



# Federal Centre for Breeding Research on Cultivated Plants

## Annual Report 2005

Aschersleben  
Braunschweig  
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](http://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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Photography and illustrations, unless otherwise noted, by institutes and photographic service of BAZ

Edited by Head Office of BAZ, April 2006

Printed by KOCH-DRUCK Halberstadt

ISSN 0948-745X

printed on paper produced without chlorine bleaching

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## Preface

Dear Sir or Madam,  
dear reader,

All times, plants have been mankind's most important resource. They are the basis of all food and animal feed as well as important raw materials for industry and, nowadays, industrial countries attribute a growing attention to plants in their search for an alternative to fossil fuels. Philippe Busquin, the former Commissioner for Research of the European Union, recently wrote in his preface to the brochure „Plants for the future“: „Today, in the face of important challenges at the European and global levels, we must pay renewed attention to plants“.

To conduct breeding research for the development of cultivated crops and varieties that have the potential to meet future challenges – this has been the clearly defined mission and commitment of BAZ since its founding in 1992.

Today I would like to present you the report reviewing the activities of the Federal Centre in the year 2005. With its look, it takes up the graphic design and content presentation of its 2004 precedent, which met widespread approval from a broad range of users.

Obviously we were able to reach not only the experts from our field of work but also the general public, which was definitely the aim we wanted to achieve with the revised and more image-based Report format. We are very glad about this.



The report provides the reader with a summarized review of BAZ activities in the year 2005. More detailed information are available on our website [www.bafz.de](http://www.bafz.de).

The German version of the Annual Report was published in book 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.

Acting Head of BAZ:

Dr. rer. nat. habil. Thomas Kühne



# I. The Federal Centre for Breeding Research on Cultivated Plants in the year 2005

## 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, fossil fuels) or the CO<sub>2</sub> 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

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

and the working group

- Gene bank (Braunschweig).

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 Federal Centre for Breeding Research on Cultivated Plants (BAZ) could start the year 2005 with a very pleasant event. After a construction period of only 16 months, the new research greenhouse with the adjacent central utility unit on the Moorberg site at Quedlinburg was put into service. In the presence of Dr. Gerhard Thalheim, Parliamentary Secretary in the Federal Ministry of Consumer Protection, Food and Agriculture, Tilo Braune, the State Secretary in the Federal Ministry of Transport, Building and Housing, and Dr. Karl-Heinz Dähre, Minister of Building and Transport of the Land Saxony-Anhalt, and many other guests, the greenhouse was handed over to its users on 9 February 2005. This research greenhouse mirrors the latest technological progress made in this field and, thus, meets highest standards of cultivating test crops under controlled conditions. It is one of the biggest of its kind in Europe. The scientists of BAZ can make use of altogether 108 separate cubicles of different size and technical equipment, but all individually adjustable to provide controlled environment conditions. Moreover, 32 ultra-modern climatic chambers provide cutting-edge conditions for experimental work. Before, the BAZ had abandoned its old greenhouse complex in the Stumpfsburger Garten at Quedlinburg and gradually transferred the majority of its test crops from the Aschersleben site to the new Moorberg complex, which made it possible to come very early to a certain routine in running the new facility. The complete occupancy of the area available

Inauguration of the new greenhouse at Quedlinburg on 09.02.2005



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Grit Lautenbach  
librarian



Topping out of the new laboratory and office building at Quedlinburg on 01.09.2005

BUGA 2005 at Munich



is scheduled for the end of the year 2006 when the two institutes now located at Aschersleben will have been moved to the new BAZ site at the outskirts of Quedlinburg.

The topping-out ceremony on 1 September 2005, which was again celebrated in the presence of numerous personalities of science and politics, marked the last building stage in the construction of the new laboratory and office building. Shortly before, a jury had decided in favour of two out of 444 art objects that were submitted following a European-wide invitation to make proposals for art objects to be later integrated on the new premises. The manufacturing of the two prize-winning works of art will be started by the end of 2006.

On 30 June 2005, thus a bit earlier than originally planned, the BAZ Institute of Ornamental Plant Breeding at Ahrensburg was closed. With the retirement of Professor Dr. J. Grunewaldt, who was the head of the institute for many years, and several other scientific employees leaving the institute at the same time, the personnel background for continuing the research at the institute until the planned move to the new building at Quedlinburg was not given anymore. All technical employees of the Ahrensburg institute found new employments nearby. Due to the support of our partners in the research sector affiliated to the Federal Ministry, the majority of them could take up their new occupations in the Federal Research Centre for Forestry and Forest Products and in the Federal Agricultural Research Centre. Although the closure of the Ahrensburg site entailed a drastic reduction in the number of specialized staff, the Institute of Horticultural Crops, now in charge of research on ornamentals, could launch its new breeding programme without major difficulties. For the time being, the main focus of

activities will be on *Pelargonium*, hydrangea, several *Erica* species and *Rhododendron simsii*.

All in all, the staff working at BAZ can look back on another successful year of research. Guideline of all scientific activities was again the BMELV research plan. Complying with its mission statement in the BAZ statute, the Federal Centre contributed again with excellent results and performances to the implementation of the following main objectives of the BMELV research plan:

- 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

Compared with other sciences, a specific characteristic of breeding research and plant breeding is the relatively long period of intensive work before the project aims set are successfully accomplished – a fact conditioned by the complex character of this specific object of research and work. Depending on the problem to be approached, this period may stretch from a few years up to three decades, which is a quite usual period in the breeding of new fruit and grapevine varieties. It clearly shows that an indispensable prerequisite for success in this field is a thorough and foresighted planning as well as a high but undogmatic continuity in scientific work and enduring breeding efforts. From the very beginning, the concept underlying research at BAZ in the field of evaluating and unlocking plant genetic resources for food and other agricultural applications has been focused on the priorities



- Increase of resistance to pests and crop diseases and tolerance to abiotic stress factors,
- Increase of product quality.

Moreover, with its research the BAZ also assumes responsibility for expanding the genetic diversity in agriculturally used ecosystems as well as for the development of strategies for the preservation and sustainable use of plant genetic resources. The appropriateness of the path taken in 1992 finds evidence in various, recently published documents, for example the strategic paper “Pflanzen für die Zukunft” (Plants for the future) issued by the GFP, an association for the promotion of German private plant breeding, or the concept of the newly founded technology platform “Plants for the future”.

With their ambitious work and with the scientific progress achieved so far, the BAZ staff members assured in 2005 again that the Federal Ministry will continue to be provided with high-quality advice on all issues relevant to breeding research and plant breeding. The expertise of BAZ is also increasingly sought after in order to provide assistance to the Bundessortenamt (Federal Office of Plant Varieties); recently this collaboration has included variety identifications and differentiation by molecular methods as well. Needless to say that the research results accomplished in the period under review are again put at the disposal of a wide range of medium-sized breeding companies in various ways. In that sense, the BAZ sees itself in the role of a connector or a mediator between basic research and practical breeding.

The successful scientific work in the year 2005 finds evidence in the achievements stated in the individual reports of the BAZ institutes. Some of the results shall be already highlighted here:

- From the pool of genetic resources of *Triticum durum*, 4 accessions with high *Fusarium* resistance and 6 with low susceptibility to soil-borne viruses could be identified. They are valuable basic materials for the further enhancement of disease resistance in durum wheat, which meets growing interest among German farmers.
- In research that was part of an EU-CRAFT project scientists could prove for the first time that it is a monogenic inheritance that underlies the translocation resistance in baking wheat (*T. aestivum*) against the European-wide spread fungus-transmitted *Soil-borne cereal mosaic virus*. For mapping the resistance-conferring gene, BAZ scientists succeeded in developing first PCR markers.

- Considerable progress was also made in the combination of late blight of potato (*Phytophthora infestans*) with the quality traits of a table potato and of deep-frying. A total of 22 new breeding strains as well as 84 seed populations could be handed over to potato breeders affiliated to GFP.
- Furthermore, it was revealed that the transfer of a single radish chromosome into the rape genome generates plants conferring resistance to the beet cyst nematode (*Heterodera schachtii*). These plants used as catch crops could play a major role in future with their potential of drastically reducing the contamination of cultivated areas.
- To enhance the urgently required extension of the genetic basis of *Pelargonium*, important methodical prerequisites were provided with the development and establishment of methods of protoplast fusion.
- For the first time, German fruit growers have a comprehensive survey on the fertility of sweet cherry cultivars at their disposal, which is the results of a systematic determination and classification of sterility alleles by means of molecular markers. In future, the survey will surely help to prevent fertility problems and resulting loss of yield.
- In apple, researchers succeeded in proving two new genes in wild species that are conferring resistance to mildew (*Podosphaera leucotricha*). In addition, a gene technological approach led to a considerable shortening of the juvenile, i.e. flowerless developmental stage of apple trees. Due to the fast flower formation, the resulting crossing products allow a much earlier beginning of research, e.g., on the elucidation of genome functions or on the metabolic cascades.
- In a collaborative project with partners in Spain and France for which the *Vitis* collections of the three countries were the basis, the establishment of a European core collection of *Vitis* was successfully launched. The backbone of the collection will be extensive molecular data on the genetic diversity.

Taking the international development in the commercial cultivation of transgenic plants into account, the Federal Ministry initiated in 2005 a “Research programme to ensure the protection of GM-free and GM-based agriculture and of biodiversity”. From the very beginning, the BAZ as well as its scientific partners FAL and BBA have been involved in drafting the programme as well as in planning and implementing the field trials with transgenic and conventional GM-free maize. However, significant results can only be expected after several years of test practice.



BUGA 2005 at Munich – ‚Pilot‘, a new apple cultivar from the breeding programme at Dresden-Pillnitz



IGW 2005 – promotion of young talents

The research activities of BAZ in the period reviewed were again flanked by hosting a number of scientific events, among others:

- Electrical Penetration Graph (EPG)-Workshop at Aschersleben (19-20 April)
- Festive colloquium on the occasion of the retirement of the head of the Institute of Abiotic Stress Tolerance in Groß Lüsewitz, Prof. Dr. Wilhelm Flamme (14 June)
- Summer meeting of the “Potato Breeding and Seed Potatoes Production” section of the Society of Plant Breeding (GPZ) at Groß Lüsewitz (13-14 June)
- Colloquium to mark the 100<sup>th</sup> return of anniversary of Professor Becker, the founder of plant breeding research at Quedlinburg
- Meeting of the “Fruit and Grapevine” section of GPZ at Siebeldingen (18-19 September)
- Meeting of the “Medicinal and Aromatic Plants” section of GPZ at Quedlinburg (16 November)

With its broad public relations work, the BAZ continued to make people aware of the general assignment as well as the potentials and methods of breeding research and plant breeding. Addressing the general public in many ways, BAZ researchers explain the relevance of their work, that among others guarantees an agricultural production characterized by reliability of high-yields, high quality and sustainable production methods, contributes to the generation of alternative energy sources and raw materials and to the protection of our genetic resources and, last not least,

influences the laying out of future agricultural landscapes. Therefore the BAZ is an active participator in events such as

- International Green Week, Berlin
- German Horticultural Show (BUGA), Munich
- Long Night of Sciences, Dresden
- European Day in the Land of Saxony-Anhalt, Quedlinburg

GW 2005 – in the wine-cellar of the Institute of Grapevine Breeding Geilweilerhof





Girls' Day 2005

On 1 October, the Institute of Fruit Breeding at Dresden-Pillnitz organized its first so-called Apple Day under the motto “The apple in the course of time”. The many visitors in Dresden, but also our guests attending the numerous other presentations or popular scientific lectures given by the scientists of BAZ clearly show the growing interest of the general public in topics related to the breeding and production of cultivated plants.

In 2005, the BAZ organized again a so-called “Girls' Day”. This special campaign as well as the visits of several groups of school and university students to the BAZ institutes are organized by our staff to allow the up-and-coming generation of young scientists 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 this future-oriented field of science that breeding research and breeding of plants represent.

As far as vocational training is concerned, BAZ could manage to hold its high rate of the previous years. As shown in the survey, altogether 34 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)	21
Agriculturist	2
Cellarman	1
Winegrower	4
Assistant in office communication	4
Graduate in biotechnology (Dipl.-Ing.)	2
<b>Total</b>	<b>34</b>

The 14<sup>th</sup> year in the existence of BAZ was also marked by two more events. Almost a year after entering retirement, the former head of BAZ, Dr. Manfred Neumann, was decorated with the Cross of the Order of Merit of the Federal Republic of Germany. The medal was handed over to him by the Minister-President of Saxony-Anhalt, Professor Dr. Wolfgang Böhmer. We sincerely congratulate Dr. Neumann on this high honour that acknowledges his outstanding commitment to the BAZ and to the site of Quedlinburg.

His predecessor in office, the first head of BAZ and long-time director of the Institute of Grapevine Breeding Geilweilerhof, Prof. Dr. Dr. h.c. Gerhardt Alleweldt, died on 28 March 2005 at the age of 78. From January 1992 to July 1995, he was the director of the at that time young federal centre and laid the decisive foundations for the development and scientific priorities of the BAZ. The scientists and employees will gratefully remember Professor Alleweldt's commitment to BAZ.





**Institute  
of  
Resistance Research and  
Pathogen Diagnostics**

**Aschersleben**

# Institute of Resistance Research and Pathogen Diagnostics

The tasks of the Institute of Resistance Research and Pathogen Diagnostics (IRP) are comprehensive and tightly linked to projects of other institutes of the BAZ which deal with the improvement of resistance of crops.

Research activities of the institute's working groups – pathogen diagnostics and resistance research – are directed on the development of methods of diagnostics and resistance testing as well as their utilisation. In addition, mechanisms of resistance are investigated too.

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## Resistance testing, mechanisms of resistance and improvement of resistance

To provide breeders with useful resistant material it has to be selected from a larger number of wild forms. Appropriate methods have to be developed for this which give the opportunity for a fast and reliable selection of desired genotypes.

Investigation of mechanisms of resistance provides the opportunity for its targeted improvement.

### Viruses as a serious threat for potato growing

Potato belongs to the most important food items in Germany. Unfortunately, it can suffer from several diseases, especially those caused by viruses. Actually, the most important potato virus is the aphid transmitted *Potato virus Y* (PVY). During the last years it was observed, that new highly virulent strains permanently spread which cause severe damages on potato tubers even after primary infection (Fig. 1). In Germany, actually registered cultivars are only partially resistant to PVY. For this reason material with improved resistance will be developed for breeders in co-operation with the Institute of Agricultural Crops Groß Luesewitz (ILK). Virus resistances will be transferred from wild *Solanum* species into the cultivated potato using somatic hybridisation. Before launching back-crossing programs the fusion products have to be examined for their interspecific hybrid character (wild species x cultivated form). Therefore, different molecular techniques (SSR, AFLP, MFLP) were established which permit a reliable identification of somatic hybrids.

Using SSR primers amplifying polymorphic DNA fragments of the fusion partners (Fig. 2) as well as the AFLP technique, more than 800 hybrids could be identified unambiguously.

After this, the selected hybrids and their back-crosses were evaluated for PVY resistance and late blight (*Phytophthora infestans*).

Fig. 1 : Tuber necrosis at late stage induced by PVY<sup>NTN</sup>

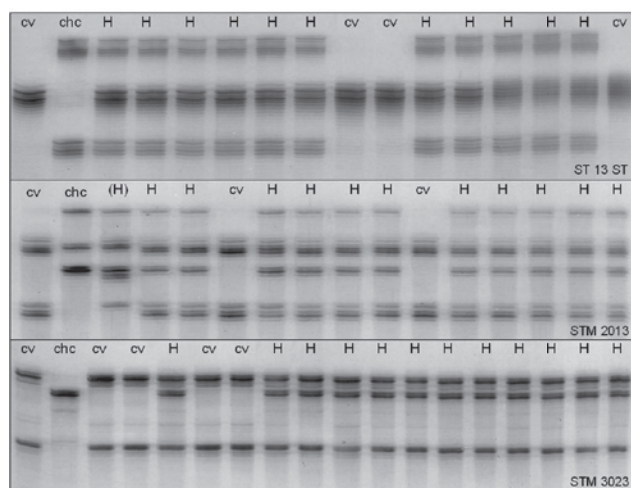


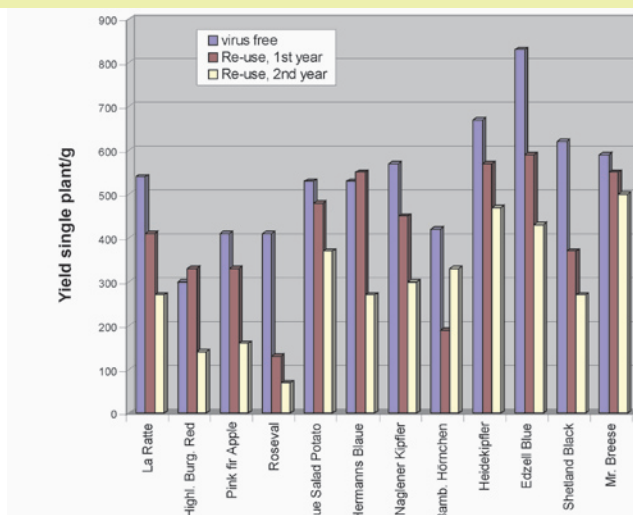
Fig. 2: SSR analysis for identification of somatic hybrids (H) from the fusion 'Delikat' (cv) X *S. chacoense*(chc).

First results of resistance testing are encouraging, as a large number of new sources of resistance could be identified. Among them no genotypes were found, which revealed resistance only to PVY<sup>N</sup> or PVY<sup>NTN</sup> what would have been of special interest for practical breeding. Several sources have been identified which provide resistance to all tested strains.

### Are viruses really as harmful as reported?

Organic farmers often take the view that potatoes grown in this kind of agriculture will recover from virus infection or suffer only slightly. In the framework of a project it will be tested which yield losses can be expected in organic farming for different organic cultivars after virus infection. Preliminary results demonstrated (Fig. 3) that even under organic farming conditions yield depressions have to be expected. Potato cultivars which might represent an interest for organic farming have been tested for susceptibility to tuber

Fig. 3: Yield reduction of potato grown under organic conditions caused by virus infection. Mean values of single plant yield in 2005 are shown.



necrosis caused by PVY<sup>NTN</sup> also in 2005. Compared to control cultivars non of the tested cultivars reacted on artificial infection with tuber necrosis.

The collection of old cultivars suited for organic farming was extended for further numbers. All samples hold in the collection are free of *Potato spindle tuber viroid* and most were already freed from potato viruses.

### ■ Understanding mechanisms of plant defence to viruses – basis for targeted improvement of resistance

Beside unravelling molecular basics of plant defence reactions a detailed knowledge on ultrastructural changes in infected tissues is of great importance for the direct improvement of resistance.

### ■ Special features in ultrastructure as result of resistance reactions

In previous investigations we have shown by scanning electron microscopy, that in barley plants of the cultivar ‘Salome’, resistant to *Blumeria graminis*, germinated mildew spores form appressoria, penetration of leaves, however, did not occur. In the contact areas we frequently observed the formation of papillae. It was shown by X-ray microanalysis that in these papillae amounts of silicon are accumulated

(Fig. 4). The specific accumulation of Si in the area of papillae suggested, that Si is important for the expression of mlo-resistance of the cultivar ‘Salome’.

To prove this hypothesis, plants of the cultivar ‘Salome’ were grown up in a medium free of Si. After inoculation, the plants showed distinct mildew symptoms (Fig. 5), the resistance was broken. Indeed, on the sheets papillae were detected, silicon enrichments in the papillae were not observed. After addition of sodium / potassium silicate to the culture medium no mildew symptoms were found. Si-enrichments were found in the area of the papillae of these plants. These findings show that the mlo-resistance in barley is really based on a Si enrichment at the penetration place.

### ■ The characterisation of a defence protein family

The thaumatin-like proteins (TLPs) belong to the defence proteins of plants. The sequences and structures of the barley TLPs were compiled to get hints for their functions. Transcripts encoding eight different barley members were identified and cloned. All the TLPs from the infected leaves (Fig. 6) were subjected to MALDI-TOF mass spectrometric measurements resulting in fragments, which were found to be in accordance with the deduced peptide sequences. The members of the family fall into two subgroups.

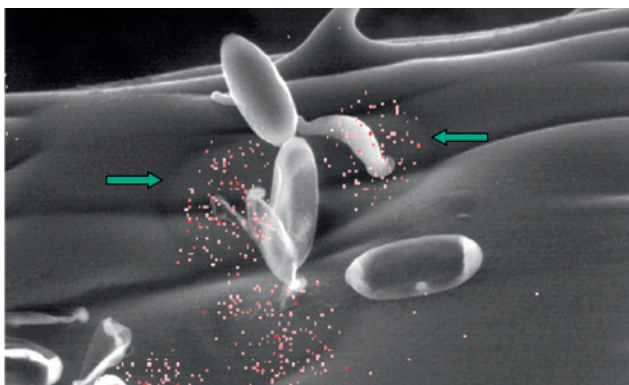


Fig. 4: Germinated mildew spores on the leaf surface of a barley plant (cv 'Salome') with papillae (arrows). Red labels: X-ray signals for silicon accumulation.

Fig. 5: Surface of a leaf from a barley plant (cv 'Salome'), cultured on a silicon free medium and inoculated with spores of powdery mildew.

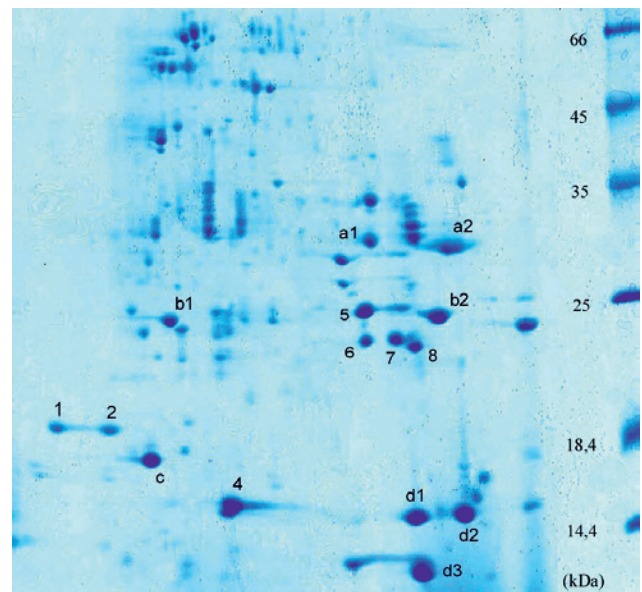
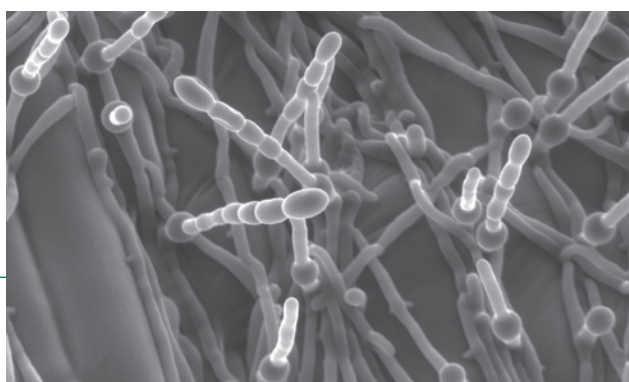
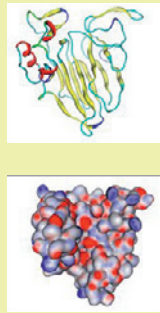


Fig. 6: Coomassie stained 2-D PAGE gel of acidic extracted barley leaf proteins. First dimension (left to right pH 3-10): IEF; second dimension (top to bottom): SDS-PAGE. The spots of the PR-5 proteins are numbered 1, 2, 4-8 according to TLP1, TLP2, and TLPs 4 – 8, respectively. Other pathogenesis-related proteins, which also have been identified by MALDI-TOF MS, are indicated by ‘a’ for  $\beta$ -1,3-glucanases, ‘b’ for chitinases, ‘c’ for superoxididismutase, and ‘d’ for the three spots of PR1 proteins.

Fig. 7:

**Molecular modelling of barley TLP7. Top: Representation of the secondary structure elements of the TLP7 (yellow arrows indicate beta sheets, red are alpha helices and the remaining regions are coil loop structures). Bottom: In identical orientation to the secondary structure the calculated molecular electrostatic potentials of TLP7 are indicated. Basic regions are shown in blue and acidic regions are shown in red.**



In co-operation with the Leibniz Institute of Plant Biochemistry Halle modelling experiments were performed for secondary structures and molecular electrostatic potentials of all eight barley TLPs, based on zeamatin as a homology model. The secondary structure of the studied proteins is characterised by an extended beta sheet in the centre of the proteins. In addition, within the bigger TLPs 5–8 there is at least one  $\alpha$ -helix (i.e. TLP7 in Fig. 7). All TLPs except TLP3 show a negatively charged cleft caused by acidic residues, which may represent a binding site for not yet known ligands. Furthermore, the TLP isoforms show small differences in proposed topology and surface electrostatic potential around the acidic cleft and in other structural regions, which have to be considered as determinants for specificities of the TLPs towards putative receptor targets.

From transgenic rape plants showing strong overexpression of barley TLP8 and enhanced resistance against *Plasmodiophora brassicae*, DH lines were produced by means of microspore culture. Resistant lines should be used for crossing with transformed rape lines with improved resistance due to the overexpression of barley  $\beta$ -1,3-glucanase gene. In addition, potato plants transformed with TLP8-gene were subjected to a second transformation using a construct containing a gene coding for barley  $\beta$ -1,3-glucanase. These studies are aimed to detect synergy effects between these two barley PR-proteins in potato and rape plants.

Together with the IPK Gatersleben experiments on the improvement of virus resistance by expression of single chain variable fragment antibodies (scFv) have been continued. ScFv are directed against non constitutive proteins of the viruses. Enhancement of virus resistance observed in the first pedigree generation was not stable in further generations.

### ■ Bacterial diseases cause concern of growers

Leaf spots on corn salad are caused by *Acidovorax valerianellae* sp. nov. The effective method to restrict the spread of the disease is the breeding and cultivation of resistant cultivars. The species *Valerianella rimosa* and *V. dentata* (basic breeding material) proved to be resistant against isolates from *A. valerianellae* from cultivation areas in Germany.

In further examinations the two species were tested against the isolate CFBP 4730 from France (aggressive strain). The detection of CFBP 4730 (Fig. 8) in the wild forms was not possible. Thus, the resistance properties of *V. rimosa* and *V. dentata* provide an excellent genetic basis for the development (creation) of resistant cultivars. In the next step the developed method for resistance screening has to be adapted for application under field conditions.

### ■ Sources of the resistance to soil-borne viruses

So far, the chemical control of the soil-borne virus vector *Polymyxa graminis* has remained unsuccessful. Therefore the cultivation of cultivars with resistance to the furoviruses *Soil-borne cereal mosaic virus* (SBCMV) and *Soil-borne wheat mosaic virus* (SBWMV) and the bymovirus *Wheat spindle streak mosaic virus* (WSSMV) is the only effective method for the protection of cereals against these virus diseases.



Fig. 8: Symptoms of leaf spots caused by *A. valerianellae* sp. nov. (CFBP 4730) on corn salad.

In barley (*Hordeum bulbosum* L.), *Polymyxa* resistant forms were selected already in previous years. In a collaborative project with the Saatzuchtgesellschaft Streng's Erben GmbH&CoKG, these materials were used to establish mapping populations.

In wheat (*Triticum aestivum* L.) and triticale, test methods allowing an effective resistance screening to soil-borne viruses were developed and applied to respective gene bank materials. These methodological works were successfully finished in 2005.

Investigations on the resistance type to furoviruses were carried out in climatic chambers. Under these controlled conditions, it could be demonstrated that roots of wheat varieties that were classified as resistant so far showed infection symptoms after virus transmission by vector. In numerous single plants tested, the SBCMV spread to leaves (appr. 25%). This



fact is contrary to the proposed translocation resistance in wheat genotypes, i.e. the prevention of virus movement from the root to the upper parts of the plant. After mechanical leaf inoculation of resistant varieties, a high percentage (20% to 70%) of SBCMV infection was observed.

In the course of a resistance selection in different infested locations in Saxony-Anhalt, one field was identified showing infection of wheat forms (varieties, DH-lines and wild forms) that used to be resistant in other infested areas (Table 1).

This is the first evidence for the occurrence of different virulent forms of the SBCMV. The reason for this resistance reaction is still to be elucidated in order to know whether the environment conditions, or genetic variability of wheat materials or differences in virulence between pathogen populations are involved in this event.

### ■ Is the cultivation of durum wheat an option for agriculture?

The durum wheat (*Triticum durum* Desf.) supplies the raw material for pasta production. The loess soils of arid regions of Saxony-Anhalt are particularly suitable for the cultivation of durum wheat. The stabilisation of winter hardiness, the improvement of different quality traits and the resistance to diseases are important prerequisites for the increase of durum wheat production. Therefore investigations of resistance to fungal leaf and ear diseases and to soil-borne viruses were carried out. The results of resistance screenings showed that only a few durum wheat varieties had a low susceptibility to important fungal pathogens. The newly developed breeding lines of the project partner (Südwestsaat GbR, Rastatt) conferred a high level of resistance. During an evaluation of genetic resources of durum wheat, 157 gene bank accessions were identified with diminished disease development after *Fusarium* infection. Thereof 55 forms were classified as

Fig. 9: Genetic diversity of *Triticum durum* Desf. as revealed by spike morphology and stalk length.



Tab.1: Infection level of different wheat accessions with SBCMV and WSSMV at different locations.

<i>Triticum aestivum</i>	Extinction <sup>#</sup>			
	SBCMV		WSSMV	
	Gö*	WN*	Gö	WN
<b>cultivars</b>				
<i>Autan</i>	0	0,21	0	0
<i>Caesar</i>	0	0,66	0	0
<i>Charger</i>	0	1,09	0	0,28
<i>Claire</i>	0	0,42	0,24	0
<i>Hereward</i>	0	0,93	0	0
<i>Ökostar</i>	0	0,38	0	0
<i>Tremie</i>	0	0,23	0	0
<b>DH-lines</b>				
7	0	0,18	0	0
8	0	1,08	0	0
9	0	0,31	0	0
50	0	1,28	0	0
78	0	1,8	0	0
<b>susceptible standard</b>	<b>1,72</b>	<b>1,91</b>	<b>0,76</b>	<b>1,26</b>

\* Locations Gö - Gödnitz and WN - Walternienburg. # - Extinctions for DAS-ELISA measured at 405nm, mean values from 4 repeats.

susceptibility class 1 (very low susceptibility); 4 accessions resisted infection. More than 60 accessions showed a very low infection level after inoculation by *Septoria tritici* and *Stagonospora nodorum*. This gene bank material is very heterogeneous (Fig. 9) and therefore still requires considerable breeding efforts.

The tested durum varieties are normally highly susceptible to soil-borne viruses. Among the examined accessions, 6 durum wheat forms with a low level of virus infection could be selected. This material can be used for subsequent resistance breeding.

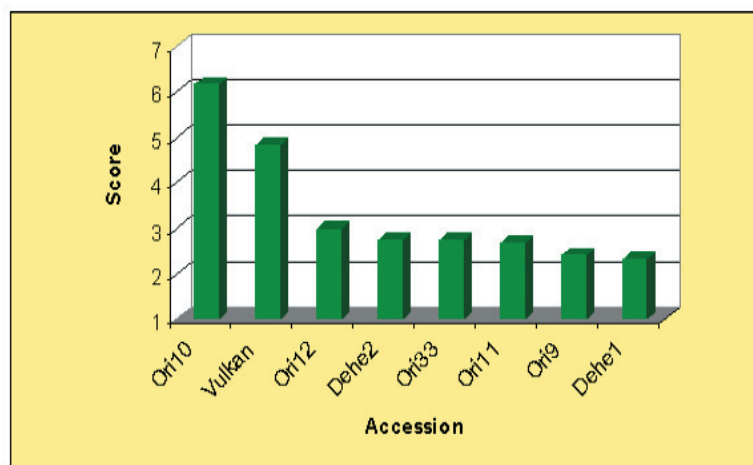
### ■ Spice plants have to be particularly healthy

In connection with an increased awareness of the consumer for use of healthy foods, medicinal and aromatic plants are of utmost importance. It is assumed especially in this case that they are hygienically absolutely harmless, and that they have mostly even constitutional characteristics. Therefore, their quality is subjected to special requirements. The cultivation of cultivars with resistance to diseases contributes not only to reduce the application of pesticides and the resulting risk of residues but it prevents also the formation and enrichment of toxic compounds from pathogens in plant tissue.



Fig. 10:

Evaluation of resistance of oregano accessions to *Phoma* sp. performed in trays with detached shoots.



In 2002, a massive outbreak of diseases was observed in oregano crops (*Origanum vulgare* ssp. *hirtum*) in the traditional Aschersleben marjoram cultivation area caused especially by an attack with *Phoma* sp. Fungicides for direct control of the pathogen are not available. ‘Vulkan’, the only approved cultivar in Germany, proved to be highly susceptible to this pathogen. Therefore, the development of new, resistant cultivars is necessary. A practicable method for resistance screening to *Phoma* has to be developed. Detached shoots of plants cultivated in the greenhouse are used in this test. These are inoculated with pycnospores of the pathogen. A close positive correlation was usually established between the scores and the ELISA values indicating the mycelium concentration. In some cases, weak symptoms corresponded with unexpected high ELISA values what can be considered as an indicator for pathogen tolerance. Most accessions proved until now showed a significant higher resistance level than the cultivar ‘Vulkan’ (Fig. 10). These could be the basis for cultivars with improved resistance.

#### ■ *Monilia*-twig blight is an increasing problem

The *Monilia*-twig dieback, the most important disease of sour cherry, occurs to an increasing degree in the plantations. The problem cannot be controlled alone by application of fungicides. Relief could be produced by sour cherry cultivars with improved resistance or tolerance to *Monilia laxa*. Therefore, the development of a resistance screening method was started. A PTA-ELISA was developed for pathogen detection in the plant using polyclonal antisera. A variant of the Tissue Print Immuno Assay proved to be also suitable to localize the pathogen in infected shoots. First resistance studies using knip trees of 10 sour cherry cultivars (Fig. 11) provided encouraging results. Between the cultivars, differences in the percentage of infected flowers and shoots with

dying symptoms were established. The methods developed will be applied in the BAZ-Institute of Fruit Breeding Dresden-Pillnitz.

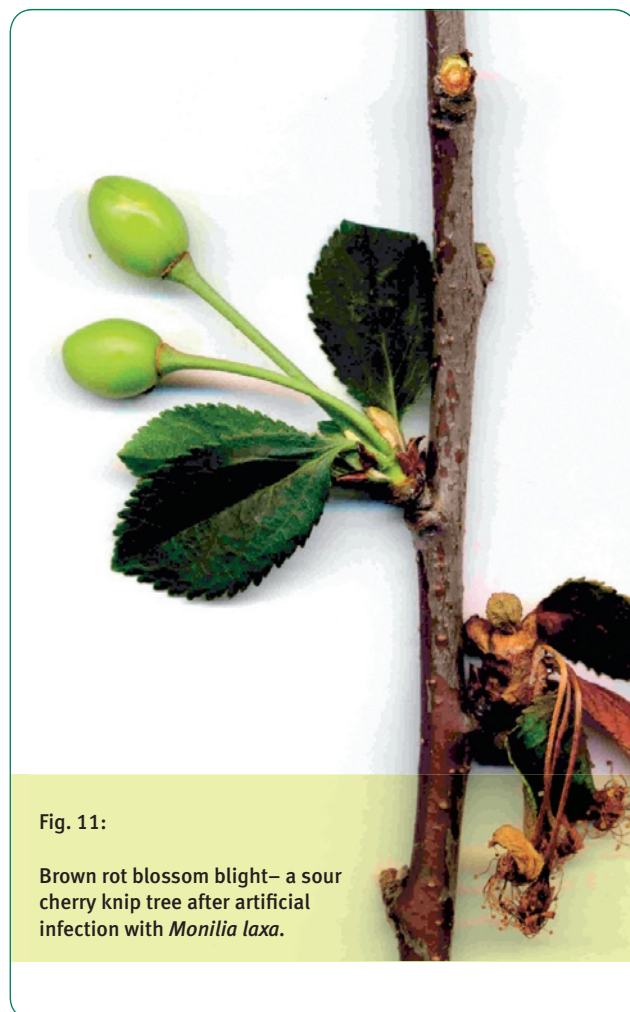


Fig. 11:

Brown rot blossom blight – a sour cherry knip tree after artificial infection with *Monilia laxa*.

## Development of diagnostic methods and diagnostics

Antibody based test methods (immunoassays) possess by virtue of their sensitivity and practicability still a great importance. Antibodies also form the basis for application of IC-RT-PCR which is a highly sensitive and specific diagnostic tool for detection of viruses. Polyclonal antisera (PAS) and monoclonal antibodies (MAbs) were generated against several pathogens.

### ■ Diagnostic methods for differentiation of plant viruses

#### Differentiation of *Wheat dwarf virus* types

*Wheat dwarf virus* (WDV) exists in two main pathotypes infecting either barley or wheat. Both types can be differentiated by PCR-methods. Sequence data comparisons revealed that the coat proteins of the two forms differ in amino acid sequence in some regions so that it appears to be feasible to generate differentiating MAbs. An isolate of WDV transmissible by the leafhopper vector only to barley but not to wheat was purified and used as antigen for production of PAS and MAbs. As expected, the polyclonal DAS-ELISA reacted with all tested WDV pathotypes whereas a selected MAb in TAS-ELISA exclusively recognized all samples originating from barley but never reacted with WDV pathotypes infecting wheat or triticale.

#### Improvement of diagnosis and differentiation of soil-borne cereal viruses

Furoviruses were isolated from plants of rye and wheat varieties grown in different regions in Germany. By means of RT-PCR and specific primer combinations the isolates were identified either as *Soil-borne wheat mosaic virus* (isolate 'Heddesheim', SBWMV-Hed) or as isolates of *Soil-borne cereal mosaic virus* (SBCMV). With specific polyclonal antisera from other laboratories a serological differentiation of both virus species was not possible. Therefore, 8 PAS were produced in the own lab, of which only 2 reacted specifically with the homologous virus. However, at high virus concentrations a differentiation was still difficult. Therefore, MAbs to both pathogens were produced. One of the generated MAbs was suitable for detection of SBWMV in a MAb-based DAS-ELISA detection system and another one can be applied for the determination of SBCMV by TAS-ELISA.

### ■ Development of diagnostic methods for fungal antigens

#### *Fusarium* head blight and *Fusarium* species – formidable toxin producers

Workings on improvement of detection systems for fungal exoantigens (ExAg), accumulated in the mycelium of *Fusarium* species grown in small cereal grains, were continued in the frame of an externally financed project. The application of polyclonal antisera to ExAg preparations of the two species *F. graminearum* and *F. culmorum* in PTA-ELISA allowed the genus-specific detection of all investigated *Fusarium* species. Even though the polyclonal test system was further optimized problems exist still in regard to test sensitivity at low amounts of mycelium in the grain. In order to improve this situation and to configure the assay more sensitive and specific a panel of MAbs was generated to ExAg of two *Fusarium* species and one antibody was selected which is applicable for routine analyses of wheat flour. This antibody can be applied in different ELISA formats and is particularly suitable for the preferred variant of DAS-ELISA.

#### Leaf blight of carrot

Carrot leaf blight or leaf spot of carrot is caused by the fungus *Alternaria dauci* (Kühn), Groves & Skolko. In co-operation with the Institute of Horticultural Crops in Quedlinburg, for the evaluation of resistance resources in carrots, several PAS to the fungus were produced and successfully used in PTA-ELISA. In ELISA and Western blotting (WB) experiments the antisera showed in fact conspicuous cross-reactions with cultures of all tested *Alternaria* species, however the characteristic patterns produced by each species on the WB membrane could be used for discrimination. By serological quantification of the relative amount of mycelium the process of resistance evaluation can be accelerated.

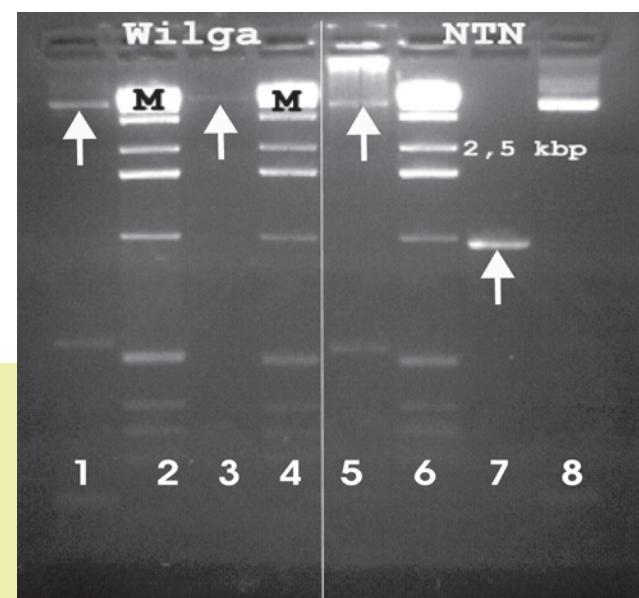


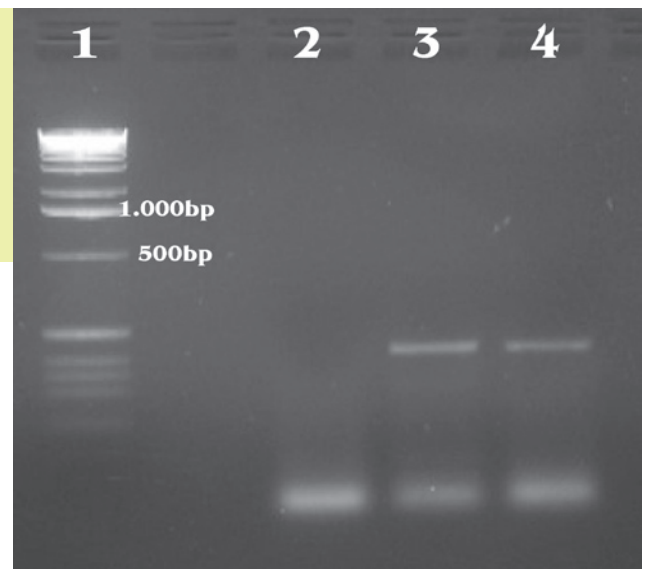
Fig. 12:

Detection of isolates of PVY<sup>W</sup> by means of long range PCR. Notice the unusual large size of the PCR fragments.

Fig. 13:

**Detection of BYDV in single aphids.**

- 1 – marker,
- 2 – aphid not carrying virus,
- 3 – detection in living aphid,
- 4 – detection in an aphid fixed in ethanol.



### ■ About the use of sequence data of virus genomes

For resistance testing of potato hybrids PVY isolates had to be chosen which are representing the whole range of existing strains. To achieve this besides their biological data also data on their molecular structure had to be included. The genomic structure of 13 isolates was analysed by means of complete sequencing. We were able to detect for the first time a North-American strain of PVY<sup>NTN</sup> in Germany. A number of field isolates, which were able to overcome transgenic PVY resistance, showed an exceptional structure. For purposes of resistance testing one isolate of each of the known 6 PVY strains was chosen.

Based on the sequence data primers were deduced for differentiation of PVY strains. Together with partners their reliability was tested on a set of biologically and serologically well defined isolates from Poland, New Zealand and Germany. PCR data matched with the expected results or some mixed infection could be detected. Identification of isolates of PVY<sup>NW</sup> was complicated as in this case a fragment of 4,2kbp had to be amplified. An example is given in Fig. 12. Analysis of the strain spectrum revealed that strains PVY<sup>NW</sup> and PVY<sup>NTN</sup> predominate in Germany and Poland, while in New Zealand mainly O-, N- and C-strains could be identified.

Very often we are faced with the question, why in some cases aphids do not transfer viruses. For a better understanding of this problem it was necessary to develop a method for detection of viruses in a single aphid. In the framework of an externally financed project together with the Institute of Epidemiology and Resistance Resources (IER) and the company BTL Sagerheide a simple method was developed for detection of *Barley yellow dwarf virus* in a single aphid. Result of a RT-PCR-analysis is shown in Fig. 13. This work is based on sequence data previously collected.

### A look into the future work

It is our endeavour to link our research potential more closely with the scientific work of other institutes of BAZ. Based on the collaboration with numerous partners the objectives of research will be quite diverse in future, too.

Crossing populations of barley segregating for *Polymyxa*-resistance will be characterised pheno- and genotypically. In co-operation with the ILK we plan to identify and map the relevant resistance gene(s).

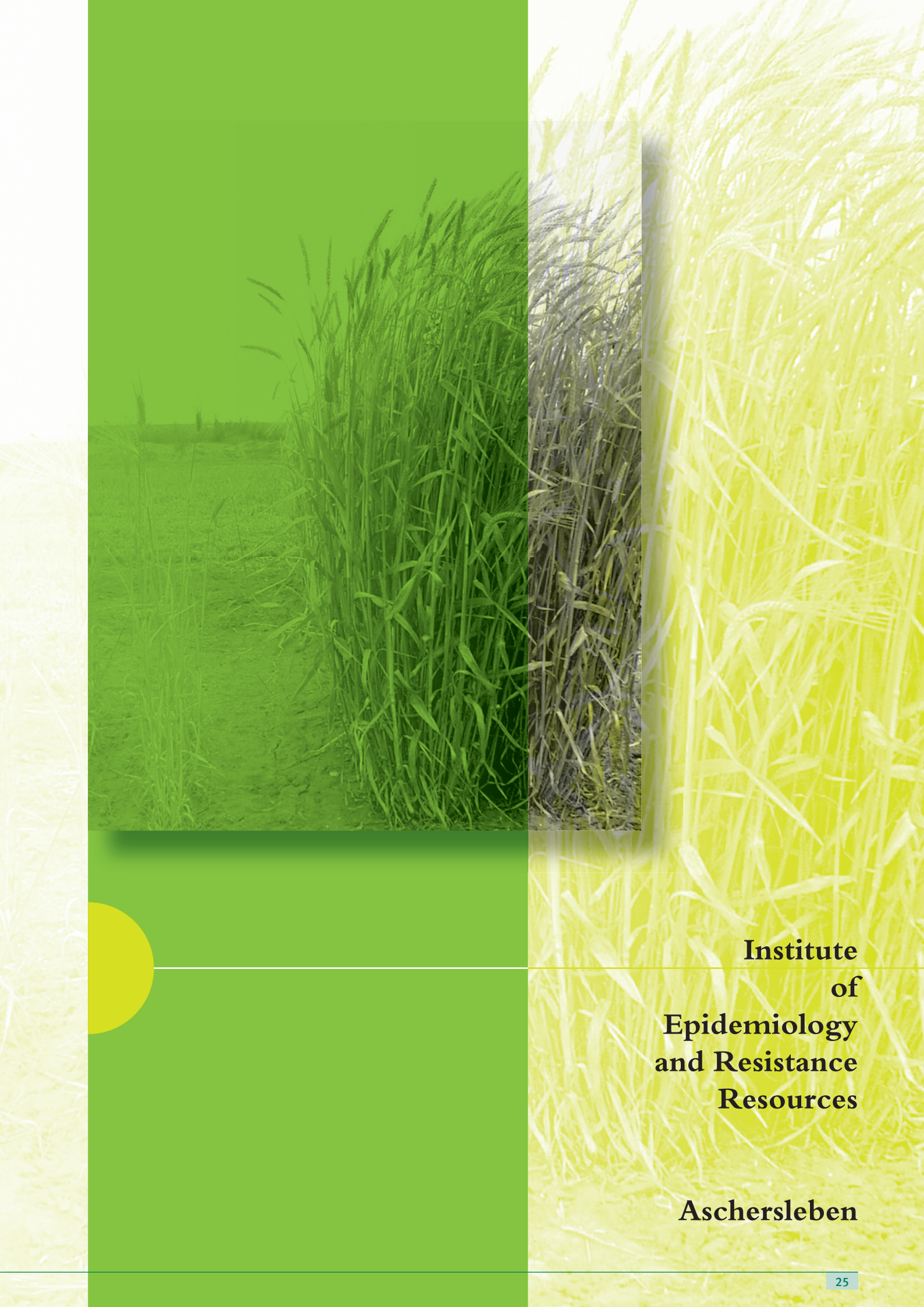
Contamination caused by infection with *Fusarium* spp. continues to be an important topic of our research work. In co-operation with the Institute of Plant Analysis express methods for detection of *Fusarium* infection at wheat and determination of toxin content will be developed.

In the framework of a project support from BMBF the method for differentiation of PVY-strains will be adopted for analysis of changes in virus structure in transgenic plants together with a partner.

Method of detection of viruses in aphids will be extended for quantification of the virus content. Using this approach together with IER we will investigate feeding behaviour of aphids and acquisition of the virus.

Experiments for selection of resistant oregano accessions will be continued in 2006. It is of particular interest to verify the results of bioassays in field tests.





**Institute  
of  
Epidemiology  
and Resistance  
Resources**

**Aschersleben**

# 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 essential for sustainable plant production. With respect to soil-borne pathogens – e.g. viruses – which cannot be combated by chemical measures, resistant cultivars are a prerequisite for ensuring wide and economic crop rotations.

Therefore, research of the Institute of Epidemiology and Resistance Resources (IER) aims at improving resistance of crop plants by the analyses of virulence of pathogens of agronomic importance (fungi, viruses, bacteria, insects) and the evaluation of 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. Research carried out at the IER contributes to the “National programme for the maintenance 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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## Viruses and invertebrate pests

At present, soil-borne viruses of barley, i.e. *Barley mild mosaic virus* (BaMMV) and *Barley yellow mosaic virus* (BaYMV), and of wheat [*Soil-borne cereal mosaic virus* (SBCMV) and *Wheat spindle streak mosaic virus* (WSSMV)], which cannot be combated by chemical measures, as well as the insect transmitted *Barley yellow dwarf virus* (BYDV) and *Wheat dwarf virus* (WDV) are in the focus of epidemiological and resistance research. Similar work is carried out on *Turnip yellows virus* (TuYV) which is an important pathogen on rape seed in Germany. With respect to insects in cereals, virus vectoring aphids and blossom midges (*Sitodiplosis mosellana*, *Contarinia tritici*) are under investigation.

In the growing season 2003/2004 a BaMMV isolate has been detected for the first time in Germany overcoming the resistance gene *rym5*. However, it turned out in additional growth chamber experiments that some resistance genes, e.g. *rym9*, *rym11*, *rym13* as well as the dominant resistance genes *Rym14<sup>Hb</sup>* and *Rym16<sup>Hb</sup>* are still effective against this strain. With respect to the emergence of new resistance breaking strains, pyramiding strategies of respective resistance genes, which in the case of barley yellow mosaic virus have proven their efficiency already (Werner, K., W. Friedt, F. Ordon, 2005: Mol. Breeding 16, 45-55) may become of special importance in the future in order to prolong the usability of partly overcome resistance genes (Fig. 1). First results give hint, that lines derived from this pyramiding programme carrying *rym5* and *rym9* are resistant to all strains of BaMMV and BaYMV known in Europe.

In France *Soil-borne cereal mosaic virus* and *Wheat spindle streak mosaic virus* are important pathogens of wheat, already and the same is expected for Germany in the near future. In the frame of the EU funded project WHEATPROTECT it turned out by analyses of DH-lines that resistance to *Soil-borne cereal mosaic virus* is inherited in a monogenic manner. Based on these phenotypic data, SSR markers have been developed facilitating efficient marker based selection procedures. This is of special importance for wheat breeding in Germany as up to now no fields facilitating efficient phenotypic selection are available.

In 2005 the project "Development and use of efficient screening methods for *Wheat dwarf virus* tolerance in barley, wheat and oats" ended. In the frame of this project efficient screening methods for field and growth chamber conditions were established including rearing of the vectoring leaf hopper *Psammotettix alienus* and the development of a polyclonal antiserum for virus detection. Besides this, in collaboration with Dr. Jörg Schubert and Dr. Frank Rabenstein (Institute of Resistance and Pathogen Diagnostics) serological and PCR based methods were developed allowing differentia-

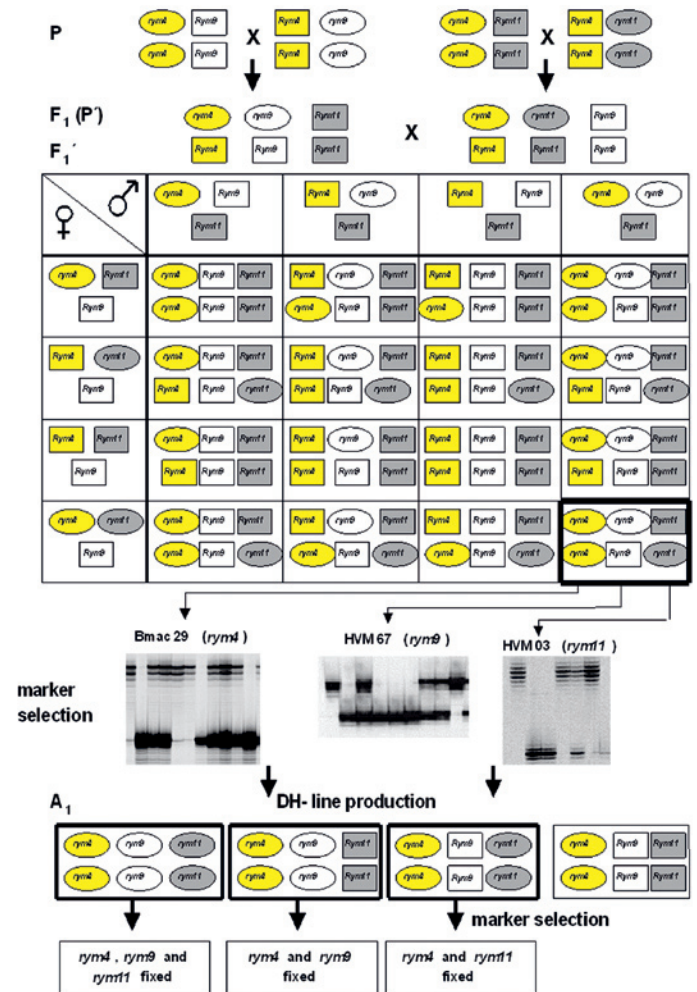


Fig. 1.: Pyramiding different resistance genes against the barley yellow mosaic virus complex using one haploid step (Werner, K., W. Friedt, F. Ordon, 2005: Mol. Breeding 16, 45-55.)

tion of the wheat and barley strains of WDV. In field tests the cultivar 'Post', which already exhibited a high level of tolerance to BYDV, also turned out to be quite tolerant to WDV (Fig. 2).

In 2005 also the project "Development of winter durum wheat with superior quality characteristics and resistance to viral and fungal pathogens" ended. It turned out that within the set of released cultivars no genetic variation is present with respect to BYDV and WDV tolerance, i.e. all cultivars are susceptible. But, three breeding lines and four genebank accessions with a high level of tolerance to BYDV and winter hardiness were detected being the basis to improve these traits in durum wheat (Fig. 3).





Fig. 2.: Screening for WDV tolerance – Reaction of 'Post' (right) in comparison to 'Okal' (center) and the highly susceptible cultivar 'sigra' (left).

Besides cereal viruses, resistance of rape seed to *Turnip yellows virus* is investigated. Assuming a threshold for resistance of  $E_{405}=0.1$  in December, which has been published already, a monogenic mode of inheritance for resistance was detected by artificial inoculation of DH-lines using virus bearing aphids. However, within the set of susceptible lines a broad variation was observed with respect to the virus titre. Repeating these ELISA measurements from April to June results 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 a first differentiating SSR has been identified. In addition to this project, the efficiency of *Myzus persicae* with respect to transmitting TuYV is investigated in relation to environmental conditions. First results give hint that the efficiency is influenced by acquisition and inoculation time as well as temperature.

With respect to *Rhopalosiphum padi* vectoring BYDV-PAV, significant differences between clones were detected on the molecular level by AFLPs as well as with respect to the number of larvae/female (14.2-37.8 larvae/female) and the BYDV infection rate per single aphid (47.9-97.9 %). These results give hint that the epidemiology of BYDV may be strongly influenced by the genotype of the vector.

Besides this, some aphids e.g. *Brevicoryne brassicae* on cabbage, are directly damaging plants. This aphid is of special importance in eco cabbage growing. By evaluating 552 different cabbage genotypes derived from different gene banks, a range of 9.4 to 331 aphids per plant was observed. Out of



Fig. 3a.: Field test of *Triticum durum* for BYDV tolerance; inoculation with virus bearing aphids.

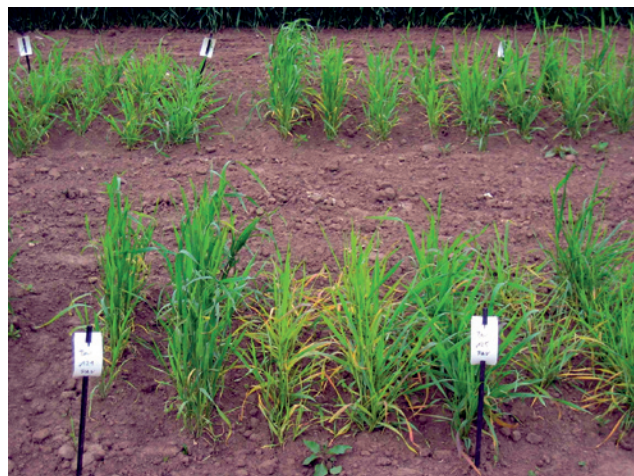


Fig. 3b.: Field test of *Triticum durum* for BYDV tolerance; genotypic differences



Fig. 4.: Blossom midge larvae on wheat

these, five accessions revealed a significantly lower number of *Brevicoryne brassicae* per plant. These genotypes may be used directly in eco growing of cabbage, but are also suited as the basis for incorporating quantitative resistance to this aphid into adapted cabbage breeding lines.

In some parts of middle and northern Germany blossom midges (Fig. 4), i.e. *Contarinia tritici* (Yellow blossom midge) and *Sitodiplosis mosellana* (Orange blossom midge), are quite frequently detected during the last years and may cause damages like this is known in the UK, already. After first genotypic differences concerning susceptibility have been detected already in 2003/2004 by analysing a set of 133 genotypes within the EVAII programme, a set of 20 cultivars was tested in replicated field trials in 2004/2005. On average between 0.7 and 4.9 larvae/ear were detected resulting in a proportion of affected kernel between 4.2 and 25%. Both parameters are strongly correlated. These experiments are replicated in 2005/2006 and first crosses have been conducted to elucidate the genetics of resistance to *Sitodiplosis mosellana*.

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 resistance against *Puccinia hordei* and *Pyrenophora teres* as well as on wheat with respect to *Puccinia triticina*, *Pseudocercospora herpotrichoides*, *Ustilago tritici* and *P. tritici-repentis*. These studies also include the collection of isolates and analyses of virulence each year, e.g. concerning rusts. Respective isolates are included in official trials for cultivar release and in trials for the evaluation of genetic resources. Respective pathogens are hosted at the Institute of Epidemiology and Resistance Resources in several collections.

Due to ending of the funding period of the “German network for the evaluation of genetic resources of cereals for disease resistance (Eva II)”, this project which is co-ordinated by the Institute of Epidemiology and Resistance Resources and carried out in collaboration with private cereal breeding companies and ZADI, had to be intergrated into the institute in 2005 as it is regarded as a permanent task of the BAZ. This was successfully achieved by several internal measures so that EVAII will contribute to the evaluation and use of genetic resources of barley and wheat in plant breeding also in the future. Detailed information can be gained at <http://www.genres.de/eva>.

In the frame of evaluating genetic resources for resistance, a barley landrace derived from the former Yugoslavia has been identified being completely resistant to *Puccinia hordei* and expressing a high level of resistance to net blotch (*Pyrenophora teres*). First results using differentiating isolates give hint that resistance to *P. hordei* is different from all resistance genes known up to now and follows a monogenic recessive mode of inheritance. Based on phenotypic data available on 90 DH-lines, marker development was started using bulked segregant analysis. Similar analyses were started for net blotch resistance of this germplasm.

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. Based on F<sub>2</sub>-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 – as several distinct classes were observed (Fig. 5). F<sub>2</sub>-plants are re-tested in F<sub>3</sub> at the moment in order to get reliable results on the genetics of pre-haustorial resistance to *P. triticina*. Results up to now hint to complementary gene action.

Besides foliar diseases, soilborne fungi, e.g. *Oculimacula yallundae* (syn. *Tapesia yallundae*, anamorph *Pseudocercospora herpotrichoides* var. *herpotrichoides*) and *O. aciformis* (syn. *T.*



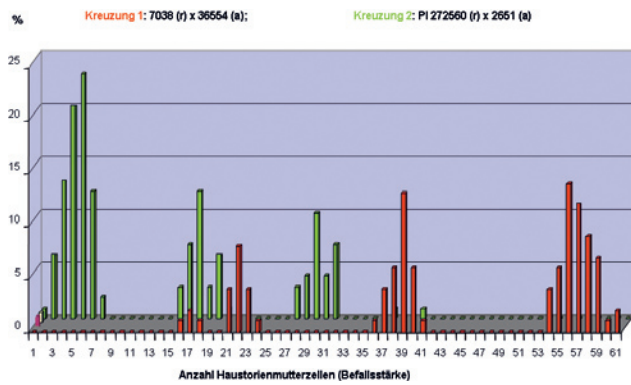


Fig. 5: Segregation of  $F_2$  plants derived from crosses of resistant (r) and susceptible (s) lines of *T. monococtum* after infection with leaf rust (*P. triticina*) giving hint to different genetics of resistance.

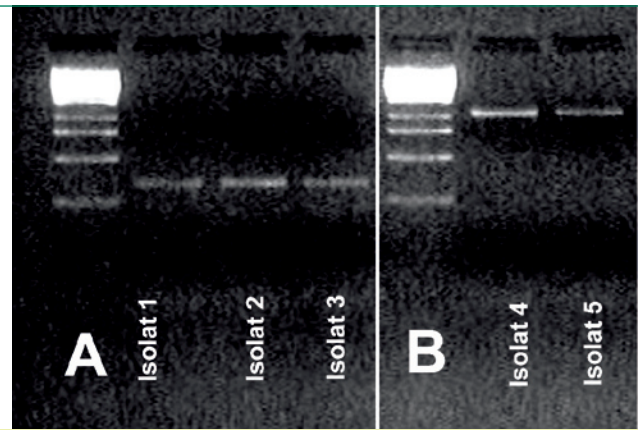


Fig. 6: Molecular identification of  
A) *Pseudocercospora herpotrichoides* var. *acufiformis* (teleomorph *O. acufiformis*);  
B) *Pseudocercospora herpotrichoides* var. *herpotrichoides* (*O. yallundae*).

*acufiformis*, anamorph: *P. herpotrichoides* var. *acufiformis*) are gaining importance due to an increasing portion of cereals in crop rotations. In order to differentiate isolates of *Oculimacula* ssp. molecular techniques were established (Fig. 6), and for reliable selection of genotypes with a higher level of resistance, a selection scheme has been developed in growth chambers in which plants grow without tillering and in which a standardised suspension of spores is applied in the first leaf stage (Fig. 7). This procedure facilitates a reliable evaluation prior to heading, which is a prerequisite for the development of molecular markers for different 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”. Up to now, five spring wheat genotypes did not show symptoms of an *U. tritici* infection after artificial inoculation in 2003/2004. These genotypes are well suited for eco-farming and as parental lines in breeding programmes for *U. tritici* resistance. In order to screen for resistance prior to heading, additional attempts are carried out to develop an efficient ELISA procedure. For this purpose three isolates of *U. tritici* are available which have been transferred into *in vitro* culture (Fig. 8) and will be characterized by a set of differential cultivars. Due to the assumed global warming, bacterial diseases may become of special importance. 61 isolates of *Erwinia amylovora*, the causal agent of fire blight, were analysed for virulence and those being most virulent (3) were selected for testing wild *Malus* ssp. and apple breeding lines of the Institute of Fruit Breeding for resistance. Additional studies aim at the development of molecular markers for resistance

to *E. amylovora*. For this reason, two populations comprising 150 seedlings each, were inoculated (10 scions/seedling) with a defined isolate of *E. amylovora* and screened for resistance. On average 23% of the seedlings analysed did not show any symptoms of fire blight and within the susceptible genotypes a large range of symptom expression was observed.

In cabbage (*Brassica* spp), *Xanthomonas campestris* pv. *campestris* is a pathogen of economic importance for a long time, already. However, up to now nothing is known about the susceptibility/resistance of rape seed (*Brassica napus*) to this pathogen. In very favourable greenhouse conditions all out of 15 rape seed cultivars tested turned out to be susceptible to *Xanthomonas campestris* pv. *campestris* expressing typical symptoms known from cabbage (Fig. 9). With respect to

Fig. 7.: Left: Inoculation of 8 days old wheat seedlings with *Pseudocercospora herpotrichoides*  
Right: Single culm wheat plants 8 weeks after infection

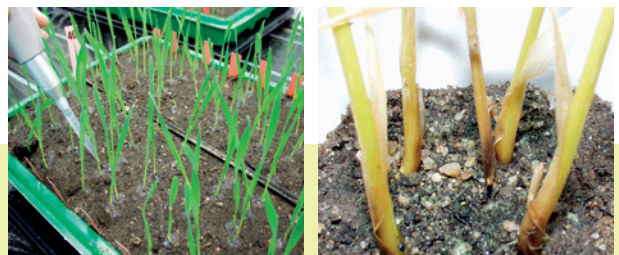




Fig. 8 Left: Smut (*Ustilago tritici*) in a wheat field  
Right: Growth of *U. tritici* on different media

*Xcc* race 1, differences between cultivars regarding symptom expression were observed, while all cultivars were highly susceptible to *Xcc* race 4. Additional analyses revealed that plants get systemically infected by *Xcc*, as *Xcc* could be re-isolated from young leaves. Further analyses now aim at getting information on yield reductions caused by *Xcc* and the identification of donors of resistance.

Especially in southern Germany *Xanthomonas fragariae* has gained evident importance in strawberry production. Therefore, a common project together with the Institute of Fruit Breeding was started in 2005 to determine virulence of different *Xanthomonas fragariae* isolates. Especially two isolates from southern Germany and Switzerland resulted in severe symptoms (Fig. 10) and will be used in future analyses to identify donors of resistance.

## Future perspectives

Due to their economic importance, virus diseases of cereals will be one of the main focuses of the institute. Therefore, at the end of 2005 a new project within the programme PROINNO II 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*” was started. Besides this, in collaboration with the IPK (Prof. A. Graner/Dr. N. Stein) and the group of Rothamsted (K. Hammond-Kosack, K. Kanyuka, M. Adams) future activities will focus on the isolation of additional resistance genes (*rym9*, *rym11*) to BaMMV, BaYMV and BaYMV-2. Similar analysis will be carried out in the EU-CRAFT project “Structural and functional analysis of virus resistance in wheat (*Triticum aestivum* L.) (WHEATPROTECT)“. With respect to the isolated BaMMV/BaYMV resistance locus *Rym4/Rym5* (Stein et al. 2005, Plant J. 42, 912-922), additional analyses in collaboration with the IPK (Prof. Graner/Dr. Steiner) aim at estimating the allelic diversity at this locus and the specificity of these alleles to the different members of the barley yellow mosaic virus complex. With respect to improving tolerance to BYDV, crosses to combine *Ryd2*, *Ryd3* and a QTL derived from cv. ‘Post’ were carried out and subjected to DH-line production. It is expected that pyramiding of the genes may lead to a higher level of tolerance to BYDV due to additive effects. This will result in less spraying of chemicals. Further analyses with respect to virus diseases aim at the identification and mapping of differentially expressed genes. In order to quantify respective differences, a Real-Time-PCR is available at the institute since the end of 2005.



Fig. 9.: Rape seed plant infected by *Xanthomonas campestris* pv. *campestris*



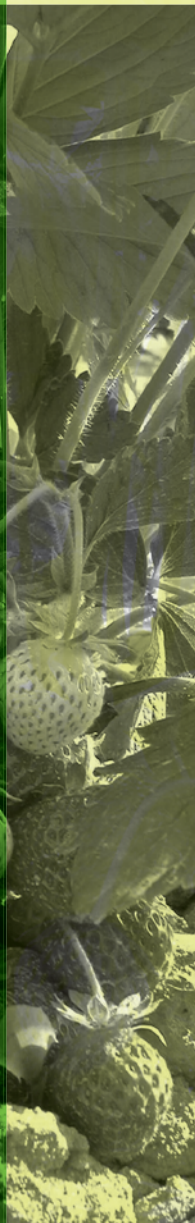
Fig. 10: Bacterial angular leaf spot of strawberry (*Xanthomonas fragariae*)

With respect to fungal diseases, the project “Development of molecular markers for resistance to *Pseudocercospora herpotrichoides* and marker based combination of resistance genes *Pch1*, *Pch2* and a resistance derived from *Aegilops kotschy*” has been started in 2005. By combination of these resistances the project aims at enhancing the level of resistance against this pathogen, which is of special importance due to a constant spread of the area cultivated with cereals. In the frame of exploiting resistance derived from genetic resources, *T. monococcum* will be in the focus in the near future to improve resistance of *T. durum* and *T. aestivum*. Based on the results obtained on the genetics of pre-haustorial resistance to *P. triticina*, future work now aims at the development of molecular markers facilitating an efficient marker based transfer of this resistance to *T. durum* and *T. aestivum*. Additional analyses concerning *T. monococcum* will be carried out in 2006 with respect to *Fusarium* ssp. within the Canadian German Agrobiotec Teamworking project “Reducing fusarium toxins in wheat through genomics guided strategies”. Furthermore, in co-operation with Dr. Bernd Rodemann (Federal Biological Research Centre, BBA) attempts to establish an efficient screening system for resistance to *Gaeumanomyces graminis*, which like *Oculimacula* ssp.

is of growing importance due to ceareal rich rotations, will be carried out. Also *Septoria* ssp. are of rising importance in German wheat production. Consequently, analyses of the efficiency of known resistance genes to German isolates of *Septoria tritici* will start in 2006. Besides this, based on DH-lines, which will be available in 2006, analyses on the genetics of resistance to *Pyrenophora tritici-repentis* will be conducted followed by the development of molecular markers. Additional research activities will deal with 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 DFG-funded project “Estimation of yield functions of selected crop species in relation to genotype and site factors” which is mainly carried out at the University of Giessen and deals with the phenotypic and genotypic evaluation of important winter barley cultivars being the basis for studies on association genetics, has been prolonged for another three years.

Besides these scientific aspects, the Institute of Epidemiology and Resistance Resources will move to new facilities at Quedlinburg in 2006 resulting in a considerable improvement of working conditions.





**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. Scientific work focuses 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 research which allows to increase the efficiency in selection, to evaluate and to improve the resistance to biotic and abiotic factors in breeding material and to increase nutrition 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 was as in the same way as in the year before a reliable partner for collaborations with universities and academies of the city of Dresden and the state Saxony. In 2005, eighteen students got a practical training in different working groups of the institute. Four students were coached during their work for the diploma thesis.

Following, the areas of important research progress in 2005 are highlighted:

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Silke Lesemann  
agricultural engineer (project contract)

Stefanie Reim  
agricultural engineer (project contract)

Matthias Vitten  
agricultural engineer (project contract)



## Genetic resources

The institute is a federal institution responsible for the collection, preservation and evaluation of fruit genetic resources. Due to the long reproductive cycle of fruit crops and the peculiarity of vegetative propagation, fruit genetic resources are preserved in field collections. New plantations are initiated regularly according a timetable based on the development of the individual fruit species. In 2005, a new plantation of the wild species collection in pear (*Pyrus*) was established and new plantations of apple and pear cultivars were initiated. New cultivars with unknown phytosanitary status, including budwood material from orchard meadows, pass an internal health control in the greenhouse for one year before transfer to field plantations. The new planted apple collection will include 686 cultivars and the pear collection 150 cultivars. About 70 % of the cultivars were first mentioned before 1900 and represent valuable fruit genetic resources of Germany.

In addition to preservation, the evaluation of individual collections is of great importance for the gene bank. At the end of April 2005 night temperatures decreased in three consecutive nights to  $-3.2^{\circ}\text{C}$ . This event occurred during blossom of cherries and apples; therefore it was possible to determine the percentage of surviving flowers as an indicator for resistance of flowers to spring frost. The *Malus sieversii* collection (main progenitor of the domesticated apple cultivars) consists of 35 single populations from the centre of origin in Kazakhstan. Survival of flowers at the 'green bud' stage up to the 'balloon stage' of 664 seedlings was between 0 and 100% after spring frost. Frost tolerance of three groups of apple flowers was estimated, and assigned to the areas of seed collection using a cluster analysis. The same evaluations

Fig. 1: Excursion through the collections of fruit genetic resources and presentations of the breeding material are manifold duties of the institute's scientists.



were done in the cultivar collections of the sweet and sour cherries. In general, the sour cherry is more tolerant to frost during blossom time than sweet cherry. In sour cherry, 25 % of 92 investigated cultivars revealed 30 % of flowers being damaged, while in sweet cherry (191 cultivars) there were found only two frost resistant cultivars.

In cooperation with the University of Applied Science in Dresden, an evaluation project is being conducted for the identification of strawberry cultivars regarding the most important morphological parameters of leaves, flowers and fruits. At this point, 87 cultivars planted in special trials in the field have been evaluated for 53 parameters.

Comprehensive recording of fruit quality data was started in 41 strawberry and 48 German apple cultivars to evaluate variability in the available germplasm.

A proposal "Inventorying and documentation of fruit genetic resources in Germany" was prepared for the call "Inventorying of collections and non scientific evaluation in the field of biological diversity" for grants awarded by the Federal Agency of Agriculture and Food.

The goal of the gene bank - preservation of fruit genetic resources - was presented in four lectures or posters, nine demonstrations in the orchard and five exhibitions.

The gene bank, among others, was involved in designing a part of the new permanent exhibition of the Hygienemuseum Dresden and organized actions in this museum (Figure 1 and 2).



Fig. 2: New and old apple varieties presented at the Deutsches Hygienemuseum.

## Breeding of new cultivars

### ■ Apple

The new 'apple year' in 2005 was started with sowing of seeds obtained from crosses. In total 4.623 seeds of 48 hybridizations were used. All seedlings were grown up in the greenhouse under optimal conditions to get rapidly scion for grafting. Seeds of crosses aimed for multiple scab resistance were screened for resistance by artificial inoculation in the greenhouse. Resistant seedlings were selected for grafting into the orchard.

Besides seeds obtained by crossings in the orchard, seeds resulting from crosses with transgenic apple lines were also used. The segregation and heritability of transgenic traits were determined by PCR analysis. Five plants could be detected carrying three resistance related transgenic traits: *Nag70* (exochitinase) and *Ech42* (endochitinase) from *Trichoderma harzianum* and *Attacin E* from *Hyalophora cecropia*. For the first time the combination of three resistances related transgenes could be established by crossing. Transcription analyses verified the expression of mRNA of all three genes only for one plant.

A considerable breeding program for 2005 could be performed only in small parts due to heavy spring frost. Some fruits from crosses were provided by W. Baab (Kompetenzzentrum Bad Neuenahr/Ahrweiler). The process of selection in the orchard was continued. A total of 1.609 graftings were performed in the orchard in 2005.

A main topic in the apple breeding program in 2005 was again fire blight resistance. Comparison of an *in vitro* leaf assay and artificial shoot inoculation resulted in differences between both methods regarding susceptibility to fire blight. The main problem is a reliable artificial infection of leaves. For early selection, the development of molecular markers for fire blight resistance seems to be more promising. In cooperation with the Austrian Research Centres Seibersdorf, a preliminary genetic linkage map for a segregating progeny was established. With a high probability a part of one linkage group is responsible for resistance to fire blight. The suitability of markers of this region as diagnostic markers for resistance to fire blight will be proved. The phenotypic assessment of susceptibility to *Erwinia amylovora* of progenies of the segregating population and of cultivars, advanced selections and wild species was done in cooperation with the Institute of Epidemiology and Resistance Resources Aschersleben.

Some promising breeding selections were included into fruit quality analyses. In addition to favourite amounts of substances related to taste and attractive appearances of the fruit, at least three of the new apple selections are characterized by very satisfying textures of their fruit flesh. Nowadays texture is an essential attribute for consumer's popularity of cultivars.

Apple breeding as well as new cultivars were presented in numerous lectures and some exhibitions.

### ■ Sour cherry

In the focus of sour cherry breeding are the improvement of fruit quality and processing ability, tolerance to biotic stress factors and high yield. To achieve these goals, hybridizations between selected cultivars and wild species were realized (Figure 3). The trees obtained from seeds were evaluated for specific characteristics. The best seedlings from populations were selected and propagated clonally to be planted in test plots for secondary selection.

Besides classical breeding, research is also focused on resistance to leaf spot (*Blumeriella jaapii*) and blossom blight (*Monilinia laxa*). For this feature cross populations with resistant sour cherry cultivars and the wild species *P. maackii* were generated (Figure 4). The progenies will be evaluated and selected based on phytopathological and genetic studies. A large sour cherry collection was evaluated additionally for diseases under field conditions. Aroused by the partially low fruit set of sour cherry cultivars and seedlings, specific investigations were carried out on fruit set.

The sour cherry selections 'Achat' and 'Jade' were registered as protected varieties in Germany and the rights for plant propagation are announced for application. Registration of 'Rubellit' is expected for 2006.

Studies of fruit quality traits that have been started several years ago were continued. Much effort was concentrated on the latest cultivars from Pillnitz 'Jade', 'Achat' and 'Rubellit'. Especially 'Jade' and 'Achat' were found to be very tasteful sour cherries characterized by favorable amounts of soluble solids and acids. In this way, they are estimated to be superior to the cultivar 'Schattenmorelle' which has been grown most frequently until now.

### ■ Sweet cherry

The goals in sweet cherry breeding are improvement of fruit quality, prolongation of the ripening period, self-compatibility and resistance against pest diseases combined with a high yield potential. Populations of seedlings were generated. The cherry season was characterized by strong spring frost in Dresden-Pillnitz in April 2005. In result of spring frost, crosses were interrupted and in general fruit set was damaged in the field.

In the field of breeding research accompanying classical breeding, the main objectives are: determination of sterility S-allele combinations present in sweet cherry cultivars; evaluation of resistance reactions of different sweet and sour cherry varieties and wild cherry species against the causal agent of cherry leaf spot (*Blumeriella jaapii*). The determination of S-alleles in German and foreign cherry cultivars is carried out by DNA marker analysis. By this, it is possible



to assess this characteristic trait independently on the phenological state of the tree and season. During the last years the S-alleles from a large number of sweet cherry cultivars and clones were determined. These results give an extensive overview about the S-allele combinations present in sweet cherries with importance for both, growers and breeders. Knowledge of S-allele combinations enables to avoid problems in pollination and resulting yield losses by a systematically choice of cultivars.

For expansion of the genetic variability and the introduction of new sources of resistances, crosses have been carried out between cultivars and the wild species *Prunus canescens*.

### ■ Strawberry

Hybridizations within 74 breeding groups resulted in 29.000 seeds, 12.900 seedlings and after primary selection in 7.400 plants which were already planted in the field for evaluation in 2006. Selections from the last years consist of approx. 900 A- and B-clones. Among those, there are promising selections which will be further evaluated in respect to the requirements of both commercial strawberry growers and traders (Figure 5). In cooperation with the working group Berry Breeding of the Federal Fruit Growers Association (Bundesverband Obst), an evaluation of the breeding level achieved until now will take place in Dresden in June

2006. A propagation field was established in order to supply healthy clones and cultivars for evaluation in and out off the research station of Dresden-Pillnitz. In cooperation with the BAZ Institute of Plant Analysis, basic analysis in inheritance of flavor compounds was carried out based on a model population of *Fragaria x ananassa* 'Mieze Schindler' x 'Elsanta', consisting of 200 clones. Since 2005, analysis of flavor compounds coincides with selection at the berry garden and contributes to the choice of breeding partners.

The mentioned model population was also used for studies on inheritance of dry matter content and for analysis of metabolites by mass spectrometry in cooperation with the SCRI in Dundee (Scotland).

In the area of resistance evaluation, the strawberry selections were exposed to Verticillium wilt (*Verticillium dahliae*) by greenhouse inoculation and planting at an inoculated field. Since *Xanthomonas* becomes more and more important also for strawberry production in Germany, a new project will be started in cooperation with the BAZ Institute for Epidemiology und Resistance Aschersleben. The genpool of the genus *Fragaria* will be analyzed for resistance resources to *Xanthomonas fragariae*. To tap new resources of resistance to *Colletotrichum acutatum* is the ambition for mutation breeding using a specific accession of *Fragaria vesca* (wild strawberry). This diploid wild species was established meanwhile at a tet-

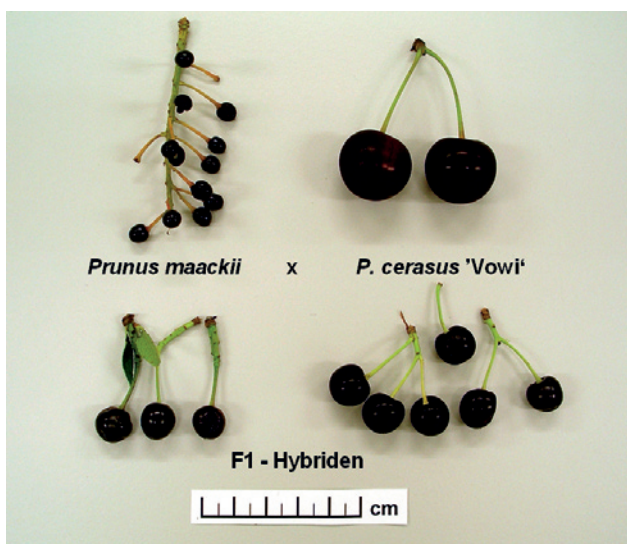


Fig. 3: Interspecific hybridisation of *Prunus maackii* and *Prunus cerasus* : Fruit size and morphology of the inflorescence are inherited intermediate.



Fig. 4: Crossing of cherries in the field : Flowers are isolated before opening in special bags to avoid fertilisation by bees. The breeder applies pollen of the variety which was chosen as father on the stigma of the mother plant using a brush.

raploid level in cooperation with the Humboldt-Universität Berlin and the University of Applied Science Dresden. The tetraploid level is an intermediate step in order to achieve the crossable octoploid level of the contemporary high performance cultivars (Figure 6).

## Biotechnological approach in breeding

### ■ Molecular methods

Combining durable disease resistance with best fruit quality is a great challenge for practical apple breeding. Molecular breeding may help to develop efficient tools for that goal. Molecular research is aimed to both fungal diseases and fruit quality traits. Regarding fungal pathogens, apple scab (*Venturia inaequalis*) and powdery mildew (*Podosphaera leucotricha*), new races of both fungi have been described which are able to overcome resistance genes used in the past in apple breeding. On the host site, currently new resistance sources

are being searched that can extend the genetic basis for apple resistance breeding. Genetic analyses of new genes and their location in the apple genome by molecular mapping are a prerequisite for practical applications in molecular breeding such as marker assisted selection (MAS). On the site of the pathogen, the work is focused on the phytopathological and molecular characterization of virulence differences, in both pathogens under the involvement of monosporic isolates. Regarding apple scab, new races of the fungus occurred in German apple growing areas which are able to overcome the *Vf* resistance used in the past within most apple breeding programs worldwide. One of the most promising alternative scab resistance sources is the Russian seedling R12740-7A. A scab resistance gene (called *Vr1*) was identified and mapped in several populations. A multiallelic SCAR marker developed for MAS was tested successfully for its usefulness under practical conditions. Other promising scab resistance genes are present in *Malus sieversii*, the assumed wild progenitor of the cultivated apples. Race-specific scab tests are applied to mapping populations and the genetics of the resistance are studied. Several putative major genes have been



Fig. 5: The new strawberry breeding clone P4121 which is characterized by a rich flower number, upright inflorescences and healthy leaves.

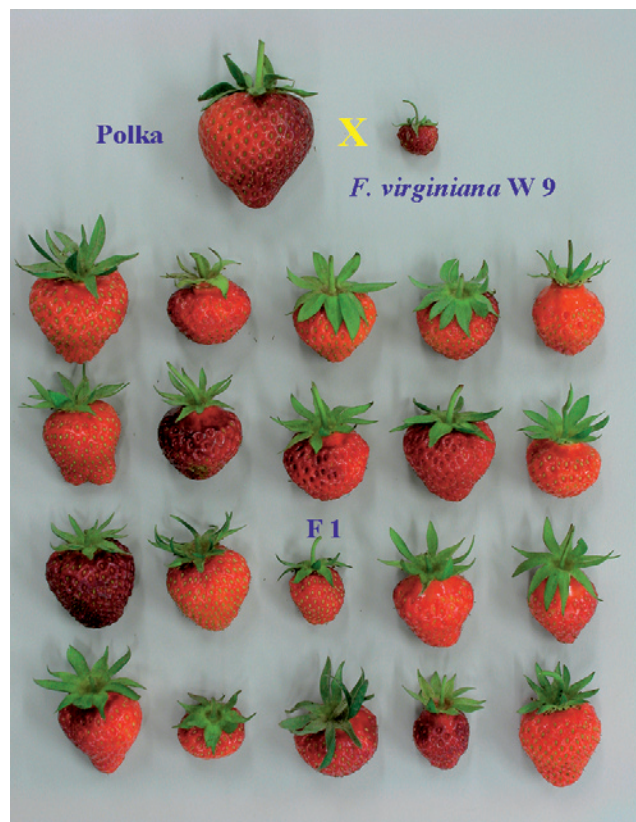


Fig. 6: Hybridisation between the strawberry cultivar Polka and the wild species *Fragaria virginiana* – fruits vary in size and form.



identified, at least two of them being effective against race 7. As a functional molecular approach on apple scab resistance genes, a series of *HcrVf* gene analogs have been cloned, sequenced and analyzed for gene expression. Interestingly, a considerable number of expressed variants of *HcrVf* genes seem to be present in the apple genome. Also susceptible cultivars do obviously express constitutively some highly specific scab resistance genes. Resistance to powdery mildew is one of the other major aims in apple breeding. The current breeding strategies are focused on the development of apple cultivars suitable for a sustainable fruit production. Prerequisite of successful resistance breeding is a good understanding of host-pathogen-relationships, including the population structures of fungal pathogens and the virulence behavior of different races. Several new major resistance genes have been identified in *Malus* species. Their genetic mapping and the development of molecular markers is in progress. Among others, a major gene has been identified in a *M. baccata* accession (called *Plb1*) which is tightly linked to an identified AFLP marker. Regarding the apple powdery mildew resistance gene *Pl1*, also some progress was made concerning its location in a resistance gene cluster on the apple linkage group 12. As shown earlier, a high level of diversity in terms of virulence does exist in the apple powdery mildew fungus, although the overall genetic diversity evaluated on a molecular level appeared to be low in Europe. The main task during the EC project SMADIA was the use of molecular marker techniques such as RAPD, SSR and AFLP to compare isolates and field samples of the fungus collected from European and Asian populations of apple powdery mildew. The isolates have been tested for their pathogenicity on a differential *Malus* set consisting of different resistance gene donors as well as some susceptible control cultivars. The results again displayed a high level of variability regarding the pathogenicity of the tested new isolates. Twelve isolates have repeatedly been tested on a collection of about 50 *Malus* genotypes. All isolates showed different infection patterns. This alludes to the possibility that many races exist for apple powdery mildew and it was possible to identify further isolates with new virulence types. The results also showed that the resistances of *Pl1* and *Pl2*-donor plants are overcome. It was also shown that *Pl1-Pl2* gene combinations are resistant to isolates with virulence types that could overcome the single resistances. On the molecular level it was possible to distinguish between two separate major groups of isolates which is a similar situation published for the grape powdery mildew fungus *Uncinula necator*.

A major part of the work on molecular breeding research is presently running within the EC project HiDRAS on fruit quality traits. HiDRAS is based on a pedigree-based QTL-analysis of the most important parameters of fruit quality.

Traits considered in the project are: fruit size, taste, fruit firmness, juiciness, acidity, sugar content, vitamin C, flesh texture, storability, and flavor. A part of the project is directed to a functional genome analysis. In 2005, the major part of the work in HiDRAS was the realization of large-scale SSR analysis. Twenty-eight selected microsatellite loci were analyzed on the whole set of 1.800 apple genotypes consisting of cultivars and progenies by using PCR multiplexing protocols. The SSR work will be completed in winter 2006. During the last stage of the project, a statistical evaluation will be performed on the basis of all phenotypic and molecular data collected in the past three years (Figure 7).

### ■ Genetic engineering

In future, genetic engineering will become increasingly important as a tool in plant breeding. Contrary to the conventional breeding, genetic engineering allows the targeted introduction of desired genes. Furthermore, it is also possible to prevent the expression of existing genes. However, genetic engineering which enables the clarification of gene functions and metabolism cascades will be of particular interest.

In woody plant breeding, especially apple, the juvenile phase exhibits a special importance due to its long duration up to 10 years. Therefore, the assessment of trees resulted from classical breeding is only possible after several years. This leads to extensive breeding programs. At the Institute of Fruit Breeding research was performed to manipulate the juvenile phase of apple using genetic engineering. Several genes which are responsible for the flower bud induction were transformed into the apple genome. The transformation of the *BpMADS4* gene originated from birch (*Betula pendula* L.), initiated flower buds in *in vitro* apple plants. The

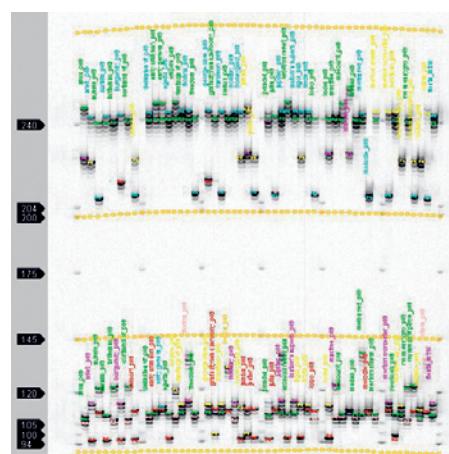


Fig. 7: Microsatellite DNA fragment analysis of 40 different apple varieties. The figure shows two different SSR loci with several alleles each (left: Size of the fragments in base pairs).

flowers showed morphological fully developed organs (Figure 8). Also, after transfer into the greenhouse, these plants soon started to flower (Figure 9). No differences were found in vitality and germination capacity between the transgenic pollen and pollen of non-transgenic apple plants. At the moment, fruit development is investigated after hybridization. Based on these results, it is assumed that the hybridization programs to introduce resistance genes will be more efficient. This assumption will be verified in backcross programs.

To improve the analysis of transgene expression, Real Time PCR technique was established in apple. Primers were derived from known gene sequences. After preliminary experiments, the expression of 10 transgenes and 20 breeding relevant *Malus* genes can be quantified. Seven housekeeping genes of apple are used as standard.

### ■ Risk assessment in genetic engineering

Within a project financed by the Federal Ministry of Education und Research (BMBF), examinations were performed to prevent the gene escape from genetically engineered apple plants. Different approaches were established. One possibility is the establishment of male sterility to prevent the transport of transgenic pollen. Another alternative is the establishment of parthenocarpic (seedless fruits) to avoid the distribution of transgenic seeds. For both approaches a large number of transgenic lines were produced. These lines were analyzed for stability of the integration and expression of the transgenes. After induction of roots, several lines were transferred into the greenhouse and grafted in combination with non-transgenic rootstocks. A number of plants were selected for special trials on flower bud development to evaluate the success of genetic engineering. The first blossoms for these plants are expected in 2006.

Another project on the potential risk of gene escape in apple was started in 2005. This project is engaged with the risk minimization in field grown transgenic apple plants. This research is focused on the distribution of pollen and seeds under natural conditions. A non-transgenic apple species is used as pollen dispenser plant. This species exhibits a gene which is responsible for red coloration of all plant organs and can be used as a morphological marker in progenies (Figure 10). The examination of pollen distribution is performed in a commercial apple orchard. Preliminary investigations were realized in a previous project. Because of the frost damage of flowers in spring 2005, the experiment was not carried out as proposed. The analysis on pollen transport by wind showed a transport distance of apple pollen over 20 m, therefore the experimental field has to be enlarged next year. The pollination biology was determined using transgenic apple plants in



Fig. 8: Induction of flowers on *in vitro* shoots of apple.

Fig. 9: Flower formation after breaking the juvenile phase due to overexpression of the flower induction gene *BpMADS4* of birch *Betula pendula* L. on 4 weeks old apple plants propagated *in vitro* and transferred to the greenhouse.





the greenhouse. The transgenic pollen showed no differences in the fertilization in comparison to non-transgenic pollen. In addition, the potential risk of pollination with flowers generated after June drop was examined. 900 apple cultivars and selections of the gene bank were used. For some selected cultivars the fertilization and the ripening of the fruits were analyzed. Another focus of this research is the determination of transgene distribution by seeds. In autumn 2005, apple fruits were laid out in different environmental conditions and will be examined in spring 2006. The contamination of honey by transgenic DNA sequences was also studied. Different protocols to isolate DNA from honey were tested. So far no method was satisfactory.

### ■ The First Apple Day

In 2005, the “1. Pillnitzer Apfeltag” (The First Apple Day) themed “The Apple in the Course of Time” was organized (Figure 11). Besides lectures concerning “Old Apple Cultivars”, “Apple Breeding” and “Resistance to Diseases and Pests”, poster exhibiting different research areas of the institute were presented: cultivar breeding for apple, strawberry, sweet and sour cherry, collection and evaluation of genetic resources, analyses fruit quality and ingredients (vitamin C, aromatic compounds, et al.), molecular genetic and genetic engineering. Guided tours visiting the pome fruit plots of the orchard, determination of apple cultivars (Mr. R. Lebe, Bundessortenamt, Versuchsstation Wurzen) and demonstrations of techniques determining fruit quality completed the program.

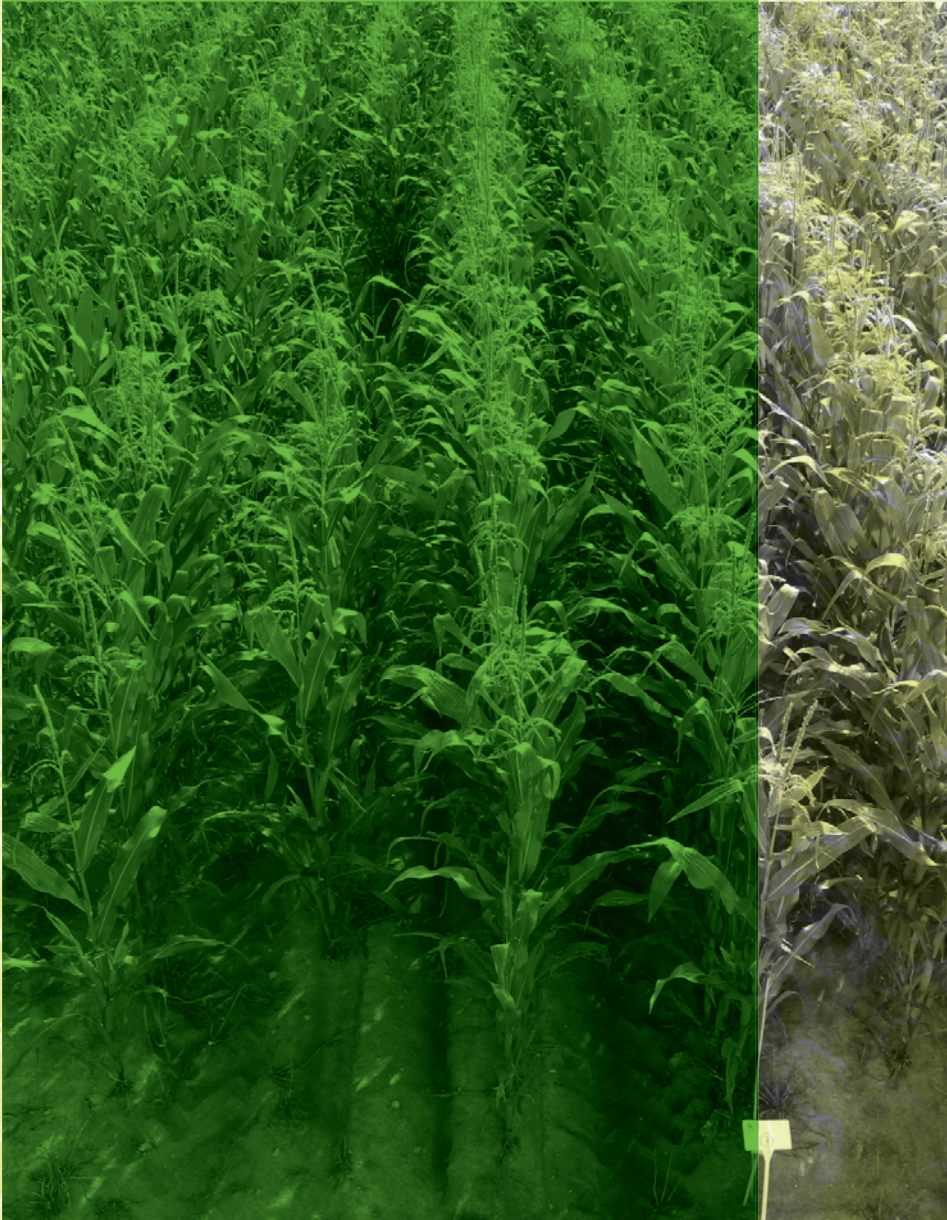


Fig. 10:  
The apple wild species *Malus pumila* var. *Niedzwetzkyana* is used as a morphological marker in outcrossing experiments. Seedlings originating from fertilization with pollen of the wild species show also a red tissue coloration.



Fig. 11: The youngest apple tester at the 1st apple day, October 1<sup>st</sup> 2005.





**Institute  
of  
Agricultural  
Crops**

**Groß Lüsewitz**



# Institute of Agricultural Crops

## ■ Tasks

The Institute of Agricultural Crops (ILK) is charged with characterizing and unlocking plant genetic resources for food, feed and agriculture by use of 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. Adapted germplasm created under these aspects as well as other scientific results of our research are meant to support federal policies in warranting environmentally friendly and sustainable agriculture as well as agricultural produce which meet the consumers' demands. 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. The spectra of agricultural crops considered is a function of long-term requirements of breeding research in Germany. In the period under review, this spectra comprised potato, rye, barley, triticale, oat, ryegrass, narrow-leafed lupin, and oilseed rape as well as other Brassicaceae. In addition, maize was included in the frame of a large-scale coexistence field trial. To allow for an efficient research on these crop species, the institute is organized in three cooperating working groups with specific methodical expertise, namely the groups of 'Classical Breeding Methods', 'Molecular Breeding Methods' and 'Biotechnology'.

## ■ Groß Lüsewitz – a location for plant-breeding research

Of the eight research institutes at the Federal Centre for Breeding Research on Cultivated Plants (BAZ), two institutes, namely the Institute of Abiotic Stress Tolerance and the Institute of Agricultural Crops, are situated in Mecklenburg-West Pomerania, at the site of Groß Lüsewitz near the Hanseatic town of Rostock (Figs. 1 and 2). The location of Groß Lüsewitz

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Philipp Ackermann  
agricultural ecologist (project contract until 14.03.2005)

Rayko Becher  
biologist (project contract)



Fig. 1 BAZ location of Groß Lüsewitz in a bird's-eye-view



Fig. 2 Partial view of the trial field of Groß Lüsewitz

stands in a long tradition of plant breeding in agricultural crops which traces back to 1948 when the former Institute of Plant Breeding was founded with its first director Rudolf Schick, a disciple of the famous Erwin Baur. On 9 April 2005, a commemoration on the occasion of the 100<sup>th</sup> birthday of R. Schick was held, with a public day to demonstrate current research activities at Groß Lüsewitz (Fig. 3). After the reunification of Germany and following the advice of the German Science Council to reorganize the agricultural research in the New Länder, the location of Groß Lüsewitz with its BAZ institutes became a centre for breeding research on agricultural crops in the scope of the present Federal Ministry of Food, Agriculture and Consumer Protection, and (BMELV).

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 proprietary 58 ha trial field is flanked by continuous grassland and, thus, provides excellent control in respect to gene flow and pathogen pressure as well as self-reliance with regard to fertilization and plant-protection regimes, crop rotations and cultivation pauses. 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 township of Sanitz, where Groß Lüsewitz belongs to, is situated in an officially acknowledged healthy region for potato growing. Within this healthy region, solely Groß Lüsewitz marks a core zone defined as high-grade region where phytosanitary conditions for potato farming and propagation are strictly regulated. Crops like potato, oilseed rape and cereals profit from the advantageous damp climatic conditions with 680 mm precipitation per year, which also provides excellent conditions for disease-resistance breeding, since 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 and yield meaningful results in most cases due to the high air-humidity. This is an essential, which allows for efficient and directed research on 'genetic plant protection' approaches in agricultural crops.

The Groß Lüsewitz trial-field area (Fig. 2) is of diluvial origin and has a homogeneous structure, with a soil-classification score of 47 (German scoring system), making it representative in agricultural 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. This is important with regard to the policy advice BAZ has to provide via its research to BMELV. Breeding research of BAZ institutes in Groß Lüsewitz profits from the close cooperation with the

Fig. 3 Public day on 9 April, 2005







**Fig. 4 Professional education of Biological Technical Assistants in Groß Lüsewitz**

Gatersleben Genebank external locations nearby, namely in Groß Lüsewitz (potato) and Malchow/Isle of Poel (oil and forage plants).

The BAZ location of Groß Lüsewitz is engaged in the education of trainees for the profession of Biological Laboratory Assistant. In 2005, 16 trainees of educational terms 1-4 passed through the two institutes (Fig. 4). 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 locations where trainees for the farmer profession may be educated. In 2005 three trainees of terms 1-3 were educated in this facility.

## Research at the ILK

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

Due to the increasing demands for environmentally friendly and consumer-oriented agricultural production, disease resistance is gaining importance as a means to reduce chemical plant protection. In potato, late-blight resistance is of

highest priority in the breeding research of ILK. As to our current knowledge, polygenic quantitative resistance is the only basis for durable resistance. To achieve this, pre-breeding programmes have to be run where resistance genes are transferred from non-adapted wild species and brought together with a number of agronomical and quality traits, which on their part are also most often quantitatively inherited (Fig. 5). The resistance sources are drawn from the genebank, External Station North in Groß Lüsewitz, of the IPK Gatersleben. Resistance screening of genebank materials is done in a joint effort of ILK and IPK genebank. Defined *Phytophthora* isolates are provided by the Federal Biological Research Centre (BBA), Institute for Plant Protection in Field Crops and Grassland. BBA also performs resistance testing with regard to soft rot (*Erwinia carotovora*) and potato wart disease (*Synchytrium endobioticum*).

In the period under review, the breeding programme at ILK comprised 7500 seedlings in the greenhouse, 1720 single plants in the field, 964 A-clones, 101 B-clones, 94 C-clones, 66 D-clones as well as 191 older clones. About 70 % of these materials was dedicated to *Phytophthora* resistance, 20 % to table quality, processing quality and starch content (prevalently on the diploid level), and 10 % to *Globodera pallida* and virus resistances. There was breeding progress with the combination of late-blight resistance and table quality in respect to visual impression after cooking, discolouration after cooking, disintegration during cooking, disposition to blue spots and colour of tuber flesh. With some resistance donors of *S. stoloniferum* and *S. demissum*, an acceptable level of culinary quality could be combined with late-blight resistance after only two or three backcrosses. A sub-programme dedicated to suitability for processing yielded promising results with the combination of late-blight resistance and reduced darkening upon deep-frying after storage at 4° C. With regard to the combination of *G. pallida* resistance and

**Fig. 5**

Pre-breeding in potato – a long yet promising way from the resistant non-adapted wild species (left-hand side) to a presentable breeding clone with quantitative disease resistance (right-hand side).







**Fig. 6 Breeding clones from the Groß Lüsewitz pre-breeding programme with resistance to *Phytophthora infestans* (Pi) and good adaptation in diverse characters**

high starch yield as well as late-blight resistance, we are using since three years the diploid nematode resistant *S. spegazzinii* and *S. vemei*. Nematode-resistance testing is done in cooperation with the State Office for Agriculture, Food Safety and Fisheries, Rostock.

Our cooperation in the EU initiative EUCABLIGHT, which is meant to contribute to the EU-wide harmonization of *Phytophthora*-resistance testing, comprised a three-years screening of 25 potato cultivars for late-blight resistance at our location. From 4-5 August 2005 the ILK organized a Host Resistance Meeting, with 24 participants from 10 countries. The meeting addressed methodical issues of data collection and data management in the EUCABLIGHT data base ([www.eucablight.org](http://www.eucablight.org)). ILK contributed results to this database on race-specific late-blight resistant genes present in commercial potato cultivars. Computational elimination of maturity effects from the resistance-test data presently is done solely at BAZ whereas internationally, there is no such correction for maturity. Lack of correction for maturity constitutes a major obstacle for successful resistance breeding due to selection for late maturity instead of late-blight resistance. ILK made proposals for methodical improvements to circumvent the correlation between resistance and maturity. Additional proposals concerned methodology of tuber testing and assessment of maturity time.

In the period under review, 22 BAZ breeding clones and 84 seed populations were handed over to potato breeders via the Gemeinschaft zur Förderung der privaten deutschen Pflanzenzüchtung e.V. (GFP), Bonn (Fig. 6). Among these were 5 tetraploid clones with high resistance to *Phytophthora*, middle-early to middle-late maturity and suitability for table, starch or processing. Three dihaploid clones with late-blight resistance also displayed good virus and soft-rot resistance, whereas processing quality was still low. Four

tetraploid and 10 dihaploid inheritors with suitability for chips and French fries processing proved to be prevalently middle-early. Characterization of resistant BAZ breeding clones by ILK in a total of 44 traits helps potato breeders to choose and use these clones for variety breeding. The 2005 offer of tetraploid seeds comprised 51 combinations in the breeding direction of table or processing quality, 14 combinations for high starch, as well as 20 combinations for high starch *plus* resistance to *G. pallida*. The entire offer of BAZ breeding materials in 2005 enjoyed popularity among commercial potato breeders.

On 13 and 14 July, 2005 the summer meeting of the GPZ Work Group for Potato Breeding and Seed Potato Production took place in Groß Lüsewitz. On this occasion potato breeders presented an assessment of breeding clones which they had received from BAZ over the years. Positive ratings of BAZ breeding materials were given for speedy haulm growth, good haulm architecture, crossability, high foliage blight resistance as compared to variety-breeders' materials, combination of late-blight resistance with early to second-early maturity. The German potato breeders expressed their strong interest in the continuation of pre-breeding at BAZ against *Phytophthora infestans*. They use the polygenic resistance because of its durability, despite the unfavourable mode of inheritance of this resistance type. Conventional as well as organic farming will profit from this specific genetic material. Results of our pre-breeding activities in potato were presented to the public, e.g. at the International Green Week Berlin (Fig. 7).

**Fig. 7 Demonstration of ILK research activities in potato at the International Green Week in Berlin**



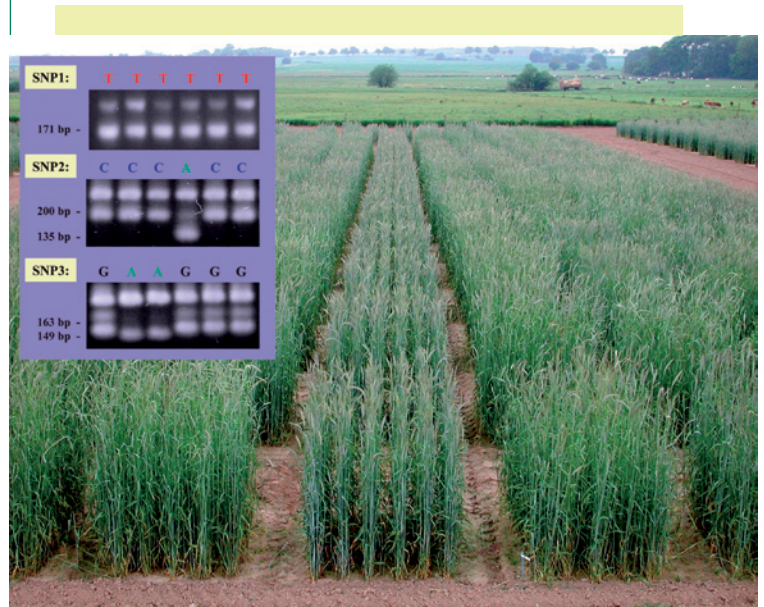
## Rye (*Secale cereale* L.)

Research activity to unlock plant genetic resources (PGR) with regard to leaf-rust resistance was continued successfully in 2005. Genetic analyses led to the identification of two additional dominant resistance genes, which were given the preliminary designations *Pr-s* and *Pr-t*. Altogether, 15 *Pr* genes have been identified from PGR to-date. For genes *Pr-n* and *Pr-s*, adult-plant resistance could be demonstrated in growth-chamber experiments, with a correlation of 1.0 and 0.7, respectively, between the results of detached-leaf resistance tests in the seedling stage and resistance in the adult-plant stage of individual plants. To address effectivity of *Pr*-gene pyramidization and yield relevance of *Pr* genes, our efforts in establishing a standard set of near-isogenic lines (NILs) each carrying a single *Pr* gene were continued. After NILs for the published resistance genes of *Pr1*, *Pr2*, *Pr3*, *Pr4*, and *Pr5* have been available, additional NILs for genes *Pr-d*, *Pr-e*, and *Pr-f* will be accomplished soon. In the period under review, resistance genes *Pr-d* and *Pr-e* were mapped to rye chromosomes 2R and 6R, respectively, with the aid of genomically anchored molecular markers. For *Pr-e*, a closely linked marker (2.1 cM) is available for marker-assisted selection. In total, 9 *Pr* genes have been mapped by us in the rye genome to-date.

Another research project is dealing with molecular-marker development for genetic and breeding purposes. A molecular-marker class with increasing importance is constituted by single-nucleotide polymorphisms (SNPs). The wealth of sequence information from EST projects in a number of crop species allows for a directed search for SNPs in the genome. SNP display, though, still requires costly laboratory procedures which appear worthwhile not for every crop. In an attempt to allow for SNP analyses in rye, we established a method which allows for cheap and robust SNP display on agarose gels (Fig. 8) and, thus, opens the possibility to characterize gene variants or haplotypes among PGR in a simple way.

## Barley (*Hordeum vulgare* L. *sensu lato*) and bulbosum barley (*H. bulbosum* L. *ssp. bulbosum*)

To strengthen the position of “genetic plant protection” in the context of an integrated concept for barley growing, we investigate the secondary gene pool of barley as a potential genetic resource which could be used to broaden the genetic diversity within the barley gene pool with regard to a variety of disease-resistances. The secondary gene pool of barley is represented by a single wild-barley species, namely *H. bulbosum*. Using interspecific crosses of *H. vulgare* and *H. bulbosum* we have investigated a number of introgression lines which carry *H. bulbosum* chromatin at telomeric sites of specific barley chromosomes. These introgressions confer dominantly expressed resistance to different pathogens (Ta-



**Fig. 8** Evaluation of plant genetic resources of rye – as depicted here in evaluation plots on the Groß Lüsewitz trial field – may profit from the use of molecular markers. Insert, SNP alleles (SNP1-3) from three different rye genes with display via agarose gel electrophoresis (genes #1 and #2 show allelic variation among the plants sampled whereas gene #1 does not).

ble 1), among them resistances to the most threatening soil-borne yellow mosaic virus complex. *Rym14<sup>Hb</sup>* and *Rym16<sup>Hb</sup>* represent two novel, dominantly expressed virus resistance genes. These two genes are effective against BaMMV, BaYMV-1, BaYMV-2 as well as against the novel BaMMV strain, the latter of which has newly arisen in Germany. This broad effectiveness of *Rym14<sup>Hb</sup>* and *Rym16<sup>Hb</sup>* is important since the recessive gene *rym5*, which has increasingly been used in plant breeding during the last years, is not effective against the novel virus strain. The introgressed resistances have been tagged by molecular markers (Table 1), some of which are already used in breeders’ backcross programmes.

## Triticale (*x Triticosecale* Wittm.)

A long-termed ILK project addresses to the ‘Generation of adapted germplasm in winter triticale with high resistance to lodging and diseases and with good kernel quality’. In 2005, offspring from crosses involving primary F1 triticales was second-year evaluated in our nursery. As expected, most of the offspring ranged considerably below the level of standard cultivars with regard to kernel filling, hectolitre weight, yield, sprouting resistance and lodging resistance. A number of lines, though, were distinguished by simplex or complex disease resistance to powdery mildew, leaf rust, and ear septoria. These lines should prove valuable for plant breeding since powdery mildew and leaf rust are currently emerging as relatively novel challenges in triticale growing. An-



Table 1

Resistance genes introgressed from *Hordeum bulbosum* at ILK

Introgression	Resistance Gene	Pathogen	Molecular Marker	Genetic Distance to R-Gene (cM)	Cooperation
6HS	<i>Rym14<sup>Hb</sup></i>	BaMMV, BaYMV-1, -2	<i>Xiac500</i>	0.0	1, 2
2HL	<i>Rym16<sup>Hb</sup></i>	BaMMV, BaYMV-1, -2	<i>MWG949</i>	3.6	2
2HS	<i>Rph20Hb</i> <i>Ml<sup>Hb</sup></i>	<i>Puccinia hordei</i>	<i>Xiac503</i>	0.8	2, 3
		<i>Erysiphe graminis</i> f.sp. <i>hordei</i>	<i>Xiac503</i>	0.5	
2HL	<i>Rph21<sup>Hb</sup></i>	<i>P. hordei</i>	<i>Xmwg2076</i>	1.0	2
5HL	<i>Rph22<sup>Hb</sup></i>	<i>P. hordei</i>	<i>MWG602</i>	1.8	2
4HS	<i>Rrs16<sup>Hb</sup></i>	<i>Rhynchosporium secalis</i>	<i>Xiac511</i>	0.1	1, 4

1, Crop & Food Research, Christchurch, New Zealand

2, BAZ, Institute of Epidemiology and Resistance Resources, Aschersleben, Germany

3, BBA, Institute for Plant Protection in Field Crops and Grassland, Kleinmachnow, Germany

4, Bavarian State Research Centre for Agriculture, Institute for Agronomy and Plant Breeding

other point of interest is that despite weak kernel filling, some of the resistant offspring lines reached the yield level of the presently highest yielding cultivars ('SW Talentro', 'Benetto', 'Magnat' or 'Lamberto'). Since these lines can be assumed to be genetically distant to the current panel of registered cultivars they should constitute an interesting genetic material for plant breeding. A third-year evaluation and further crosses are envisaged for 2006.

### ■ Oat (*Avena sativa* L.)

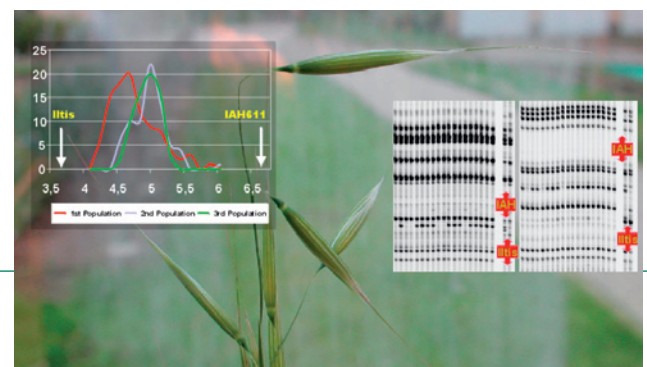
The dietary value of the oat kernel is determined by its valuable protein composition, favourable ratio of unsaturated to saturated fatty acids and the high fibre content. As in barley, oat fibre is predominantly made of (1-3, 1-4)- $\beta$ -D-glucan, which is a main constituent of the endosperm cell walls.  $\beta$ -glucan is ascribed a number of positive health effects, e.g., reduction in serum cholesterol, regulating effects on the blood sugar level, and consequently risk reduction with regard to cardiovascular diseases.

To generate efficient oat lines with high fibre the high- $\beta$ -glucan genebank accession IAH611-447 (PI 502955) was backcrossed with the high-yielding cv. 'Iltis'. In BC<sub>2</sub>F<sub>2.5</sub> and BC<sub>2</sub>F<sub>2.6</sub> lines, 11 agronomic traits as well as other quality-related traits were evaluated at three locations in 2003 and 2004. In the period under review, these lines were genotyped using 144 microsatellite and 256 AFLP markers and QTL analysis was accomplished (Fig. 9). Simple-Interval Mapping revealed 4 QTLs for high  $\beta$ -glucan, contributed by positive-effect alleles from the donor IAH611-447 and each explaining 20-30 % of the phenotypic variation in  $\beta$ -glucan contents. These results demonstrate that advantageous QTLs for  $\beta$ -glucan were introduced into the genetic background of cv. 'Iltis'. In addition, novel genetic resources could be unlocked for agronomic traits like ripening time, thousand-kernel weight, hectolitre weight, and hull

content. These results are of practical use for the breeding of efficient, high-quality oat. The research work is part of a joint project funded by BMBF and involving the Martin Luther University Halle-Wittenberg, Institute for Plant Breeding and Plant Protection, as well as the Nordsaat Saat-zucht GmbH, Böhnshausen.

Another project part of this research activity was addressing to establishing novel microsatellite markers for oat breeding research. In 2005, a total of 234 microsatellite markers could be established, most of them (195) derived from publicly accessible oat ESTs (Expressed Sequence Tags; <http://www.ncbi.nlm.nih.gov/entrez>). As compared to the hitherto published number of 114 SSR markers our results make an essential contribution to the genomic resources for oat. Of the 195 EST-based microsatellites, 107 proved polymorphic among 12 oat cultivars screened. Fifty-one of these were mapped by us in the reference genomic map of 'Kanota' x 'Ogle', which was kindly provided to us by Agriculture & Agri-Food Canada (N. Tinker).

Fig. 9 Marker-assisted improvement of  $\beta$ -glucan content in oat. Left-hand side, Continuous variation of  $\beta$ -glucan contents in three mapping populations (contents of the cross parents are indicated); right-hand side, AFLP marker analysis of a mapping population





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

In view of the potentials of narrow-leafed lupin with regard to sustainable forage-plant production in Germany and to the high protein value of the seed we decided to include this legume in the ILK research activity (cf. Annual Report 2004). In the period under review, four main activities can be recorded.

Firstly, F2 and F3 mapping populations were generated which segregate for anthracnose resistance. As potential resistance donors, German cultivars were used as cross parents, as well as the Australian cv. 'Tanjil' which carries the resistance gene *Lanr1*.

Secondly, a meaningful and reproducible greenhouse resistance test, which allows for phenotyping the F2 and F3 mapping populations, was adopted from Australian colleagues and adapted to regional lupin germplasm. This was possible thanks to the kind support by the Department of Agriculture, Western Australia, Perth, and included cooperation with the Federal Biological Research Centre, Institute for Plant Virology, Microbiology and Biological Safety, Berlin-Dahlem (Fig. 10).

A third main focus was directed to the development of molecular resistance markers. To make use of the resistance gene *Lanr1* from cv. 'Tanjil', this gene was introduced via marker-assisted backcrossing into German breeding lines, using a molecular marker which had been developed at the Department of Agriculture, Western Australia (by courtesy of H. Yang; Fig. 11). In addition, a resource of 150 markers, most of them EST-based, are available from the University of Western Australia, Perth, for tagging further resistance genes to anthracnose.

Finally, a lupin work collection was established in 2005. In total, 69 accessions were received from the genebank of the IPK Gatersleben, Germany, 1 accession from the botanical

Fig. 11

Trial plot of cross progeny in narrow-leafed lupin. Insert, Detection of the molecular anthracnose-resistance marker allele in F1 cross progeny from the cross of cv. 'Tanjil' (resistant) x cv. 'Borlu' (susceptible)



garden of the University of Bayreuth, Germany, 10 accessions of Plant Breeding Station Wiatrowo, Poland, 146 accessions from the Australian Lupin Collection, Department of Agriculture, Western Australia, as well as 32 accessions of the Western Regional Plant Introduction Station, Washington State University, USA (Fig. 12). These accessions were evaluated for a number of traits, e.g., seed germination and emergence, infestation by diseases and pests under our local conditions. A total of 46 wild-lupin species as well as a number of various cultivated lupin origins were left as a core collection which subsequently will be screened for their potential as genetic resources in the breeding of narrow-leafed lupin.

### ■ Oilseed rape (*Brassica napus* L. (partim))

In September 2005 a novel research activity was launched at ILK for providing scientific support to a joint effort involving the Bundessortenamt (German Federal Plant Variety Rights Office, BSA) and the Federal Association of German Plant Breeders (BDP). The effort aims at elucidating technical feasibility to distinguish hybrids (including so-called half-sib hybrids) by means of molecular markers. Specifically,

Fig. 10 Greenhouse test for anthracnose resistance in narrow-leafed lupin. Right-hand side, resistant plant; left-hand side, susceptible plant with typical symptoms

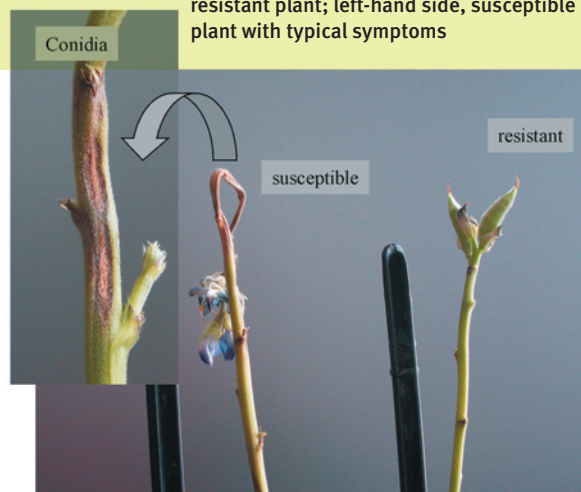
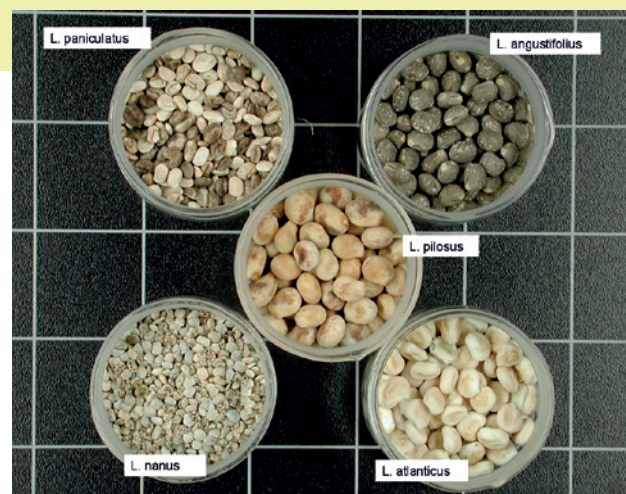


Fig. 12 Diversity of seed traits among species of the genus *Lupinus*



the effort shall 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 markers was to be determined in this joint effort. To this end, 96 samples of oilseed-rape hybrids and their parent lines were examined at ILK and a BDP partner 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.cssp.la-trobe.edu.au/>). In the period under review, 27 informative SSR markers were identified which differentiate between the parent lines of a given hybrid (Fig. 13). In a next step, assessment of these and additional markers will be done for their ability to distinguish oilseed-rape hybrids in official variety registration testing.

### ■ Maize (*Zea mays* L.)

In the period under review a large-scale coexistence field trial in maize was initiated by the Federal Ministry of Food, Agriculture and Consumer Protection, BMELV (formerly BMVEL). This field trial was designed by three research centres in the scope of BMELV, namely, the Federal Agricultural Research Centre (FAL), the Federal Biological Research Centre (BBA), and the Federal Centre for Breeding Research on Cultivated Plants (BAZ). 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. In 2005, the field trial was scaled to a total of 70 ha at 4 locations (Braunschweig, Groß Lüsewitz, Mariensee and Wendhausen). To measure gene flow from donor-maize to

recipient-maize plots, Bt-maize (MON810) as well as conventional maize with a colour marker (white maize) and with a molecular marker, respectively, was planted next to conventional recipient maize. Various experimental designs at the locations and involvement of clover/grass and sunflower plantings between the plots were used to address the influence of distance, natural barriers, and field crop interplantings on transgenic maize pollen flow into neighbour plots. In the trial field at Groß Lüsewitz, a 9.8 ha experimental design was run comprising 3.5 ha of Bt maize as a donor, 4.5 ha of conventional maize as recipient, and 1.8 ha of clover/grass growing in varying depth between the plots. The trial was sown on 3 May and the cobs of the recipient plot harvested on 24 October (Fig. 14). Determination of donor admixtures is accomplished by accredited laboratories and will be completed by January or February, 2006. The large-scale coexistence field trial shall be repeated in 2006.

## Prospects

Utilization of plant-genetic resources for food and agriculture (PGRFA) to generate crop germplasms with novel trait genes and better agronomic adaptation is a long-termed, costly and scientifically demanding process which, in view of globally dwindling biotic and abiotic resources needed for agriculture, is gaining growing importance for the public. In the period under review we rigorously went ahead with a number of research activities which had been started or planned only in 2004. Some of these novelties for ILK concern the successful implementation of narrow-leafed lupin in our research portfolio, the scientific support of joint BSA/BDP efforts to establish marker-assisted differentiation of oilseed-hybrids in official variety testing, the genomic work

Fig. 13 Distinguishing parent lines (P1, P2) of oilseed-rape hybrids (H) by use of microsatellite markers

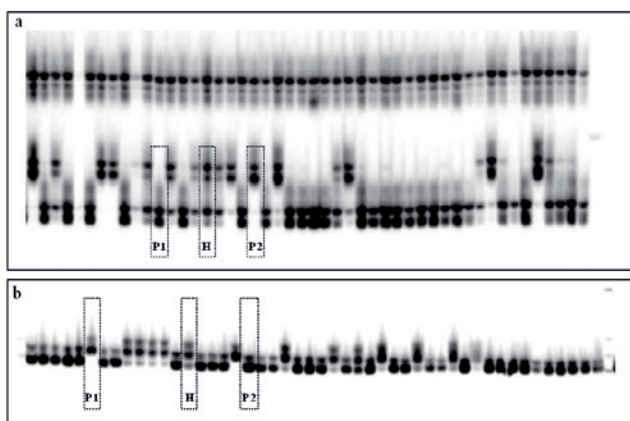


Fig. 14 Sampling of corn cobs from the recipient-maize plot in Groß Lüsewitz at the end of the large-scale coexistence field trial in October, 2005



done in oat, and participation in the large-scale coexistence field trial in maize. Another aspect to be emphasized is the intensive cooperation with other research institutions at an international scale as well as with private plant breeders. It is this kind of close external linking which is a pre-requisite for meaningful plant breeding research and for a knowledge transfer that is of practical relevance.

Present issues of plant breeding as well as ongoing long-termed developments will define our research focus for the coming years. 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 and pests. Furthermore, the increasing role 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 novel topics, we will not lose sight of "old" albeit still important issues like, e.g., late-blight resistance in potato or management, characterization and unlocking of plant genetic resources for food and agriculture.





**Institute  
of Abiotic  
Stress Tolerance**

**Groß Lüsewitz**

# Institute of Abiotic Stress Tolerance

The objective of the institute is to characterize and to diminish the effect of abiotic stress factors on the performance of crop plants, especially on yield, quality of raw materials, nutrient efficiency and disposition to diseases under consideration of genetic resources. Investigations aim to promote a competitive and multi-functional agriculture, which is able to produce highly nutritious, healthy and safe food and feed and has the potential of supplying industry with raw materials for a broad range of industrial applications.

This is of special importance in view of the world-wide shortage of natural resources and the prognosticated climate changes and the following complex consequences for an economic and at the same time environmentally friendly agriculture.

The development and adaptation of suitable methods, the analysis of genetic resources as well as the long-term observation of indicator assortments (cereals, potatoes, legumes, oilseed crops) under varying environmental conditions with regard to conventional and organic farming are an important contribution to a sustainable agriculture and consumer protection.

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## Abiotic Stress

Abiotic stress is a complex factor whose influence on yield and quality affects the agricultural production process and therefore also the economic and political decision-making. Abiotic stress occurs in connection with spontaneously appearing short term weather events (summer drought, frost event etc.) as well as – in the longer term – with regard to the predicted climate change.

Important aspects are damage prognosis – in relation to yield and increasingly with regard to quality (industrial application) as well as damage diminishing by breeding for abiotic stress tolerance.

This includes

- test of quality and yield stability influenced by abiotic stress factors
- long-term monitoring of indicator assortments
- evaluation of genetic resources for relevant characters
- development of breeding-relevant stress markers

### ■ Drought tolerance and yield stability in faba beans

Faba beans belong to the high yielding legumes and they are interesting elements of crop rotations especially in view of organic farming. The seeds have high contents of starch and protein and breeding has already done a lot to improve their quality for food and feed – for instance by reducing the content of antinutritive substances. Nevertheless, cultivation of this crop shows a declining tendency in Central Europe and mainly in Germany. One reason for that is a lack in yield stability caused by poor drought tolerance.

Investigations under stress and control conditions in field and pot trials have shown variability in yield stability of faba beans measured by various indices (Fig. 1). Out of a range of physiological parameters measured as indirect selection criteria, accumulation of free proline and the effective quantum yield  $\Delta F/F_m'$  of chlorophyll fluorescence had the closest relation to yield stability.



Fig. 1: Drought stress trials of faba beans in a rain out shelter

On the other hand, a relatively high correlation has been found between yield under control conditions and that under stress conditions, the higher yielding genotypes being characterized by a lower yield stability.

Physiologically, this could be put down to the low potential for osmotic adaptation of faba bean genotypes and therefore to their inability of improving water use efficiency under drought stress – as shown by investigations under controlled stress conditions.

Progress in this field could arise from the evaluation of so called ‘exotic genotypes’ from marginal locations (habitats) on one side and from breeding of winter beans, which are able to use winter and spring precipitation more effectively, on the other side.

### ■ Drought tolerance and quality stability in potatoes

Potatoes are known to react relatively sensitively to water deficit. Depending on the stress intensity and the physiological conditions of whole plants, drought stress induces various changes in their metabolism. Amongst the accumulation of so-called compatible solutes especially the nitrogenous compounds show a marked variation in their concentrations and activities, respectively. Changes in yield, yield stability and quality of the tubers are the consequence.

In order to determine the extent of these changes a test assortment of 23 genotypes were cultivated under stress and control conditions (Fig. 2).



Fig. 2: Influence of drought stress on seven-week-old potato plants



Yield and quality parameters were captured. Drought stress caused yield reductions of 25–90%. In the tubers significant lower contents of dry matter, starch and starch yield as well as a significant higher content of protein were observed.

In the starch, lower gelatinization maximum and mean particle diameters as well as higher amylose contents appeared. All important parameters of the raw material and the starch correlated with the relative yield under stress.

In the selection process regarding drought tolerance selection criteria of an early developmental stage of the plant are favoured. It could be found that protein loss in stressed leaves (7 weeks old) correlated with the relative yield.

## Organic farming

Organic agriculture as a particularly sustainable type of land management gains in competitiveness by specific, adapted genotypes. Breeding research can make a contribution to that.

Furthermore long-term cultivation tests of different assortments of agricultural plants regarding quality and yield provide objective criteria to classify the organic compared with the conventional agriculture.

### ■ Comparison of organically and conventionally grown agricultural crops

In case of the evaluation of genetic resources, landraces and relevant varieties, principles of organic farming were taken into account. For that purpose, an organic test field was established in Groß Lüsewitz in 2000. The analysis of agricultural products over several years under the same environmental conditions should clarify the differences in the quality of raw material dependent on the kind of cultivation. Investigations will result in statements about the suitability of available varieties (potatoes, cereals, legumes) for the production of specific qualities and the possibility of their improvement for organic farming. The cultivated assortments include winter and spring wheat, rye, triticale, spelt, winter and spring barley, peas, field beans and potatoes. Whereas seed lots and seed quantities are identical in both farming systems, the used crop rotations are different (organic: potatoes, spring grain, legumes, winter grain, grass ley, grass ley; conventional: potatoes, legumes, winter/spring grain, oat, grass ley). The valuations and measurements in the standing crop occur up to harvest and include especially characters of the growth and observed diseases. Yield and quality parameters are comprehensively determined in kernels as well as in the whole meal and the tubers, respectively. In addition, the value of the food potatoes is investigated (Fig. 3).

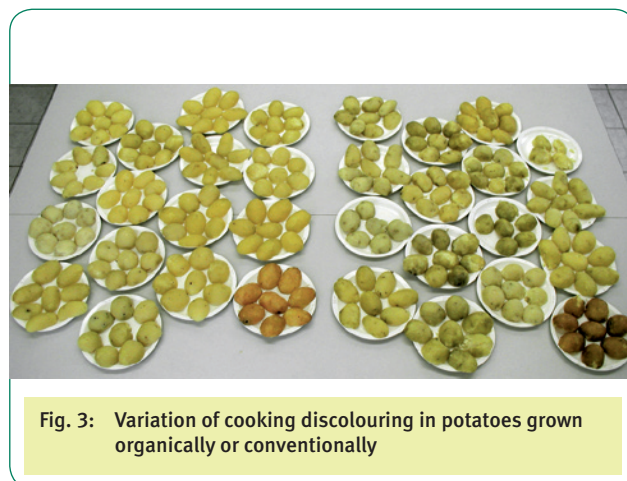


Fig. 3: Variation of cooking discolouring in potatoes grown organically or conventionally

### ■ Improvement of feeding quality of sweet lupin seeds for utilization in organic farming

Organic farmers are striving for a closed cycle in their companies. Besides field beans and peas, sweet lupins are a very important supplier of vegetable protein in organic farming. Lupins can make a contribution to solve problems by the use of organic feeding stuffs in animal nutrition. Prerequisite is an optimal and stable feeding quality. Besides the genetic variability of sweet lupin seeds, the influence of different organic locations on yield and on quality parameters such as crude protein, starch, sugar and oil content are analyzed. The protein quality and the fatty acids are also investigated (Fig. 4). A further aim is the determination of antinutritive substances, such as non starch polysaccharids and alkaloids. Primarily, current varieties and breeding material of blue lupins are taken into account.

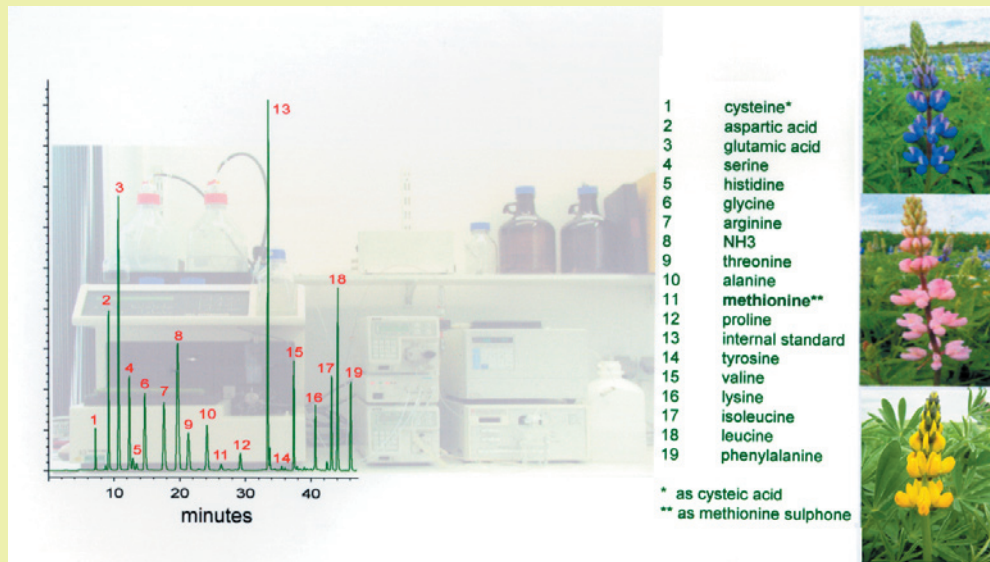
## Quality

Besides the supply of high quality food and feed, the production of industrial raw materials with specific properties develops a further important agricultural market. The protection and evaluation of such qualities can only be conducted by means of efficient, breeding-relevant methods. For this reason a system of analysis comprising spectroscopy, chromatography and a wide range of biochemical and biotechnological methods was established over the years. This enables a comprehensive evaluation of genetic resources.

### ■ Evaluation of genetic resources regarding specific quality parameters in rapeseed

Rapeseed is the most important oil crop in North and Central Europe today, mainly due to the successful breeding of erucic acid-free and low glucosinolate cultivars. Its competitive position is additionally improved by a commercialization of the protein rich residues of the oil production as a valuable plant-derived animal feed. Besides the oil content the crude protein is the most important quality parameter;

Fig. 4: Protein quality – amino acid composition in lupines



however, there is a significant, negative correlation between both. A high amount of crude fibre, which is mainly located in the seed coat, and the resulting low content of usable energy reduces the utilization especially in the feed of monogasters like pigs. On the other hand the content of essential amino acids, particularly sulphurous amino acids such as methionine and cysteine, as well as minerals and vitamins is enhanced in rapeseed compared to soybean - another important reason for the extended investigations which have been carried out in our institute.

The aim of the evaluation of genetic resources with respect to value determining ingredients is the search for outliers in the regression analysis between oil and protein content. In this context the colour of rape seed coat plays a key role (Fig. 5).

Thus, investigations of the coat thickness in relation to the colour have shown that the yellow seed types have a lower coat proportion and consequently an enhanced content of oil and protein.

### ■ Safeguarding a healthy nutrition by breeding in the food sector

Currently, we satisfy 2/3 of our energy requirements by plant derived foods. In this context also potatoes play an important role. Due to their valuable ingredients such as the vitamins B1, B2 and C, minerals (potassium, calcium, magnesium), proteins and essential amino acids they rank among the most healthy foods. In the interest of a good health policy it is important to stop the regressive tendency of potato consumption or to reverse it as far as possible. This



Fig. 5: Seed colour of rapeseed as important parameter for oil content



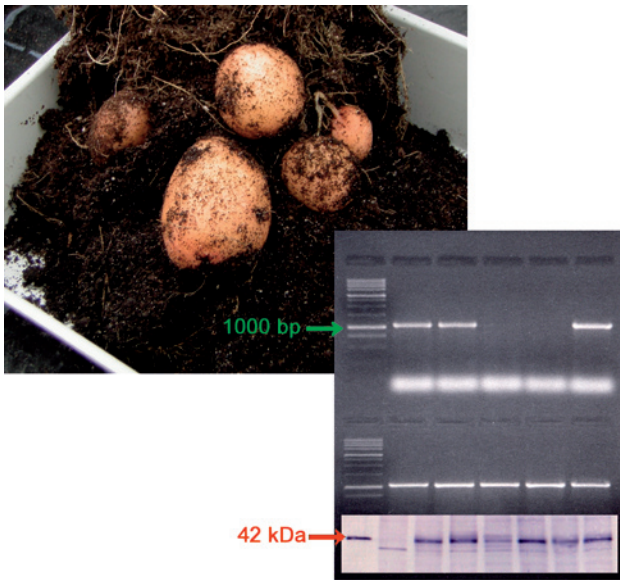


Fig. 6: Harvest of tubers and molecular analysis

makes high demands on the quality standards of the goods offered on the market. But very often tuber soft rot caused by *Erwinia carotovora* bacteria leads to considerable quality problems and great economic losses – especially in wet years. Washing procedures, long transport and subsequent storage under unfavourable conditions promote the spread of this disease. The *Erwinia* bacteria, which are always present on the surface of tubers, enter the tissue via wounds and lenticells and produce a set of cell wall degrading enzymes such as pectinases, cellulases and proteases. The enzymatic maceration of plant tissue leads to typical soft rot symptoms. The potato cultivars are all more or less susceptible to this

disease. Therefore, during many years the improvement of resistance is an important goal in breeding and breeding research. The activities of our institute are focussed on the design of evaluation parameters for plant resistance reactions. Besides traditional, biochemical methods also molecular techniques are valuable tools. Thus, in previous projects an *Erwinia*-derived pectate lyase (PL) gene was transferred by means of *Agrobacterium* into potatoes of cv. Désirée. In the generated transgenic potato lines expression of PL3 protein mediated an advanced activation of plant defence mechanisms, combined with an enhanced resistance of tuber tissue to *Erwinia* soft rot. In PL3 expressing potato lines the phenylalanine ammonia-lyase (PAL) activity was significantly enhanced compared with the non-transgenic counterparts. The PAL, a key enzyme in the phenylpropan metabolism, acts as an important regulator in the biosynthesis of phenolic compounds and is widely seen as a marker for the induction of plant defence mechanisms. In the meantime the *Solanum tuberosum* cvs. Agave and Adretta with a moderate level of soft rot resistance were crossed with three PL3 transgenic potato lines. The resulting progenies were assessed with respect to plant and tuber characteristics (Fig. 6) since 1998. Besides molecular analysis (Fig. 6), which confirmed the inheritance of the *pel3* gene, lines with acceptable agronomic traits were evaluated for their biochemical composition (dry mass, starch, proteins, amino acids, phenols etc.) as well as their resistance properties. The group of PL3-active progeny revealed a better resistance to *Erwinia* bacteria than the non-transgenic parental cultivars. Again the PL3 expression was coincident with enhanced activities of PAL in tuber tissue. Future research activities will be focussed on the effect of abiotic stress on the expression of foreign genes in potatoes and on enzymes of the phenylpropan metabolism.



Fig. 7:  
Pre-breeding material of wheat containing specific starch qualities



### ■ Specific qualities in cereals for the non food area

Wheat as starch supplier has an important position in Europe and will get more relevancy in future because of its high and reliable yield.

With the production of waxy-wheat (Fig. 7), wheat with a changed ratio in main components of starch is available. Because of the absence of amylose the substantial, chemical, physical and because of that technological properties are changed. Breeding relevant methods are developed to characterize the breeding products of waxy-wheat mutants with efficient spring and winter wheat.

In the interest of a highly added value beside the raw material and starch also the gluten was characterized. Simultaneously, the investigations on waxy-wheat are focused on the reduction of pre-harvest sprouting. Furthermore, stress factors (temperature, water) and their influence on stability of quality are taken into account. Because of the complex characterization and the improved properties of waxy-wheat, the use of wheat in food and industrial area can be expanded.

## Outlook

The research activities of the Institute of Abiotic Stress Tolerance, which are concentrated on stress physiological questions as well as those of product quality, make a contribution to the progress in breeding research and adduce consulting for political decisions of the Federal Ministry of Food, Agriculture and Consumer Protection (BMELV). The prominence of the “applied basic research” performed in the institute lies mainly in the origination of objective eligibility criteria for political decisions with respect to consumer protection, food and agricultural policy as well as foreign aid for third world countries. The 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 the area of responsibility of the BMELV, with gene banks, universities, regional research centres and breeders inland and abroad (Fig. 8). In future, abiotic stress tolerance of crop plants will gain more importance, especially due to more and more scarce resources world-wide (water, energy) and prognosticated climate changes. In this context, not only crop yield will be regarded, but also quality of agricultural raw materials, taking into account the increasing application of agro-products in the industrial sector and the high consumer requirements (safety, healthy nutrition).



Fig. 8: Discussion with breeders and guests from the People's Republic of China and Japan in the test field



**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 and 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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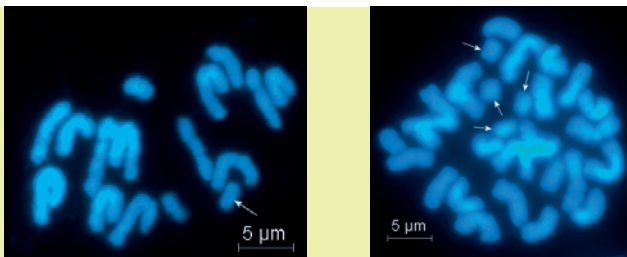
Susanne Gürtler  
horticultural engineer (project contract from 01.07.2005)



## Sovereign Duties

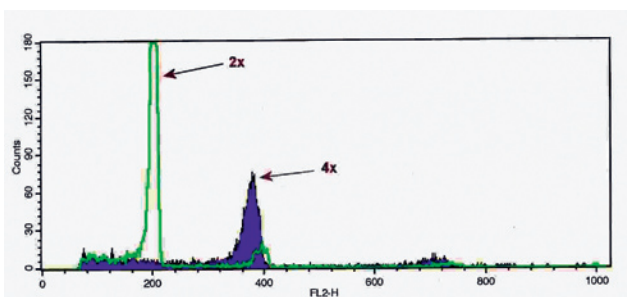
Within the scope of registration for breeders' rights, the Bundessortenamt needs exact information on the level of ploidy of several gramineous plants, sugar beets, fodder beets, red clover and in particular cases on miscellaneous species, e. g. asparagus. In the case of red fescue (*Festuca rubra*), colonial bent-grass (*Agrostis*), sheep fescue (*Festuca ovina*), tufted hair-grass (*Deschampsia caespitosa*) and English blue grass (*Festuca pratensis*), due to their chromosome size and cytological aberration, the analysis of the ploidy level is

Fig. 1: Metaphases of rye-grass varieties (*Lolium perenne*): 'Action' diploid (left) and 'Proton' tetraploid (right) with 1 and 4 B-chromosomes (arrows), respectively



labour-intensive and needs besides the diagnostic routines scientific steering. This work has been assumed in the report period by the institute and the technical prerequisites have been established. First results in cytogenetic stability of ploidy levels were obtained in different varieties of ryegrass and meadow-grasses as well as red fescue. In samples of 5 single plants each, no deviation from the expected ploidy levels was noted. However, as described in the literature on other

Fig. 2: Histogram of rye-grass varieties (*Lolium perenne*): 'Action' (diploid, green) and 'Merkem' (tetraploid, blue)



cultivated grasses, e.g. in rye, the accessory chromosomes (B-chromosomes) had the potential to change the chromosome numbers in all levels of ploidy (2x, 4x, 6x and 8x). Thus the diploid and tetraploid ryegrasses are characterized with one to six additional B-chromosomes (Figs. 1 and 3A). This can change the results of DNA measurements in the flow cytometry and lead to deviations from the expected 1:2 relation (Fig. 2). Within the diploid rye grass variety 'Greenfair', a variation of the number of B-chromosomes between zero and six (Fig. 3A) was shown. Furthermore, this variety exhibited differences in the morphology of the autosomic chromosome pairs after fluorescence *in situ* hy-

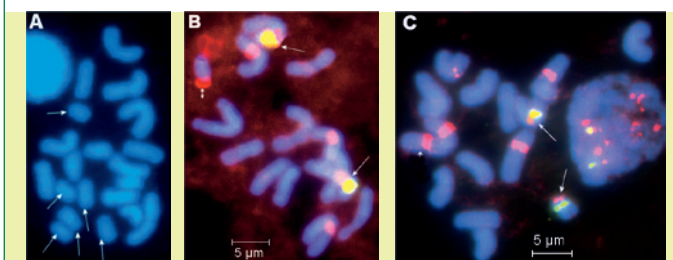


Fig. 3: Rye-grass variety 'Greenfair' (*Lolium perenne*)  $2n = 14 + B$ ; A: six B-chromosomes (arrows); B and C: FISH with gene-specific DNA probes - Yellow 5S and red 18/25S rDNA with double marked chromosomes (arrows) and one very short chromosome (arrow heads); in C the double marked chromosome pair is heteromorphic.

bridization (FISH) with DNA probes specific for 5S and 18/25S rDNA genes (Fig. 3B-C). This indicates considerable karyotypic dynamism in this variety.

## 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.

## ■ Vegetable Brassicas (*Brassica oleracea*) and its Relatives

### Resistance Improvement in Vegetable Brassicas

A sustainable reduction of plant protecting agents in the cultivation of cabbage is dependent on the transfer of effective disease resistance. For this reason further work was done to characterise cabbage (*Brassica oleracea*) and *Raphanobrassica* hybrids resistance donors to *Turnip mosaic virus* (TuMV), clubroot (*Plasmodiophora brassicae*) as well as to *Phoma* leaf spot (*Phoma lingam*, teleomorph: *Leptosphaeria maculans*).



Fig. 4: Clubroot (*Plasmodiophora brassicae*) on Chinese cabbage (*Brassica rapa* ssp. *pekinensis*)

Fig. 5: Resistance screening in cabbage lines (*Brassica oleracea*) to *Turnip mosaic virus*



Resources with new resistance to TuMV have been identified in cabbage primitive forms (*B. oleracea* var. *ramosa*), in a cabbage landrace and in radish (*Raphanus sativus*). From cabbage primitive forms homozygous lines ( $I_8$ ) have been generated with resistance to three different TuMV pathotypes (pathotyped by Jenner and Walsh, Wellesbourne, UK). Resistance in these homozygous lines ( $I_8$ ) was effective to both mechanical inoculation and exposure to viruliferous aphids in the field. From the cabbage landrace lines ( $I_7$ ) revealed resistance (infection rate 0 %) to five TuMV pathotypes. The produced *B. oleracea* lines possess broad-spectrum resistance to TuMV.

Protoplast fusions between *B. oleracea* and *R. sativus* were used for transferring and stabilising resistance in *Raphanobrassica* hybrids. The progenies of these *Raphanobrassica* hybrids showed resistance to TuMV pathotypes, to different races and isolates of *Plasmodiophora* and *Phoma* respectively. The different ways to generate and characterize new resistance donors will enable the establishment of resistance to different pathogens as well as to races and pathotypes of these pathogens in *Brassica*-vegetables.

### Addition of Alien Chromosomes in Brassica Species

Addition lines are plants carrying a chromosome (monosomic) or a pair of homologous chromosomes (disomic) of an alien donor species additionally to their normal chromosome complement. A complete set of addition lines consists of a line for each non-homologous chromosome. In this way, the genetic information of a donor plant is dissected physically and functionally on chromosome level. To produce addition lines, recipient and donor species have to be related and crossable. Therefore, they belong mostly to the same taxonomic genus or family. After initial cross between both species, the number of donor chromosomes will be reduced with backcrosses to the recipient from the full complement to single chromosomes. Often, strong barriers of low fertility have to be overcome. Following each cross cycle, extensive genetic characterization of progenies is necessary. Using methods of molecular biology and cytogenetics, it has to be determined which plants possess alien chromosomes, their number and specificity of the extra chromosomes. From the known addition lines, not all are in a full set. Disomic lines have been produced seldomly. In the Institute of Horticultural Crops a complete series of additions of radish (*Raphanus sativus*) chromosomes on genetic background of *Brassica napus* was developed (Fig. 1). Because of radish chromosome number  $n=9$ , the series has nine lines ( $a, b, \ddot{O}, i$ ). At first, the monosomic lines with  $2n=38+1$  chromosomes were obtained, from these subsequently the disomic set of additions ( $2n=38+2$ ) was developed. Disomic lines are easier to reproduce because of no segregation for the alien chromosome. The integrity of the added chromosome is protected against changes by recombination between homoeologous chromosomes of recipient and donor species. Radish as chromosome donor represents an interesting genetic resource for *Brassica* crops such as cabbage and rapeseed. The cytoplasm of radish has been used to induce male sterility, which is important for the breeding of cms hybrid varieties. The restorer genes for CMS have been also introduced from radish. Radish has some further characters that are interesting for *Brassica* crop breeding. For the identification of the chromosome additions molecular and cytogenetic methods have been used. The cytological analysis by fluorescence *in situ* hybridization (FISH) with

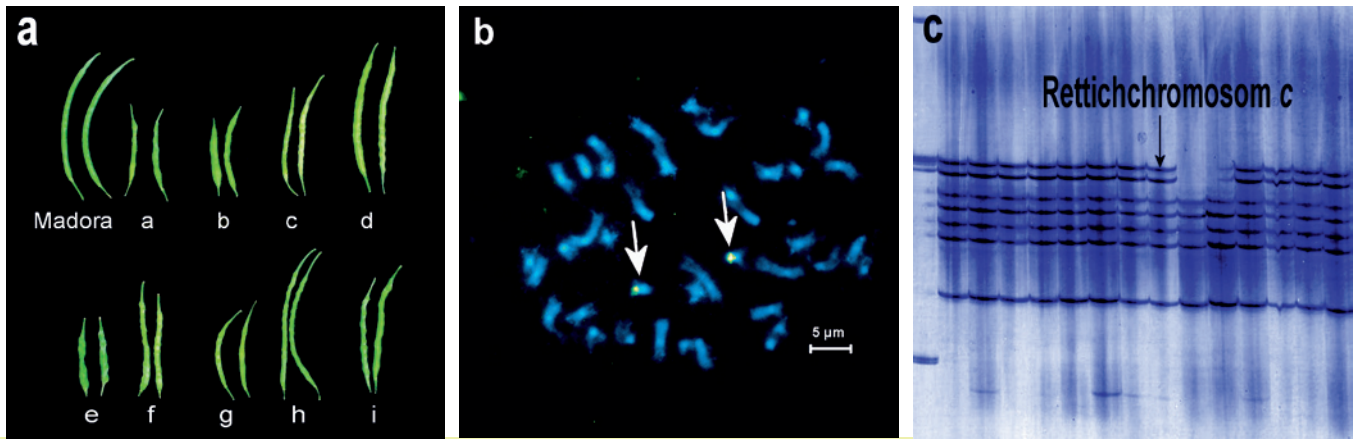


Fig. 6: Recipient and radish additions (a); cytological labelling of extra chromosomes (b); control of chromosome transmission with a molecular marker (c)

radish-specific DNA probe pURsN allowed the detection of all the homologous and non-homologous radish chromosomes in an addition plant, even in interphase nuclei. With further probes, 5S-rDNA and 18/25S-rDNA, a more detailed description of karyotypes was given. Furthermore, molecular markers (RAPD, AFLP) have been assigned to each specific non-homeologous radish chromosome. The reliability of the results was increased by multiple markers per chromosome. With the molecular methods used, it was possible to screen effectively large backcross progenies of several hundreds of plant individuals to identify the desired genotypes. The process of meiosis in generative tissue of addition plants was not influenced visibly by the extra chromosomes. Studies of the extra chromosome transmission in disomic additions were conducted showing a nearly undisturbed transmission of radish chromosomes through female (egg cell) as well as male (pollen) side. Comparisons between parental species and addition lines allowed the identification of chromosomes controlling the expression of characters. The resistance in radish against the beet cyst nematode (*Heterodera schachtii*) is transferred to rape by a single chromosome. Thus it seems possible to transform the susceptible recipient species into a nematode trap crop plant (biological plant protection). First field trails (carried out by BBA Institute of Nematology and Vertebrate Research) have verified the decreasing effect on nematode population in the soil. The growth of nematode-resistant addition line *d* reduced significantly, compared to that of normal rape, the pathogen density in a highly infested soil. In contrast, the reaction to another pathogenic nematode species, the root-knot nematode *Meloidogyne hapla*, was influenced by the effect of nearly all radish chromosomes but in different directions. Some extra chromosomes in rapeseed enhanced nematode resistance, whereas the others had the opposite or no effect. Specific radish chromosomes modified also biochemical characters such as glucosinolate content and composition in root, leaves and seeds and fatty acid synthe-

sis in seeds. Some characters of the donor species had not been expressed in any of the addition lines. All nine addition lines showed the same susceptibility as the recipient species, though the donor species radish was resistant to clubroot (*Plasmiodiophora brassicae*) and to TuMV (*Turnip Mosaic Virus*). We have some indications that radish-chromosome mediated effects for these resistances will be expressed on different genetic backgrounds. Therefore, we started to transfer radish chromosomes to the diploid background of cabbage (*Brassica oleracea*).

### ■ Carrot (*Daucus carota*)

Carrot is throughout the world one of the important kinds of vegetables and it is used fresh and in processed form. The high content of carotene or provitamin A, other vitamins (B, C, D, E), antioxidatives and essential trace elements make carrots important for human health. To open up these potentials methodically, an exact knowledge of the inheritance is essential. The selection process of plants with well-defined characters can be simplified with the help of molecular markers. Since the development of the DNA-fingerprinting techniques, molecular markers can be used. Molecular markers are generally established in modern plant breeding but the application in research and breeding is highly cor-



Fig. 7: Phenotype classes in the  $F_2$  – progenies of the double mutant assay. A – wild-type with green and normal leaf structure; B – yellow leaf mutant; C – compressed lamina mutant; D – double mutant yellow + cola leaf



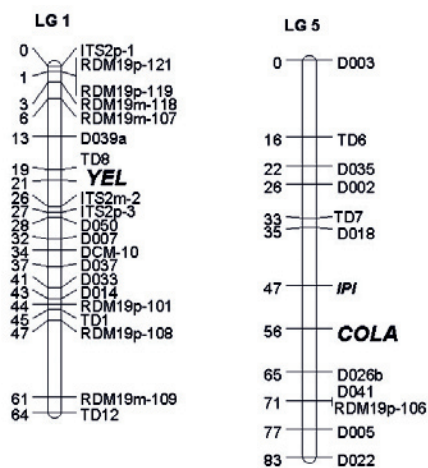


Fig. 8: Part of the preliminary linkage map. Linkage group 1 and 5 with mapped target genes *YEL* and *COLA*

mapping) were prepared.  $F_2$  plants of the mapping population segregated into four distinct phenotype classes, exactly in a Mendelian fashion expected for two independent genes (9:3:3:1; Fig. 7). Genomic DNA used for molecular evaluation was isolated from leaves of the individual  $F_2$  plants. A total of 28 RAPD and 41 AFLP markers were developed for the population and used for construction a preliminary skeletal linkage map. Additionally, 10 published co-dominant SSR markers and 14 dominant retro-transposon markers could be introduced in the map. Furthermore, 6 gene-specific markers were generated and mapped. The preliminary map contains 100 markers distributed over nine linkage groups for a total length of 494 cM. Both target genes were mapped on separate linkage groups (Fig. 8), very interesting as morphological anchor loci in future. Activities for the molecular cytology (physical mapping) are in progress.

## Medicinal and Aromatic Plants

Medicinal and aromatic plants are used as raw material of a vast variety of products, among them herbal medicinal products, seasonings and other food additives, cosmetic preparations and natural plant protection products. They act to a lesser extent as sources of energy, vitamins and dietary fiber for human nutrition. However, they contribute to the improvement of our well-being, because they protect our health and make our food tasty and more digestible. About 100 different species of medicinal and aromatic plants are cultivated in Germany providing a market niche for farmers in a very special sector of minor crops. Covering this group of alternative crops the Institute of Horticultural Crops contributes to the maintenance of genetic diversity in agriculture, to breaking-up crop rotation, to safety and quality of the products. Hitherto medicinal and aromatic



Fig. 9: Fruits of annual caraway



Fig. 10: Polycross of 40 annual caraway inbred lines for testing the general combining ability

plants have been only marginally the object of plant breeding and breeding research. Most species are yet in the stage of wild plants. Therefore, research focuses on collection and evaluation of numerous different accessions to investigate the high natural variability available and to point out ways how to exploit accessions as donors of valuable characteristics for breeding.

### ■ Caraway (*Carum carvi*)

Caraway fruits (Fig. 9) are used as spice but also as herbal medicinal product. In Central Europe prevails a biennial caraway form with the scientific name *Carum carvi* growing also in the wild on meadows. Biennial caraway makes a leaf rosette in the first year only. Therefore, the farmer has no revenues in this year. Endemic in the Mediterranean is an annual caraway form (*C. carvi* var. *annuum* hort) that can be harvested already in September in the first year under German climatic conditions when sown in April. The obstacle of the introduction of this - from the economic point of view - more advantageous annual form was hitherto the low essential oil content of the fruits. The essential oil content is the most important quality determining characteristic. The results of collection and evaluation of different accessions of annual and biennial caraway revealed that the aspired high essential oil content is not primarily available in annual caraway, but in biennial caraway forms. The following methods for the development of new annual forms with a high essential oil content level together with good agronomical characteristics have been tested: continuous recurrent selection in one population of annual caraway and crossing of biennial and annual caraway cultivars with subsequent selection of types with the aspired trait expressions. Recurrent selection resulted in significant improvement of the essential oil content from 3 to 5%. The improved populations could be used for the development of the first German annual caraway variety and it has been already widely introduced in practice. Populations originating from the crossing experiments shall be tested in the following years for particularly favourable combinations of high essential oil content and good agronomical characteristics. In 2005, 40 individual plants of each line developed from the crossing progeny of annual and biennial caraway types were cultivated in a field experiment according to an polycross arrangement that exposes each plant to the same probability of being pollinated by an individual plant of another line (Fig. 10). This experiment is the first step of the combining ability test of the lines and will be completed with a performance test of the progeny arisen under these conditions. Progenies with high essential oil content, fruit yield and good agronomic characteristics will point out the good general combining ability of the mother lines. These lines are particularly qualified as genetic components of a synthetic variety.

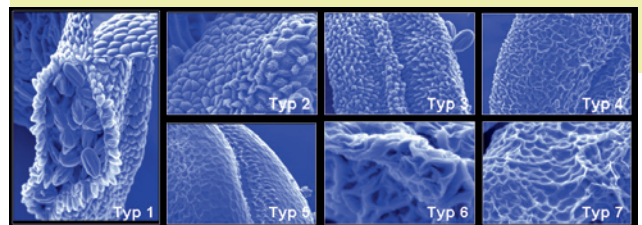


Fig. 11: Flowering thyme plant



Fig. 12: Different reproductive types of thyme: (type 1 = hermaphroditic, types 2-7 intermediate with atrophied anthers, type 8 = male sterile)

Fig. 13: SEM micrograph of the anther surfaces



### ■ Thyme (*Thymus vulgaris*)

Thyme is an evergreen semi shrub (Fig. 11) endemic in Central and South Europe whose leaves and flowers are used as spice but primarily also as remedy. The active principles with antimicrobial and antioxidative properties are the phenols thymol and carvacrol, which are contained in the essential oil. The in Germany currently cultivated thyme is very heterogeneous. But, the industry requires a homogeneous raw material with high content of important constituents. The research project aims at the exploitation of the reproductive specifics for the development of lines as genetic components of hybrid varieties. Hybrid varieties whose seeds are generated by consistently new crossings of two parental lines provide the best prerequisites to overcome



the heterogeneity. Controlled pollination of certain parental lines is facilitated e.g. by male sterility of the maternal parent line. The frequent occurrence of such male sterility by nature in case of thyme provides good prerequisites to exploit this flower specific particularity for this purpose. The Institute is accomplishing investigations on flower biology and on the specifics of the reproduction behavior as basis for future variety breeding by the participating partner company in the frame of the InnoRegio-Initiative of the Ministry of Education and Research. The investigation of the flower biology revealed that there are numerous medium forms not suitable as parental lines for a hybrid variety. The varying forms can be classified by the shape of the anthers, by the morphology and vitality of the pollen and by the shape of the flower (Fig. 11). Most recent investigations on longitudinal sections of the anthers revealed that their shape and their deformation shift from spheroid to star-shaped/frayed. Scanning electron microscope recordings showed that the degeneration is observable not only by the shape and color of the anthers, but that the cells of the anther surfaces appear more distorted with increasing male sterility (Fig. 13). The clear differentiation of the level of male sterility allows an improved selection strictness selecting appropriate genotypes for hybrid varieties. We succeeded in establishing systems for maintenance of male sterile lines by test crossings of appropriate pollinators and male sterile plants. In 2003 and 2004, accomplished test crossings resulted in the following reproductive types among 126 progenies: 18 totally male sterile and 93 progenies with atrophied anthers.

### ■ Summer Savory (*Satureja hortensis*)

Summer savory is traditionally cultivated in the region north of the Harz mountains for spice production. The main component of its essential oil - carvacrol - is responsible for the spicily flavor. In addition, carvacrol has antioxidative and

antimicrobial properties and therefore it is an alternative to the antibiotic animal feed additives whose use will be thoroughly prohibited in the EU in 2006. The short developmental vegetation period of savory facilitates its flexible arrangement in the crop rotation as catch crop and provides good prerequisites for the raw material production with low costs. The joint research project is accomplished together with companies in the frame of the InnoRegio-Initiative of the Ministry of Education and Research and aims at the development of savory populations with high yield and content of carvacrol rich essential oil. The natural variability of the important characteristics has been investigated by evaluation of 58 accessions cultivated in summer and in autumn as well (Fig. 14). Two cycles of recurrent selection resulted in a significant performance improvement of the best populations (Fig. 15). Investigations on the harvest stage in summer and autumn conditions revealed that savory achieves the highest essential oil yield with an appropriate carvacrol content when harvested shortly before full flowering. Savory can be cultivated in summer before a catch crop or after a main crop. Besides agronomical traits, the running investigations cover the following characteristics: developmental period, yield and content of essential oil, and carvacrol content of the essential oil. As result of the selection, the carvacrol content could be improved to 64-67% in the best populations where the basic requirement is 60%. Despite the ascertained negative correlation between essential oil content and carvacrol content, high essential oil yielding populations with an appropriate carvacrol content of the essential oil could be developed.

## 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

Fig. 14: Evaluation of a summer savory collection



Fig. 15: Improvement of the essential oil content of summer savory by recurrent selection

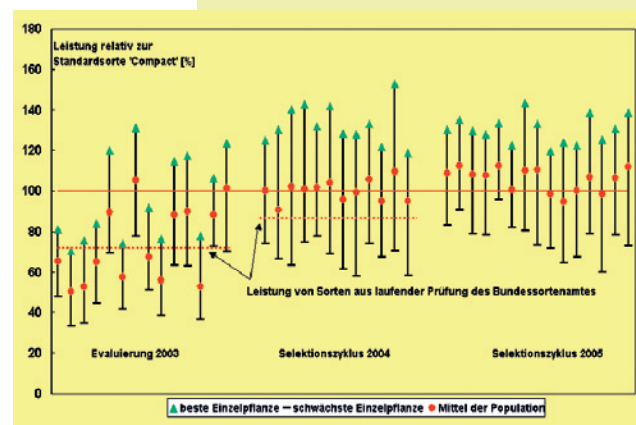






Fig. 16: Diversity of wild species as a genetic resource of *Pelargonium* (from left to right *P. fulgidum*, *P. acetosum*, *P. cucullatum*, *P. schizopetalum*)

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

*Pelargonium* (also called Geranium) holds under the bedding and balcony plants the largest market position. This ornamental plant has developed within the last centuries from a botanical curiosity grown as an amateur plant into a cultivated plant with economic importance. Crosses between wild species were at the beginning of the development and, presumably, only a few parental species with good crossability were used. Therefore, the genetic basis of the large numbers of modern varieties might be narrow for creating new variability. The genus *Pelargonium* consists of much more than 200 species that could be used for the development of new varieties (Fig. 16). Molecular and biotechnological methods could help to exploit these genetic resources.

### Sexual Hybridization

The wild species of *Pelargonium* are subdivided in 16 sections and show a great range of diversity. They differ in chromosome number, ploidy level, growth habit and a number of morphological characters (e.g. shape and colours of leaves and flowers), as well as in their secondary biochemical substances and physiological requirements. Sexual hybridization between cultivated varieties and wild species could lead to new basic material for breeding if existing cross barriers will be overcome. Such incongruities have to be analyzed by

investigations on generative tissues after wide hybridizations (Fig. 17). For genetic characterization of new hybrids molecular and cytogenetic methods are adapted that have been proven useful in other cultivated plants. The development of marker systems for early and reliable screening of the hybrid character constitutes an important part of this work.

In practical breeding, crosses between varieties of the *Pelargonium* ñ *hortorum* (zonal) and *Pelargonium* ñ *peltatum* (ivy) groups are used to produce new combinations of characters. From a breeders point of view it is important to know the genetic proportion of parental genotypes in progenies resulting from such a breeding programme for an effective selection. To evaluate methods for discrimination of parental genetic material, the experimental hybrids were produced from defined genotypes of zonal and ivy hybrids. Furthermore, experimental interspecific crosses with wild species from section *Ciconium* and cultivated varieties have been carried out. Pollen grain germination and tube growth were observed by means of a fluorescence microscope to search for progamic incompatibility. Because of failure to observe all stages, this method has to be adapted even more to *Pelargonium* ovaries. Strong barriers seem to exist after fertilization. Interspecific embryos isolated 14 days after pollination showed mostly disturbed differentiation during *in vitro* culture, but some hybrid plants were obtained. Molecular analyses at the plantlets *in vitro* allowed the discrimination between mother-like and hybrid plants very early. Generally, the DNA polymorphism was lower than expected. Genomic fluorescence *in situ* hybridization (GISH) was started to determine the hybrid character of the new *Pelargonium* genotypes. To investigate the effect of ploidy level on seed



Fig. 17:

Sexual interspecific hybridization in *Pelargonium*. Locule with two ovules (a); stigmas with pollen (b); hybrid embryo *in vitro* (c)

fertility in cultivated *Pelargonium*, selected diploid varieties with  $2n=18$  were treated by colchicine both as cuttings and as seedlings. Chromosome counting on root tips showed tetraploid cells in about 25 % of treated plants.

### Somatic Hybridization

In *Pelargonium* scented-leaved pelargonium and wild species have a lot of valuable characters, especially resistances against different pathogens. However, sexual incompatibility between different *Pelargonium* species prevents improvement by crossing. Somatic hybridization may be a viable alternative to overcome these difficulties. Beside that the process of protoplast fusion may be a useful tool for the induction of genetic variability and the combination of traits of the plastome and genome of both parents. A prerequisite of that is the development of procedures for protoplast isolation, protoplast culture and plant regeneration. To work out optimal protocols for protoplast fusion, the using of mesophyll protoplast and protoplast originating from cell suspension cultures (Fig. 18) is advantageous. Such visible markers allow easy examination of the fusion process and control of the efficiency by microscope. An *in vitro* culture system of different pelargonium species has been built up. Mesophyll protoplasts from micro-propagated plants from different species were successfully isolated, grown into colonies and regenerated to plants. A lot of cell suspension cultures could be established which provided excellent materials for isolating protoplasts. These protoplasts were grown into colonies and regenerated to plants, too. First experiments of protoplast fusion by using PEG as a fusogen and by electrofusion with *Pelargonium zonale* (+) different scented-leaved pelargoniums and different wild species have been carried out.

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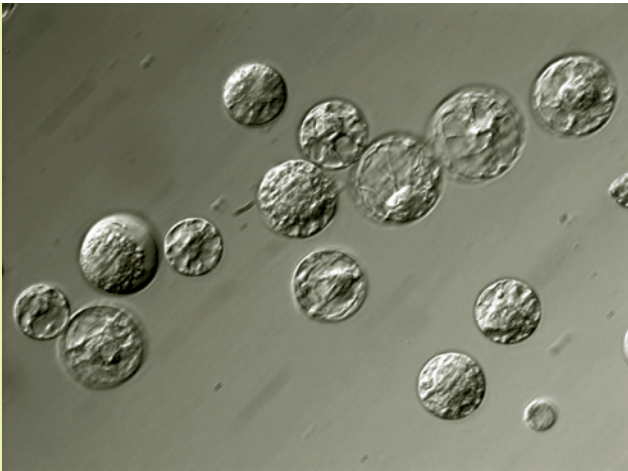


Fig. 18: Protoplast from cell suspension of *Pelargonium*

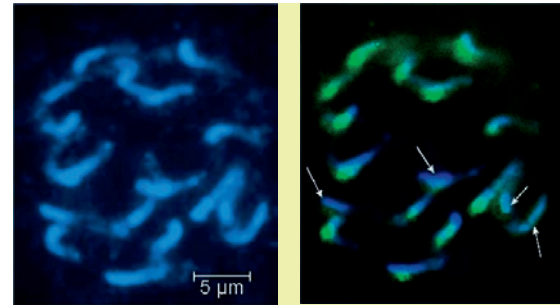


Fig. 20: Genomic in-situ-hybridization (GISH) with genomic DNA of *Pelargonium inquinans* (yellow) in metaphase chromosomes of variety 'Ville de Paris' ( $2n=18$ ). Four chromosomes (arrows) have no hybridization signals

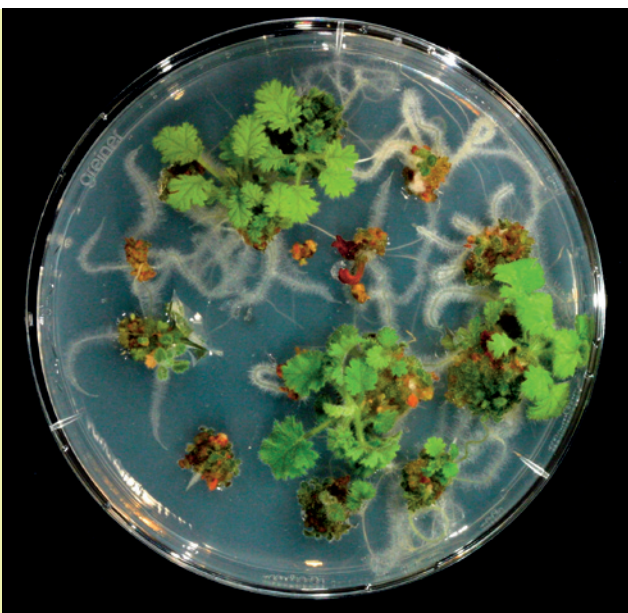


Fig. 19: Plant regeneration from protoplast

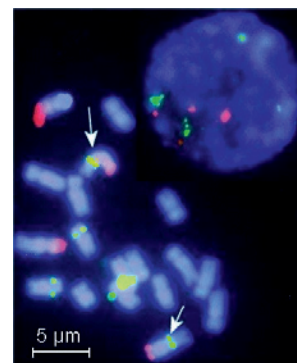


Fig. 21: Fluorescence in-situ-hybridization (FISH) with gene-specific probes in metaphase chromosomes of *Pelargonium acetosum* ( $2n=18$ ). The 5S-rDNA (yellow) is located in six and the 18/25S-rDNA (red) in four chromosomes. In two chromosomes both gene sequences are present (arrows).

### Cytological Analyses

To investigate the unknown origin of variety 'Ville de Paris', the ribosomal RNA-specific genes of 5S- and 18/25S-rDNA were used as probes in the fluorescence in-situ-hybridization (FISH). *P. acetosum* as one of the possible donor species has with six chromosomes labelled by the 5S-rDNA (Fig. 20) four more than 'Ville de Paris'. From this it follows that not all 5S-rDNA carrying chromosomes of *P. acetosum* are present in the variety 'Ville de Paris'. Similar results were also obtained by genomic in-situ-hybridization (GISH) (Fig. 21). After hybridization with genomic DNA of *P. inquinans* four chromosomes were not labelled in 'Ville de Paris'. Further investigations with other possible donor species such as *P. zonale* and *P. peltatum* are in progress.

### ■ Hydrangea

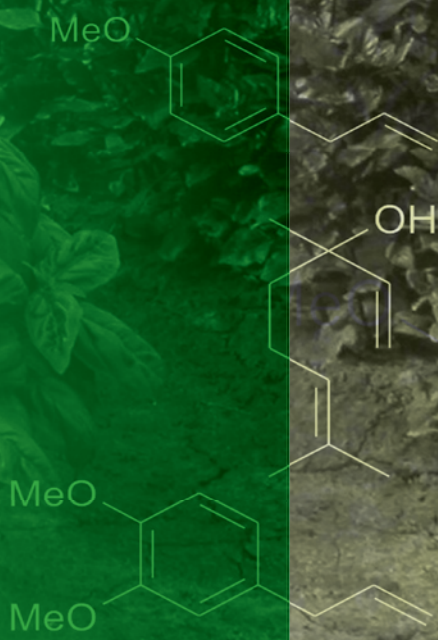
Among classic garden shrubs, the genus of *Hydrangea* (Fig. 22) comprises species with a high ornamental value and variability. These plants, known as 'lacecap' or 'mophead' Hydrangeas, do not only experience a renaissance in today's gardens, but are also of great interest as potted plants. In Europe, Hydrangeas are mainly cultivated in France, the Netherlands and Germany. Marketing criteria for a cultivar value encompass colour and size of the inflorescence, flower endurance, compact but vigorous plant growth, ramification and finally disease resistance. The development of new cultivars attracts the interest of the breeders and plant producers. Particularly, remontant cultivars are of high value as they do not require any time- and cost-intensive cold treatment for flower induction and therefore are characterized by a shorter production cycle. The aim of this project is the broadening of the available breeding methods and the development of new cultivars of *Hydrangea macrophylla*. The project is supported by the Arbeitsgemeinschaft industriell-

ler Forschungsvereinigungen „Otto von Guericke“ e. V. (AiF, German Federation of Industrial Research Associations), and it will be realized in a close cooperation with the University of Hannover and the breeding company Synergy Breeding GmbH und Co KG Billerbeck. The concerted and integrative implementation of biotechnological, cytogenetical and molecular techniques should contribute to the breeding process of new genotypes with desirable attributes. The development of new breeding strategies offers the possibility to use them not only for the genus *Hydrangea*. A transfer of the successfully applied methods will be also useful for the increase of the genetic variability of other ornamentals. Besides the breeding research for new and modern cultivars, the project partners are working with old genetic resources of *Hydrangea*. This is an important contribution for the preservation of genetic resources of this culturally and historically valuable plant. At the beginning of the project, the experiments on mutagenesis were commenced. For that purpose, cuttings of standard cultivars were radiated *in vivo* by X-rays. At present, the cuttings are cultivated in the greenhouse and their comprehensive exploitation is scheduled for spring 2006. For crossing activities the knowledge of ploidy of the breeding material is an important prerequisite. The cytogenetic characterisation could be established successfully by flow cytometry using the DNA dye propidium iodide. Molecular markers will be used to determine genetic distances between potential crossing parents. In addition, DNA-fingerprinting will be applied for characterisation of species and cultivars. So far, DNA of 90 genotypes of different species was isolated. First attempts showed a good standardization and reproducibility of the generated RAPD patterns. For the next year further radiation experiments, RAPD- and AFLP-analyses, as well as polyploidisation of *in vitro* material are planned.

Fig. 22: Two kinds of *Hydrangea macrophylla* cultivars







**Institute  
of  
Plant Analysis**

**Quedlinburg**

# Institute of Plant Analysis

Within the BAZ the Institute of Plant Analysis is occupied with the whole spectrum of quality and breeding research dealing with fruit and vegetable as well as medicinal and spice plants. Also special aspects of wine quality are part of the research work. The individual tasks are mainly related to genetically determined quality properties of plant raw materials and products considering both the specific demands of the consumer and the claims of the processing industry to the same degree. Furthermore, some research studies are also dealing with changes in the composition of certain components induced by plant pathogens.

Working on the individual research projects is performed in closed cooperation with other institutes of the BAZ, but also with other national and international research partners. At present main emphasis is placed on the following tasks:

- development of efficient analysis methods for selection of improved genotypes achieved by breeding processes
- screening of genetic resources with respect to valuable and toxicologically relevant substances
- formulation of a molecular basis for the biosynthesis of important secondary metabolites
- evaluation of sensory quality and instrumental-analytical determination of flavour and healthy substances
- investigation of changes in the plant metabolism induced by various pathogens (e. g. expression of specific repellents)
- characterization of postharvest effects as well as quality changes induced by technological treatments.

Furthermore, scientists of the institute are in direct dialogue with breeders, farmers and industrial as well as consumers' associations. Consequently, important inputs are supplied to improve the quality standards of plant products in Europe and to develop specific analytical techniques for their objective measurement.

The topics of the 40<sup>th</sup> symposium of the "German So-

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Dr. rer. nat. Detlef Ulrich  
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Kristin Ziegert  
chemist (BMBF-funded project)

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

ciety for Quality Research (DGQ)”, which in this year was organized in cooperation with the Federal Research Centre for Nutrition and Food, were mainly focused on the comparatively low consumer acceptance of novel products with high nutritional value. In this context, it was discussed in which manner the marketing of “healthy foods” could be improved in the near future.

This year Dr. Kammerer from the University of Hohenheim was awarded the “DGQ Prize for Young Scientists”, amounting to 1000 € (Fig. 1). The main topic of the next DGQ symposium in Wädenswil (Switzerland) will be dedicated to the aspects “freshness and quality of plant foods”. The research studies within the area “aroma, taste and sensory properties/evaluation” were focused especially on the cultivated species strawberry, carrot, asparagus, parsley and potato as well as various *Allium* species. In doing so main emphasis was laid on sensory quality in context with the individual genetic biodiversity (Fig. 2).



Fig. 1: Awarding the “DGQ Prize for Young Scientists” by the head of the IPA and president of the association.

Projects initiated in this regard predominantly aim to counter the impending genetic erosion of sensoric attributes by detailed investigation of flavour quality as well as application of suitable analysis methods in plant breeding.

### ■ Efficient analysis of wine aroma

In the framework of methodic studies new sample clean-up techniques and analysis methods for determination of health and aroma value of grape juice and wine were developed. For the isolation of aroma substances, solvent extraction with subsequent gas chromatography has been successfully applied already for several decades. In this con-

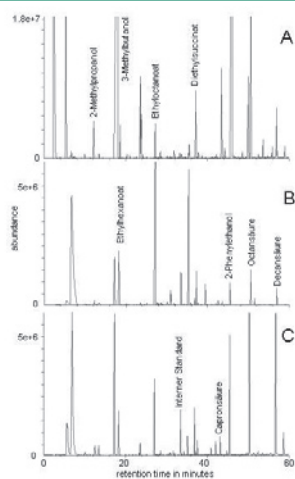


Fig. 2:

Sensory testing is the standard method for the evaluation of flavour not only for fruit and vegetable but also for wine.

nection, especially chlorofluorocarbonhydrates have been used, because they present best extraction properties and they are neither combustible nor toxic. Because of aspects endangering the environment it is no longer allowed to use these solvents in the future, but in spite of this fact no alternative analysis techniques are available today. Therefore, the effectiveness of modern, solvent-free sample clean-up procedures for the isolation of aroma substances from various white wine varieties was examined in a comparative study. In this context two extraction techniques, solid-phase microextraction (SPME) and stir bar sorptive extraction (SBSE), which are both available in the Institute of Plant Analysis, were applied. At first the analyte is adsorbed on different polymeric materials and in a subsequent step it is thermally desorbed after injection into the gas chromatograph. Whereas SPME since its introduction more than 10 years ago has achieved broad application in nearly all fields of analysis, SBSE is available as a routine methods not until a few years. Both techniques can be largely automatized, but sometimes the adsorption on the polymeric matrix may lead to negative effects such as a discrimination of certain analytes. Furthermore, competing adsorption effects may occur. The technical efforts in terms of (semi)-quantitative measurements are quite high, especially for SBSE analyses. When applying SPME usually only half of those substances that are available by classic liquid extraction are detected. Certain chemical groups such as furanones, which represent important aroma substances, are detected only in low amounts, whereas several terpenes are found in high yields. SBSE is more comparable to the usual liquid extraction, but principally this technique shows the same disadvantages in terms of discrimination





**Fig. 3:**

Gas chromatography analysis of aroma substances in white wine. The application of three different sample clean-up methods results in completely different gas chromatogrammes. A: solvent extraction using Freon 11; B: Headspace SPME using a 100 µm PDMS fibre; C: SBSE coupled with thermo-desorption and cold injection.

effects (Fig. 3). At present, the aimed substitution of solvent extraction is only possible if the alternative methods are adapted to the individual tasks in an optimal way. For high-throughput measurements, as they are for instance applied in breeding research and genome mapping, only SPME can be recommended as a reliable alternative to the classic solvent-extraction procedure.

### ■ Improvement of sensoric quality of tropical fruits

In cooperation with the University of Bogor, Indonesia, Centre for Tropical Fruits Studies, various new breeding lines of salak [*Salacca zaluca* (Gaert.) Voss] and *papaya* (*Carina papaya* L.) have been analysed for their aroma properties. Main tasks of these cooperation projects consist in describing the biodiversity of sensory attributes for tropical fruits as well as developing efficient analysis methods for plant breeding. According to gas chromatography results, salak fruits contain numerous volatile substances of which 24 show sensory effects; furthermore 19 of them have been identified by gas chromatography mass spectrometry as so-called key aroma substances. It has been found that the aroma of salak is mainly determined by 2-methyl butyric acid. This compound is characterized by an intense odour which shows besides fruity-sweet notes also unpleasant, overripe and caseous aspects. Depending on the cultural environment, the acceptance of such flavours can be really different. Whereas in Europe fruit with a caseous odour are rejected, in Asia those products are particularly popular. Therefore, in order to increase the export of salak into EU countries it is important to select genotypes with a preferably low content of 2-methyl butyric acid. One main goal of the common project performed with the University of Bogor is to select *papaya* plants with low height producing fruits with high aroma quality (Fig. 5). So far, a negative correlation between plant height and positive sensory properties has been found. In a first step it is therefore necessary to establish the sensory pro-

**Fig. 4:** The genetic diversity of salak fruits becomes manifest not only in certain resistance characteristics but also in terms of habitus and sensory quality.



file and to determine key aroma substances in *papaya* cultivars and breeding lines. Subsequently, the obtained sensory and instrumental methods have to be applied in extensive aroma studies of crossbred populations.

### ■ Twisted garlic – a new cultivated species in Germany?

During the past 4 years numerous *Allium* species have been analysed with respect to medicinal-therapeutic as well as flavour aspects. In this context main interest was focused on specially selected accessions of garlic (*A. sativum*) and twisted garlic (*A. obliquum*) which were reproduced by in-vitro technique and subsequently transferred to the open land (Fig. 6 and 7). Furthermore, commercial cultivars of onion (*A. cepa*) were analysed regarding valuable components (e. g. isoalliin) and sensory properties. In cooperation with the University of Magdeburg extracts of the three *Allium* species mentioned above have been developed on pilot plant

**Fig. 5:** *Papaya* fruits of different cultivars and crossbred populations (Centre for Tropical Fruits studies, Bogor, Indonesia).





Fig. 6: The bulbs of twisted-garlic (*A. obliquum*) contain high amounts of sulphurous substances which are responsible not only for the pungent taste but also for the pharmaceutical value. The aroma of the green plant tissue also evokes the smell of ramson (*A. ursinum*).



Fig. 7: Applying vegetative reproduction techniques genetically identical clones of selected twisted-garlic single plants can be obtained.

scale using various vegetable oils as extraction solvents. Due to the applied highly gentle treatment the obtained plant extracts reflect the individual authentic flavour profiles in an excellent way. Thermal degradation products, which often determine the sensory impression of *Allium* oils, can be detected in these novel products only in traces. After extraction into the used vegetable oil the valuable cystein sulphoxides (e. g. alliin, isoalliin, allicin) are present in high concentration, so that the resulting extracts can be principally applied as phytopharmaceuticals or food supplements. In the meantime for all novel *Allium* plant extracts data sheets have been created, which provide detailed information regarding specification ranges as well as possible fields of application. Furthermore, first contacts with potential buyers in industry have been established in order to develop a common marketing strategy for the novel *Allium* product range.

### ■ Natural antibiotics for animal nutrition

Also this year the Institute of Plant Analysis was involved in several third-party funds which aimed to increase the content of individual secondary metabolites in basil, savory, fennel, caraway, marjoram, oregano and thyme. In this context different objectives play a role of which only a few will be mentioned here:

Since the use of synthetically modified antibiotics in animal production has been banned, natural antibiotic substances such as carvacrol and thymol, isolated from savory, oregano or thyme by distillation or extraction, become more and more important for animal nutrition.

For basil, the Scientific Committee on Food (SCF) of the EU recommends to lower the limits for methyleugenol and estragole, because both substances are known for their carcinogenic potential.

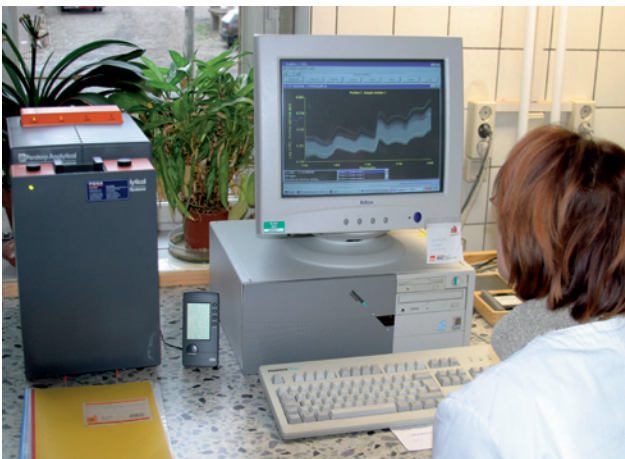


Fig. 8: Near-infrared spectroscopy as a high-throughput method allows to evaluate thousands of medicinal and spice plants per year with special regard to their valuable substances.



Fig. 9: When the non-destructive NIRS measurement is finished, the fennel fruits collected from single plants are made available to the breeders for further crossing experiments.





**Fig. 10:** During education of laboratory technicians performed at the Institute of Plant Analysis the most important chemical-analytical methods are imparted.

Furthermore, for several years fennel and caraway have been in the focus of breeders aiming to increase the yield of annual forms and to optimize the quality parameters as well as resistance towards pathogens.

In Germany marjoram as a cultured species is established only in Saxony-Anhalt. If attempts to increase the content of tertiary alcohols by breeding are successful in the near future, marjoram, which is known for its spicy properties, could be also commercially used as a medicinal plant.

All described topics need the support by powerful analytical methods which allow to determine secondary metabolites non-destructively and reliably within a short time. During the last years near-infrared spectroscopy was found to fulfil these demands in an optimal way (Fig. 8 and Fig. 9).

From breeding experiments as well as analyses performed on behalf of the “Bundessortenamt” meanwhile an extensive knowledge exists in the Institute of Plant Analysis regarding the biodiversity of medicinal plants.

This experience is not only reflected in numerous scientific publications but it is also used for discussions in the BAZ working groups dealing with “genetic resources” and “renewable resources”.

Furthermore, latest research results are published in popular scientific journals or presented at fairs such as “Grüne Woche” (International Green Week Berlin) or “Bundesgartenschau” (German Horticultural Show). Last but not least, characterization of medicinal plants and their components contributes considerably to the education of laboratory assistants in analytical chemistry (Fig. 10).

### ■ Specific cabbage species are known to prevent cancer

*Brassicaceae* represent a plant family rich in species of which several have commercial importance. Beside well-known forms such as white cabbage, red cabbage, broccoli, cauliflower, pak choy, cabbage turnip, radish, mustard, horseradish and cress (Fig. 11) also some common ornamental plants such as wallflower, purple gem rock cress and dame’s rocket as well as a few wild *Brassica* species (e. g. thale cress) belong to this botanical family. Various parts of the individual cabbage species are used for human nutrition: Leaves of curly kale and Chinese cabbage, the main sprout of red cabbage, savoy and pointed cabbage, the buds of Brussels sprout and the flowers of broccoli and cauliflower. The taste of cabbage is mainly determined by sulphurous aroma substances which are formed from various glucosinolates during preparation in the kitchen. Fig. 12 demonstrates the profile of most important glucosinolates in selected wild forms of *Brassica oleracea* as well as white cabbage and broccoli. The red columns represent the sum of progoitrin (PRO), sinigrin (SIN) and gluconapin (GNA). These so-called alkenyl glucosinolates, which are classified as unhealthy, have a strong and pungent taste. Contrary to that, indol glucosinolates are desirable plant substances (green columns), which possess anticarcinogenic properties, especially in the case of colon cancer. Also glucoiberin (IBER) and glucoraphanin (RAP) are estimated as healthy substances due to their anticancer activity (green columns). Including the gene pool of wild and primitive forms of *Brassica oleracea* it is not only possible to transfer resistance traits but there is also the chance to use the high variability of individual plant components. Usually, an amount of approx. 10 % indol glucosinolates is ingested

**Fig. 11:** Glucosinolates present in radish are not only responsible for its pungent taste but they also contribute to the health value of this *Brassica* species.





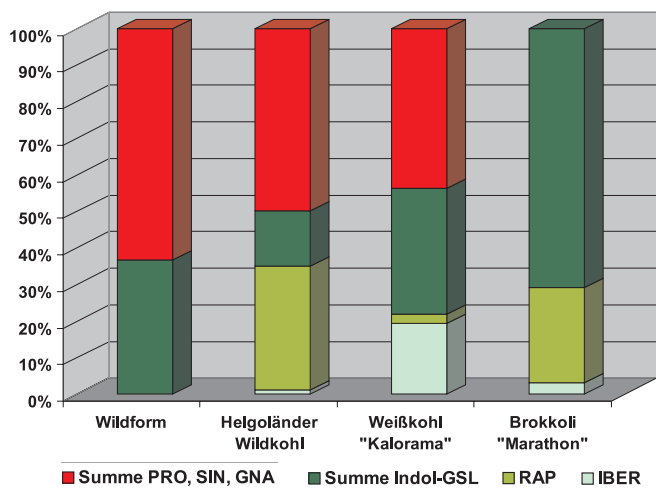


Fig. 12: Wild forms of *Brassica oleracea* show significantly different distributions of glucosinolates. The red columns represent the part of undesirable alkenyl glucosinolates, whereas the green columns reflect the content of indol glucosinolates which are known for their anticarcinogenic properties.

with human consumption. If other cabbage cultivars with higher amount of indol glucosinolates would be used, a significant increase of the health value could be achieved.

Presently the international cooperation with VIR in St. Petersburg (Russia) is focused on the investigation of glucosinolate contents and profiles and the occurrence of flavonoids in different Chinese cabbage forms. Due to their antioxidative properties, some of these substances are also important for human nutrition. Applying the sophisticated HPLC-MS-technique, which is available in the Institute of Plant Analysis for a short while, those plant substances can be characterized more detailed. Based on the obtained results, suitable selection criteria for breeding cabbage species with improved health value can be precisely defined.

### ■ Non-destructive identification of plant substances

The initiated studies to evaluate possible applications of micro Raman spectroscopy in plant analysis gave new, interesting results, which were published in several scientific journals. Raman spectra obtained from measurements of plant tissues are usually well-structured and often show characteristic key bands of the analyte molecules. Based on such "marker signals" rapid studies of different plant species can be performed and in some cases also a discrimination of different chemotypes belonging to the same species is possible. So, the main components in the essential oils isolated from various marjoram and origanum chemotypes could be identified applying hierarchic cluster analysis of the resulting Raman data. In an analogous approach, a taxonomic classification of selected single-fruits of *Umbelliferae* species could be successfully performed. Fig. 13 presents a dendrogramme developed on the basis of spectral data, which proves clearly that a discrimination of different species belonging to the genus *Daucus* can be principally achieved. Raman meas-

urements on root tissue of carrots (*Daucus carota* L.) allow to detect simultaneously carotenoids, polysaccharides and polyacetylenes without applying any sample pre-treatments. Because the mentioned plant substances show intense, specific key bands in the Raman spectrum, it is possible to develop so-called "Raman maps" that reflect the spatial concentration profiles for individual plant substances (Fig. 14 and Fig. 15). Thus, for the first time the spatial distribution of two polyacetylenes occurring in carrot (falcarinol and falcarindiol), which have been found to be responsible for bitter taste as well as healthy properties, could be impressively illustrated. Beside the described qualitative measurements also quantitative analyses of selected substances can be performed, if a calibration equation for the individual analyte has been successfully established before. So, it is usually possible to reliably quantify main essential oil substances in plant extracts by Raman or ATR-IR spectroscopy, if the samples are homogeneous enough.

### ■ Which genes are responsible for the typical carrot aroma?

In this year research studies dealing with carrots focus on further development of the genetic map. Here, a main topic is the integration of quantitative traits (so-called QTLs) in the existing map. It is well-known that carrots show a very complex aroma profile and it has been also described that numerous influencing factors (e. g. sugar content, substances with bitter taste, free amino acids and volatile components) affect their sensory quality. Furthermore, it is expected that many volatile aroma substances follow a quantitative heredity. Due to the development of molecular markers for  $F_2$  plants, an opportunity principally exists to localize QTL ar-

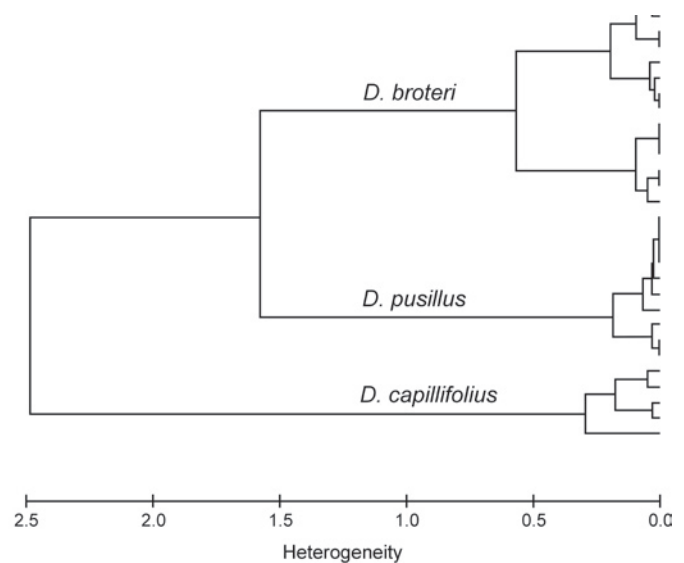


Fig. 13: Applying Raman spectroscopy in combination with statistic interpretation it is possible to distinguish single fruits of various *Umbelliferae* species on the basis of their specific spectral data.

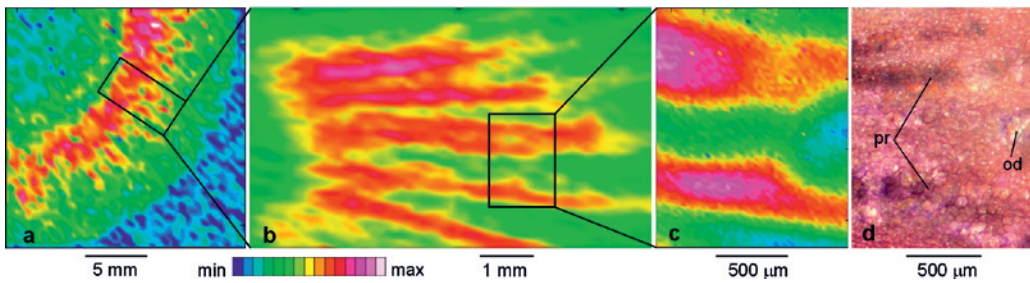


Fig. 14: The distribution of beta-carotene in plant tissue of carrots (cultivar 'Bolero') can be analysed by Raman spectroscopy at different spatial resolutions (a to c) in cellular dimensions (d microscope image of the analysed tissue sample, od oil ducts, pr phloem rays).

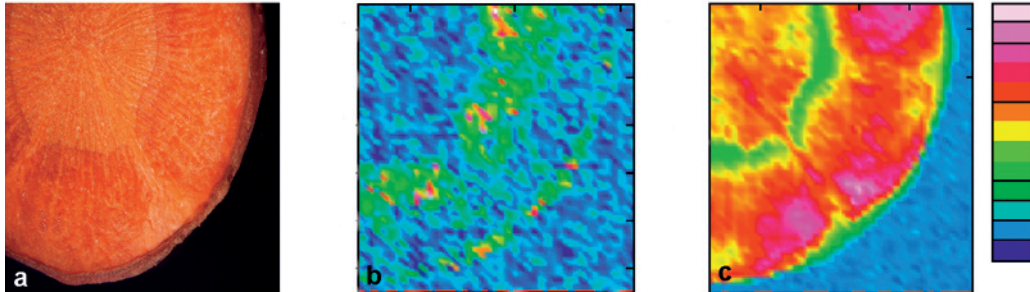


Fig. 15: The sophisticated Raman-Mapping technique allows to determine simultaneously the distribution of polyacetylenes (b) and carotenoids (c) in carrot roots (a).

cas for aroma substances within the genetic map of carrot using linkage analysis. For this, crossings were performed with single plants of two cultivars containing a significantly different amount of aroma substances. Furthermore, an  $F_2$  population was obtained performing self-pollination of an  $F_1$  single plant. From this population 200 single plants were analysed with respect to their aroma substances and molecular marker analyses (AFLP) were simultaneously performed. More than 50 different volatile aroma substances were detected in these  $F_2$  single plants, of which 20 were used for the development of the genetic map. Within the scope of AFLP-analyses 64 primer pairs were tested and 58 of them showed polymorphic bands which could be used for mapping. For the time being a preliminary genetic map based on 20 aroma substances was established which presents one linkage between a marker and an aroma component.

### Future prospects

Medium-term research activities will be focused on the biodiversity of various substances in wild plants and on the identification of functional genes/proteins as well as their correlation with plant components and sensory attributes. In this context it will be very important to develop new method which allow a fast and simultaneous determination of plant components in cellular dimensions (e. g. Raman and IR microscopy). Finally, it will be necessary to study intensively possible effects of technological processes just from the beginning of new breeding programmes.





**Institute  
of  
Grapevine Breeding  
Geilweilerhof**

**Siebeldingen**



# 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 of 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 1993, the Institute of Grapevine Breeding Geilweilerhof became a member of this Centre.

Grapevine breeding has the task to develop new varieties with high resistance to pests 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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Further activities are indexing and abstracting of the worldwide 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.

## Breeding resistant grapevines

Breeding of new wine varieties was motivated by events in the 19<sup>th</sup> century which affected deeply traditional European viticulture and, thus, led to the onset of breeding resistant grapevine varieties.

New fungal parasites and phylloxera which had been transferred from North America to Europe by importing ornamental and subsequently other grapevines were spreading out and devastating rapidly European vineyards. Imported parasites were powdery mildew (*Uncinula necator*, observed for the first time in England in 1845), phylloxera (*Dactylosphaera vitifoliae*, observed for the first time in France in 1863) and downy mildew (*Plasmopara viticola*, observed for the first time in France in 1878).

Reductions of yield and of viticultural area exceeded all former experience with other cultural plants and menaced the existence of millions of people living on viticulture in Europe. Still today these events are the reason for growing grafted vines (defence of phylloxera) and for an intensive chemical plant protection management.

Breeding resistant grapevines is a time consuming task (25 to 30 years) due to the long duration of plant development, the low rate of vegetative propagation, the high demand for area and labour and the polygenic inheritance of essential characters like resistance and quality. To optimize combination of essential characters several steps of crossing are necessary.

The continuous improvement of breeding material led to varieties with a high resistance level and – at the same time – high wine quality. E.g. the variety ‘Regent’, bred by G. Alleweldt, was classified in 1996 for the first time in some areas in Germany. Meanwhile it has reached a growing area of more than 2,000 ha. Using ‘Regent’, crossings with fungus-susceptible varieties, e.g. ‘Lemberger’ and ‘Domina’ were performed. From these crossings two genotypes ‘Calandro’ and ‘Reberger’, were selected which now are to be introduced to growers.

Besides these red wine varieties breeding of white wine varieties continued. For the first time combination of parents, which both are quite resistant and produce good quality wines, led to remarkable progress with regard to those characters. One parent is ‘Sirius’, which crossed with ‘Vidal blanc’, led to the variety ‘Felicia’. Combining ‘Sirius’ and ‘Villard blanc’ led to the variety ‘Villaris’.

In the meantime three new cultivars derived from the resistance breeding program of the Institute of Grapevine Breeding Geilweilerhof received variety protection (‘Reberger’, ‘Felicia’, ‘Villaris’)(Fig. 2–4). For ‘Calandro’ (Fig. 1), the fourth variety, the application for variety protection is pending. Concerning the most important mildew diseases these varieties show a degree of resistance which allows a considerable reduction of plant protection treatments. Regarding

Fig. 1 – 4:



‘Calandro’

‘Reberger’

‘Felicia’

‘Villaris’

the performance data especially the high sugar content of the new varieties is to be pointed out which is for the white varieties 'Villaris' and 'Felicia' in the average of 10 years about 15% higher compared to 'Müller-Thurgau'. Even the sugar content of the cultivar 'Regent' which is known to accumulate sugar to a high level is exceeded by the new red cultivars 'Calandro' and 'Reberger' (5% resp. 10% in the average of 10 years). The first data obtained in the frame of suitability tests on different locations in different vine growing areas confirm the results attained up to now in the test plots of the institute. Within the frame of resistance breeding analytical tools for an early characterization of cultivars will be used. Thus, the use of molecular markers in grape breeding is of special interest for those characteristics whose phenotypical evaluation is difficult and labour intensive resp. whose parameter are polygenic meaning that several mechanisms (genes) are involved in the degree of the expression of the characteristic. The latter fact applies to the resistance against the mildews in grapes which can be traced back to different defence mechanisms. The identification of different resistance genes by the use of molecular markers enables the selection with combined resistance characteristics within the progeny of appropriate crosses.

First investigations aligned to this fact were accomplished in descendants of the crossing by 'Regent' x 'VHR 3082-1-42'. (Fig. 5) 'VHR 3082-1-42' carries the gene *nun1* originating from *Muscadinia rotundifolia*, which causes a resistance against powdery mildew. Further markers correlating with the resistance against powdery mildew are known from 'Regent'. First results confirm the possibility of the identification of genotypes from descendants with pyramided resistance genes.



Fig. 5: Different genotypes out of the cross 'Regent' x 'VHR 3082-1-42' with different degree of resistance against powdery mildew.

## Drought resistance of grapevine varieties

Compared to other cultural plants grapevine is referred to be relatively resistant to climatic stress factors. Nevertheless, processes in ripening berries leading to quality are menaced by drought. Very often low precipitation during the season, soils with low water storage capacity, e.g. on steep slopes, and permanent green-cover cause water deficiency stress in grapes, with negative effects on wine quality. In recent years this situation has become more dramatic due to climatic changes: Increases of temperature, and - associated herewith - higher evaporation rates as well as an unfavourable distribution of rainfall have caused growers to install irrigation systems in many areas. In viticulture irrigation is very often limited due to economic reasons, so that breeding of drought resistant grapes has become an interesting alternative. A prerequisite are appropriate methods to evaluate drought resistance of new genotypes. In this context determination of the water use efficiency plays a major role. In leaves drought leads to stomatal closure and hence to a reduction of transpiration ('cost'); simultaneously  $\text{CO}_2$  uptake ('benefit') is reduced as well. To maintain high rates of photosynthesis and herewith production of sugar under

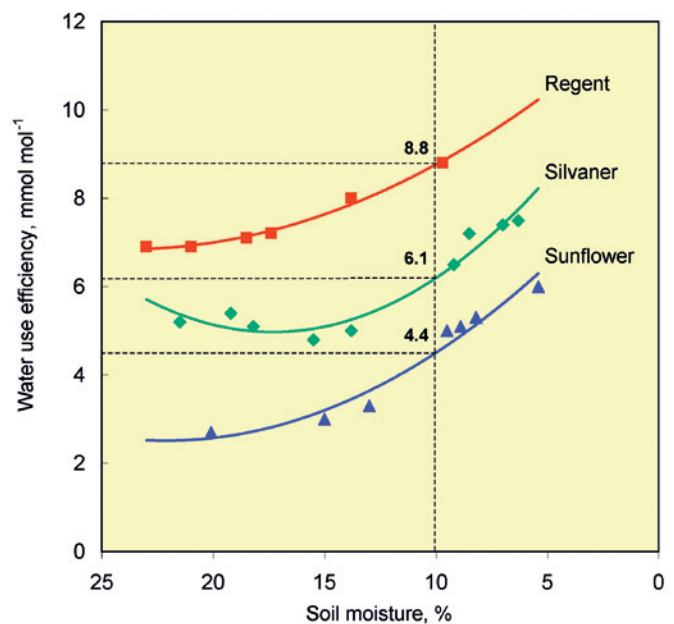


Fig. 6: According to the economic principle of a cost-benefit analysis the water use efficiency, i.e. the relationship between photosynthesis ( $\text{CO}_2$  uptake, 'benefit') and transpiration (water loss, 'cost') can be used as an indicator of drought resistance. At the same degree of drought, e.g. 10% soil moisture, the cv. 'Riesling', known to be drought resistant, shows a higher water use efficiency compared to cv. 'Silvaner' (drought sensitive) and, more important, to the very sensitive sunflower. At decreasing soil moisture, water use efficiency increases. In the fine-tuning between  $\text{CO}_2$  uptake and water loss stomatal pores at the lower side of leaves but also pores in the cell membranes ('aquaporines') are involved.



drought conditions, breeders will select genotypes which are able to optimise stomatal aperture and which have a low resistance for CO<sub>2</sub> to be transported to the sites of CO<sub>2</sub> assimilation in chloroplasts.

Under conditions of mild water stress drought resistant grape varieties 'Regent' and 'Riesling' had a distinctly higher water use efficiency (rate of photosynthesis / rate of transpiration) than the drought sensitive varieties 'Silvaner' and 'Müller-Thurgau' or (as control) sunflower (Fig. 6). This was caused by the higher rates of photosynthesis and simultaneously lower rates of transpiration of drought resistant varieties.

In addition, mild water stress led to an increase of CO<sub>2</sub> transfer into chloroplasts. Only severe water deficiency induced almost complete stomatal closure and a decline of CO<sub>2</sub> transfer in leaves.

It has been reported that CO<sub>2</sub> transfer in leaves is varied by the expression of 'aquaporines', a group of membrane proteins, which control water and ion transport through cell membranes; thus 'aquaporines' may have direct effects on photosynthesis and stomatal aperture. These data are assumed to be ascribable to grapevine, as well.

### ■ Mapping in 'Regent' x 'Lemberger'/'Regent' BAC library screening

'Regent' as a new red cultivar combining high wine quality and fungal disease resistances to powdery mildew (*Ucinula necator*) and downy mildew (*Plasmopara viticola*) has been investigated. The aims of these efforts are to localize factors determining resistance in the genome, to label these regions with molecular markers for practical applications in breeding and to isolate the corresponding genes. An earlier constructed map (Fischer et al., TAG 108, 501-515; 2004) has recently been improved by integration of microsatellite (SSR, simple sequence repeat) markers to render it comparable to other genetic maps developed in grapevine. 212 SSR markers were tested, 120 could be mapped in the population of the cross progeny consisting of 140 individuals. Efficient multiplex assays were developed. In addition, published resistance gene analogs (RGAs, DiGasparo and Cipriani, MGG 269, 612-623; 2003) were employed for mapping. The results show an integrated genetic map with 19 linkage groups, corresponding to the number of chromosomes of the haploid set in grape. Some of the RGAs could be mapped.

This improved genetic map was employed for QTL analysis of resistance factors to the two fungal pathogens using phenotypic data from several years of field evaluation. Two genomic regions identified previously to carry factors of resistance to downy mildew (*P. viticola*) and one earlier identified region with factors antagonising powdery mildew (*U. necator*) could be confirmed and were flanked by newly mapped

### 'Regent' x 'Lemberger' linkage group 15 (IGGP15)

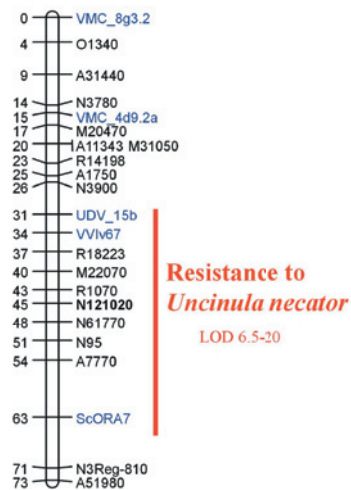


Fig. 7:

Linkage group 15 from the integrated map of 'Regent' x 'Lemberger'. It corresponds to IGGP15 according to the international nomenclature (see text). The red bar shows the region with resistance factors to powdery mildew, *Ucinula necator*, as it was identified by QTL analysis based on phenotypic evaluation data from leaves and fruit throughout several years with varying statistical significance (LOD values). The left numbering of the linkage group corresponds to genetic distances in centiMorgan. Abbreviations at the right hand side represent the position of various molecular markers. Newly mapped markers are indicated in blue.

markers (Fig. 7). A representative BAC library of 'Regent' organised into pools was then screened with QTL-flanking markers in PCR assays. Several marker-positive clones are currently under molecular analysis. This is the first time that a link between the genetic and the physical map has been generated and the way to gene isolation was opened.

### ■ Mapping in 'Gf.Ga-47-42' x 'Villard blanc'

Supplementary to the analysis of 'Regent' investigations on a second population derived from 'Gf.Ga-47-42' (a breeding line, Fig. 8) crossed to 'Villard blanc' has been performed. In this case, both parental types transmit fungal disease characteristics that segregate in the progeny. Furthermore, 'Gf.Ga-47-42' produces muscat-type flavour compounds (mainly monoterpenes) in its must, that are absent in 'Villard blanc'. The progeny of roughly 150 individuals was analysed with SSR markers in addition to earlier AFLP analyses. RGA markers were also used. The integrated map currently shows 21 linkage groups with 233 markers (including 6 RGAs and 86 SSRs). QTL analysis based on that map with phenotypic data from two years of field scoring shows factors determining resistance to *P.viticola* on four linkage groups. One of these regions, localised on linkage group 5, coincides with an QTL for resistance to *U. necator*. In contrast to results obtained in 'Regent', in this case resistance factors directed against both fungi seem to overlap partially in one genomic region. Two of the four QTL regions of *P. viticola* resistance also include RGA markers. This finding hints at a possible functional relevance of these genes, that needs to be stud-



**Fig. 8:** Picture of the breeding line 'Gf.Ga-47-42'. It was generated through a cross of 'Bacchus' x 'Seyval blanc', has fungal resistance traits and produces white berries. This breeding line has a pronounced muscat-type flavour in its must, which is absent in the partner of the cross, 'Villard blanc'. In addition, 'Gf.Ga-47-42' produces small berries in a loose cluster structure with early ripening in contrast to 'Villard blanc'.

ied. A first look for factors influencing the synthesis of flavour compounds indicated QTLs on five of the 21 linkage groups. These results need further confirmation using additional analyses of terpene contents in must in the progeny.

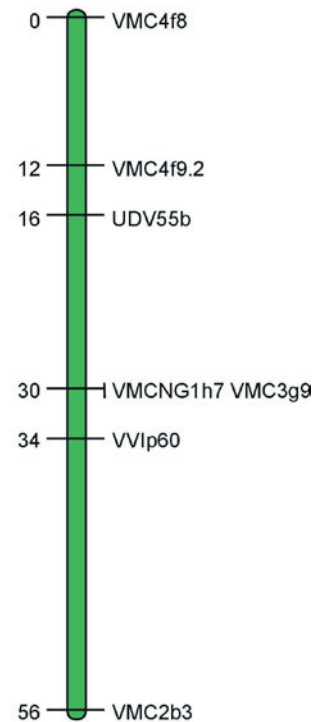
### ■ Mapping V3125 x 'Börner'/'Börner' BAC library organisation

Besides the fungal disease resistances resistance to phylloxera (*Dactulospira vitifoliae*) damage on roots is very important for grapevine breeding. The rootstock variety 'Börner' (derived from a cross of *Vitis riparia* x *Vitis cinerea*) shows excellent phylloxera resistance. In addition, this variety has fungal resistances directed against both mildew fungi *U. necator* and *P. viticola*. It was hence crossed to a susceptible breeding line V3125 ('Trollinger' x 'Riesling'), to study inheritance of the resistance traits. The phenotypic evaluation of the progeny has not yet been completed. The individual plants, however, were used to construct a genetic map as framework for further investigations. 250 SSR markers were tested with 178 genotypes; 109 could so far be mapped at a statistical stringency of LOD 4.0 in 19 linkage groups. Due to the transferability of SSR markers, this map is easily comparable with other genetic maps developed in grapevine and data from the literature. It can very well be homologized with the international reference map (Fig. 9) deduced from the cross of 'Riesling' x 'Cabernet Sauvignon' (Riaz et al., TAG 108, 864-872; 2004; the basis of numbering of linkage groups according to the International Grape Genome Program, IGGP).

A BAC library of 'Börner' was also constructed. The clones were plated and organised into a library. It covers 68.000 clones with an average insert size of 93 kb, representing 13-fold genome coverage in total. This library will be helpful to isolate important genomic regions in the future.

'V3125' x 'Börner'  
linkage group 10

IGGP1  
VMC4f8  
VMC4f9.2  
VMC3g9  
VMC2g3



**Fig. 9:**

Comparison of linkage group 10 from the integrated mapping of breeding line V3125 with the rootstock cultivar 'Börner'. The left numbering at the bar indicates genetic distances deduced from recombination analysis in centiMorgan. The right hand abbreviations correspond to various SSR markers. The light blue inset shows the marker sequence in the reference map (see text). This linkage group could hence be homologized with linkage group 1 (IGGP1) from the progeny of 'Riesling' x 'Cabernet Sauvignon'.

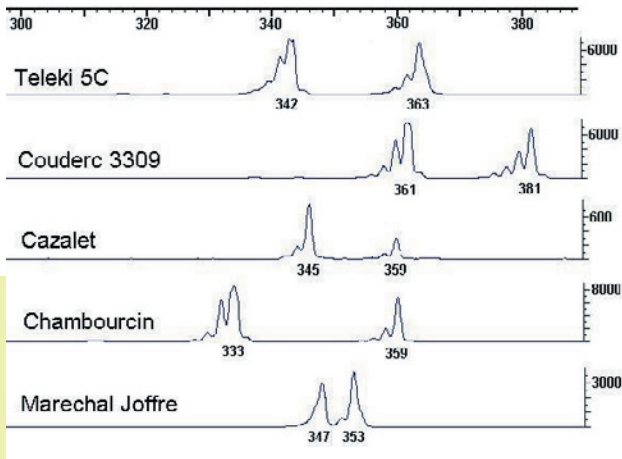


Fig. 10: Microsatellite profiles of SSR VV1v67 (Merdinoglu et al., 2005) on an automatic capillary sequencer showing grape genotypes with different resistance.

### CoregrapeGene Project

With respect to development and breeding of new quality and equally fungal resistant grapevines, French, Spanish and German grapevine collections represent most important genetic resources on the European level. In order to get a deeper understanding of the complex mechanisms of resistance or quality parameters, a characterization of the genetic diversity of a selected collection of European grape accessions will be performed in a trilateral cooperation together with France and Spain. Primarily, the project focuses on

the establishment of a European grapevine CoreCollection representing all in all the genetic diversity represented by the collections of the three countries localized at Montpellier (F), Siebeldingen (G) and El Encin (E).

The analysis of the genetic diversity has been based on twenty microsatellite loci, while in parallel the evaluation of the phenotypic resistance correlated data is performed according to the internationally accepted OIV descriptors. This part of the project contributes to a defined and molecular characterized *Vitis* core collection generating an valuable instrument for the extended use of the naturally existing *Vitis* gene pool. At the same time the characterization of candidate genes in association with phenotypic essential traits will be possible and the analysis of allelic variation of respective candidate genes as well as new knowledge of the extend of nucleotide diversity and Linkage Disequilibrium will be collected (Fig. 10).

### Documentation of Viticultural Research and Germplasm Repository

Three large databases are produced by the Institute and made available on the internet: "VITIS-VEA" is an international literature database on viticulture and related disciplines, "European VITIS Database" describes grapevine accessions in several European germplasm repositories and "*Vitis* International Variety Catalogue" is based on facts on grapevine varieties from literature.

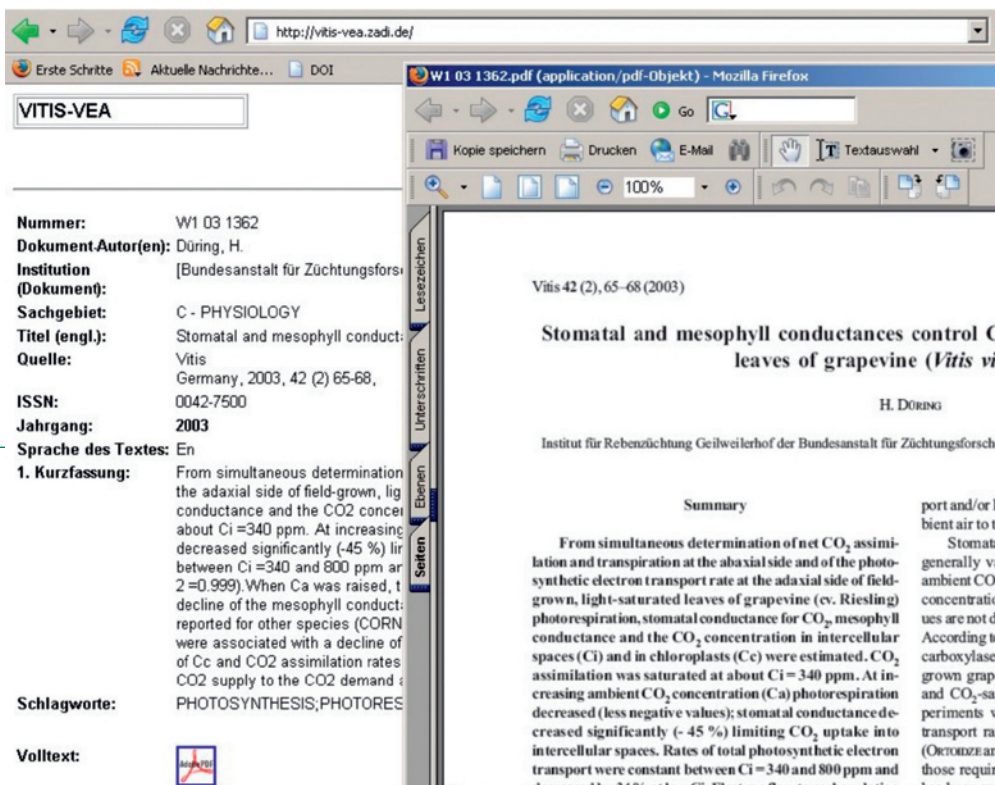


Fig. 11:

Screenshot of a document stored in VITIS-VEA. The left side shows the bibliographic information in the database, on the right a pop-up window with the associated full text is displayed.



## VITIS-VEA literature database

Knowledge in all disciplines of science, economy, and society has grown exponentially in recent decades. The Library of Congress, Washington, today the largest library worldwide, holds 58 million accessions of manuscripts. Publications in the field of vine and wine add up to the hundreds of periodicals, conference proceedings or individual papers being published in one of the thousands of international publications appearing monthly. The working groups 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 publicly accessible. This knowledge database VITIS-VEA (Fig. 11) with at present almost 51,000 accessions is available on the internet at <http://vitis-vea.zadi.de>. The back-issues of the periodical VITIS – Journal of Grapevine Research, published at Geilweilerhof, are successively converted into electronic documents and stored as full text in the database along with bibliographical information. At present, volumes from 1970–2003 are freely available, the preparation of further back is in progress. Next step will be the update of the journal homepage within the frame of the institutional web presence with contents of back issues and linkage to the database.

## Vitis International Variety Catalogue

The database holds passport data of more than 22,500 entries (wild grapevines, cultivars, selections) and was founded in 1984. Since 2004, a new database structure is developed in collaboration with the IT-department in Quedlinburg featuring further data on characterisation and evaluation, pictures, herbarium specimen, distribution and breeder. 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. A subset of this database with multiple search options will be published on the internet addressing curators, scientists, breeders, winemakers and wine enthusiasts. The update of “Vitis International Variety Catalogue” (Fig. 12) (<http://www.genres.de/idb/vitis>) by this new database is scheduled for 2006.

The screenshot displays the Vitis International Variety Catalogue interface. On the left is a navigation menu with options like 'Online Search on', 'Offline Database', and 'Content'. The main area shows the entry for 'Regent' with the following details:

<b>Accession ID:</b>	4572
<b>Accession name (Variety):</b>	REGENT
<b>Species:</b>	V. VINIFERA
<b>Pedigree:</b>	DIANA X CHAMBOURCIN
<b>Synonyms:</b>	GEILWEILERHOF 67-198-3
<b>Holding Institution(s):</b>	<a href="#">AUT 01</a> ; <a href="#">CAN 03</a> ; <a href="#">CZE 01</a> ; <a href="#">DEU 01</a> ; <a href="#">DEU 02</a> ; <a href="#">DEU 04</a> ; <a href="#">DEU 06</a> ; <a href="#">DEU 10</a> ; <a href="#">ESP 02</a> ; <a href="#">HUN 01</a> ; <a href="#">HUN 05</a> ; <a href="#">ITA 01</a>
<b>Country of Origin:</b>	DEU
<b>Berry Length:</b>	15.5
<b>Berry Width:</b>	15.8
<b>Color of Berry:</b>	N
<b>Single Berry Weight:</b>	2.18
<b>Utilization:</b>	Wine
<b>Mildew L:</b>	6
<b>Mildew LC:</b>	7
<b>Oidium L:</b>	8
<b>Oidium C:</b>	7

Below the table, there are links for 'Link to Morphological Data' (Leaf, Berry), 'Link to Bibliography' (See bibliography), and 'Link to Pictures' (Sprout, Cluster, Leaf). A photograph of a grape cluster is shown, with a legend below it:

<b>Part of the Plant:</b>	Cluster
<b>Accession ID:</b>	4572
<b>Variety:</b>	REGENT

At the bottom, the footer reads: © German Centre for Documentation and Information in Agriculture (ZADI) [http://www.genres.de/VITIS/foics/SDF?ACC\\_ID=C=6&ACC\\_ID=4572](http://www.genres.de/VITIS/foics/SDF?ACC_ID=C=6&ACC_ID=4572)

Fig. 12:

Screenshot of a dataset on the cultivar 'Regent' from Vitis International Variety Catalogue



**Gene Bank**

**Braunschweig**



# Gene Bank Braunschweig

The protection of biodiversity including agrobiodiversity shaped under the influence of mankind is mainly understood as a challenge to the whole society today. The alarming loss of species diversity and genetic variability within species has no biological causes, it is rather the consequence of political and economic targets. Visualising undesirable developments caused by these targets is as much a task of science as the search for a way out of this biological crisis. Our cultivated species and varieties as well as wild species closely related to these crops are described as plant genetic resources for food and agriculture. To safeguard genetic resources of fruit crops and grapevine the Institute of Fruit Breeding and the Institute of Grapevine Breeding of the BAZ apply the method of *ex situ* conservation. In view of the undiminished high rate of loss and the limited capacities of *ex-situ* holdings obviously this method can only reduce the impact of the societies' targets, but cannot solve the problem itself. Therefore a strategic reorientation began in the course of the negotiations on the international Convention on Biological Diversity about 15 years ago circumscribed with the term *in situ* conservation. This method places the natural environment, in which the wild species and cultivated forms have evolved their specific features, as well as the process of evolution itself in the focus. Countries like Turkey set an example and have started implementing this conservation strategy at the national level. The Ministry of Food, Agriculture and Consumer Protection (BMELV) charged the group at Braunschweig with the elaboration of a national management strategy for plant genetic resources *in situ* and on farm, complementing *ex situ* conservation.

An efficient conservation of genetic resources is only possible through international task-sharing. The promotion of the European co-operation is a steady concern of the group at Braunschweig supporting the European Co-operative Programme for Crop Genetic Resources Networks (ECP/GR) for 23 years, amongst others by operating central crop specific databases for the genera *Avena* and *Beta*. On the basis of these experiences the group shall presumably develop a global conservation strategy for oat. It will be one of the 35

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crop specific conservation strategies promoted by the Global Crop Diversity Trust with the aim to make more efficient use of financial resources. The project negotiations with the Trust began this year.

The conservation of plant genetic resources is part of the state-sponsored existence provisions. The BMELV, being the responsible Ministry for genetic resources for food and agriculture, requires for the planning of regulations data, information and assessments as to evaluate the effect of state-sponsored maintenance programs on the status of genetic resources. Information is also needed as to evaluate and prioritise maintenance measures correctly. The question which species and cultivated forms are to be maintained and with which justification is a recurrent theme in the German history of plant genetic resources. One factor always had a major significance when resources are ranked: the use value. This value is being determined by BAZ institutes through evaluation. The diverse and numerous data however do not flow into a public and readily accessible information system as it could be and can therefore benefit the consulting of BMELV and other institutions only conditionally. The joint working group “data management” of the BAZ institutes developed a strategy for the improvement of the data management infrastructure of the BAZ as to enforce the sector of data storage and information provision. In this field the group at Braunschweig and the data processing unit at Quedlinburg play a leading role in the BAZ. The BMELV is supporting the project and thereby acknowledged the specific needs of the BAZ.

## Management of plant genetic resources

The 7<sup>th</sup> Conference of the Parties (COP 7) of the Convention on Biological Diversity (CBD) contracted the parties to seize measures that will lead to a significant reduction of the biodiversity loss rate by the year 2010. The loss of species in the course of the 21<sup>st</sup> century shall presumably amount to up to 25% of the current global stock of species. It can readily be imagined that species important for agriculture, horticulture and grapevine production will likewise be affected. An example is the wild grapevine, *Vitis sylvestris*, classified as highly endangered in Germany. This species is an important genetic resource for grapevine breeders. Without doubts the specific needs of genetic resources of plant breeders could add arguments for specific protection measures and strengthen the position of nature conservation projects for *V. sylvestris*. Due to the federal organisation of Germany responsibilities are shared between the federal government and the states and there is no formal organisational struc-

ture as precondition for an intensive co-operation between agriculture and nature conservation in the field of plant genetic resources for food and agriculture. The co-operation is not formalised but is based at best on individual interest and initiative, as was already noticed in the annual report of 2004. It is however not a specific problem of Germany alone. Rather a global expert programme is lacking for the conservation of those wild species defined according to the CBD as plant genetic resources. The concept of ‘genetic reserves’ is considered an approach to the problem. According to Maxted et al. (1997) a genetic reserve is a defined site harbouring specific populations which are maintained according to specific management plans. Investigations on how this concept can be implemented were started in the year 2005 and tested in the parts of the distribution area of the genus *Beta*.

Apparently owing to a number of warm winters the wild beet *B. vulgaris* subsp. *maritima* is expanding its distribution area from the Danish Baltic sea islands to the coast of Schleswig-Holstein and the island of Fehmarn. The Rizomania resistance widely used in beet breeding was first found in Danish populations. Thus there would be an objective reason to establish a genetic reserve in the distribution area in Denmark and / or Germany. The ideal would be growing sites that are already under legal protection as for example the Natura 2000 site 1532-325 at the western coast of Fehmarn. The survey of the species distribution on Fehmarn in the year 2005 showed that large populations of the wild species only occur outside specifically protected areas. The sea beet is living in a very dynamic habitat. Populations go extinct at one site and are founded at others anew. A prerequisite for the establishment of a genetic reserve would therefore also be permanent and stable populations.



Fig. 1: A new population of *Beta vulgaris* subsp. *maritima* was found in Lemkenhafen on Fehmarn.



Fig. 2: Fehmarn has been considered with the award for innovative performance in the field of integrated environment protection concepts. Highlighted in green colour is the distribution area of LF2005-1. The balance of interest between tourism, coast protection with the establishment of a genetic reserve could be negotiated with the concerned parties and local authorities responsible for this site.

Though the species is extremely rare in Germany, it occurs in Europe very frequently and is considered as not endangered. According to the nature conservation regulations there is no reason to create protected sites for this species. A legal claim for the protection of distinct populations such as the large one in Lemkenhafen (Fig 2.) does not exist.

During the one day excursion the gathering of geographic data and data on populations was tested. The digital map (DTK50, L1532, geodetic office Schleswig-Holstein), a handheld computer, the software ArcPad and a clip-on bluetooth GPS were deployed. Data were recorded in tables that can serve as components of a relational database for *in situ* management data. The experiences gained during the trip to Fehmarn proved to be useful for a two-week plant exploration in Greece in August/September 2005 jointly planned and implemented by the USDA/ARS (Pullman, Washington), the Greek Gene Bank (Thessaloniki) and the BAZ. The goal of the mission was to survey populations of the wild beet species *Beta nana*, an endemic, rare and threatened species in Greece. *B. nana* is a genetic resource of beet breeding whose traits are insufficiently known. Due to lack of knowledge of the natural habitat genebanks have neither succeeded to maintain the species *ex situ* nor have they been able to produce sufficient amounts of seeds for evaluation projects. Above all there was the need to determine where exactly this species is still existing and to assess the conservation status. The last detailed survey was done by M.F.G. Dale in the year 1980 and 1981 who critically assessed the conservation status of the species. He often noted heavily grazed growing sites and the existence of only few plants per site.

Contrary to expectation populations of *B. nana* were encountered in the Taygetos (T), Chelmos (C), Vardoussia (V), Giona (G) and Olympos (O) mountains 25 years later. Except for few sites all populations were growing on heavily grazed, mainly disturbed sites. The population size increased from the south (Taygetos, few plants only) to the north (Olympos, >1000 plants). Estimates for the risk of genetic erosion (RGE) after Guarino (1995) never reached the maximum value of 200 points (=very high risk) but ranged around 100 points (Fig. 3). In particular the population found at the Olympos is not endangered, as the area adjacent to the nature park is only moderately grazed and

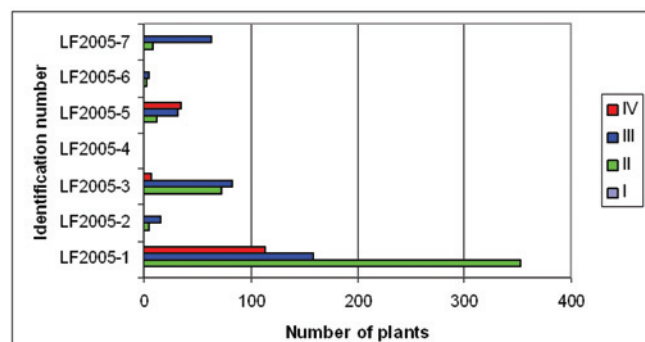


Fig. 3: Growing site of *B. vulgaris* subsp. *maritima* on Fehmarn. The populations are different in terms of size and demographic structure. In particular LF2005-1, a site not reported before, is composed of many mature annual (II), seed producing biennial (III) and seed producing perennial (IV) plants. Seedlings (I) were not observed. According to Drießen (2003) and new data the population at site 4 and 6 decreases, increases at site 3 and is stable at site 7.



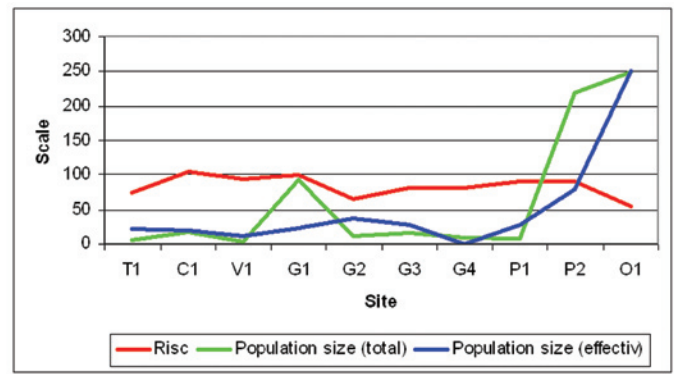


Fig. 4: The graph shows RGE values for 10 areas, the total population size (actual value /10), and the effective population size. As many factors determine the population size and population dynamic, the graph depicts the current status only. The coincidence of low RGE value and the large population size at the Olympos is however noteworthy. The photo on the left side shows *B. nana*.

the species obviously capable to keep up under these conditions. The area qualifies as genetic reserve as do two additional, small sites in the Parnassos and Giona mountain (Fig. 4). The latter are suited due to their location and shape for the establishment of a small protected site which can be purposefully grazed as to ensure the reproduction of the species.

For the first time geographic co-ordinates of growing sites of *B. nana* populations were determined with a GPS. Future surveys of the population dynamics on protected sites and in the whole distribution area, respectively, can refer to exactly the same spot. A baseline for monitoring of a en-

dangered species and genetic resources of beet breeding has been drawn. A rational conservation of *B. nana ex situ* or *in situ* will require investigations into the population ecology including the spatial and temporal genetic structure of the species. Moreover, the development of tools for data gathering and an information system to document the population management *in situ* is needed which would benefit all *Beta* species and similar projects in the whole distribution area of the genus.



Fig. 5: In the background, left side, a U-shaped site surrounded by steep rocks is located, which can be fenced and be grazed tuned with the reproduction biology of *B. nana*. Giona 1 would be an ideal site for a genetic reserve.



## Information management

The arrival of information technologies in biological sciences has generated a thrust of innovations. Modern database technologies and data analysis procedures ('data mining, knowledge discovery') contribute to the understanding of the structures of biological diversity, increasingly. The digital presentation, communication and utilisation of scientific results replace classical procedures. A multitude of knowledge based systems is available in the internet and the connection with international data warehouse systems play a key role for the BAZ. As the high flexibility of information technologies can only be used in an optimal manner in close collaboration between specialised and information scientists, outsourcing of information technology (IT) tasks is only conditionally meaningful. It is of key significance that the BAZ is further developing and expanding its competence in modern information technologies that are increasingly based on internet. The German Science Council (the Wissenschaftsrat) has criticised in its analysis of the efficiency the insufficient networking between scientific institutions of the federal government. Information systems relying on database technologies create the technical conditions for improved networking and co-ordination of research activities. Precondition for an effective interaction of the BAZ within a network is an own, sufficiently developed data management infrastructure. The considerable structural deficiencies in the field of database technology deployment within the BAZ, currently still affecting the efficiency of political consulting task, shall be overcome stepwise, for the time being, through a temporarily limited project. In preparation of this project four user groups were identified (evaluation, molecular biology, quality analysis, breeding) amongst the current scientific staff of the BAZ. Their IT requirements were surveyed groupwise. The need for actions appeared to be particularly high in the very dynamic fields of molecular biology and quality analysis. These fields are moreover characterised by complex methodological approaches requiring the use of a diversity of laboratory devices and software interface.

Within the frame of a project funded by the BMELV a requirement analysis in the sector of molecular data was started. A system was then projected, a technological database concept designed, a data model developed, the need of hard and software as well as time required for administration described and tools for the project management (central, in the BAZ intranet available communication platform as well as code and version management (CVS)) was furthermore developed. An application was built that can be used on all PC within the local network without installation of additional software. This platform can be accessed via the

internet by every authorised user who can follow the application development or steer it. The project is led by the group at Braunschweig jointly with the data processing unit at Quedlinburg and is decisively supported by the members of the data management working group representing all institutes of the BAZ.

At Braunschweig a server was available suited to establish the central communication platform, on which a productive application on the basis of the application server Zope was running. The server had to be migrated to an up-to-date software version to allow building of the platform. The scarce knowledge on the functions of the Zope based server proved to be a hindrance. This application had been developed during a predecessor project, however, the expert required for the knowledge transfer was no longer available. Yet, the server could be raised to a sufficiently new Linux version (SuSE 9.3) and the Zope application could be kept operational. The communication platform for the BAZ data management (Fig. 5) was set up on this server. It is operational on the basis of the content management system Typo 3. The data processing unit at Quedlinburg chose Typo 3 for the internet portal likewise. Apart from this, the server, on which the open source version management software Subversion is running, is used as a BAZ wide component for the software development. This Subversion is the direct successor of the well known CVS. The development of Subversion is promoted by the creator of CVS. For the implementation of Java web-applications the application Servlet-Container Tomcat was installed on it, too. The databases required for the operation of the applications to be newly developed were placed on another server. Here the well-tried schema already used by the International Data Base for *Beta* and the European *Avena* Data Base was chosen.



Fig. 6: Communication platform of the BAZ for application development

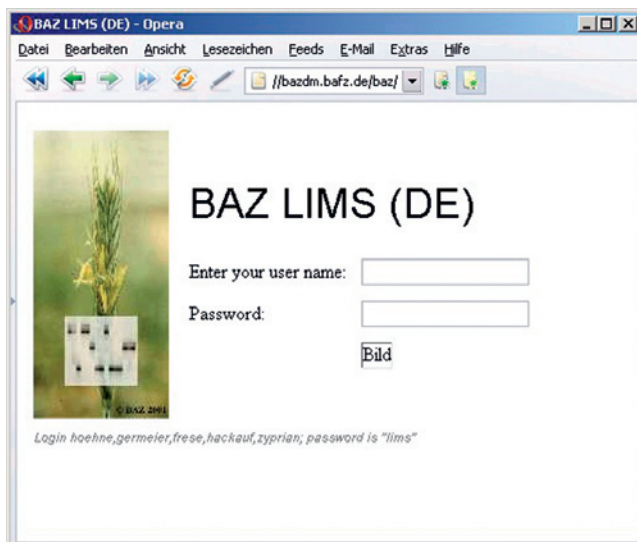
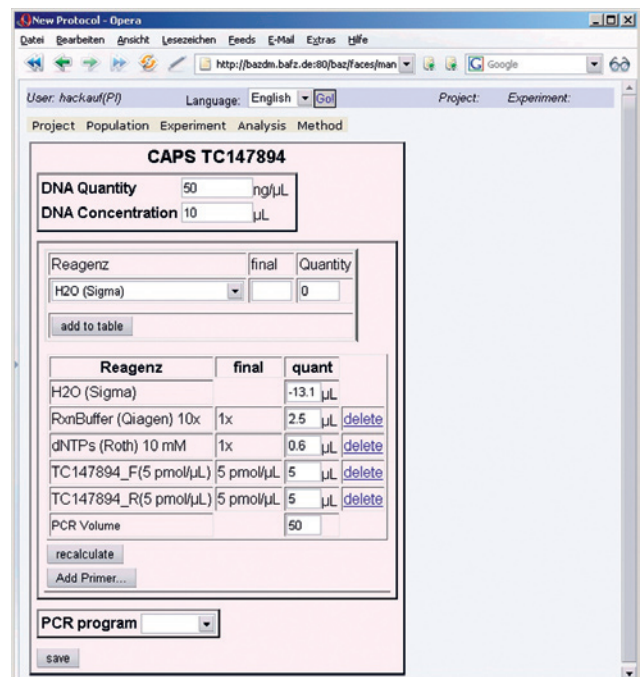


Fig. 7: Entry page guiding to the LIMS for molecular marker as well as a user interface for data input



In addition to these activities a development environment suiting the needs of BAZ was evaluated. As development platform the open source product Eclipse was chosen. This platform is readily to learn and extendable. It appeared that it is possible to extend open source products with Eclipse in a way that the platform is supporting software development work for web projects with Java Server Faces extremely well. To facilitate the work the products MyEclipse and Exadel Studio were purchased. Java version 5 is recommended as programming language. For the realisation of the user interface Java Server Faces are suitable. They protect the developer against the shallows of web programming and are very easy to learn. The Unified Modelling Language (UML) served for the modelling of applications. Finally the object relational mapping tool Hibernate version 3 was selected to image the object model arising from UML onto a relational database.

Besides the establishment of the software development frame the development of a prototype for a laboratory information system (LIMS) for molecular work was pursued (Fig. 6). In close co-operation with a specialist of the Institute of Agricultural Crops the underlying data model was built (Fig. 7).

## Perspectives

At the end of the project year a prototype of a LIMS will be available that can be deployed productively but will not fulfil all requirements of the daily laboratory routine. The underlying SAGA conform software architecture is basically developed and can be used as starting point for further, already planned projects. The project restricted to just one year was not at all sufficient for the establishment of important, the software development of the whole BAZ carrying structures. The still required components are a style guide for user interfaces (a document describing how user interfaces should look like and should function), a concept for further surveying and analysing the users needs as well as a procedure model tailored to the specific needs of the BAZ in the field of software development of SAGA conform applications. The survey and analysis would also become necessary if parts of the application development are to be out-sourced.

It appeared at the end of the project, completely in agreement with the expectations and experience of comparable research institutions, that by hiring experts on a temporary contract basis very specific applications relieving a single or

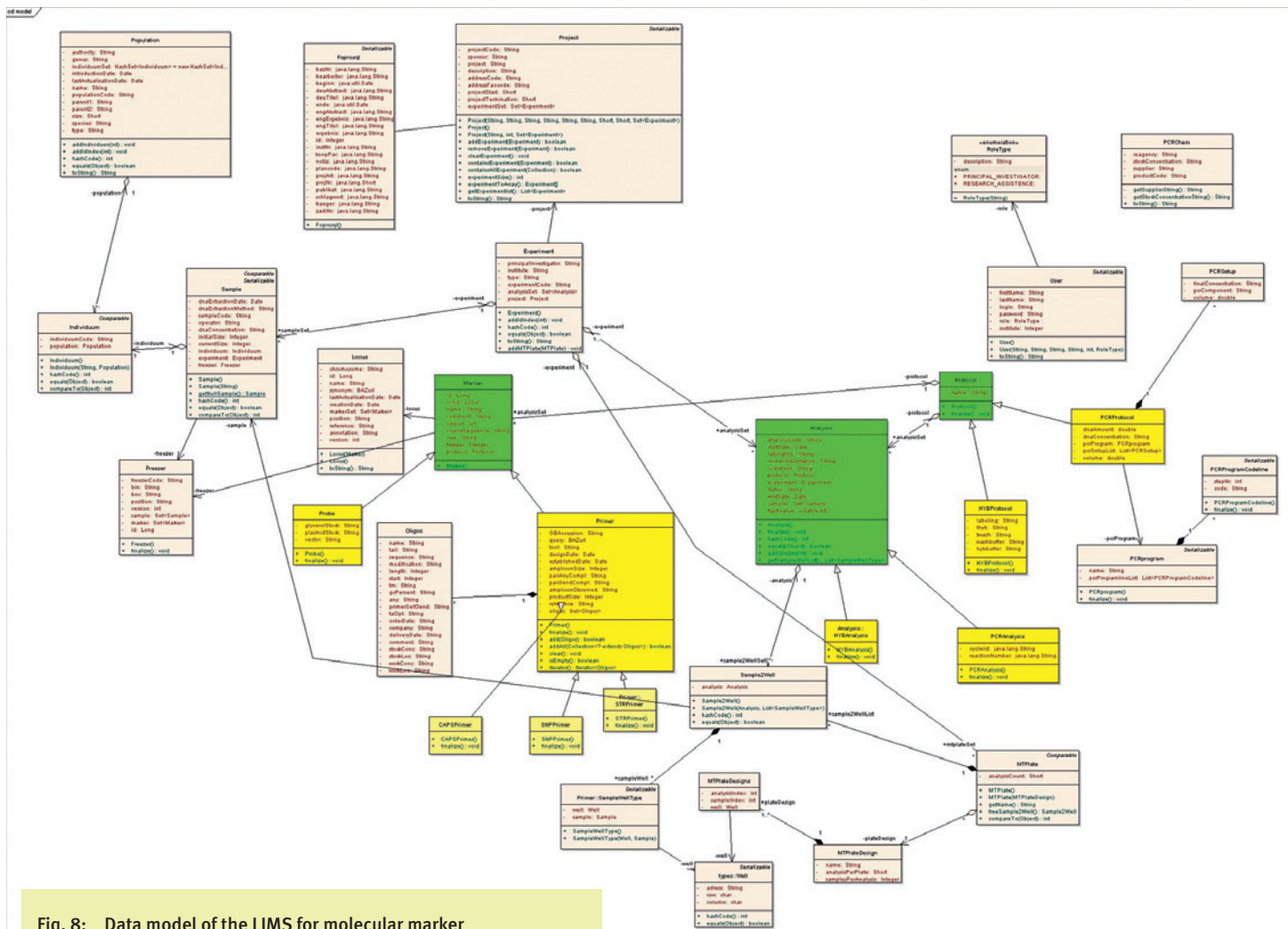
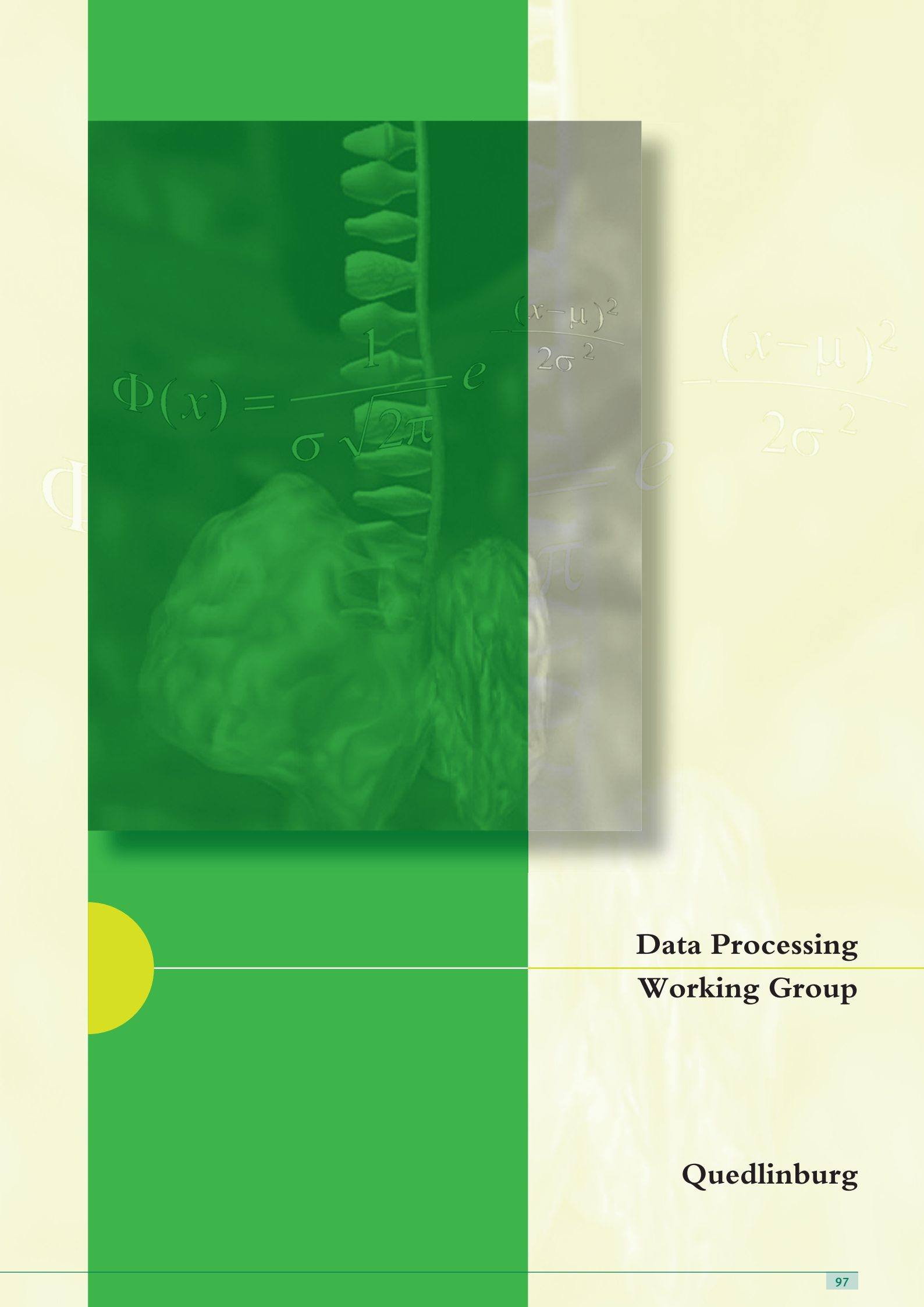


Fig. 8: Data model of the LIMS for molecular marker

several specialists can be built such as LIMS modules for molecular work. Since its foundation the BAZ is lacking sufficient expert capacities for a fundamental modernisation of the data management infrastructure as well as its continuous up-to-date development. This is in view of the very innovative information science and the significant development thrusts in information technologies a strategic disadvantage. The timely restricted project showed anew that

the working group data management of the BAZ estimated and described the BAZ needs in the internal paper 'New project data management in the BAZ' launched at the end of 2001/2002 in a realistic way. By charging the BAZ with new tasks as outlined in chapter 'Management of plant genetic resources' even new and additional needs arise such as in the field of gathering and documentation of geo-referenced data.




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

**Data Processing  
Working Group**

**Quedlinburg**

# Data Processing Working Group

## Tasks of the work group

Bioinformatics remains the central task of the work group; however, the planning of the IT (information technology) for the new building of the BAZ in Quedlinburg required considerable efforts, too.

Based on comprehensive estimations, the demand of storage, backup and archiving capacities were defined.

Basic structures of the new central IT are:

- a storage area network (SAN) with the start capacity of 5 Tbyte for flexible user data storage,
- a comprehensive backup strategy for all user data as well as the possibility of long-time data archiving,
- the continuous use of digital print and copy machines,
- the flexible integration of the PCs by means of the current e-Directory by Novell and the software distribution tool Zenworks.

These approaches including the possibility of “profile roaming” will help to make the important resource “IT” even more effective and more reliable.

With the assistance of the student André Göbel (*Hochschule Harz* – Harz University of Applied Sciences), who works at BAZ on a temporary contract, a lot of discussions and project meetings with well-known vendors could be accomplished.

The results were integrated into the IT-Concept, which has been recently confirmed.

Within the scope of **Biometrics** the SAS version 9.1x as well as the SAS Enterprise Guide have been tested and distributed. The scientists were informed about a presentation of the new module “SAS Genetics” that will take place at the BBA / Klein Machnow.

Furthermore the work group continues its active

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mathematician

## Programmer

Grazyna Marx  
mathematician

support for the efforts of the work group of biometricians of the Senate of Federal Research Centres (*Senat der Bundesforschungsanstalten*) to establish a central biometric authority.

The same as last year, the work group was again highly involved in the **Database System and Application Development** – a commitment that requires major parts of the capacities of the work group. Besides the advancement of projects in progress, the project titled “Development and implementation of a documentation system of the Vitis International Variety Catalogue” was the main activity.

The work group’s staffers made also considerable contributions to drafting and realising the BAZ-wide data management system. This system is planned to be the foundation of development of all scientific software at BAZ.

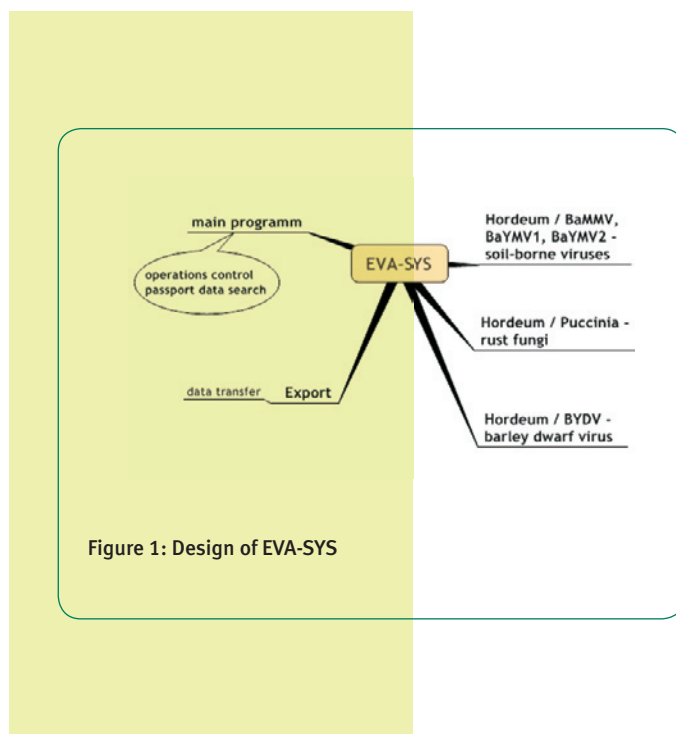
In 2005 as well as the years before, a student assisted the permanent staff in solving some of the group’s tasks. Based on an existing database he analysed the commercial software “Scopeland” as an alternative development tool for the BAZ scientists.

Respective software tools, which will be enhanced continuously, were handed over to the scientists of the institutes involved.

## ■ 9002

With the help of this software the users can feed databases with historical as well as new resistance data; the data are securely stored and consistently provided. EVA-SYS is designed in modules and consists of several programs for special tasks and data.

All modules are using a common base of passport data imported from the “Gatersleben Genebank”. The further development of EVA-SYS is aligned with the development of the infrastructure of data management in BAZ.



## Individual projects

The continuous development and completion of scientific projects, the planning of a data management solution for BAZ as well as the stepwise realisation of it were the main part of the tasks of the group.

The project 9002 (“Establishment of tools for the database input of evaluation data for the resistance of genetic resources against diseases and pests”) and 9004/1 (“Analysis and structuring of data compiled from BAZ breeding research and development of a database aided Data Storage system Plant – DSP”) have been completed.

## ■ 9004/1

The “Data Storage Plant” (DSP) gives the scientists an effective tool to store and edit plant data. In view of the data management strategy of BAZ, the increasing generalisation and modularisation of the software as well as object oriented design were in the focus of software development. The aim is to develop software modules that can be used in any other project.



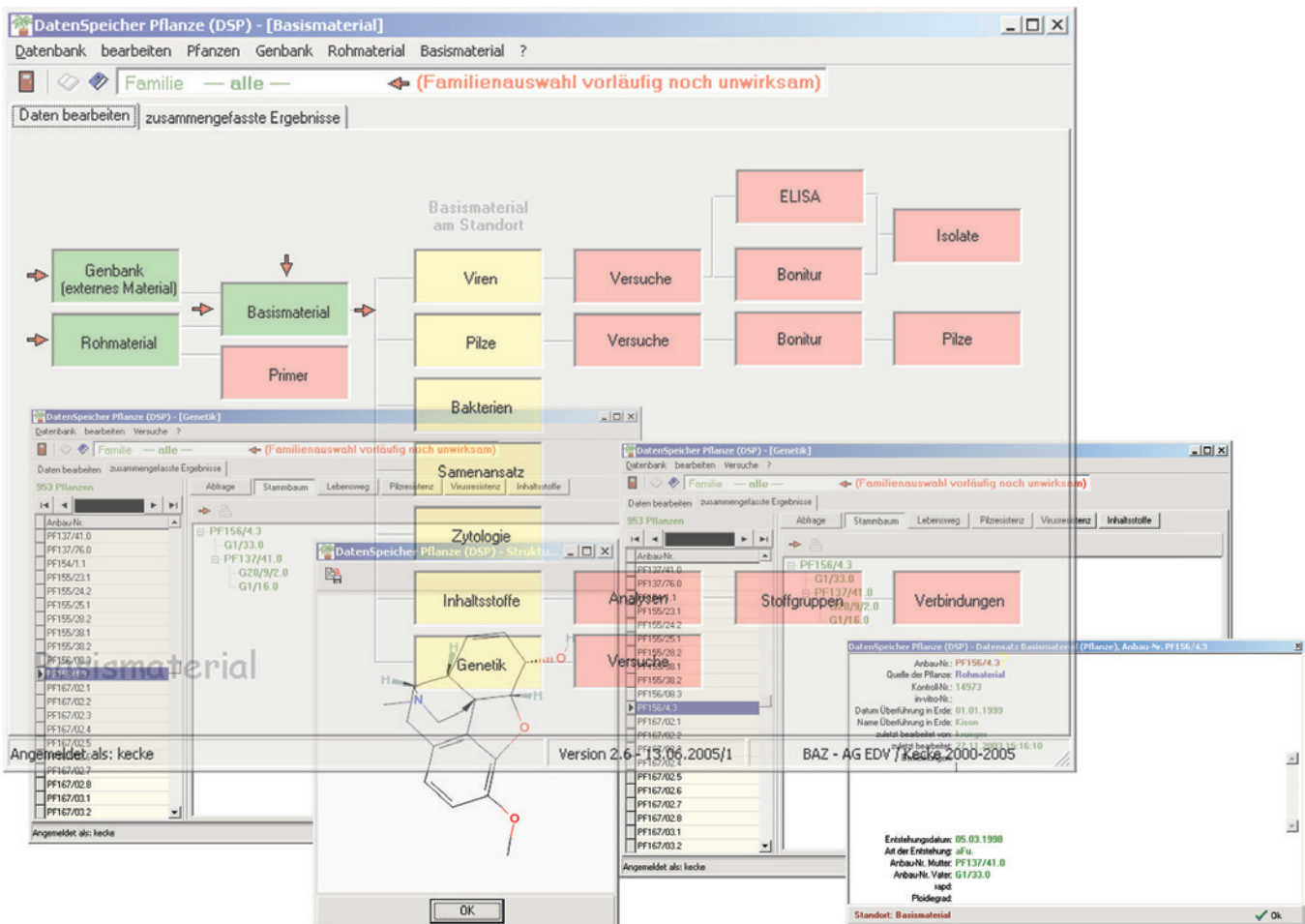


Figure 2: Data Storage Plant

This project is a continuous task (project 9004/0). The next step will be the development of a module to edit scientific evaluation data related to specific projects and experiments. The use of self defined descriptors and its free combination to form so-called surveys is the foundation for a maximum of flexible handling of data. This module will be developed as an autonomous one to be used for DSP as well as other software projects like “Genebank Vitis” (see project 9005).

### 9005

The database design and the software development “Genebank Vitis” to handle the data of the Vitis International Variety Catalogue were the main task in 2005.

There are the following subtasks:

- design of the data model,
- implementation of the database and data import,
- development of a software tool to edit data,
- enhancement with investigation modules and integration of evaluation data,
- development of a Web-based search tool

Parts 1, 2 and 3 (beta test) have been realised. The describing data could be imported into the database on a new database server located at Siebeldingen. The test run started in December 2005. Since January 2006, work on the Web-based search tool has been going on. For this specific task, the staff of the Quedlinburg work group is complemented by a software developer who works in a temporary employment at the Institute of Grapevine Breeding, Siebeldingen.

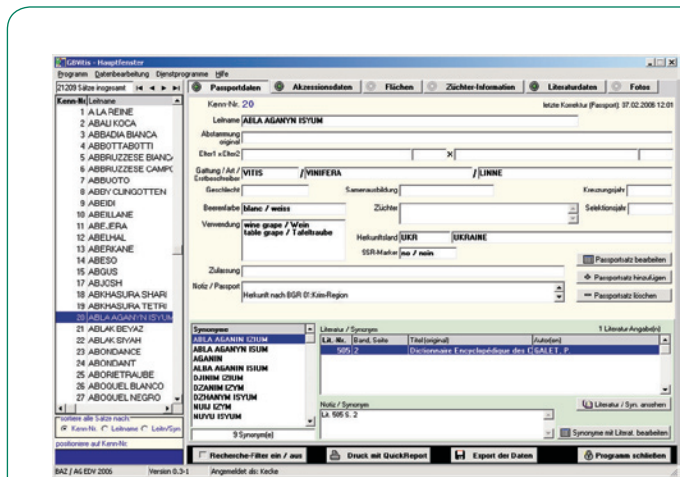


Figure 3: Genebank Vitis

## Future research objectives

In future the Data Processing work group together with the gene bank group from Braunschweig will be actively involved in establishing “biodiversity informatics” as a major part of “bioinformatics” at BAZ. The aim is to help the scientists with making a better use of bioinformatic methods than before.

Especially in molecular genetics the use of bioinformatics methods in the BAZ has to be advanced. In 2006 it remains to be seen how usable the SAS module “SAS Genetics” is. The LIMS Web-solution that is developed in Braunschweig to edit molecular data will be completed. It is a test for future software solutions at BAZ and has to be verified.

A special challenge for the work group and the whole BAZ is using the limited capacities with the maximum of efficiency.

After the establishment of the common data management system in the BAZ and an adapted software development strategy, the future priority of the group’s work will be the scientific analysis of the data with biometrical and other methods.

## III. Publications

### Scientific Publications

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FOMITCHEVA, V. W.; SCHUBERT, J.; SAALBACH, I.; HABEKUSS, A.; KUMLEHN, J.; CONRAD, U.: Bacterial expression and characterization of a single-chain variable fragment antibody specific to several replicases of plant (+)RNA viruses. *J. Phytopathol.* **153**, 2005, 633-639

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HABEKUSS, A.; KÜHNE, T.; RABENSTEIN, F.; KRÄMER, I.; EHRIG, F.; RUGE-WEHLING, B.; HUTH, W.; ORDON, F.: Detection of an rym5 resistance breaking virus strain in Germany. 6th Symp. Int. Working Group Plant Viruses with Fungal Vectors (IWGPVFFV), 05.-07.09.2005, Bologna, Italien, S. 60

JÄRVEKÜLG, L.; VILLEMSON, S.; PAALME, V.; HUNT, R.; EHRIG, F.; RABENSTEIN, F.: Identification and characterization of Pepino mosaic virus isolated from imported tomato fruits. *Pflanzenschutzber.* **61** (2), 2005, 33-42

KASTIRR, U.; MÜLLER, E.; RÖMER, P.; SCHACHSCHNEIDER, R.; HAMMANN, T.: Selection of durum and common wheat accessions for resistance to furoviruses under controlled environmental conditions. 6th Symp. Int. Working Group Plant Viruses with Fungal Vectors (IWGPVFFV), 05.-07.09.2005, Bologna, Italien, S. 58

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## Lectures and Posters

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- EHRIG, F.: Was macht unsere Pflanzen krank? BUGA, 04.10.2005, Munich, lecture
- GABLER, J.: Phytopathogene an Kümmel und Resistenztests. Vortrags- und Diskussionstagung der GPZ „Züchtungsforschung an Arznei- u. Gewürzpflanzen aus der Familie der Umbelliferen“, AG Arznei- u. Gewürzpflanzen, 16.11.2005, Quedlinburg, lecture
- GABLER, J.: Krankheiten an Arzneipflanzen, BUGA, 04.10.2005, Munich, lecture
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- HABEKUSS, A.; KASTIRR, U.; SCHACHSCHNEIDER, R.; HAMMANN, T.: Entwicklung und Anwendung von Methoden zur Bewertung der Virusresistenz bzw. -toleranz bei Getreidearten, Statusseminar InnoPlanta, 05.10.2005, Gatersleben, lecture
- KASTIRR, U.: Erschließung genetischer Ressourcen für die Züchtung von Weizensorten mit *Fusarium*-Resistenz. GFP-Workshop „Fusariosen an Weizen“, 03.-04.02.2005, Freising, lecture
- KASTIRR, U.; GÖTZ, R.; SPANAKAKIS, A.: Vergleichende Untersuchungen zur Resistenz von Winterweizen gegen bodenbürtige Viren in unterschiedlichen Befallsstandorten. GFP-Sommertagung, Abteilung Getreide, 27.06.2005, Hohenheim, lecture
- KASTIRR, U.; RABENSTEIN, F.; EHRIG, F.; KÜHNE, T.: Bodenbürtige Getreideviren – Diagnose, Verbreitung, Gegenmaßnahmen. Seminar „Pflanzenschutz im Ackerbau und Grünland“, 7. bis 9. November 2005, Emmelshausen, lecture
- KASTIRR, U.; RABENSTEIN, F.; KÜHNE, T.: Epidemiological aspects of soil-borne viruses of wheat, triticale and rye in Germany, 6th Symp. Int. Working Group Plant Viruses with Fungal Vectors (IWGPVFFV), 05.-07.09.2005, Bologna, Italy, lecture
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- KASTIRR, U.; WORTMANN, H.; RABENSTEIN, F.; SCHLIEPHAKE, E.; EHRIG, F.; KÜHNE, T.: Epidemiology of soil-borne viruses of wheat, triticale and rye. Seminarveranstaltung, 14.03.2005, Justus-Liebig-Universität Gießen, lecture
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- AHLEMEYER, J.; KÖHLER, W.; FRIEDT, W.; ORDON, F.: Genetic gain and genetic diversity in winter barley. Multifunctionality of landscapes - Analysis, evaluation and decision support, 18.-20.05.2005, Universität Gießen, poster
- HABEKUSS, A.: Zum Auftreten des WDV in Sachsen-Anhalt und erste Ansätze in der Züchtungsforschung, 15. Tagung der AG „Schädlinge in Getreide und Mais“ des AK Integrierter Pflanzenschutz der DPG, 23.-24.02.2005, Braunschweig, lecture
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- ORDON, F.: Züchtungsstrategien zur Verbesserung der Pathogenresistenz von Kulturpflanzen, Wissenschaftliche Tagung des Dachverbandes Agrarforschung (DAF), 26.-27.10.2005, Braunschweig, lecture
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- RICHTER, K.; PEIL, A.; HÖFER, M.; FISCHER, C.: Identification of resistance donors for fire blight in *Malus*. First Int. Symposium on Biological Control of Bacterial Plant Diseases, 23.-26.10.2005, Darmstadt/Seeheim, poster
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- BOUDICHEVSKAIA, A.; DUNEMANN, F.: Phänotypische und molekularbiologische Charakterisierung von Fruchtqualitätsmerkmalen des Apfels – Das EU-Projekt HiDRAS. Tagung der Deutschen Gartenbaulichen Gesellschaft, 23.-26.02.2005, Geisenheim, poster
- DUNEMANN, F.: Molekulare Forschung für die Züchtung von krankheitsresistenten Sorten mit hoher Fruchtqualität beim Apfel. 12. Jahrestagung der AG Genomanalyse der GPZ, 22.-23.02.2005, Bonn, lecture
- DUNEMANN, F.: Genetische und molekularbiologische Untersuchungen zur Schorf- und Mehlauresistenz beim Apfel. Kolloquium „Pflanzenzüchtung/Pflanzenschutz“, Martin-Luther-Universität Halle-Wittenberg, 22.06.2005, Halle und Tagung der AG Obst/Gehölze/Reben der GPZ, 18.-19.10.2005, Großhansdorf, lecture
- DUNEMANN, F.; BOUDICHEVSKAIA, A.; LESEMANN, S.: Molecular research for breeding disease resistant apple cultivars with high fruit quality. Int. Workshop „Application of biotechnology in breeding cultivars suitable for sustainable fruit production“, 12.-13.05.2005, Teresin, Poland, lecture
- FLACHOWSKY, H.: Die Bewertung der Gentechnik als Verfahren für die Apfelzüchtung. Kolloquium des Institutes für Allgemeine Botanik, Universität Hannover, 07.02.2005, Hannover, lecture
- FLACHOWSKY, H.; ELO, A.; SOPANEN, T.; HANKE, V.: BpMADS4 – a MADS box gene of birch induces flowers on in vitro shoots of transgenic apple lines. ISHS Symp., Int. Symp. on Biotechnology of Temperate Fruit Crops and Tropical Species, 10.-14.10.2005, Daytona Beach, Florida, USA, lecture
- FLACHOWSKY, H.; HANKE, V.: Gene transfer as an important approach to resistance breeding in apple. Workshop on application of biotechnology in breeding cultivars suitable for sustainable fruit production, 12.-14.05.2005, Skierniewice, Poland, lecture
- FLACHOWSKY, H.; RIEDEL, M.; REIM, S.; HANKE, V.: Untersuchungen zu den Ursachen des Verlustes eines Transgens bzw. seiner Funktion bei Apfel während der In-vitro-Kultur und im Gewächshaus. 42. Gartenbauwissenschaftliche Tagung, 23.-26.02.2005, Geisenheim, lecture
- GRAFE, C.: Untersuchungen zur Fruchtqualität. 1. Apfeltag im Institut für Obstzüchtung: Der Apfel im Wandel der Zeit, 01.10.2005, Dresden, poster
- HALBWIRTH, H.; MILCEVICOVA, R.; STRISSEL, T.; TREUTTER, D.; PEIL, A.; HANKE, V.; RICHTER, K.; WILHELM, E.; STICH, K.: Influence of polyphenols on fire blight resistance in apple. Identification of resistance donors for fire blight in *Malus*. 1st Int. Symp. on Biolog. Control of Bacterial Diseases, BBA, 23.-26.10.2005, Darmstadt, lecture
- HALBWIRTH, H.; PUHL, I.; GOSCH, C.; MIOSIC, S.; PIEBER, S.; TREUTTER, D.; OLBRICHT, K.; HANKE, V.; STICH, K.: Flavonoid biosynthesis in different strawberry cultivars and species. 5. Symposium Phytomedizin und Pflanzenschutz im Gartenbau, 21.09.2005, Vienna, Austria, poster
- HANKE, V.: Gentechnik in der Obstzüchtung. Fachtagung der Sächs. Landesanst. für Landwirt. zur Weiterbildung für Lehrer „Gentechnik in der Land- und Ernährungswirtschaft“, 02.03.2005, Dresden-Pillnitz und Tagung Staatl. Amt für Landwirt., 02.11.2005, Zwickau, lecture
- HANKE, V.; HÖFER, M.: Erhaltungs- und Nutzungsstrategien pflanzengenetischer Ressourcen bei Obst. GPZ-Tagung, 15.11.2005, Gatersleben, lecture
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- SCHUSTER, M.: Vom Zufalls sämling zur modernen Kirschenzüchtung. BUGA, 30.05.2005, Munich, lecture
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- SCHUSTER, M.: Sauerkirschen-Unterlagen-Versuch. Tagung AK Obstbauliche Leistungsprüfungen, 15.–16.06.2005, Jork, lecture
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- DARSOW, U.: Vorzüchtung (pre-breeding) bei der Kartoffel am ILK. Sommertagung der AG Kartoffelzüchtung und Pflanzguterzeugung in der GPZ, 13.-14.07.2005, Groß Lüsewitz, lecture
- DARSOW, U.: Combining of quantitative blight resistance of potato with table potato quality. 16th Triennial Conf. of the European Association for Potato Research (EAPR), 17.-22.07.2005, Bilbao, Spain, lecture
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- HERRMANN, M.: Ergebnisse zur Resistenz von Hafer gegen Flugbrand (*Ustilago avenae*), GPZ-Tagung, Universität Hohenheim, 27.06.2005, lecture
- HERRMANN, M.; LEITHOLD, B.: Aktuelle Ergebnisse zur Flugbrandresistenz von Nackthafer. 8. Wissenschaftstagung Ökologischer Landbau, 01.-04.03.2005, Kassel, poster
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- RUGE, B.: Unlocking the secondary gene pool of barley, *Hordeum bulbosum*, for a marker-assisted transfer of novel resistance genes into cultivated barley. Vavilov-Seminar, 22.06.2005, Gatersleben, lecture
- RUGE, B.: Resistenz gegenüber Anthraknose bei der Blauen Süßlupine. Projekttreffen ILK Groß Lüsewitz, 13.07.2005, lecture

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- SONNTAG, K.: Biotechnologie im Pflanzenbau. Gymnasium Sanitz, 10.01.2005, lecture
- SONNTAG, K.: Embryokultur in weiten Kreuzungen mit *Lupinus angustifolius*, Projekttreffen ILK Groß Lüsewitz, 13.07.2005, lecture
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- THIEME, R.; ANTONOVA, O.: New sources of resistance to late blight and PVY. EUCABLIGHT -meeting about host resistance to late blight of potato, 05.08.2005, Rostock/Groß Lüsewitz, lecture and poster
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- BALKO, C.: Durch Züchtungsfortschritt zu angepassten Kulturpflanzen? Trockentoleranz bei Kartoffeln und Ackerbohnen. Bayerische Jungbauernschaft e. V., Grainauer Tage „Klimawandel – Folgen für die deutsche Landwirtschaft“, 25.-27.11.2005, Grainau, lecture
- JANSEN, G.: Rohstoff- und Stärkequalität von Wintergerste aus dem CO<sub>2</sub>-Anreicherungsversuch 2000/2003. 5. FACE-Treffen, 20.01.2005, Braunschweig, lecture
- JANSEN, G.: Rohstoff- und Stärkequalität von Weizen aus den CO<sub>2</sub>-Anreicherungsversuchen 2002 und 2005. 6. FACE-Treffen, 08.12.2005, Braunschweig, lecture
- JANSEN, G.; JÜRGENS, H.-U.; KUHLMANN, J.; FLAMME, W.: Züchterische Bearbeitung von Süßlupinen für den ökologischen Landbau : Erste Ergebnisse zu Ertrags- und Qualitätsuntersuchungen. 8. Wissenschaftstagung „Ökologischer Landbau – Ende der Nische“, 01.-04.03.2005, Kassel, poster
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- SCHUM, A.: Mutation induction: An efficient method for breeding of new cultivars in ornamentals. Int. Symposium on Genetic Improvement of Ornamental Plants, 29.08.2005, Buenos Aires, Argentina, lecture
- SEDDIG, S.; JANSEN, G.; FLAMME, W.: Drought stress in potatoes – consequences and selection possibilities. InterDrought-II, The 2nd Conf. on integrate approaches to sustain and improve plant production under drought stress, 24.-28.09.2005, Rom, Italy, poster
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- WEGENER, C. B.: Crosses between pectate lyase transgenic potato lines of cv. Désirée and *S. tuberosum* cultivars – assessment of progeny for resistance to *Erwinia* soft rot. 16th Triennial Conference of the EAPR, 17.-22.07.2005, Bilbao, Spain, lecture
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- BUDAHN, H.; PETERKA, H.; SCHRADER, O.: Identification of disomic additions of *Raphanus* chromosomes in rape background. Xishuangbanna State Agricultural Institute, 19.04.2005, Jinghong, China, lecture
- BUDAHN, H.; PETERKA, H.; SCHRADER, O.: Molecular and cytological characterization of *Raphanobrassica* hybrids. Deut./chin. Kooperation an der Yunnan Academy of Agricultural Sciences, 18.04.2005, Kunming, China, lecture
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- BUDAHN, H.; PETERKA, H.; SCHRADER, O.; DING, Y.: RAPD and dpRAPD-analysis as tools for characterization of *Raphanobrassica* material. Beijing Vegetable Research Center, 25.04.2005, Beijing, China, lecture
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- KLOCKE, E.: Federal Centre for Breeding Research – a Portrait. Arbeitstreffen im Rahmen der deutsch/russischen Kooperation, 17.08.2005, Allrussisches Institut für Phytopathologie Golitsino, Moskauer Region, lecture
- KLOCKE, E.: Prospects for somatic hybridization between various *Apiaceae*. Conference “Progress in carrot genetics – from basic to applied research”, Agricultural University, 24.-25.11.2005, Krakow, Poland, lecture
- KRÄMER, R.; MARTHE, F.; NOTHNAGEL, T.; RYSCHKA, U.; SCHUMANN, G.; PETERKA, H.; BUDAHN, H.; KLOCKE, E.; RICHTER, K.: Die Bedeutung der Resistenzzüchtung bei Gemüse für den Ökolandbau. Fachtagung des Thüringer Ökoherz e. V. Naturerlebnishof Hausen, 13.12.2005, Hausen i. Wipf-ratal, lecture
- KRÄMER, R.; SCHUMANN, G.: Krankheitsresistenz – ein Weg zu gesunden Zierpflanzen. Internationale Pflanzenmesse, 26.-27.01.2005, Essen, poster
- LINKE, B.; WAMBUTT, J.; NOTHNAGEL, T.; BÖRNER, T.: Gene expression in homeotic flowers of carrot CMS plants. XVII Int. Botanical Congress, 17.-23.07.2005, Vienna, Austria, poster
- MARTHE, F.: Gibt es nutzbare Resistenz in Petersilie (*Petroselinum crispum*) gegen den Erreger der Septoria-Blattfleckenkrankheit (*Septoria petroselinii*)?, Tagung der AG 17 GPZ Züchtungsforschung an Arznei- und Gewürzpflanzen aus der Familie der Umbelliferen, 16.11.2005, Quedlinburg, lecture
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- STOLL, C.; LÜHS, W.; ZARHLOUL, K. M.; BRUMMEL, M.; SPENER, F.; HAUSMANN, L.; TÖPFER, R.; FRIEDT, W.: Accumulation of medium-chain fatty acids in oilseed rape (*Brassica napus* L.) due to heterologous gene expression. 2. European Symp. on Plant Lipids, 17.-20.08.2005, Copenhagen, Denmark, lecture
- STOLL, C.; ZARHLOUL, M. K.; HAUSMANN, L.; SPENER, F.; TÖPFER, R.; FRIEDT, W.; LÜHS, W.: Entwicklung von genetisch verändertem Raps mit optimiertem Gehalt an mittelkettigen Fettsäuren, 7. Tagung der Gesellschaft für Pflanzenzüchtung e. V., 03.-05.03.2004, Halle/Saale, poster
- TÖPFER, R.: Möglichkeiten und Ziele der Gentechnologie in der Landwirtschaft, Vortragsveranstaltung „Gentechnologie in der Landwirtschaft – Zukunft für den Menschen?“, 15.11.2004, Saarlouis, lecture
- WELTER, L.; GLISSANT, D.; EIBACH, R.; TÖPFER, R.; DELROT, S.; ZYPRIAN, E.: Transcriptional analysis in grapevine in response to infection with powdery mildew (*Uncinula necator*) using oligo-microarrays. COST 858 Workshop “Functional Gene Analysis in Grapevine”, 06.-07.10.2005, Siebeldingen, poster
- ZYPRIAN, E.: Genetic mapping in grapevine for the analysis of disease resistance and flavour compounds. 13. Plant and Animal Genome Konferenz, 15.-19.01.2005, San Diego, California, USA, lecture
- ZYPRIAN, E.: Genetische Analyse und Markerentwicklung für Pilzresistenzigenschaften der Weinrebe. 12. Jahrestagung der AG Genomanalyse der Gesellschaft für Pflanzenzüchtung e. V., 22.-23.02.2005, Bonn, lecture
- ZYPRIAN, E.: Marker für Pilzresistenz – Werkzeuge für Züchtung und Forschung. 32. Mitgliederversammlung der Gemeinschaft der Förderer und Freunde des Instituts für Rebenzüchtung Geilweilerhof e. V., 04.03.2005, Siebeldingen, lecture
- ZYPRIAN, E.: Genetic analysis of disease resistance factors in grapevine. NCCR Leysin Conference „Plant Survival“, 31.03.-03.04.2005, Leysin, Switzerland, lecture
- ZYPRIAN, E.: Identifikation und Isolierung von Genomabschnitten für Resistenz gegen den Echten Mehltau (*Uncinula necator*). 44. Arbeitstagung des Forschungsrings des Deutschen Weinbaus bei der DLG, 03.-04.05.2005, Veitshöchheim, lecture
- ZYPRIAN, E.: Das Genom der Weinrebe – Forschung zum praktischen Nutzen. Akademie für Ältere der Volkshochschule Landau, 31.05.2005, Siebeldingen, lecture
- ZYPRIAN, E.; AKKURT, M.; FISCHER, B.; SALAKHUTDINOV, I.; EIBACH, R.; TÖPFER, R.: Molekulare Kartierung der Weinrebe, Versammlung der AG Genomanalyse der BAZ, 15.-16.06.2006, Dresden, lecture
- ZYPRIAN, E.; AKKURT, M.; FISCHER, B.; SALAKHUTDINOV, I.; WELTER, L.; KORTEKAMP, A.; EIBACH, R.; TÖPFER, R.: Fundamental research meets practical breeding: Genetics of disease resistance in grapevine. Int. Grape Genomics Symposium, 12.-14.07.2005, St. Louis, Missouri, USA, lecture and poster
- ZYPRIAN, E.; EIBACH, R.; AKKURT, M.; TÖPFER, R.: Genetic mapping in grapevine for the analysis of disease resistance and flavour compounds. 13. Plant and Animal Genome Konferenz des Int. Grape Genome Projects, 15.-19.01.2005, San Diego, USA, poster
- ZYPRIAN, E.; MURRAT, A.; SALAKHUTDINOV, I.; VOGT, S.; KORTEKAMP, A.; FISCHER, B.; EIBACH, R.; TÖPFER, R.: Genetic bases of fungal disease resistance in Grapevine. COST 858 Workshop: Defence Reactions of Grapevine Toward Biotic Stress, 06.-07.05.2005, Piacenza, Italy, lecture
- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EIBACH, R.; TÖPFER, R.: Mapping of QTLs for fungal disease resistances in grapevines. COST 858 Workshop “Functional Gene Analysis in Grapevine”, 06.-07.10.2005, Siebeldingen, lecture
- ZYPRIAN, E.; WELTER, L.; AKKURT, M.; EIBACH, R.; TÖPFER, R.: Genetische Analyse von Pilzresistenzigenschaften der Weinrebe. GPZ-Tagung der AG Obst, Gehölze, Reben, 18.-19.10.2005, Großhansdorf, lecture



## ■ Gene Bank Braunschweig

- FRESE, L.: Dynamic management of PGRFA: review of a concept. ECP/GR workshop on conservation, management and regeneration methods for grain legume genetic resources, 23.09.2005, Valladolid, Spain, lecture
- FRESE, L.: Netzwerk zur Erhaltung und Förderung der Anpassungsfähigkeit von Kulturpflanzen. Jahrestagung der GFP, interne Sitzung der Abt. Getreide, 03.11.2005, Bonn, lecture
- FRESE, L.; GERMEIER, C.: Wild beet germplasm on islands: conservation and potential use EUCARPIA Genetic Resources Section Meeting, PGR of geographical and other „islands“ (conservation, evaluation and use for plant breeding), 30.03.-02.04.2005 Castelsardo, Italy, lecture
- GERMEIER, C. U.: Aims of the meeting: a generalised approach for two central crop databases. ECP/GR sugar, starch and fibre crops network coordinating group meeting, 23.06.2005, Braunschweig, lecture
- GERMEIER, C. U.; FRESE, L.: Erhaltung genetischer Ressourcen - Bedeutung landwirtschaftlicher und gartenbaulicher Kulturen. Bundesgartenschau, 13.06.2005, Munich, lecture
- GERMEIER, C. U.; FRESE, L.: Crop wild relatives in the ECP/GR Central Crop Databases - a case study in *Beta* and *Avena*. First Int. Conf. on Crop Wild Relative Conservation and Use, 14.-17.09.2005, Agrigento, Italy, 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 Epidemiology and Resistance Resources Aschersleben

University of Giessen

PD Dr. F. Ordon, „Pflanzenzüchtung“, obligatory BSc course

#### ■ Institute of Resistance Research and Pathogen Diagnostics Aschersleben

University of Halle

Dr. habil. T. Kühne, „Viruskrankheiten bei landwirtschaftlichen Kulturen“, lecture

University of Halle

Dr. rer. nat. F. Rabenstein, „Polyklonale Antiseren und monoklonale Antikörper in der Pathogendiagnostik“, lecture

University of Halle

Dr. rer. nat. F. Rabenstein, „Viruskrankheiten an Kern- und Steinobst“, lecture

University of Halle

Dr. rer. nat. F. Rabenstein, „Virusdiagnosemethoden“, lecture

University of Halle

Dr. habil. J. Schubert, „Gemüsevirosen“, lecture

University of Halle

Dr. habil. J. Schubert, „Molekulare Nachweistechiken für Pflanzenviren“, lecture

#### ■ Institute of Fruit Breeding Dresden

University of Applied Sciences Dresden

Dr. habil. V. Hanke, „Grundlagen der Pflanzenzüchtung“, lectures, basic course

Technical University of Dresden

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

University of Applied Sciences Dresden

Dr. rer. hort. K. Olbricht, „Angewandte Pflanzenzüchtung“, lecture

## ■ Institute of Horticultural Crops Quedlinburg

University of Halle

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

University of Hohenheim

Prof. Dr. H. Düring, „Biologie der Kulturpflanze“,  
comprehensive practical course

University of Karlsruhe

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

## 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

Austria

Belgium

Bulgaria

Canada

China

Croatia

Czech Republic

Denmark

Egypt

Finland

France

Greece

Hungary

India

Israel

Italy

Japan

Lithuania

Moldova

the Netherlands

New Zealand

Norway

Poland

Portugal

Romania

Russia

Slovenia

South Africa

Spain

Sweden

Switzerland

Turkey

Ukraine

United Kingdom

USA

## Guest scientists at BAZ

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

### ■ Institute of Resistance Research and Pathogen Diagnostics, Aschersleben

Dr. Havva Ilbagi

Department of Plant Protection, Tekirdag Faculty of  
Agriculture, Trakya University,  
Tekirdak, Turkey, 10/2004-01/2005

Kwang Hyok Ju

Academy of Agricultural Sciences, Institute of Plant  
Protection,  
Pjöngjang, Korea, 03/2005-09/2005

Dr. Audrius Kacergius

Institute of Botany,  
Vilnius, Lithuania, 05/2005-07/2005

Petra Kozlova

Institute of Plant Molecular Biology,  
Budweiss, Czech Republic, 10/2005-11/2005

Zhenghe Li

University Hangzhou, Institute of Botany,  
Hangzhou, China, 10/2004-02/2005

Dr. Jaroslav Matousek

Institute of Plant Molecular Biology,  
Budweiss, Czech Republic, 03/2005 und 10/2005-  
11/2005

Dr. Ayodeji T. Owolabi

University of Calabar, Department of Botany,  
Calabar, Nigeria, 03/2005-04/2005

Galina Snihur

Kyiv National University by Taras Shevschenko,  
Kyiv, Ukraine, 05/-07/2005; 11/2005

Dr. Joanna Sztangret

Plant Breeding and Acclimatization Institute,  
Mlochow, Poland, 05/2005-06/2005

### ■ Institute of Epidemiology and Resistance Resources Aschersleben

Dr. Havva Ilbagi

Department of Plant Protection, Tekirdag Faculty of  
Agriculture, Trakya University,  
Tekirdak, Turkey, 10/2004-01/2005

Kwang Hyok Ju

Academy of Agricultural Sciences, Institute of Plant  
Protection,  
Pjöngjang, Korea, 03/2005-09/2005

Dr. Audrius Kacergius

Institute of Botany,  
Vilnius, Lithuania, 05/2005-07/2005



Petra Kozlova  
Institute of Plant Molecular Biology,  
Budweis, Czech Republic, 10/2005-11/2005

Zhenghe Li  
University Hangzhou, Institute of Botany,  
Hangzhou, China, 10/2004-02/2005

Dr. Jaroslav Matousek  
Institute of Plant Molecular Biology,  
Budweis, Czech Republic, 03/2005 und 10/2005-  
11/2005

Dr. Ayodeji T. Owolabi  
University of Calabar, Department of Botany,  
Calabar, Nigeria, 03/2005-04/2005

Galina Snihur  
Kyiv National University by Taras Shevchenko,  
Kyiv, Ukraine, 05/-07/2005; 11/2005

Dr. Joanna Sztangret  
Plant Breeding and Acclimatization Institute,  
Mlochow, Poland, 05/2005-06/2005

### ■ Institute of Fruit Breeding Dresden-Pillnitz

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

Tania Garcia  
Austrian Research Centres,  
Seibersdorf, Austria, 06/2005

Houhua Li  
Universität Hannover, Institut für Obstbau,  
Hannover, Germany, 11/2005

Agnes Masny  
Research Institute of Pomology and Floriculture,  
Skierniewice, Poland, 05/2005

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

### ■ Institute of Agricultural Crops Groß Lüsewitz

Dr. Olga Antonova  
N.I. Vavilov Institute of Plant Industry,  
St. Petersburg, Russia, 06/2005-09/2005

Dr. Catherine Chatot-Balandras  
Association des Créateurs de Variétés Nouvelles de  
pomme de Terre (ACVNPT),  
Chateauneuf-du-Faou, France, 08/2005

Dr. Leontine Colon  
Plant Research International B.V. (PRI),  
Wageningen, Netherlands, 08/2005

Dr. Kvetoslava Foriseková  
Potato Research & Breeding Institute (VSUZ),  
Velka Lomnica, Slovakia, 08/2005

Dr. Jens Grønbech Hansen  
Danish Institute of Agricultural Sciences (DIAS),  
Research Centre,  
Foulum, Denmark, 08/2005

Dr. Jan Heldak  
Potato Research & Breeding Institute (VSUZ),  
Velka Lomnica, Slovakia, 08/2005

Dr. Arne Hermansen  
Norwegian Crop Research Institute (NCRI),  
As, Norway, 08/2005

Dr. Renata Lebecka  
Plant Breeding & Acclimatization Institute (IHAR),  
Mlochow Research Center,  
Mlochow, Poland, 08/2005

Dr. Galina Pendenin  
N.I. Vavilov Institute of Plant Industry,  
St. Petersburg, Russia, 04/2005-06/2005

Jan Plich  
Plant Breeding & Acclimatization Institute (IHAR),  
Mlochow Research Center,  
Mlochow, Poland, 08/2005

Dr. Zsolt Polgar  
University of Veszprem Georgikon Faculty of  
Agriculture,  
Keszthely, Hungary, 08/2005

Ruth Salomon-Blackborn  
Scottish Crop Research Institute (SCRI) Invergowrie,  
Dundee, United Kingdom, 08/2005

Dr. Istvan Sarvari  
Sarvari Research Trust,  
Zirc, Hungary, 08/2005

Zoltan Sarvari  
Sarvari Research Trust,  
Zirc, Hungary, 08/2005

Dr. Huub Schepers  
Applied Plant Research (PPO),  
Lelystad, Netherlands, 08/2005

Prof. Dr. David Shaw  
Sarvari Research Trust,  
Siambra Gwynion, Llandygai Bangor, United  
Kingdom, 08/2005

Dr. Bodo Trognitz  
Austrian Research Centre (ARC), Seibersdorf  
Research GmbH,  
Seibersdorf, Austria, 08/2005

Dr. Istvan Wolf  
University of Veszprem Georgikon Faculty of  
Agriculture,  
Keszthely, Hungary, 08/2005

Jianzhong Yu  
University Peking,  
Peking, China, 10/2005

Prof. Dr. Ewa Zimnoch-Guzowska

Plant Breeding & Acclimatization Institute (IHAR),  
Mlochow Research Center,  
Mlochow, Poland, 08/2005

■ **Institute of Horticultural Crops  
Quedlinburg**

Dr. Anna Artemyeva

N.I. Vavilov Institute of Plant Industry,  
St. Petersburg, Russia, 03/2005-10/2005

Dr. Rafal Baranski

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 04/2004-12/2005

Prof. Liu Fan

Beijing Vegetable Research Centre,  
Beijing, China, 11/2004-06/2005

Karol Gladysz

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Production,  
Krakow, Poland, 01/2005-09/2005

Dr. Dariusz Grzebelus

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 07/2005-08/2005

Dr. Ewa Grzebelus

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 07/2005-08/2005

Zhao Hong

Beijing Vegetable Research Centre,  
Beijing, China, 10/2005 ñ 02/2006

Angnieszka Kielkowska

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 09/2004-03/2005

Daria Shumilina

All-Russian Research Institute of Phytopathology,  
Golitsino, Russia, 05/2005-09/2005

Liang Yi

Beijing Vegetable Research Centre,  
Beijing, China, 11/2004-02/2005

■ **Institute of Plant Analysis  
Quedlinburg**

Dr. Grayna. Balcerowska

University of Technology and Agriculture, Institute of  
Mathematics and Physics,  
Bydgoszcz, Poland, 05/2005

Dr. Rafal Baranski

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 08/2005-10/2005

Dr. Darek Grzebelus

Krakow Agricultural University, Department of  
Genetics Plant Breeding and Seed Science,  
Krakow, Poland, 07/2005-08/2005

Agnieszka Kielkowska

Krakow Agricultural University, Department of  
Genetics, Plant Breeding and Seed Science,  
Krakow, Poland, 09/2004-03/2005

Dr. Bogusława. Kupcewicz

University of Technology and Agriculture, Faculty of  
Zootechnics,  
Bydgoszcz, Poland, 05/2005

Prof. Dr. Ryszard Siuda

University of Technology and Agriculture, Institute of  
Mathematics and Physics,  
Bydgoszcz, Poland, 05/2005

Liang Yi

Beijing Vegetable Research Centre,  
Beijing, China, 12/2004-02/2005

■ **Institute of Grapevine Breeding Geilweilerhof  
Siebeldingen**

Leocir José Welter

Universität Karlsruhe, Botanisches Institut II,  
Karlsruhe, Germany, 04/2004 – 03/2006

■ **Gene Bank  
Braunschweig**

Marcin Zaczynski

Plant Breeding and Acclimatization Institute, National  
Centre for Plant Genetic Resources,  
Radzikow, Poland, 12/2005

## V. Scientific Advisory Board

The Scientific Advisory Board advises the Federal Centre for Breeding Research on Cultivated Plants on research issues. It promotes the relations of BAZ with scientists and research establishments working in the same or related fields as well as with practical breeders.

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.

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.

### ■ Members of the Scientific Advisory Board

In the reporting period, the following members were on the Scientific Advisory Board of BAZ:

#### Chairman

Prof. Dr. Dr. h.c. W. Friedt

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

#### Members

Prof. Dr. H. Becker

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

Dr. Dr. h.c. A. Büchting

KWS SAAT AG, Einbeck

N. L. Chrestensen

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

former member of the Landesbauernverband Sachsen-Anhalt, Magdeburg

Prof. Dr. H. Lörz

Universität Hamburg, Institut für Allgemeine Botanik, Hamburg

Dr. W. Müller

BLW delegate for International Agricultural Research, 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



## VI. BAZ collections and banks

### ■ Collection of plant pathogens

The Institute of Epidemiology and Resistance Resources at Aschersleben maintains a large collection of pathogen isolates, pathotypes, races, combinations of virulences, and aphids. The collection is continuously being supplemented with new isolates related to BAZ projects. The isolates of viruses, bacteria and fungi as well as aphid species are mainly used for studies within the BAZ, but they are also made available to users from other research institutions on the basis of the BAZ Scale of Fees.

For more information on the collection see our website [www.bafz.de](http://www.bafz.de) under **Research**.

### ■ Serum bank

The Institute of Resistance Research and Pathogen Diagnostics at Aschersleben maintains a collection of monoclonal antibodies and polyclonal antisera. The sera are used in BAZ research projects, but they are made available to other research institutions for non-commercial purposes, too.

For more information on the Serum bank see our website [www.bafz.de](http://www.bafz.de) under **Research**.

### ■ Probe bank

For BAZ, the Institute of Resistance Research and Pathogen Diagnostics at Aschersleben is in charge of a DNA probe repository. The probes have been developed from *Hordeum vulgare* at this and other institutes. The probes are made available to other research institutions free of charge, private companies have to pay a license fee.

For more information on the Probe bank see our website [www.bafz.de](http://www.bafz.de) under **Research**.

### ■ Grapevine gene bank

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

For more information on the Grapevine gene bank see our website [www.bafz.de](http://www.bafz.de) under **Research** or go to <http://www.genres.de/idb/vitis/>.

### ■ Fruit gene bank

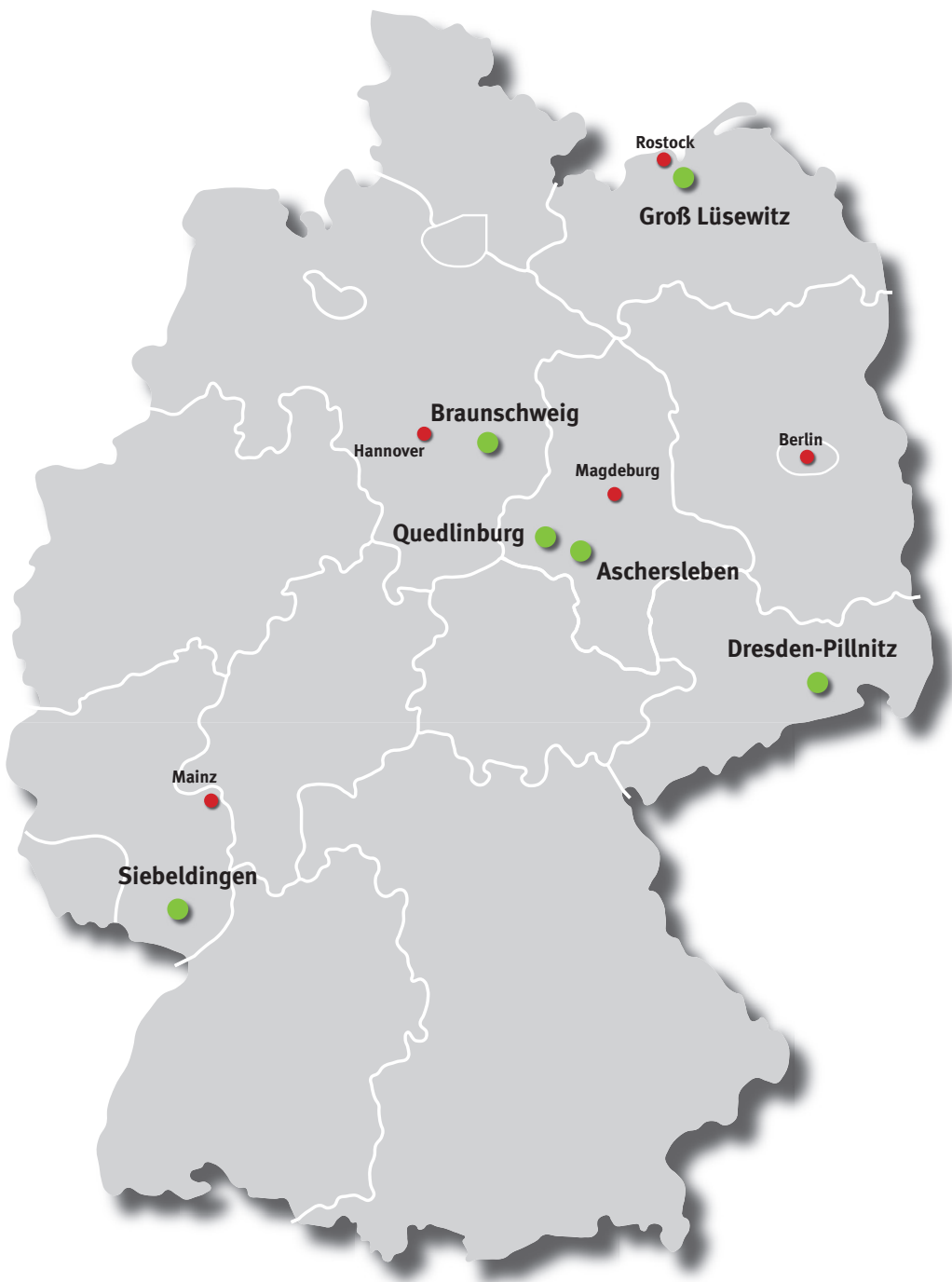
The Institute of Fruit Breeding runs the Fruit Gene Bank. More information on the apple, pear, sweet and sour cherry and strawberry varieties listed and the special collections of wild species of *Malus*, *Pyrus*, *Prunus* and *Fragaria* are found on the pages of the Institute of Fruit Breeding under [www.bafz.de](http://www.bafz.de).

The Fruit Gene Bank contains

797	apple varieties ( <i>Malus x domestica</i> )
130	pear varieties ( <i>Pyrus communis</i> )
341	strawberry varieties ( <i>Fragaria x ananassa</i> )
191	sweet cherry varieties ( <i>Prunus avium</i> )
92	sour cherry varieties ( <i>Prunus cerasus</i> )
165	plum varieties ( <i>Prunus domestica</i> )
25	sea buckthorn varieties and clones ( <i>Hippophae rhamnoides</i> )
372	accessions of <i>Malus</i>
220	accessions of <i>Fragaria</i>
85	accessions of <i>Prunus</i>
56	accessions of <i>Pyrus</i>
7	accessions of <i>Sorbus</i>

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

## Geographic location of BAZ institutes



**Institute of Resistance Research and Pathogen Diagnostics Aschersleben**  
Theodor-Roemer-Weg 4  
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Fax: +49(0)3473 879-200  
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06449 Aschersleben  
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**Institute of Fruit Breeding Dresden**  
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01326 Dresden  
Tel.: +49(0)351 2 61 62-14  
Fax: +49(0)351 2 61 62-13  
E-Mail: bafz-oz@bafz.de

**Institute of Agricultural Crops Groß Lüsewitz**  
Rudolf-Schick-Platz 3a  
18190 Groß Lüsewitz  
Tel.: +49(0)38209 45-200  
Fax: +49(0)38209 45-222  
E-Mail: bafz-lk@bafz.de

**Institute of Abiotic Stress Tolerance Groß Lüsewitz**  
Rudolf-Schick-Platz 3  
18190 Groß Lüsewitz  
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Fax: +49(0)38209 45-120  
E-Mail: bafz-st@bafz.de

**Institute of Grapevine Breeding Geilweilerhof**  
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**Institute of Horticultural Crops Quedlinburg**  
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**Administration Quedlinburg**  
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