ausprägung und Vererbung der Gynodiözie bei Thymian (*T. vulgaris* L.). Martin-Luther-Universität Halle-Wittenberg, 19.01.2006, Halle, lecture
- MEWES, S.; JUNGHANNS, W.: Entwicklung von Thy-mianhybriden mit gesteigertem Ertrag und Ätherisch-öl-Gehalt. Saluplanta, Bernburger Winterseminar, 21.–22.02.2006, Bernburg, lecture
- MEWES, S.: Entwicklung von Linien eines Hybridsor-tensystems von Thymian. Bundesanstalt für Züch-tungsforschung an Kulturpflanzen. Institut für garten-bauliche Kulturen. Institutskolloquium, 18.05.2006, lecture
- MEWES, S.; PANK, F.: Genetik der Gynodiözie des Thy-mians (*Thymus vulgaris* L.) und Ergebnisse der Entwick-lung cytoplasmatisch männlich steriler Linien mit ihren Maintainern. GPZ-Tagung, AG Arznei- und Gewürzpflanzen, 23.08.2006, BAZ Quedlinburg, lecture
- NOTHNAGEL, T.: Research on *Daucus carota* L. at the Fed-eral Centre of Breeding Research on Cultivated Plants (BAZ). Einladung durch EU Chair Prof. B. Arnoldt-Schmitt, University of Evora, Portugal, 01.03.2006, Evora, Portugal, lecture
- NOTHNAGEL, T.: Aktuelle Forschungsarbeiten an der Möhre *Daucus carota* L. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture
- NOTHNAGEL, T.: Möhrenzüchtung im Wandel der Zeit. Landesgartenschau Wernigerode, 09.09.2006, Wernige-rode, lecture
- NOTHNAGEL, T.; MARTHE, F.; KLOCKE, E.: Blütenbi-ologische Untersuchungen im Vorfeld eines Screenings auf männliche Sterilität bei Sellerie (*Apium graveolens* L.) und Petersilie (*Petroselinum crispum* (Mill.) Nym.). GPZ-Tagung, AG Arznei- und Gewürzpflanzen, 23.08.2006, BAZ Quedlinburg, lecture
- NOTHNAGEL, T.; STRAKA, P.; ULRICH D.: Molecular characterisation of different aroma types of carrot. Deutsch-israelisches Symposium „Aroma - a Key Quality Attribute in Plants“, 27.03.-01.04.2006, Bet-Dagan, Israel, lecture
- NOTHNAGEL, T.; ULRICH, D.; QUILITZSCH, R.; STRAKA, P.: Molecular characterization of different aroma types in *Daucus*. 2006 Israel-Germany Bi-Na-tional Workshop on Aroma – a key quality attribute in plants, 27.03.-01.04.2006, Bet Dagan, Israel, lecture
- PANK, F.: Resistenzzüchtung an Arznei- und Gewürzpflan-zen an Beispielen aus der Arbeit der BAZ und aus der Literatur. Anwenderseminar der Landesanstalt für Land-wirtschaft und Gartenbau Sachsen-Anhalt in Bernburg, 31.01.2006, Bernburg, lecture
- PANK, F.: Züchtung von Arznei- und Gewürzpflanzen für den ökologischen Anbau. Tagung „Die Heilkräuter – Gegenwart und Zukunft einer Realität in den Alpen“. 24.-26.08.2006, Poschiavo, Switzerland, lecture
- PANK, F.: Ergebnisse des InnoPlanta-Forschungsprojektes „Carvacrolhaltige Bohnenkrautextrakte (*Satureja hortens-isis* L.) für Naturstoffprodukte mit antimikrobieller und antioxidativer Wirkung für Pharmazie, Lebensmittelin-dustrie und Kosmetik“. Statusseminar-InnoPlanta im IPK Gatersleben, 19.10.2006, Gatersleben, lecture
- PANK, F.: Ergebnisse des InnoPlanta-Forschungsprojektes „Entwicklung von *Mycosphaerella* - resistenten Arznei-fenchel-Sorten (*Foeniculum vulgare* MILL. ssp. *vulgare* var. *vulgare*) und einer wettbewerbsfähigen Technologie der Produktion der Früchte und des ätherischen Öls im An-bau von Sachsen-Anhalt“. Statusseminar-InnoPlanta im IPK Gatersleben, 19.10.2006, Gatersleben, lecture
- PANK, F.: Ergebnisse des InnoPlanta-Forschungsprojektes „Rohstoffoptimierung für die Herstellung von Thymi-anfluidextrakt und Thymi herba unter Berücksichtigung der Bedingungen im traditionellen Anbaugbiet des Harzvorlandes“. Statusseminar-InnoPlanta im IPK Gatersleben, 19.10.2006, Gatersleben, lecture
- PANK, F.; QUILITZSCH, R.; KRÜGER, H.: Variabilität der Ausprägung der Gynodiözie an ausgewählten Fen-chelpopulationen (*Foeniculum vulgare* MILL.) und Ein-fluss der Fertilitätstypen auf wirtschaftlich bedeutende Merkmale. GPZ-Tagung, AG Arznei- und Gewürz-pflanzen, 23.08.2006, BAZ Quedlinburg, lecture
- PETERKA, H.; BUDAHN, H.: Erschließung genetischer Ressourcen bei *Pelargonium* durch Artkreuzungen. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture

- PFEFFERKORN, A.: Einfluss von Entwicklungsstadium auf Ertrag und Carvacrolgehalt des ätherischen Öles von Bohnenkraut (*Satureja hortensis* L.). 16. Bernburger Winterseminar Arznei- und Gewürzpflanzen, 21.-22.02.2006, Bernburg, lecture
- PFEFFERKORN, A.: Ergebnisse eines Prebreeding-Programms für Einjähriges Bohnenkraut (*Satureja hortensis* L.) zur Entwicklung öl- und carvacrolreicher Genotypen. BAZ, Institut für gartenbauliche Kulturen. 25.04.2006, lecture
- PLASCHIL, S.: Übersicht der geplanten Arbeiten an *Rhododendron simsii* und *Erica gracilis*. GFP-Sommertagung, 20.06.2006, BAZ Quedlinburg, lecture
- PLASCHIL, S.: Übersicht über die geplanten Projekte an *Erica gracilis* und *Rhododendron simsii*, Treffen AG Zierpflanzen der GPZ, 14.07.2006, Hillscheid, lecture
- PLASCHIL, S.: Übersicht der geplanten Arbeiten an *Erica gracilis* und *Rhododendron simsii*, Azerca-Züchtungsausschuss, 07.11.2006, Bad Zwischenahn, lecture
- QUILITZSCH, R.; NOTHNAGEL, T.: Spektroskopische Identifizierung von epikutikulären Wachsschichten an Laubblättern von *Daucus* ssp., XXXXI. Vortragstagung der Deut. Ges. für Qualitätsforschung (Pflanzliche Nahrungsmittel) e. V. (DGQ), 20.-21.03.2006, Wädenswil, Switzerland, poster
- RYSCHKA, U.: Protoplastenfusion bei *Pelargonium*. Treffen AG Zierpflanzen der GPZ, 14.07.2006, Hillscheid, lecture
- SCHRADER, O.: Genomic and fluorescence in situ hybridization (GISH & FISH) detecting species differences of karyotypes in hybrids of horticultural plants. XVII Annual Meeting of the Botanical Society of Chile, 16.-19.01.2006, Talca, Chile, lecture
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- ULRICH, D.; NOTHNAGEL, T.; STRAKA, P.: Bestimmung von Aromamustern zur Genomkartierung bei Möhren (*Daucus carota* L.). Pflanzenzüchtung für bessere Lebensmittel und Futtermittel. 8. GPZ-Tagung mit Mitgliederversammlung 14.-16.03.2006, Freising /Weihenstephan, poster
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- AHLEMAYER, J.; HOBERT, M.; KÖHLER, W.; FRIEDT, W.; ORDON, F.: Zuchtfortschritt und genetische Diversität bei Wintergerste. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
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- HABEKUSS, A.; KÜHNE, T.; KRÄMER, I.; RABENSTEIN, F.; EHRIG, F.; RUGE-WEHLING, B.; HUTH, W.; ORDON, F.: Wirksamkeit bekannter Resistenzgene gegenüber einem neuen *rym5*-resistenzbrechenden deutschen BaMMV-Isolat. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
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- HOBERT, M.: Identifikation differenziell exprimierter Gene der Gerste nach BYDV-Infektion. Pflanzenzüchterisches Seminar, 25.06.2006, Universität Gießen, lecture
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- KOMATSUDA, T.; POURKHEIRANDISH, M.; AZHAGUVEL, P.; HE, C.; TAGIRI, A.; FUJIMURA, T.; STEIN, N.; PEROVIC, D.; KANAMORI, H.; WICKER, T.; MATSUOKA, M.; MATSUMOTO, T.: The origins of six-rowed barley. 5th Plant Genomics European Meetings, Session 5, 10.-14.10.2006, Venice, Italy, poster
- LEISTNER, H.-U.; SCHLIEPHAKE, E.; KUSTERER, A.; HARRER, S.; ORDON, F.: Etablierung eines nationalen Evaluierungsprogramms pflanzengenetischer Ressourcen bei Getreide EVA II. 8. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
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- LIND, V.: Speltoide bei Winterweizen. Besprechung auf Einladung des BDP, 10.04.2006, Bundessortenamt Braunschweig, lecture
- MEYER, N.; KARLOVSKY, P.; LIND, V.: Entwicklung einer Real-Time-PCR basierten Quantifizierung des Befalls von *Oculimacula yallundae* und *Oculimacula aciformis* an *Triticum aestivum*. 55. Deut. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
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- NAZ, A.; KUNERT, A.; KERWER, P.; LIND, V.; FLATH, K.; PILLEN, K.; LÉON, J.: Comparative mapping of QTLs for plant disease resistances in wheat advanced backcross populations. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
- ORDON, F.: Von Mendel zum Gentransfer - Moderne Pflanzenzüchtung. Lions Club Goslar - Bad Harzburg, 06.03.2006, Goslar, lecture
- ORDON, F.: Molecular breeding for virus resistance in barley. Invitation University of Uppsala, 22.03.2006, Uppsala, Sweden, lecture
- ORDON, F.; PEROVIC, D.: Mapping of Soil-borne cereal mosaic virus resistance (SBCMV) in wheat. Meeting of the EU-CRAFT Project WHEATPROTECT, 29.-30.03.2006, Capelle en Pevelle, France, lecture
- ORDON, F.: Was kann moderne Pflanzenzüchtung leisten - Wissenschaftliche Einblicke. 09.09.2006, Landesgartenschau Wernigerode, lecture
- ORDON, F.; PEROVIC, D.; HABEKUSS, A.; KRÄMER, I.; HARIRI, D.; FÖRSTER, J.; DEVAUX, P.; FEUERHELM, D.; STEIN, N.; GRANER, A.; FRIEDT, W.: Molecular breeding for virus resistance in cereals. Eucarpia Cereal Science and Technology for Feeding Ten Billion People: Genomics Era and Beyond, 14.11.2006, Lleida, Spain, lecture
- ORDON, F.: Molekulare Nutzung genetischer Vielfalt - Züchtungsstrategie der Zukunft. Abschlusskol-

- loquium „Zwischen Tradition und Fortschritt – die bundeszentrale *Ex-situ*-Genbank am IPK Gatersleben“, 15.12.2006, lecture
- PEIL, A.; FLACHOWSKY, H.; GARCIA, T.; RICHTER, K.; TROGNITZ, B.; HANKE, V.: Kartierung der Feuerbrandresistenz in *Malus* und weitere Analysen zum Feuerbrand. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
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- RICHTER, K.: Erste Untersuchungen zur Adernschwärze (*Xanthomonas campestris* pv. *campestris*) an Raps. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
- RICHTER, K.: Untersuchungen zur Resistenz von Brassicaceen gegenüber dem Erreger der Schwarzadrigkeit (*Xanthomonas campestris* pv. *campestris*). GFP-Tagung, 20.06.2006, Quedlinburg, lecture
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- BARANSKA, M.; SCHULZ, H.: Rapid quantifikation of carotenoids in tomatoes and tomato products by Raman Spectroscopy. ICOPVS, 25.-28.02.2006, Meerut, India, poster
- EICHHOLZ, I.; ROHN, S.; KROH, L. W.; ULRICH, D.; ALEXANDER, A.; HUYSKENS-KEIL, S.: Beziehungen zwischen Antioxidantien und sensorischen Qualitätseigenschaften von Kultur Heidelbeeren (*Vaccinium corymbosum* L.) und deren Beeinflussung durch Elicitoren. XXXXI. Vortragsstagung der Deut. Ges. für Qualitätsforschung (Pflanzliche Nahrungsmittel) e. V. (DGQ), 20.-21.03.2006, Wädenswil, Switzerland, poster
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- GAMSJÄGER, S.; BARANSKA, M.; SCHULZ, H.; HEISELMAYER, P.; MUSSO, M.: NIR-FT-Raman mapping spectroscopy of *Viola x wittrockiana* as method to study carotenoid and flavonoid content in living plant tissue. ICORS 2006, 20.-25.08.2006, Yokohama, Japan, poster
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- HOBERG, E.: Vielfalt regt die Sinne an. Int. Grüne Woche 13.-22.01.2006, lecture
- HOBERG, E.: Bewertung der Einflüsse auf den Spargelgeschmack im Betrieb. Unterfränkischer Spargeltag, 15.02.2006, Amt für Landwirtschaft und Forsten Kitzingen, Alitzheim, lecture
- HOBERG, E.: Auswirkung des Anlagenalters auf den Geschmack. Arbeitskreis Spargel der Bundesfachgruppe Gemüsebau, 18.-19.09.2006, Hannover-Ahlem, lecture
- HOBERG, E.; ENGEL, M.; SCHMIDT, A.: Qualität des Spargels in der Einschätzung junger Konsumenten., DGQ – Vortragstagung, Qualität und Frische pflanzlicher Lebensmittel aus ökologischer und konventioneller Produktion. 20.-21.03.2006, Agroscope Changins, Wädenswil, Switzerland, poster
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- HOBERG, E.; SCHMIDT, A.: Korrelationen zwischen Wahrnehmungen der Süße und analytisch bestimmten Zuckerwerten. Arbeitskreis Spargel der Bundesfachgruppe Gemüsebau, 18.-19.09.2006, Hannover-Ahlem, lecture
- HOBERG, E.; ULRICH, D.: Wichtigste Ergebnisse der Geschmacksforschung an Spargel und ihre Umsetzung in die Praxis. Jahresmitgliederversammlung der Niedersächsischen Spargelvereinigung e.V. Walsrode, 19.01.2006, Walsrode, lecture
- HOBERG, E.; ULRICH, D.: Erdbeer- und Spargelqualität – Einfluss der Züchtung – Forschung an der BAZ. Veranstaltung an der Landesvolkshochschule Freckenhorst, 08.02.2006, Freckenhorst, lecture
- HOBERG, E.; ULRICH, D.: Dynamik der sensorischen Qualität von *Asparagus off.* L. unter dem Einfluss des Anlagenalters. 43. Gartenbau. Tagung 2006 der Deut. Gartenbauwiss. Ges. e.V., 22.-24.02.2006, Potsdam, lecture
- HOBERG, E.; ULRICH, D.: Monitoring des Spargelgeschmacks. Workshop im BAZ, Institut für Pflanzenanalytik, 01.-02.03.2006, Quedlinburg, lecture
- HOBERG, E.; ULRICH, D.: Vergleichende Qualitätsuntersuchungen an alten und neuen Gemüsesorten. BNN-Seminar „Sensorik von Ökolebensmitteln“ 09.-10.11.2006, Frankfurt/Main, lecture
- KRÜGER, H.: Losses of active substances of essential chamomile oils during steam distillation. I. Int. Symp. on Chamomile Research, Development and Production, 07.-10.06.2006, Universität Presov, Slovakia, lecture
- KRÜGER, H.: Verlust und Schädigung von ätherischen Ölen durch den Entkeimungsprozess am Beispiel von Majoran. 4. Lemgoer Nachmittag zu Entkeimungsfragen, Fachhochschule Lippe und Höxter, 01.12.2006, Lemgo, lecture
- OLBRICHT, K.; ULRICH, D.; HOBERG, E.; STAUDT, G.: Züchtungsbegleitende Aromaanalytik bei Erdbeeren. GPZ-Vortragstagung „Pflanzenzüchtung für bessere Lebens- u. Futtermittel“, 14.-16.03.2006, Freising-Weißenstephan, lecture
- QUILITZSCH, R.; NOTHNAGEL, T.: Spektroskopische Identifizierung von epikutikulären Wachsschichten an Laubblättern von *Daucus* sp. XXXXI. Vortragstagung der Deut. Ges. für Qualitätsforschung (Pflanzliche Nahrungsmittel) e. V. (DGQ), 20.-21.03.2006, Wädenswil, Switzerland, poster
- QUILITZSCH, R.; SCHÜTZE, W.: Comparison of spectroscopic and chromatographic methods for mycotoxin determination in samples of winter wheat. 3rd Int. Secd. Health Conference, 06.-08.09.2006, Univ. Technol. and Agriculture, Bydgoszcz, Poland, lecture
- SCHULZ, H.: Effiziente Charakterisierung von Pflanzeninhaltsstoffen mittels Infrarot- und Raman-Spektroskopie. Öffentliche Sitzung der Abteilung Öl- und Eiweißpflanzen im IPK Gatersleben, 07.-08.02.2006, Gatersleben, lecture
- SCHULZ, H.: Möglichkeiten und Grenzen schwingungsspektroskopischer Methoden bei der Ermittlung pflanzlicher Qualitätsparameter. Öffentliche Sitzung der Abteilung Futterpflanzen bei der Norddeutschen Pflanzenzucht, Zweigniederlassung Saatzucht Hans Lembke, 25.04.2006, Malchow/Poel, lecture
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- SCHULZ, H.; BARANSKA, M.: Raman studies on various dyeing plants. ICOPVS, 25.-28.02.2006, Meerut, India, poster
- SCHULZ, H.; BARANSKA, M.: The use of ATR-IR and Raman Spectroscopy for the characterisation of valuable plant substances. ICOPVS, 25.-28.02.2006, Meerut, India, lecture
- SCHULZ, H.; BARANSKA, M.: Antioxidants in plant foods investigated by FT Raman Spectroscopy. Spec 2006 – Shedding Light on Disease: Optical Diagnosis for the New Millennium, 20.-24.05.2006, Heidelberg, poster
- SCHULZ, H.; BARANSKA, M.: Rapid evaluation of quality parameters in plant products applying ATR-IR and

- Raman Spectroscopy. Int. Conf. Managing Quality in Chains (MQUIC 2006), 07.-10.08.2006, Bangkok, Thailand, lecture
- SCHULZ, H.; BARANSKA, M.: Polyacetylene distribution can be observed and mapped in living plant tissue applying micro-Raman Spectroscopy. ISEO 2006, 10.-13.09.2006, Grasse, France, poster
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- ULRICH, D.: Aromaanalytik von Erdbeeren. Ergebnisse der Geschmacksforschung an der Bundesanstalt für Züchtungsforschung. 7. Beerenobsttag im DLR Rheinland Pfalz, 03.03.2006, Neustadt, lecture
- ULRICH, D.: Internationale Geschmacksforschung - eigene Erfahrungen. Arbeitskreis Spargel der Bundesfachgruppe Gemüsebau, 18.-19.09.2006, Hannover-Ahlem, lecture
- ULRICH, D.; HOBERG, E.: Variabilität des Spargelaromas. Arbeitskreis Spargel der Bundesfachgruppe Gemüsebau, 18.-19.09.2006, Hannover-Ahlem, lecture
- ULRICH, D.; NOTHNAGEL, T.; HOBERG, E.: Effective screening of aroma pattern in carrots. Int. Conf. Managing Quality in Chains (MQUIC 2006), 07.-10.08.2006, Bangkok, Thailand, poster
- ULRICH, D.; OLBRICHT, K.; ROUDEILLAC, P.: Inheritance of bioactive terpenoid compounds in *Fragaria*. COST 863 Euroberry, Genetic bases for bioactive compounds affecting human health in berry fruits, 28.-30.09.2006, Barcelona, Spain, lecture
- ULRICH, D.; HOBERG, E.: Aromaanalytik von Erdbeeren. Ergebnisse der Forschungen zum Erdbeergeschmack an der BAZ. 7. Beerenobsttag Rheinland-Pfalz, 03.03.2006, DLR Rheinpfalz, Neustadt/W., lecture
- VITTEN, M.; OLBRICHT, K.; ULRICH, D.; HOBERG, E.; TIEDKE, F.: Quality traits in freeze dried strawberries. 1st Joint Meeting of WGI and WG4, Genetic bases for bioactive compounds affecting human health in berry fruits, 28.-30.09.2006, Barcelona, Spain, poster
- ZIEGERT, K.: Entwicklung neuer Aromaextrakte und phytopharmazeutischer Produkte aus *Allium*-Arten. Institutskolloquium des IPA in der BAZ Quedlinburg, 08.06.2006, Quedlinburg, lecture
- ZIEGERT, K.; SCHULZ, H.: Development of new products based on *Allium* extracts. NAROSSA 2006, 12th Int. Conf. for Renewable Resources and Plant Biotechnology, 12.-13.06.2006, Magdeburg, poster
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- BARCHEND, G.: Blattfleckenkrankheit am Feldsalat (*Valerianella locusta L.*) 8. GPZ-Tagung, 14.-16.03.2006, Freising-Weißenstephan, poster
- BARCHEND, G.: Arbeiten am Feldsalat. GFP-Sommertagung Abteilung Gemüse-, Heil- und Gewürzpflanzen, 20.06.2006, Quedlinburg, lecture
- BARCHEND, G.: Resistenzprüfung von Feldsalat (*Valerianella locusta L.*) gegen *Acidovorax valerianellae* sp. No 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- EHRIG F.: Resistenzreaktion bei Gerste gegen *Blumeria graminis*: Rasterelektronenmikroskopische und röntgenmikroanalytische Beobachtungen. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- EHRIG, F.; KÜHNE, T.: Elektronenmikroskopische Untersuchungen zur Übertragung des BaMMV durch *Polymyxa graminis*. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- FOMITCHEVA, V. W.; SCHUBERT, J.; SZTANGRET-WISNIEWSKA, J.; LINDNER, K.: Development of a method for the molecular differentiation of strains in potato virus Y populations. Jahrestreffen DPG-Arbeitskreis "Viruskrankheiten der Pflanzen", 30.-31.03.2006, Lauterbad-Freudenstadt, poster
- GABLER, J.: Krankheiten an Gewürzkräutern. Anwenderseminar Pflanzenschutz/Pflanzenbau, 31.01.2006, Bernburg-Strenzfeld, lecture
- GABLER, J.: Krankheiten an Oregano und Majoran. Sitzung der Projektgruppe „Arznei-, Duft- u. Gewürzpflanzen des AK „Phytomedizin im Gartenbau“ der DPG, 21.02.2006, Bernburg, lecture
- GABLER, J.: Wichtige Schaderreger bei Gewürzpflanzen. Gartenbauberatung, Anbauerschulung für Heil- und Gewürzpflanzenanbauer, 10.03.2006, Ahrweiler, lecture
- GABLER, J.: Resistance assessment in pathosystem *Origanum vulgare/Phoma* sp. 12th Mediterranean Phytopathol. Congr. 11.-15.06.2006, Rhodos, Greece, poster
- GÖTZ, R.; RABENSTEIN, F.; HUTH, W.; SPANAKAKIS, A.; DEML, G.: Nachweis und Differenzierung bodenbürtiger Weizenviren. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- KASTIRR, U.; MÜLLER, E.; RÖMER, P.: Erschließung von Winterdurumformen mit verbesserter Resistenz gegen pilzliche Krankheitserreger. GPZ-Tagung, 14.-16.03.2006, Freising, poster
- KASTIRR, U.; SCHACHSCHNEIDER, R.; HAMANN, T.; WORTMANN, H.; SCHMIEDCHEN, B.: Selektion von Getreidearten auf Resistenz gegen Furoviren. GPZ-Tagung, 14.-16.03.2006, Freising, poster

- KASTIRR, U.; WORTMANN, H.: Untersuchungen zum Verlauf der Infektion durch bodenbürtige Viren an Weizen, Triticale, Roggen und Indikatorpflanzen. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, lecture
- KASTIRR, U.; WORTMANN, H.; SCHMIEDCHEN, B.; RABENSTEIN, F.; KÜHNE, T.: Occurrence of soil-borne viruses in rye and prospects for the improving of resistance to these viruses. Eucarpia Symp. on Rye Breeding & Genetics, 28.-30.06.2006, Rostock, lecture
- KELLERER, T.; SEDLMEIER, M.; RABENSTEIN, F.; KILLERMANN, B.: Development of immunochemical and PCR methods for qualitative detection of *Tilletia* species in organic seeds. XVth Biennial Workshop on the Smut fungi, 11.-14.06.2006, Prag, Czech Republic, poster
- KÜHNE, T.: Spezielle Anforderungen an die Forschung auf dem Gebiet der Pflanzenbiotechnologie in Sachsen-Anhalt. Int. Wissenschaftliche Konferenz anlässlich des 70. Geburtstages von Prof. Dr. Georg Kratzsch, 19.04.2006, Bernburg, lecture
- LINDNER, K.; RABENSTEIN, F.; VETTEN, H. J.: Evaluierung monoklonaler Antikörper zum Nachweis des Potato virus Y. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- OWOLABI, A. T.; SCHLIEPHAKE, E.; EHRIG, F.; RABENSTEIN, F.: Identifizierung und Charakterisierung von Viren in Cucurbitaceen aus Nigeria. Jahrestreffen DPG-Arbeitskreis „Viruskrankheiten der Pflanzen“, 30.-31.03.2006, Lauterbad-Freudenstadt, poster
- RABENSTEIN, F.: Entwicklung multiplexer immunologischer Nachweissysteme für Pathogene an Zierpflanzen als Modellobjekt. Tagung der Fachgruppe Jungpflanzen im Zentralverband Garten e. V., 15.-18.11.2006, Bremerhaven, lecture
- RABENSTEIN, F.; ROHDE, S.: Monoklonale Antikörper zum Nachweis von Pilzantigenen in *Fusarium* befallenen Getreidekörnern und deren Nutzung für die Resistenzbewertung. 8. GPZ-Tagung, 14.-16.03.2006, Freising-Weihenstephan, poster
- RABENSTEIN, F.; ROHDE, S.; VOSS, H.-H.; MIEDANER, T.: Antibodies for detection of fungal antigens in *Fusarium* infected cereal grains and their use for resistance assessment. 9th European Fusarium Seminar (EFS9), 19.-22.09.2006, Wageningen, Netherlands, poster
- RABENSTEIN, F.; SCHUBERT, J.; EHRIG, F.; HABEKUSS, A.; KRAUTHAUSEN, H.-J.; MÜLLER, J.: Identifizierung und Differenzierung von Viren an Spargel. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, poster
- RODEVA, R.; GABLER, J.: Diseases caused by *Phomopsis* spp. on cultivated *Apiaceae* hosts. 12th Mediterranean Phytopathol. Congr. 11.-16.06.2006, Rhodos, Greece, lecture
- SCHUBERT, J.: Gentechnik – Chancen und Risiken. Maschinenring, 12.05.2006, Dobareuth, lecture
- SCHUBERT, J.; FOMITCHEVA, V.; SZTANGRET, J.; THIEME, T.: Nachweis des PVY. BioOK, 07.06.2006, Groß Lüsewitz, lecture
- THIEME, R.; SCHUBERT, J.; NACHTIGALL, M.; HEIMBACH, U.; THIEME, T.: Virus- und Krautfäule-resistenz bei Nachkommen der Wildart *Solanum tarnii*. Regionale wiss. Konferenz IAPTC&B, 22.-24.03.2006, Vienna, Austria, poster
- THIEME, R.; THIEME, T.; HEIMBACH, U.; NACHTIGALL, M.; SCHUBERT, J.; SCHLIEPHAKE, E.; RAKOSY-TICAN, L.: Identifizierung von Resistenzen gegen Pathogene und Schaderreger in Wildkartoffeln und Übertragung auf die Kulturkartoffel durch Einsatz biotechnologischer Methoden. 55. Dt. Pflanzenschutztagung, 25.-28.09.2006, Göttingen, lecture

■ Institute of Grapevine Breeding Geilweilerhof Siebeldingen

- EBERT, S.; ZYPRIAN, E.; VELASCO, R.; TÖPFER, R.: Physical mapping of a QTL for Erysiphe necator resistance in *Vitis vinifera* cv. Regent. Institutsseminar am Istituto Agrario San Michele all' Adige, 14.12.2006, San Michele all' Adige, Italy, lecture
- EIBACH, R.: Entwicklung, Stand und Perspektiven der Rebenzüchtung – aktuelle Sorten aus der Resistenzzüchtung. Badischer Rebveredlertag, 10.02.2006, Breisach, lecture
- EIBACH, R.: Auswirkungen der novellierten Rebpflanzgutverordnung auf züchterische Aspekte. Klonenseminar des Dienstleistungszentrums Ländlicher Raum Rheinhessen-Nahe-Hunsrück, 02.03.2006, Oppenheim, lecture
- EIBACH, R.: Die Novellierung der Rebpflanzgutverordnung: Konsequenzen für Rebzüchter und Rebveredler. Treffen der Rebpflanzguterzeuger Mosel, 07.03.2006, Bernkastel-Kues, lecture
- EIBACH, R.: Current state of grapevine breeding at Institute for Grapevine Breeding Geilweilerhof. ITV France – Station Régionale Champagne, Pôle environment, 10.04.2006, Epernay, France, lecture
- EIBACH, R.: Weinbau und Umwelt – neue Rebsorten. Sonderseminar für Ausbilder und Dozenten des Deutschen Weininstituts, 19.06.2006, Siebeldingen, lecture
- EIBACH, R.: Stand und Perspektiven der Resistenzzüchtung bei Reben. 11. Jahrestagung der Society of Environmental Toxicology and Chemistry – German Language Branch e.V., 05.09.2006, Landau, lecture
- EIBACH, R.: Neue pilzwiderstandsfähige Rebsorten. Landesgartenschau Wernigerode, Tag der Pflanzenzüchtung, 09.09.2006, Wernigerode, lecture

- EIBACH, R.: Stand und Perspektiven der Rebenzüchtung. Thematische Weinproben-Reihe, Schloss Hoflössnitz, 30.09.2006, Radebeul, lecture
- EIBACH, R.; ZYPRIAN, E.; TÖPFER, R.: The use of molecular markers for pyramidizing resistance genes in grapevine. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, lecture
- HARST, M.; BORNHOFF, B. A.; TÖPFER, R.: Investigations of pollen dispersal and out crossing events with transgenic grapevines: a pilot study. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, poster
- HAUSMANN, L.; NEUMANN, K.; EIBACH, R.; TÖPFER, R.: Characterization of anthocyanin 5-glucosyltransferase homologous genes of grapevine. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, poster
- HAUSMANN, L.; NEUMANN, K.; EIBACH, R.; ZYPRIAN, E.; TÖPFER, R.: Development of molecular markers for the trait of malvin formation to improve breeding efforts. 24. Weltkongress für Rebe und Wein, 25.-30.06.2006, Logrono, Spain, lecture
- MAUL, E.: Welche Rebsorten sind miteinander verwandt? Der genetische Fingerabdruck schafft Klarheit. 48. Veitshöchheimer Weinbautage, 24.01.2006, Veitshöchheim, lecture
- MAUL, E.: Rebengenetische Ressourcen in alten Weinbergen. Klonenseminar des Dienstleistungszentrums Ländlicher Raum Rheinhessen-Nahe-Hunsrück, 02.03.2006, Oppenheim, lecture
- MAUL, E.: The European Vitis database. Presentation of a further development. ECP/GR-Tagung der Fruchtartenetzwerke, 29.-31.03.2006, Bonn, lecture
- MAUL, E.: Maßnahmen zur langfristigen Erhaltung reben-genetischer Ressourcen - national und international - .45. Arbeitstagung des Forschungsrings des Deutschen Weinbaus bei der DLG, 26.04.2006, Neustadt, lecture
- MAUL, E.: Erhaltung der Rebenvielfalt - Alte Rebsorten - . Sonderseminar für Ausbilder und Dozenten des Deutschen Weininstituts, 19.06.2006, Siebeldingen, lecture
- MAUL, E.: The Vitis collection at the Institute for Grapevine Breeding Geilweilerhof, a contribution to a long-term and sustainable maintenance of the grapevine genetic resources. 1. Workshop Pflanzengesundheit und genetische Ressourcen in Südosteuropa, 25.-27.09.2006, Mostar, Bosnia and Herzegovina, lecture
- MAUL, E.: Documentation of accessions, availability of information via the Vitis International Variety Catalogue. IPGRI Workshop, 19.11.2006, Luxembourg, lecture
- NEUHAUS, G.; EIBACH, R.; MAUL, E.; TÖPFER, R.; ZYPRIAN, E.: Exploitation of the genetic diversity: an approached to resistance elucidate. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, lecture
- NEUHAUS, G.; EIBACH, R.; MAUL, E.; TÖPFER, R.; ZYPRIAN, E.: Nutzung der natürlichen Diversität der Weinrebe durch funktionelle Genomik. 45. Arbeitstagung des Forschungsrings des Deutschen Weinbaus bei der DLG, 26.04.2006, Neustadt, lecture
- NEUHAUS, G.; EIBACH, R.; MAUL, E.; TÖPFER, R.; ZYPRIAN, E.; ADAM-BLONDON, A. F.; ZAPATER, J. M.: Nutzung der natürlichen genetischen Diversität: ein Instrument zur funktionellen Genomik der Weinrebe, 8. Tagung der Gesellschaft für Pflanzenzüchtung e.V., 14.-16.03.2006, Freising-Weißenstephan, poster
- STOLL, C.; HAUSMANN, L.; SPENER, F.; TÖPFER, R.; LÜHS, W.; FRIEDT, W.: Genetisch veränderter Raps mit einem erhöhten Gehalt an mittelkettigen Fettsäuren. 8. Tagung der Gesellschaft für Pflanzenzüchtung e.V., 14.-16.03.2006, Freising-Weißenstephan, poster
- TÖPFER, R.: Gentechnik in der Rebenzüchtung - eine Standortbestimmung. Fachtagung für Winzergenossen-schaften, 22.05.2006, Dresden, lecture
- WELTER, L.; AKKURT, M.; EBERT, S.; SALAKHUTDINOV, I.; EIBACH, R.; TÖPFER, R.; ZYPRIAN, E.: Genetische und molekulare Analyse der Oidiumresistenz von Regent. 45. Arbeitstagung des Forschungsrings des Deutschen Weinbaus bei der DLG, 26.04.2006, Neustadt, lecture
- WELTER, L.; SALAKHUTDINOV, I.; GÖKTÜRK-BAYDAR, N.; TÖPFER, R.; ZYPRIAN, E.: Genetic mapping of putative functional genes and RGA-derived markers in grapevine. Plant Genetics Conference, 20.-23.09.2006, Kiel, poster
- WELTER, L.; AKKURT, M.; SALAKHUTDINOV, I.; GÖKTÜRK-BAYDAR, N.; EIBACH, R.; TÖPFER, R.; ZYPRIAN, E.: Integration of Microsatellite- and Functional Gene-Based Markers for the Improvement of a Grapevine Genetic Map. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, poster
- ZYPRIAN, E.: Rebenzüchtung - Geschichte und Erfahrungen mit mehltreueren Rebsorten. Tagung des Rings des nördlichen Weinbaus, 12.-13.06.2006, Dijon, France, lecture
- ZYPRIAN, E.; ADAM-BLONDON, A.-F.; MARTINEZ-ZAPATER, J. M.: CoreGrapeGene-Exploitation of the natural diversity in grapevine functional genomics. 6th GABI Status Seminar, 21.-22.02.2006, Potsdam, lecture
- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EBERT, S.; SALAKHUTDINOV, I.; GÖKTÜRK-BAYDAR, N.; EIBACH, R.; TÖPFER, R.: Genetic analysis of fungal disease resistance in grapevine. 9th Int. Conf. on Grape Genetics and Breeding, 02.-06.07.2006, Udine, Italy, lecture
- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EIBACH, R.; TÖPFER, R.: Genetik und molekulare Analyse der Pilzresistenzigenschaften der Weinrebe. Rhein-Wein-Minisympodium, Botanik I der Universität Karlsruhe, 20.01.2006, Karlsruhe, lecture

- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EIBACH, R.; TÖPFER, R.: Genetische und molekulare Analyse der Oidiumresistenz in Regent. 45. Arbeitstagung des Forschungsrings des Deutschen Weinbaus bei der DLG, 26.-27.04.2006, Neustadt/Wstr., lecture
- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EIBACH, R.; TÖPFER, R.: Genetic analysis of fungal disease resistances in grapevine. Plant Genetics Conference, 20.-23.09.2006, Kiel, lecture

■ Research and Coordination Centre for Plant Genetic Resources Quedlinburg

- FRESE, L.: Pflanzenvielfalt – Biologischer Rohstoff für Landwirtschaft und Ernährung, Landesgartenschau, 09.09.2006, Wernigerode, lecture
- FRESE, L.; Harrer, S.; Vögel, R.: Genetisches Monitoring bei landwirtschaftlichen Kulturpflanzen und mit ihnen verwandte Wildarten, Symposium Monitoring und Indikatoren der Agrobiodiversität, BLE, 07.-08.11.2006, Bonn, lecture
- FRESE, L.: Beiträge der BAZ zur Etablierung der bundeszentralen Genbank, Mini-Symposium, IPK, 14.12.2006, Gatersleben, lecture
- GERMEIER, C.: Suggestions for a global oat genetic resources information system. Global Conservation Strategy for Oats, Canada/Americas Stakeholders and Strategy Advisory Group Workshop, 26.-27.07.2006, Fargo, ND, USA, lecture
- GERMEIER, C.: Arten- und Sortenvielfalt im Internet. Landesgartenschau, 09.09.2006, Wernigerode, lecture
- GERMEIER, C.; FRESE, L.: The international database for Beta and in situ management: potential role and functions. Third joint meeting of the ECP/GR working group on Beta and the world Beta network, 08.-11.03.2006, Puerto de la Cruz, Spain, lecture
- GERMEIER, C.; FRESE, L.; LALIBERTE B.: Towards a Global Strategy for the Conservation of Oat Genetic Resources, American Oat Workers Conference, 23.-26.07.2006, Fargo, ND, USA, lecture
- GERMEIER, C.; LALIBERTE B.: The Key Elements of a Global Conservation Strategy for Oats. Global Conservation Strategy for Oats, Canada/Americas Stakeholders and Strategy Advisory Group Workshop, 26.-27.07.2006, Fargo, ND, USA, lecture.
- GERMEIER, C.; LALIBERTE B.: Current stage of a survey. Global Conservation Strategy for Oats, Canada/Americas Stakeholders and Strategy Advisory Group Workshop, 26.-27.07.2006, Fargo, ND, USA, lecture

IV. Scientific cooperation

Cooperation in Germany

The activities of BAZ require an intensive, cross-departmental division of labour between its institutes investigating distinct plant species and its institutes concerned with applied research to support the crop-specific research groups. This internal cooperation is completed by close partnerships with other research centres affiliated to BMELV.

BAZ maintains close relationships in particular with institutions dealing with the collection, conservation and documentation of plant genetic resources. Often the institutes of BAZ cooperate with research units of the Leibniz Association, the Max Planck Society and with related university institutes. Furthermore, researchers of BAZ participate in different regional scientific networks.

BAZ scientists are also active in a number of BMELV think-tanks and they cooperate on behalf of BMELV in national and international committees and work groups. An important part of cooperation is the extensive academic teaching activity of BAZ scientists. In the reporting period, the following BAZ researchers held lectures at universities and colleges:

■ Institute of Fruit Breeding Dresden-Pillnitz

University of Applied Sciences Dresden

- Dr. habil. V. Hanke, „Grundlagen der Pflanzenzüchtung“, lectures
- Dr. rer. hort. K. Olbricht, „Angewandte Pflanzenzüchtung“, lectures

Technical University of Dresden

- Dr. habil. V. Hanke, „Pflanzliche Zell- und Gewebekultur“, lecture

■ Institute of Horticultural Crops Quedlinburg

University of Halle

- PD Dr. habil. F. Pank, „Arznei- und Gewürzpflanzen“, lecture

■ Institute of Epidemiology and Resistance Resources Quedlinburg

University of Giessen

- PD Dr. F. Ordon, „Plant Breeding“, obligatory BSc course

■ Institute of Resistance Research and Pathogen Diagnostics Quedlinburg

University of Halle

- Dr. habil. T. Kühne, „Viruskrankheiten bei landwirtschaftlichen Kulturen“, lecture
- Dr. rer. nat. F. Rabenstein, „Polyklonale Antisera und monoklonale Antikörper in der Pathogendiagnostik“, lecture
- Dr. rer. nat. F. Rabenstein, „Viruskrankheiten an Kern- und Steinobst“, lecture
- Dr. rer. nat. F. Rabenstein, „Virusdiagnosemethoden“, lecture
- Dr. habil. J. Schubert, „Gemüsevirosen“, lecture
- Dr. habil. J. Schubert, „Molekulare Nachweistechiken für Pflanzenviren“, lecture

■ Institute of Grapevine Breeding Geilweilerhof Siebeldingen

University of Giessen

- Dr. habil. R. Töpfer, „Genetische Methoden in der Pflanzenzüchtung“, lecture

University of Hohenheim

- Prof. Dr. H. Düring, „Wasserhaushalt und Gaswechsel der Rebe“, practical course
- Prof. Dr. H. Düring, „Biologie der Kulturpflanze“, comprehensive practical course

University of Karlsruhe

- PD Dr. E. Zyprian, „Angewandte Pflanzengenetik“, practical course and lecture

Cooperation abroad

The BAZ participates in research projects of the European Union and therewith strengthens its relations with teams and centres of excellence working on international level.

The researchers of BAZ maintain intensive relationships with numerous partners abroad. On the basis of two- or several-year programmes, BAZ scientists cooperate with partners in the following countries:

Australia	Hungary	Russia
Austria	India	Slovenia
Belgium	Israel	South Africa
Bulgaria	Italy	Spain
Canada	Japan	Sweden
China	Lithuania	Switzerland
Croatia	Moldova	Turkey
Czech Republic	Netherlands	Ukraine
Denmark	New Zealand	United Kingdom
Egypt	Norway	USA
Finland	Poland	
France	Portugal	
Greece	Romania	

Guest scientists at BAZ

The following foreign scientists and researchers worked at BAZ institutes in the reporting period:

■ Institute of Fruit Breeding Dresden-Pillnitz

Ewa Banaszak

Technical University of Koszalin,
Koszalin, Poland, 12/2005-03/2006

Tomasz Jecz

Institute of Pomology and Floriculture,
Skierniewice, Poland, 03/2006

Dr. Soon-Il Kwon

Apple Experiment Station, National Horticultural
Research Institute,
Gyeongbuk, Korea, 10/2006

Cheng Liu

Liaoning Institute of Pomology,
Xiongue, China, 05/2006-03/2007

Ossama Muhra

Ministry of Agriculture and Agrarian Reform,
Damascus, Syria, 03/2005-09/2005

Mathieu Rousseau-Guetin

Unité de Recherche sur les Espèces Fruitères et la Vigne,
Villenave, France, 10/2006

Jorge B. Retamales, Ph. D.

Universidad de Talca, Depto. Horticultura,
Chile, 07/2006-08/2006

Philippe Roudeillac

International fruit consultant
Bordeaux, France, 06/2006

Mohamed Ali Mohamed Saad El-Din Ali Salama

Agricultural Botany and Plant Pathology Department,
Faculty of Agriculture,
Zagazig University, Zagazig, Egypt, 09/2006-08/2010

Seba Sarhan

Damascus University, Department of Ecology and Forestry,
Damascus, Syria, 11/2006-11/2010

■ Institute of Agricultural Crops Groß Lüsewitz

Dr. Youping Wang

College of Bioscience and Biotechnology,
Yangzhou, China, 06/2006-08/2006

Dr. Lenuta Racosy-Tican

Department of Ecology-Genetics, Plant Genetics Manipulation Group, Babes-Bolyai University, Cluj-Napoca, Romania, 07/2006 – 09/2006

Dr. Zsolt Polgar
University of Veszprem, Georgikon Faculty of Agriculture,
Keszthely, Hungary, 09/2006

Istvan Wolf
University of Veszprem, Georgikon Faculty of Agriculture,
Keszthely, Hungary, 09/2006

■ Institute of Abiotic Stress Tolerance Groß Lüsewitz

Onsook Hur
National Highland Agricultural Research Institute,
Gangeron province, Korea, 07/2006–08/2006

■ Institute of Horticultural Crops Quedlinburg

Dr. Rafal Baranski
Krakow Agricultural University, Department of
Genetics, Plant Breeding and Seed Science,
Krakow, Poland, 04/2004–06/2006

Rohini Dhammika Wickrama Arachchige
Course for specialists and executives from developing
countries in Germany
(government grant), Sri Lanka, 04/2006–09/2006

Zhao Hong
Beijing Vegetable Research Centre,
Beijing, China, 10/2005 – 02/2006

Zhang Shaosong
Yunnan Academy of Agricultural Sciences,
Biotechnology Research Institute,
Kunming, China, 06/2006 – 08/2006

■ Institute of Epidemiology and Resistance Resources Quedlinburg

Dr. Anetta Kuczynska
Polish Academy, Institute of Plant Genetics,
Poznan, Poland, 10/2006

Lukasz Stepień
Institute of Plant Genetics, Polish Academy of Sciences,
Poznan, Poland, 02/2006–03/2006

Belayneh Admassu Yimer
National Plant Protection Research Center, Ethiopian
Institute of Agricultural Research,
Ambo, Ethiopia, 09/2006–09/2009

Dr. Olga Afanasenko
All-Russian Institute of Plant Protection,
St. Petersburg, Russia, 02/2006 – 06/2006

Dr. Nina Mironenko
All-Russian Institute of Plant Protection,
St. Petersburg, Russia, 02/2006 – 06/2006

Ludmilla Lebedeva
All-Russian Institute of Plant Protection,
St. Petersburg, Russia, 02/2006 – 06/2006

Dr. Elena Gulyaeva
All-Russian Institute of Plant Protection,
St. Petersburg, Russia, 02/2006 – 06/2006

■ Institute of Plant Analysis Quedlinburg

Dr. Malgorzata Baranska
Krakow Agricultural University, Department of
Genetics, Plant Breeding and Seed Science,
Krakow, Poland, 06/2006–07/2006

Luca Falchero
Università degli Studi di Torino, Dept. Agroselviter,
Grazingland Management Unit,
Turin, Italy, 05/2006

Sonja Gamsjäger
Universität Salzburg, Molekulare Biologie, Abt. Physik
und Biophysik u. Abt. Ökologie und Diversität der
Pflanzen, Salzburg, Austria, 02/2006–02/2006

Vadym Zabrodskiy
DAAD, International Association for the Exchange of
Students for Technical Experience,
Ukraine, 08/2006–10/2006

Prof. S.F. Zheng
Beijing Vegetable Research Centre,
Beijing, China, 07/2006

Prof. Avi Golan–Goldhirsch
Ben-Gurion University of the Negev, Jakob Blaustein
Institutes for Desert Research, Albert Katz
Department of Dryland Biotechnologies, Sede Boqer
Campus, Israel 06/2006

■ Institute of Resistance Research and Pathogen Diagnostics Quedlinburg

Dr. John Fletcher
New Zealand Institute for Crop Food,
Christchurch, New Zealand, 06/2006

Petra Kozlova
Institute of Plant Molecular Biology,
Budweis, Czech Republic, 06/2006

Dr. Jaroslav Matousek
Institute of Plant Molecular Biology,
Budweis, Czech Republic, 12/2006

■ **Institute of Grapevine Breeding Geilweilerhof
Siebeldingen**

Dr. Luis Fernando Revers

Empresa Brasileira de Pesquisa Agropecuária, Uva a Vinho
Bento Goncalves, Brazil, 09/2006

Leocir José Welter

DAAD/CAPES Brazil, University of Karlsruhe,
Karlsruhe, Germany, 04/2004 – 03/2007

Dr. Junke Zhang

College of Horticulture, Northwest University of
Agriculture and Forestry
Yangling,
China 09/2006-09/2007

V. Scientific Advisory Board

The Advisory Board has 15 members representing the relevant sciences and practical plant breeding.

The members of the Advisory Board are appointed by the Federal Minister for Food, Agriculture and Consumer Protection for a five-year period beginning with their first meeting.

■ Chairman

Prof. Dr. W. Friedt

Justus-Liebig-Universität Gießen, Institut für Pflanzenbau und Pflanzenzüchtung, Gießen

■ Members

Prof. Dr. H. Becker

Georg-August-Universität Göttingen, Institut für Pflanzenbau und Pflanzenzüchtung, Göttingen

Dr. A. Büchting

KWS Kleinwanzlebener Saatzucht AG, Einbeck

N. L. Chrestensen

Fa. N. L. Chrestensen, Erfurt

Prof. Dr. H.B. Deising

Martin-Luther-Universität, Landwirtschaftliche Fakultät, Institut für Pflanzenzüchtung und Pflanzenschutz, Halle

Prof. Dr. W. Diepenbrock

Martin-Luther-Universität, Landwirtschaftliche Fakultät, Institut für Acker- und Pflanzenbau, Halle

Prof. Dr. G. Forkmann

TU München, Institut für Landwirtschaftlichen und Gärtnerischen Pflanzenbau, Lehrstuhl für Zierpflanzenbau, Freising

O. Hespeler

Gärtnerei Hespeler, Wannweil

Dr. K. v. Kameke

Saka-Ragis Pflanzenzucht GbR, Windeby

K.-F. Kaufmann

Landesbauernverband Sachsen-Anhalt, Magdeburg

The Board meetings are also attended by representatives of the Ministry and by the presidents of the Federal Biological Research Centre for Agriculture and Forestry, the Federal Agricultural Research Centre, and the Federal Variety Office, who are invited as ex officio participants.

Prof. Dr. H. Lörz

Universität Hamburg, Institut für Allgemeine Botanik, Hamburg

Dr. W. Müller

Eidgenössische Forschungsanstalt für Obst-, Wein- und Gartenbau, Wädenswil

Prof. Dr. K. Schaller

Forschungsanstalt Geisenheim, Geisenheim

Dr. A. Schütte

Fachagentur Nachwachsende Rohstoffe, Gülzow

Prof. Dr. U. Wobus

Institut für Pflanzengenetik und Kulturpflanzenforschung, Gatersleben

■ Permanent Participants

Dir. u. Prof. Dr. J. M. Greef

Bundesforschungsanstalt für Landwirtschaft, Braunschweig

Präsident und Professor Dr. G. F. Backhaus

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Representative of the Federal Ministry of Food, Agriculture and Consumer Protection, Bonn

VI. BAZ gene banks

■ Grapevine gene bank

The Institute of Grapevine Breeding Geilweilerhof holds a comprehensive international grapevine database, the Vitis International Variety Catalogue.

For more information on the Grapevine database see our website <http://www.bafz.de> under Research.

The Vitis International Variety Catalogue (VIVC) contains:

<i>Vitis vinifera</i> :	11,044	varieties
<i>Vitis labrusca</i> :	322	varieties
<i>Vitis riparia</i> :	186	varieties
<i>Vitis rotundifolia</i> :	97	varieties
<i>Vitis berlandieri</i> :	57	varieties
<i>Vitis silvestris</i> :	55	varieties
<i>Vitis rupestris</i> :	50	varieties
Interspecific crossings:	7,136	varieties
Other <i>Vitis</i> species:	312	varieties
No information available:	3,022	varieties

For further information please contact the Institute of Grapevine Breeding (E-mail: bafz-rz@bafz.de).

■ Fruit gene bank

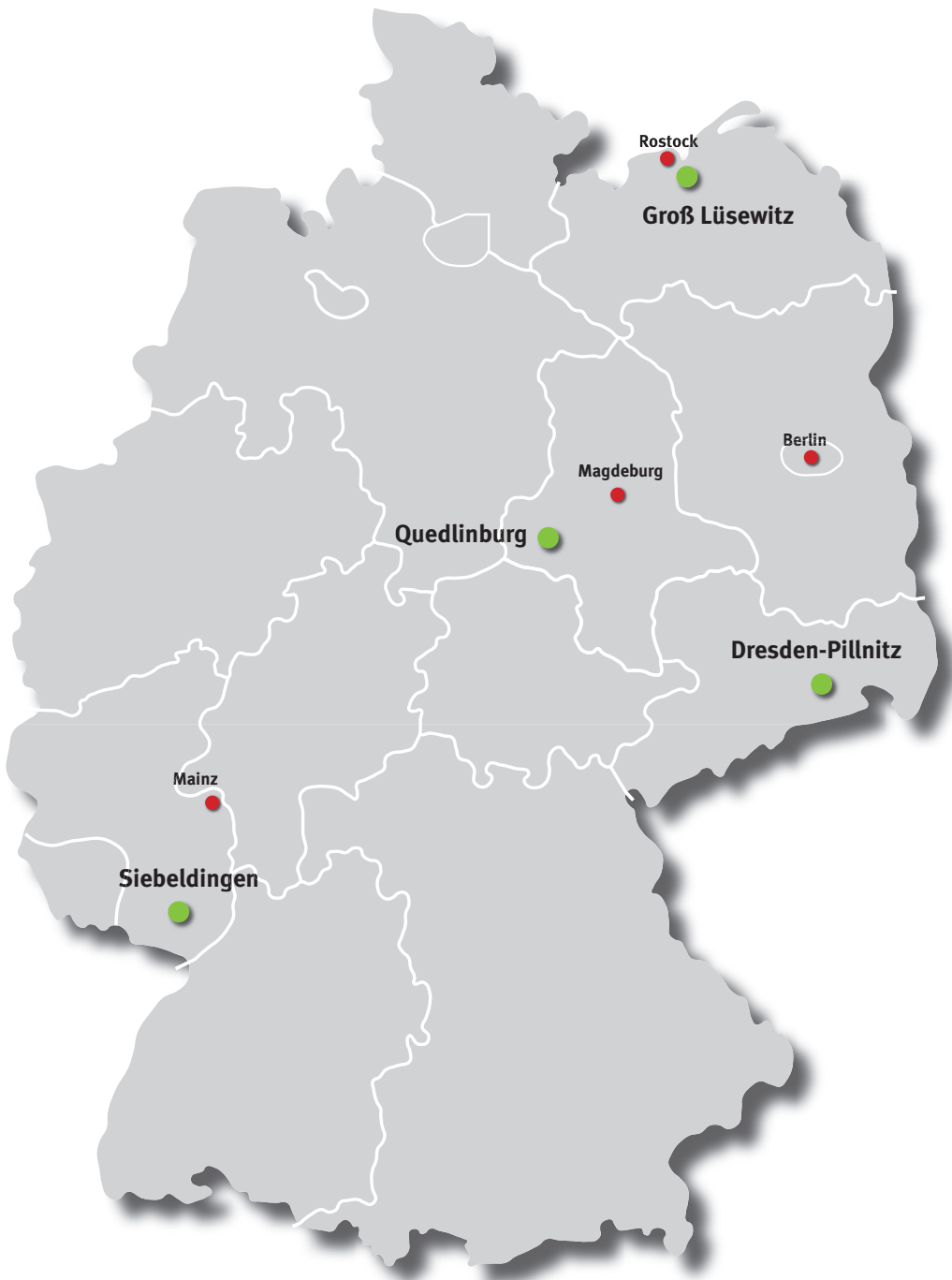
The Institute of Fruit Breeding in Dresden-Pillnitz maintains the Fruit Gene Bank. More information on the apple, pear, sweet and sour cherry and strawberry varieties listed and the special collections of wild species of *Malus*, *Pyrus*, *Prunus* and *Fragaria* are found on the pages of the Institute of Fruit Breeding under <http://www.bafz.de>.

The Fruit Gene Bank currently contains

932	apple varieties (old + new assortment)
130	pear varieties
350	strawberry varieties
210	sweet cherry varieties
92	sour cherry varieties
165	plum varieties
25	sea buckthorn varieties and clones
396	accessions of <i>Malus</i> (18 primary species, 12 interspecific hybrids + 2149 <i>Malus</i> seedlings)
317	accessions of <i>Fragaria</i>
85	accessions of <i>Prunus</i> (25 species, 9 forms, 30 clones)
56	accessions of <i>Pyrus</i> (36 species)
9	accessions of <i>Sorbus</i>

For further information please contact the Institute of Fruit Breeding (E-mail: bafz-oz@bafz.de).

Geographic location of BAZ institutes



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