Plants and People Conference

MAX-PLANCK-GESELLSCHAFT

On Roots and Fruits of Plant Biology

Philosophy and History of Science

Application of Plant Science

5-7 September 2011

Max Planck Institute
of Molecular Plant Physiology
Potsdam, Germany

Organized by PhD students

http://plants-and-people.mpg.de

IMPRS
Primary Metabolism
and Plant Growth

Max-Planck-Institut
für Molekulare Pflanzenphysiologie

Universität Potsdam

Welcome!

Dear colleagues and guests,

We are happy to welcome all participants of the “Plants and People Conference” on the Max Planck Campus Golm. The theme of our first meeting is: “Roots and Fruits of Plant Biology”, looking at both the history and present day applications of plant research. Recent findings in history and theory of plant science as well as modern plant breeding and engineering approaches will be presented in lectures and a workshop. To cover our broad range of topics, we have invited speakers from all over the world to share their knowledge and experience.

Our conference is hosted by the Max Planck Institute of Molecular Plant Physiology. The MPI-MP was founded in 1994 and has developed into one of the world’s leading plant research institutes.

“Plants and People 2011” aims to provide a platform for the participants to get together with other scientists and to discuss ideas and experiences. We hope that our inaugural meeting will become a regular series.

We wish you interesting and fruitful days with many discussions and new contacts!

The organizing team

Doctoral students of the MPI-MP and the University of Potsdam

Tobias Fleischmann
Maria Ignacia Fuentes Bustos
Ulrike Glaubitz
Dorothea Hemme
Tabea Mettler
Stefanie Schmidt
Julia Teply
Daniel Veyel

Thank you!

Marcus Thienert for web design.
Frederik Dethloff and Han-Yi Fu for poster design.
Dr. Ina Talke and the administration of the MPI-MP for support in planning and organizing.
Max Planck Society and IMPRS “Primary Metabolism and Plant Growth” for financial support.

Conference Programme

Monday, 05.09.
Applications of Plant Science

Time	
13:00 - 14:00	**Registration**
14:00 - 14:15	**Welcome**
	Breeding and Engineering Plants
14:15 - 15:00	Mark Tester (AUS)
15:00 - 15:45	Martijn Gipmans (D)
15:45 - 16:15	**Coffee break**
16:15 - 17:00	Mario Gils (D)
17:00 - 17:45	Simon Chan (US)
17:45 - 18:00	**Break**
	Evening Lecture and Reception
18:00 - 18:45	Noel Kingsbury (UK)
followed by	**Reception with cold buffet**

Tuesday, 06.09.
Applications of Plant Science

Time	
	Phyto-pharmacies – Plants as Health Factories I
09:15 – 10:00	Cathie Martin (UK)
10:00 – 10:45	Tomasz Czechowski (UK)
10:45 – 11:15	**Coffee break**
	Fueling the World
11:15 – 12:00	Marcos Buckeridge (BR)
12:00 – 12:45	Olaf Kruse (D)
12:45 – 14:15	**Lunch (not provided)**
	Challenges of Nutrition
14:15 – 15:00	Richard Sayre (US)
15:00 – 15:30	**Coffee break**
	Phyto-pharmacies – Plants as Health Factories II
15:30 - 16:15	Inga Hitzeroth (ZA)
16:15 - 17:00	Yuri Gleba (D)
17:00 - 17:20	**Concluding remarks & transition to History of Science**

Wednesday, 07.09.
History and Philosophy of Science

Time	
09:15 - 12:00	***Workshop on Philosophy of Science*** *- K. Nickelsen, R. Scholl (CH)* (see page 3 for details)
12:00 - 13:30	**Lunch (not provided)**
	History and Philosophy of Science
13:30 - 14:15	Rudolf Hagemann (D)
14:15 - 15:00	Kärin Nickelsen (CH)
15:00 - 15:30	**Coffee break**
15:30 - 16:15	Friedrich Steinle (D)
16:15 - 17:00	Raphael Scholl (CH)
17:00 - 17:15	**Closing remarks**
evening	**BBQ**

Workshop

Wednesday, 07.09.
Philosophy of Science Workshop

Time	
09:15 - 10:00	Introductory lecture on “Scientific thinking” (deduction, induction, falsification and causal inferences)
10:00 - 10:30	Choose one of the case studies presented and analyse its argument and methodology. Or, alternatively, analyse your own work or project idea (both with the help of hand-outs).
10:30 - 10:45	**Coffee break**
10:45 - 11:15	Discussion of your analysis in groups of 6-10 people
11:15 - 12:00	Fallacies and methodological pitfalls in science

This workshop is organized by Kärin Nickelsen and Raphael Scholl.

Max Planck Institute of Molecular Plant Physiology

The mission of the institute is to study plant metabolism in the context of the plant system as a whole. Since this system is more than a collection of genes and their products, we focus our efforts on understanding how these components dynamically interact over time and under different conditions.

To grasp the complexity, it is essential to determine molecular and complex parameters at different functional levels, and to analyse the resulting complex data set against the background of existing biological knowledge.

In the long run our goal is to develop a comprehensive, systems-level understanding of plant growth. To link plant growth and metabolism the institute maintains a strong interest in understanding the genetic and physiological basis of biomass formation and heterosis. Current efforts are centred on unravelling a set of complex processes that are of particular relevance to plant biomass: the bioenergetic pathways, macronutrient acquisition, nutrient signalling and resource allocation.

A detailed understanding of plant growth represents one of the greatest challenges in plant physiology. Our institute is very well prepared to accomplish this challenge.

To find out more about the Max Planck Institute of Molecular Plant Physiology, please visit our website: http://www.mpimp-golm.mpg.de/

All lectures take place in the lecture hall. The workshop takes place in the seminar room. Lecture hall and seminar room are located in building 4 (central building; yellow).

Canteen/cafeteria: Max Planck canteen in building 4
Fraunhofer canteen next to building 7

At the Max Planck canteen you pay with a pre-paid card that you can get from the machines at the entrance of the canteen. At the Fraunhofer canteen you can pay in cash.

Travel Information

Connections to Potsdam Hauptbahnhof (regional trains and the S-Bahn to/from Berlin):

Bus: 605 Wissenschaftspark Golm <> S Hauptbahnhof Potsdam

606 Alt-Golm <> S Hauptbahnhof Potsdam

Train: RB20 Bahnhof Golm <>S Hauptbahnhof Potsdam

RB21 Bahnhof Golm <>S Hauptbahnhof Potsdam

It is a 5-10 min walk between the train station and the Max Planck campus. For further information, please visit our website.

Marcos Buckeridge

LAFIECO, Department of Botany, IB-USP
National Laboratory of Science and Technology of Bioethanol, CTBE, Campinas SP, Brazil

Marcos Buckeridge is plant biologist who worked for 20 years with cell wall polysaccharide degradation focusing on the comprehension of the physiological and cellular mechanisms involved in seedling establishment in tropical biomes as well as the development of biotechnological tools to help the sustainable use of biodiversity. With the increasing importance of the impact of Global Climatic Changes in the world, Dr. Buckeridge pioneered with his team at the University of São Paulo, studies that aim at understanding how tropical species of crops and forest trees respond to the increasing carbon dioxide concentration and elevation of temperature in the atmosphere. In 2009 Dr Buckeridge became Scientific Director of the Brazilian Bioethanol Science and Technology Laboratory, in Campinas. He also coordinates the National Institute of Science and Technology of Bioethanol (INCT do Bioetanol), a virtual institute that gathers 30 laboratories in 6 states of Brazil and keeps several collaborations in the US and Europe. In 2010, he was appointed as one of the Lead Authors of WGII for the next IPCC report (AR5) to be released in 2014. He helped to create the BIOEN, the bioenergy program at FAPESP. Presently, Dr. Buckeridge is a communicating editor for Trees:structure and function (Springer), Bioenergy Research (Springer), Global Change Biology Bioenergy (Wiley).

Abstract

Understanding carbon metabolism in sugarcane to improve bioethanol production

Sugarcane is one of the most important bioenergy crops extant and any improvement in bioethanol production requires better understanding of its biochemistry, physiology and molecular biology. Some points are particularly important such as photosynthesis, sucrose metabolism and cell wall biochemistry. Sucrose metabolism has been deeply studied in varieties of sugarcane from other countries, but Brazilian varieties lack such studies. Although C4 photosynthesis has been discovered in leaves of sugarcane in the 1960s, little is known about its biochemical and genetic controls. In the case of cell walls, even less is known. Due to the great interest in the production of second-generation bioethanol, understanding its cell wall metabolism will be key to guide future agricultural and industrial process development. In this presentation I will report recent discoveries from my lab regarding photosynthesis and carbon metabolism associated to source-sink relationship in sugarcane, including work on the structure and architecture of its cell walls. Proteomics analyses of mature leaves from 45 days old plant revealed that activation of photosynthesis is followed by an increase in malate metabolism, which is one of the driving forces of the elevated CO2 effects through the sink of reducing power (NADPH and ATP) from the light reactions. As a result, electron transport increases and with that, a better use of water has been observed. Carbohydrate analyses of the diurnal variation of metabolism (including the use of metabolomics of 60 days old plants) of sugarcane revealed that leaves make starch and sucrose and export the latter to the culms, which accumulate very little starch and a large proportion of sucrose. We followed the diurnal variations of 91 substances and found that most of them vary with light-dark cycle. Starch, sucrose, raffinose, glucose and fructose (the non-structural carbohydrates) increase during the day and decrease during the night. Our results indicate that cell wall polysaccharides are synthesised during the day and wall extension occurs in the night. In 2001, we reported the discovery of 469 genes related to cell wall metabolism in sugarcane (Lima *et al.* Gen.Mol.Biol. 24:191). Since then, we have determined the chemical structure of sugarcane cell wall. We found that Beta-glucan, arabinoxylan and xyloglucan are the main hemicelluloses in sugarcane walls. Their fine structures and architecture are starting to be revealed, which are leading to a better understanding of wall biosynthesis and making possible to design strategies for its degradation in order to accomplish processes for 2nd generation biothanol. We have characterised a process in sugarcane roots (aerenchyma formation) in which walls are degraded within the context of plant metabolism. By studying the biochemistry and molecular biology of this process, we expect to understand sugarcane systems biology connections that link photosynthesis and growth through cell wall production and modifications. By studying the biochemistry and molecular biology of this process, we expect to understand sugarcane systems biology connections that link photosynthesis and growth through cell wall production and modifications. We expect this to make possible future genetic transformations that could lead to changes in carbon metabolism and a possible increase in bioethanol production.

Simon Chan

College of Biological Sciences, University of California, Davis, USA

Simon did his PhD in Elizabeth Blackburn's lab at UCSF, studying telomeres and telomerase using Saccharomyces cerevisiae. His postdoc research with Steve Jacobsen at UCLA focussed on mechanisms of gene silencing in Arabidopsis. He started his own group in the Department of Plant Biology at UC Davis in 2006, and decided to work on chromosome segregation in Arabidopsis. The lab initially studied basic mechanisms of centromere function. Recently, they have also begun to manipulate chromosome inheritance to create new plant breeding tools.

Abstract

Haploid *Arabidopsis thaliana*: power tools for plant genetics

Creating true-breeding homozygotes (e.g. recombinant inbred lines or RILs) from a heterozygous F1 typically involves many generations of inbreeding. To accelerate this process, plant breeders produce haploid plants from a heterozygous parent, then convert them into fertile diploids that are homozygous for every locus in the genome. *Arabidopsis thaliana* haploids can now be made through a simple genetic cross. When a cenh3 GFP-tailswap mutant with altered centromeres is crossed to wild type, mutant chromosomes are lost after fertilization. Up to 50% of viable progeny are haploids produced by complete genome elimination, and we have introduced dominant markers into cenh3 GFP-tailswap to facilitate their selection. Haploid Arabidopsis plants convert into fertile diploids spontaneously. Each haploid yields >50 fertile diploid seeds through random chromosome segregation during meiosis. Haploid genetics has many applications: 1) New RIL sets can be made in only two generations. 2) Multiple mutant construction: it is feasible to homozygose 8 unlinked mutations in a single generation. 3) Gametophyte lethal mutations can be studied in a haploid plant. 4) Any nuclear genome can be combined with the cytoplasmic genomes of choice. 5) Tetraploid Arabidopsis can be converted into diploids to facilitate genetic manipulations. Lastly, we are using the principle of centromere-mediated genome elimination to engineer clonal reproduction (synthetic apomixis) in Arabidopsis. Crossing a mutant with diploid gametes (spo11 rec8 osd1, or MiMe) to a mutant with altered centromeres yielded up to 34% clonal progeny with the same heterozygous genotype as their MiMe parent. Thus, clonal reproduction in an Arabidopsis cross can be created by manipulating four conserved genes. This result raises hope that apomixis can eventually be engineered in crops, allowing vigorous hybrids to be propagated through seed.

Tomasz Czechowski

University of York, UK

Tomasz Czechowski is based at the University of York in the United Kingdom. He is the genotyping manager in the CNAP Artemisia Research Project, which is developing improved varieties of the medicinal plant *Artemisia annua*. This plant is currently the sole source of the leading anti-malaria drug artemisinin. The project uses the latest genetic techniques to accelerate and enhance traditional plant breeding and create new, non-GM varieties of Artemisia with increased artemisinin yields.
Tomasz has expertise in genotyping, TILLING, and quantitative reverse transcription (qRT)-PCR analysis. He was formerly part of the Molecular Plant Nutrition Group, at the Max Planck Institute of Molecular Plant Physiology, Golm, Germany. His research interest there was transcriptional regulation of nitrogen metabolism in *Arabidopsis thaliana*.

Abstract

Fast-track breeding for improved varieties of *Artemisia annua*

Tomasz Czechowski, Deborah A Rathbone, Godfree Chigeza, Tony R Larson, Yi Li, Teresa Penfield, Anne M Rae, Thilo Winzer, Dianna J Bowles and Ian A Graham.

Centre for Novel Agricultural Products, Department of Biology, University of York, York. YO10 5DD United Kingdom

Malaria is one of the world's greatest health problems, claiming almost one million lives every year and is a principal factor in preventing the development of some of the world's poorest countries. *Artemisia annua* is, at present, the sole source of artemisinin, the active ingredient in artemisinin combination therapies (ACTs), which are currently the most effective cure for malaria. Although synthetic methods of artemisinin production, currently under development, are anticipated to meet a substantial proportion of future requirements, plant production is expected to remain an essential source of supply.

The low (<1% of the leaf dry weight) or variable yield of artemisinin from *A. annua*, however, causes problems for the ACT supply chain and there are concerns over meeting the anticipated future demands for ACTs. New varieties are needed urgently to help meet the increasing demand for affordable malaria medicines. Relatively little work has been carried out to develop *A. annua* into a domesticated crop, but high phenotypic and genotypic variation in the plant indicate the potential for improvement.

As part of the CNAP Artemisia Research Project, we performed deep sequencing on the transcriptome of *A. annua* to identify genes and molecular markers for use in fast-track breeding. A detailed genetic map was constructed (Graham *et al*., 2010. Science 327:328–331), and QTL identified for a number of key traits. In addition, over 23,000 plants have been screened for traits such as artemisinin content. Together this has enabled us to generate a collection of potential high performers, which have entered into various mating strategies for the development of new hybrids. Experimental trials under glass and in the field have been performed and have identified a number of elite parent lines with good general combining ability. Assessment of genotypic marker data has allowed the selection of hybrid parents with a large genetic distance thus maximising heterosis in new hybrid lines. Marker assisted selection has also been performed to combine positive QTL effects for major breeding traits in the new hybrids. New hybrids are currently being field trialed in the regions where *A. annua* is grown commercially. Results obtained from intermediate and advance field trials show improved yield of some CNAP hybrids when compared to the industry leader Artemis and to the locally grown varieties. Hybrid seed production is under way to produce initial hybrids with stable improved yield.

For more information on this project, please visit:
http://www.york.ac.uk/org/cnap/artemisiaproject/index.htm

Mario Gils

Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Gatersleben, Germany

Mario Gils is head of the research group “Hybrid Wheat” at the IPK Gatersleben. The work of his group is focused on:

Development of split-gene systems for hybrid breeding and gene switch-control.
Site-specific recombination systems as tools for the controlled and precise manipulation of plant genomes
Development of a high-throughput-assay system for the measurement of meiotic recombination in plants
Wheat transformation technologies and tissue culture technologies

Abstract

Transgenic pollination control systems for hybrid plant breeding

Efforts in hybrid breeding have made this technology one of the main factors contributing to the substantial global rise in agricultural output over the last few decades. For hybrid breeding, an efficient pollination control (castration-) system is necessary to avoid the unwanted self-pollination or sib-pollination of the female parental line. Castration can be carried out through mechanically removing the male flower organs or by spraying chemical hybridising agents that prevent the development of active pollen. Genetic pollination control systems are either based on mutated mitochondrial DNA leading to cytoplasmic male sterility (CMS) or else, nuclear-encoded genes or transgenes may lead to pollen ablation.

With the revolutionary development of genetic engineering methods, new options became available for the production of hybrids in various crops. In this session, biotechnological concepts for pollination control are discussed. In particular, a novel system is suggested for the industrial production of hybrid wheat. It is based on splitting a tapetum-expressed *barnase* gene, which causes male-sterility by pollen ablation, into two fragments. Eventually, it allows growing the female crossing partners as male-sterile plants, whereas the hybrid progeny is fully fertile. The concept may have the potential for a breakthrough-technology that will help to create a highly efficient, reliable and environmental-friendly method for hybrid seed production in wheat.

Martijn Gipmans

BASF Plant Science, Berlin, Germany

Martijn Gipmans studied horticulture at Wageningen University. After completing his PhD at the Max-Planck-Institute for Molecular Plant Physiology he joined BASF Plant Science in 2001. He has held several positions in research at BASF Plant Science in Ludwigshafen and at metanomics in Berlin. Since 2007 he is working in the area of government relations for BASF Plant Science.

Abstract

From basic research to products: Innovation at BASF Plant Science

BASF Plant Science forms an industry leading research and technology platform for plant biotechnology employing approximately 700 people. With subsidiaries such as CropDesign and metanomics and in an international research and technology network with universities and cooperation partners, BASF develops new traits for a more efficient agriculture, better and healthier nutrition and production of renewable resources. Projects include plants with improved yield, plants that can better resist environmental factors such as drought or disease, plants with a higher content of Omega-3 fatty acids for preventing cardiovascular diseases and plants with a higher nutritional value for animals.

Yuri Gleba

Icon Genetics GmbH, Halle, Germany & Nomad Bioscience GmbH, Munich, Germany

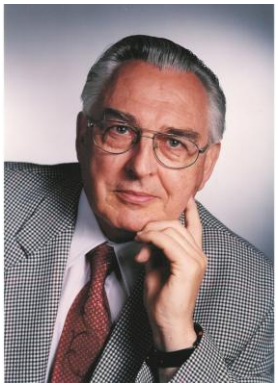
Dr. Gleba has over 30 years of research and management experience in plant genetics and biotechnology. (M. Sc., Kiev University, 1971; Ph.D., Institute of Botany, Academy of Sciences of Ukraine; D.Sc., Leningrad University, 1980).
Dr. Gleba's pioneering research in plant genetics, physiology and biotechnology was published in more than 200 research papers, books and over 30 patent families, and has earned the respect of the international scientific community as is evidenced by his election to the World Academy of Arts and Science (Rome), the European Academy (*Academia Europaea*, London), the National German Academy *Leopoldina* (Halle), the National Ukrainian Academy of Sciences (Kiev), the Lithuanian Academy of Science (Vilnius) and the Bavarian Academy of Sciences (Munich). He also received numerous international and national awards and prizes, including Koerber Prize (Hamburg), A. von Humboldt Prize (Bonn), USSR State Prize, State Prize of Ukraine (Kiev), etc.
In 1999, Dr. Gleba founded Icon Genetics, Princeton/Munich/Halle, a plant biotechnology company group; he has been serving since its inception as its CEO. Under his leadership, Icon has developed multiple plant biotechnologies, including the magnICON® transient technology that has been brought to a commercial level and cGMP compliance and is being used to support clinical trials of the product candidates developed by Icon/Bayer. Icon's IP portfolio in plant biotechnology currently includes over 300 issued patents representing 42 patent families of patents/applications. He also co-founded two other companies, Phytomedics Inc., USA, and Nomad Bioscience GmbH, Germany. Since 2009, he is also CEO of Nomad Bioscience GmbH.

Abstract

New uses for new plants

Plant biotechnology as a commercial process is a reality. During 1996-2010, the global GM crop area has grown for 15 consecutive years and has reached 120 million hectares. Such numbers undoubtedly reflect benefits enjoyed by the various participants in the business, including 10 or so million farmers. However, GM crops grown at present were modified to facilitate crop production, thus, they do not benefit the consumers. Promises to create engineered plant hosts-producers of novel materials, medicines and improved foods made by plant biotechnologists did not materialize so far. It is safe to predict that all this and more will be 'delivered' during the 21st Century, but the timing will depend on our ability to develop both the sound science leading to new products as well as the new engineering processes that satisfy the requirements of an exploiter (technical efficiency, compliance with business requirements), a government regulator (regulatory compliance, safety, sustainability), and an end user. The products most likely to reach the market in near future are high-value proteins such as biopharmaceuticals as well as new biomaterials. Several biopharmaceuticals including plant-made 'biosimilar' glucocerebrosidase, interferon alpha, insulin, flu vaccines have reached clinical trials, many more are nearing that stage. The purpose of the presentation is to review the rapid progress in this exciting area of plant biotechnology.

Rudolf Hagemann



Max Planck Institute for Breeding Research, Cologne, Germany
(Emeritus Professor)

1950 – 1955 Study of biology and genetics, University Leipzig and Halle
1955 Diploma in biology, University of Halle
1955 – 1958 Research work for the dissertation in the Institute for Research in Cultivated Plants, Gatersleben, Supervisor Prof. Hans Stubbe
1958 Doctor's degree (Dr.rer.nat.) of the Martin-Luther-University of Halle
1958 - 1967 Postdoctoral research work in the Institute of Research in Cultivated Plants Gatersleben
1966 Habilitation in Genetics (Dr.rer.nat.habil.) University of Halle
1967- 1994 Professor of Genetics and Director of the Institute of Genetics. Faculty of Natural Sciences, Martin-Luther-University in Halle
1990, 1995, 1997 Guest Professor of Molecular Genetics at the University of Salzburg, Austria, during the respective summer semesters
1994 – 1996 Professor of Genetics, Max-Planck-Society (MPI for Breeding Research Cologne)

Research Activities: Genetics and Molecular Biology of plastids and mitochondria,
Genetic instability: paramutation in tomato,
History of genetics

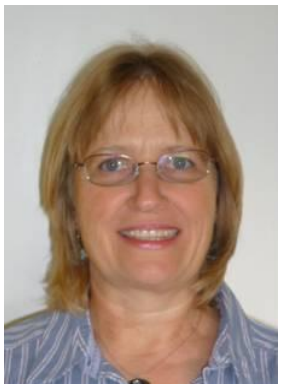
Publications: 5 books and 225 articles in scientific journals and books

Abstract

Important steps in the establishment of plastid genetics in higher and lower plants

1. Start of extranuclear genetics in 1909
2. The foundation of plastid genetics
   - The position of Erwin Baur
   - The position of Carl Correns
3. Development of the theory of plastid inheritance by Otto Renner
   - Hybrid plastid deficiency in Oenothera and other genera
   - Theory of plastid inheritance
   - Coworkers of Renner: W. Stubbe, F. Schötz
4. Contributions of Julius Schwemmle in Oenothera genetics
5. International investigations in the field of plastid genetics (in the time period 1915-1965)
   - Research workers in Great Britain, Denmark, Sweden, Japan
   - USA: Morgan, Rhoades, Ruth Sager
6. The proof of specific plastid DNA (1961-1965)

Inga Isabel Hitzeroth



University of Cape Town, South Africa

I grew up in Namibia and studied in South Africa at the University of Cape Town in Cape Town from 1980 - 1986. I did my undergraduate studies in Microbiology and Biochemistry and my PhD on hake population genetics while working for Sea Fisheries in Cape Town. My post-doctoral years I spent at medical school at UCT working on gonadotropin releasing hormone. In 2000 I started to work in Prof Rybicki's group in a then very new and novel field of expression of viral proteins in plants.
We are specifically working on production of vaccine candidates against Human papillomavirus (HPV) and development of second generation vaccines that will be cheaper by production in plants and will protect against more than one type of HPV. HPV is the cause of cervical cancer the second most prevalent cancer in women in developing countries. We also express rotavirus proteins in plants. This virus causes severe diarrhoea in children and a great loss of lives in the developing world.
Another project I am involved in is the production of a vaccine against Beak and Feather Disease Virus (BFDV). BFDV causes Psittacine Beak and Feather Disease (PBFD) in all psittacine birds (parrots). It is a highly infective and debilitating disease and to date no specific treatment exists to protect against it. BFDV affects both captive and wild populations of parrots and it is a contributing factor to the decline of wild populations and especially endangered species such as the South African Cape Parrot.
Overall the research that I have been involved in over the last ten years has come a long way from just being an idea to produce viral proteins in plants to becoming a reality with proteins being expressed in high enough levels to make it feasible to produce them as vaccines.

Abstract

Plant derived vaccines "Out of Africa"

Inga I Hitzeroth[1], Ann Meyers[1] and Edward P Rybicki[1,2]

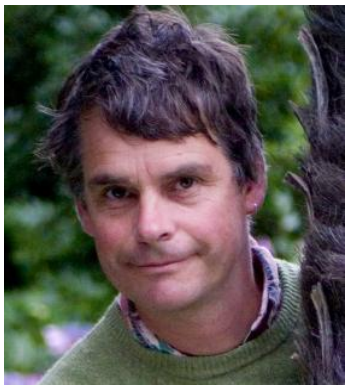
[1]Department of Molecular and Cell Biology, University of Cape Town, Cape Town, South Africa; [2]Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa

In general the costs associated with the production of new generation vaccines make them prohibitively expensive in developing countries. Plant produced vaccines are a novel and exciting development as plants provide a promising cheaper alternative to mammalian, yeast and bacterial cell culture expression systems. Plants are especially suitable as they do not require large and expensive production facilities, they are free of human pathogens, and are capable of post translational modifications absent in bacterial systems.

Plants can be efficient production hosts for cheaper vaccines if expression levels are sufficiently high, and the purification challenge is properly addressed. Our group has systematically investigated the barriers to high level expression of various viral antigens suitable for use as prophylactic and therapeutic vaccines for humans and animals. We have utilised a combination of transient expression in *Nicotiana benthamiana* via *Agrobacterium tumefaciens* infiltration, codon optimisation and intracellular localisation of expressed proteins in order to obtain high levels of expression in plants.

We have expressed a number of proteins in plants from different human and animal viruses: Human papillomavirus (HPV) coat- and onco-proteins, Avian influenza virus H5 haemagglutinin proteins, Rotavirus coat proteins and Beak and feather disease virus (BFDV) coat protein. These viruses cause very different diseases: HPV is associated with cervical cancer, avian influenza can cause an influenza pandemic in birds and humans, Rotavirus infection plays a major role in causing severe gastroenteritis and BFDV causes psittacine beak and feather disease (PBFD) which is a highly contagious and debilitating viral disease that affects parrots and other psittacine birds. What is in common among all of these, however, is that they are important diseases for which cheap vaccines are needed. Manufacture of these vaccines in plants provides the appropriate and viable method of production.

Noel Kingsbury



Plants, gardens, landscape, environment - *design, consultancy, media, education*
Associate - Department of Landscape, University of Sheffield, UK

Montpelier Cottage
Brilley
HEREFORD
HR3 6HF
ENGLAND

Dr. Noel Kingsbury is recognised internationally as a leading innovator in horticulture and landscape through his many books and journalism. His main area of interest and expertise is nature-inspired planting design, and the application of plant ecology to landscape design and garden management. He also writes and speaks about the culture and politics of gardens and about global agriculture. He is an associate of the Department of Landscape at the University of Sheffield.

www.noelkingsbury.com
Read my blog at: http://noels-garden.blogspot.com

Abstract

A genetic cornucopia - plant breeding through history

Plant breeding has been an essential prerequisite for human progress, allowing expanding populations to be fed, but also clothed - with plant fibres such as cotton, and increasingly to be supplied with plant-derived industrial raw materials. Plants grown for decorative or religious purposes have also been a strong component of many cultures and their breeding is now central to a major global industry.

The story of plant breeding is outlined as a series of distinct stages of a developing relationship with the plant world intimately linked to wider stages of human historical development: cultural, economic, philosophical and political.

Unconscious selection of plant genetic material was one of the crucial steps in the development of agriculture. This unconscious selection dominated human sifting of plant genetic material for millennia, and was often expressed spiritually. Despite being unconscious, major advances were made, with maize the most dramatic example. A long era of landrace-based arable agriculture followed; genetic improvements in crops often followed hybridisation through trade bringing together formerly separated taxa.

Conscious selection began to be articulated during the Enlightenment era, although non-European cultures had also begun to make progress in this direction too. Active breeding only became possible once the scientific bases of plant reproduction were understood; plant breeding was indeed intimately involved with the discovery of the principles of plant reproduction and heredity. Human, rather than divine, agency had to be accepted in order for progress to be seen to be possible. Deliberate hybridisation was accepted slowly in the 19th century with some indications that it was seen as immoral by religious figures (there are analogies here with current concerns over GM crops). Mendel's discovery of the principles of heredity enabled greater efficiency and productivity to be made in plant breeding; Mendelian principles were however not immediately or universally accepted – adoption was rapid in the USA, but slower in much of Europe, with attitudes in Germany an interesting precursor of many of the conflicts over the adoption of agricultural innovation in developing countries today.

The 20th century saw a cornucopia of technologies in plant breeding which have progressively expanded sources of genetic variation and the ability to hybridise between ever less closely-related species. Plant genetics has played a vital role in the modernisation of agriculture across the globe, resulting in vastly increased yields and in keeping famine at bay.

Olaf Kruse

University of Bielefeld, Germany
Chair for Algae Biotechnology and Bioenergy

Information about Prof. Kruse can be found here:
http://www.uni-bielefeld.de/biologie/Algenbiotechnologie/kruse/

Abstract

Title and abstract were not available when this abstract booklet went to press.

Cathie Martin

John Innes Centre, Norwich, UK

Cathie Martin is a group leader at the John Innes Centre, the leading plant research institute in Europe and Professor at the University of East Anglia. She has characterized the enzymes involved in starch biosynthesis and elucidated how they determine starch structure and functionality, in potato. Recently she has been co-ordinating frontier research into how diet can help to maintain health and reduce the risk of chronic disease, and how crops can be fortified to improve diets. She is Editor-in-Chief of *The Plant Cell*, the highest ranking journal for primary research articles in plant biology.

Abstract

Engineering phenylpropanoid production for healthy foods

The past 20 years has seen an enormous rise in publicity about super foods that promote health and reduce the risk of cardiovascular disease, cancer and age-related degenerative diseases, related specifically to the metabolic syndrome. These claims are supported by evidence from cell studies, animal feeding trials, human intervention studies and epidemiological studies. However, despite all the positive messages about the value of eating fruit and vegetables (the 5-aday program has been running for 25 years) the numbers of people meeting these dietary recommendations in the US remains below 25% of the population, numbers are falling, and chronic diseases, especially those associated with obesity and the metabolic syndrome, are reaching epidemic proportions in Western societies.

There is a need to engineer high levels of protective bioactives in the foods that people actually do consume, to help combat this rise in chronic diseases. Most attempts at engineering the levels of bioactives have focused on increasing the activity of key, rate-limiting steps, but such strategies usually result in only modest improvements in flux to bioactive end-products. Use of transcription factors to up-regulate entire pathways of plant secondary metabolism is a far more effective strategy and results in food material with very significantly elevated levels of health-promoting bioactives. While such improvements may, in part, be achievable for some crops through selective breeding, genetic modification offers bigger improvements because it can overcome limits in the natural variation available in transcription factor specificity and activity. Use of genetically improved foods in animal feeding studies with models of tumorigenesis has revealed that protection is afforded by diets enriched in high bioactive foods. Such health-promoting foods will offer consumers tangible improvements in the products available to them, and have the potential for public approval of genetically improved plant varieties and foods derived from them, in Europe.

Kärin Nickelsen

University of Bern, Switzerland

Kärin Nickelsen is doing teaching and research as a "Assistenzprofessorin" in History and Philosophy of Biology at the University of Bern, Switzerland. She studied Biology in Göttingen (with a major in Plant Sciences and minors in Microbiology and History of Science) and graduated with a Diploma in 1999. Kärin Nickelsen then switched fields and began doctoral studies in History and Philosophy of Science. Her dissertation thesis, finished in 2002, was on the content and function of plant drawings around 1800 (published with Springer as *Draughtsmen, Botanists and Nature: The Construction of Eighteenth Century Botanical Illustrations*), while the systematic focus of her recent projects is the historical and philosophical reconstruction of experimental research episodes in the nineteenth and twentieth centuries. Kärin Nickelsen's habilitation thesis (finished 2010) deals with the development of biochemical and biophysical models of photosynthesis (*Of Light and Darkness: Modelling Photosynthesis 1840-1960*). She was awarded several prizes for her research and is looking forward to an enjoyable workshop in September.

Abstract

In pursuit of a pathway: Collective modelling in early photosynthesis research

Photosynthesis is, arguably, the most important biological process on earth, and the way organisms accomplish this task has intrigued scientists for centuries. The first tentative (and rather simplistic) ideas were developed by organic chemists around 1850, but it was only from the 1920s onwards that noticeable progress was made in understanding the mechanism. In particular, great strides were made after 1945, and by 1960 an elaborate photosynthesis model at a molecular level had been established, including the Z-scheme of the light reactions and the Calvin-Benson-Cycle.

This paper concerns itself with the earliest attempts made in the nineteenth century to reconstruct the biochemical processes of photosynthesis. The episode is therein interpreted as a case in point of the collective construction of causal models in science. Three heuristics, which are very prominent in this type of research, are highlighted: the building block strategy, the principle of plurality and the attitude of constructive research opportunism.

I shall start with presenting the two main proposals that were advanced by German chemists to explain photosynthesis: Justus Liebig's organic acid model of 1843 and the formaldehyde model proposed by Adolf von Baeyer in 1870. Classic philosophy of science would have expected that a decision was being made between these two rival hypotheses, for which the scientists applied one of the standard criteria of theory choice, such as theoretical parsimony or explanatory power. But the scientists of the time did nothing along these lines. Instead, the set of options was multiplied, since several hybrid versions of the two original proposals were developed, all of which mixed a different set of conceptual building blocks. Many of these versions were pursued for a surprisingly long time, even though some of them did not appear at all promising – researchers seemed to consider it worth their while to examine all the possible options. Finally, it is argued that every one of these models had a definite focus on one specific aspect of the process that can be explained by referring to the individual background of those scientists who proposed the models. In this early phase of modelling photosynthesis, most, if not all, of the people contributing to the research did so on a part-time basis: their contributions to photosynthesis research were a by-product of the other work that they were pursuing, and this determined their specific modelling approach.

Richard Sayre

Director, BioCassava Plus, Phase I (2005-2010)
New Mexico Consortium
Los Alamos, New Mexico, USA

Dr. Sayre received his Ph. D. from the University of Iowa in 1978, and did post-doctoral work at Harvard University in Molecular Genetics. From September 2008-2011, he served as the Director of the Enterprise Rent-A-Car Institute for Renewable Fuels at the Donald Danforth Plant Science Center in St Louis. In 2009, Dr. Sayre became Director of the Center for Advanced Biofuel Systems, a DOE-Energy Frontier Research Center focusing on metabolic engineering of algae and camelina for oil production. Dr. Sayre is also the Scientific Director of the National Alliance for Advanced Biofuels and Bioproducts, a DOE-sponsored project on algal biofuels. He also served as the Director of the BioCassava Plus (2005-2010) program funded by the Bill and Melinda Gates Foundation. Prior to moving to the Danforth Center, Dr. Sayre was a Professor in the Department of Plant Cellular and Molecular Biology at the Ohio State University and served six years as the departmental chair. Dr. Sayre is currently Chief Technology Officer for Phycal Inc, an algal biofuels company. Dr. Sayre also serves on the editorial board of *Photosynthesis Research* and *Frontiers in Plant Physiology.* He spent the spring of 2007, at the University of Sao Paulo as a Fulbright Scholar in the Department of Chemistry and Biochemistry working on microalgal biotechnology. From 2005-2008, Dr. Sayre was the College of Biological Sciences Distinguished Professor, and in 2006, Dr Sayre was elected as an honorary member of Phi Beta Kappa. He is the author of over 90 publications in a diverse range of the biological sciences ranging from the biophysics of photosynthesis, to the bioremediation of toxic wastes, quorum sensing, and crop biofortification. Dr. Sayre serves on the Board of Directors of Logos Technologies in Cleveland. In December 2008, *Nature* identified Dr. Sayre as one of “Five Crop Researchers Who Could Change the World” (*Nature* 456: 563-569, 2008) based on the accomplishments of the BioCassava Plus team. In September, 2011, Dr. Sayre moved to Los Alamos National Labs to develop advanced biofuel systems for sustainable energy production.

Abstract

Improving cassava for nutrition, health, and sustainable development

BioCassava Plus is a multidisciplinary team of scientists developing a more nutritious cassava for sub-Saharan Africans. Inadequate nutrition is the single greatest cause of excess mortality, morbidity and suffering in sub-Saharan Africa. The objective of BioCassava Plus is to reduce malnutrition by providing complete nutrition in a single staple crop, cassava (*Manihot esculenta*). Over two hundred and fifty million Africans rely on the starchy root crop cassava as their staple food. Cassava roots, however, have the lowest protein:energy ratio of all the world’s major staple crops. A typical cassava-based diet provides less than 30% of the minimum daily requirement for protein and only 10-20% of the required amounts of iron, zinc, vitamin A and vitamin E. BioCassava Plus employs modern biotechnologies to improve the health of Africans through development and delivery of novel cassava germplasm with increased nutrient (zinc, iron, protein and vitamins A and E) levels. Effective delivery of biofortified cassava will be achieved by linking optimal nutritional traits with improved post-harvest durability of the storage roots, elimination of toxic cyanogenic glycosides, and elevated resistance to viral disease; characteristics required to provide ample amounts of foodstuffs and incentives for farmers to adopt and sustain biofortified cassava cultivars. Currently, proof-of-concept has been achieved for each of our target objectives. Transgenic plants are currently in field trials in Puerto Rico and the first confined field trail for any transgenic crop in Nigeria is underway. In phase II, BC+ will develop farmer-preferred cassava cultivars with stacked traits for enhanced pro-vitamin A, iron, protein and virus resistance for Nigeria and Kenya.

Raphael Scholl

University of Bern, Switzerland

Dr. Raphael Scholl earned degrees in Medicine and History and Philosophy of Science at the University of Bern, Switzerland. He now works on questions in the history and philosophy of biology and medicine.

Abstract

Oxidative phosphorylation and the logic of discovery

Raphael Scholl*, Rita Hidalgo Staub[y] and Kärin Nickelsen[z] April 20, 2011

Historians and philosophers of science have written extensively about the confirmation of the chemiosmotic mechanism of oxidative phosphorylation. When the mechanism was first proposed by the British biochemist Peter Dennis Mitchell in 1961, it was met with considerable skepticism. However, over the course of little more than a decade, the mechanism was experimentally validated and came to be widely accepted by the biochemical community. In 1978, Mitchell was awarded the Nobel Prize in Chemistry for the achievement. Philosophers of science have been trying to understand in detail how the choice between Mitchell's chemiosmotic mechanism and competing hypotheses was made on the basis of experimental evidence. The project is both descriptive and normative. Descriptively, it matters why the biochemical community actually accepted the mechanism around 1974. Normatively, we also wish to know when and why it was justified to accept the mechanism. Moreover, do the descriptive and the normative accounts match? In contrast to the question of confirmation, the path by which Mitchell came to formulate his mechanism has received scant attention from philosophers of science (although it has been considered in historical accounts). In the present paper, we wish to rectify the imbalance by taking a closer look at Mitchell's process of hypothesis generation. Based on our own and previous historical research, we trace the roots of the components from which Mitchell constructed his theory. In particular, Mitchell's own research on membrane transport was pivotal. We will evaluate whether the case study suggests any generalizable insights into how new scientific hypotheses are generated.

*History and Philosophy of Science, University of Bern, Länggassstr. 49a, CH-3012 Bern, Switzerland. Author e-mail: raphael.scholl@philo.unibe.ch.
[y]Department of Applied Physics, University of Bern, Sidlerstr. 5, CH-3012 Bern, Switzerland. Author e-mail: rita.hidalgo@iap.unibe.ch.
[z]History and Philosophy of Science, University of Bern, Sidlerstr. 5, CH-3012 Bern, Switzerland. Author e-mail: kaerin.nickelsen@philo.unibe.ch.

Friedrich Steinle

Technical University of Berlin, Germany

Friedrich Steinle is professor of history of science at the Technische Universität Berlin. His research focuses on the history and philosophy of experiment, on the history of electricity and magnetism, on the history of colour research, and on the dynamic of empirical concepts in research practice. His books include Newton's Manuskript 'De gravitatione' (1991) and Explorative Experimente: Ampère, Faraday und die Ursprünge der Elektrodynamik (2005), he is co-editor of Experimental Essays - Versuche zum Experiment (1998, with M. Heidelberger), of Revisiting discovery and justification. Historical and philosophical perspectives on the context distinction (2006, with J. Schickore), and of Going Amiss in Experimental Research, (2009, with G. Hon and J. Schickore)

Abstract

How do we learn from experiments? Epistemological studies of experimental practice.

Philosophers of science have long held the view that learning from experiment works by testing of hypotheses or even theories. However, the practice of research looks different. Indeed, recent studies of experimental practice, both historical and present-day, both in physical and biological sciences, have shown that there is a variety of uses of experiments that lead to new knowledge. While there have always been well-designed experiments that aimed at hypotheses testing, much experimental research takes place in situations in which there is just no theory or even hypotheses around that is to be tested. In my talk, and starting from historical cases, I shall discuss those ways of gaining knowledge from experiments.

Mark Tester

University of Adelaide and Australian Centre for Plant Functional Genomics, Australia

Mark Tester is Professor of Plant Physiology in the School of Agriculture, Food & Wine, University of Adelaide, Director of the Australian Plant Phenomics Facility and chair of the Node Management Group of the Australian Centre for Plant Functional Genomics Pty Ltd. Mark led the establishment of the APPF, a $55m organisation that develops and delivers cutting-edge phenotyping facilities for plant science, including The Plant Accelerator, an innovative 4,500 m^2 plant growth and analysis facility. He also leads a large academic research group ($9m in the past 7 years) to understand salinity and drought tolerance, and how to improve this in crops such as wheat.

Some recent relevant publications:

Rivandi J, Miyazaki J, Hrmova M, Pallotta M, **Tester** M, Collins NC (2011) A SOS3 homologue maps to HvNax4, a barley locus controlling an environmentally-sensitive Na^+ exclusion trait. Journal of Experimental Botany **62:** 201–1216 [with cover image]

Cotsaftis, O., Plett, D., Johnson, A.A.T., Walia, H., Wilson, C., Ismail, A.M., Close, T.J., **Tester**, M. & Baumann, U. (2011) Root-specific transcript profiling of contrasting rice genotypes in response to salinity stress. Molecular Plant **4:** 25–41

Roy, S.J., Tucker, E. & **Tester**, M. (2011) Genetic analysis of abiotic stress tolerance in crops. Current Opinion in Plant Biology **14:** 1-8

Tester, M. & Langridge, P. (2010) Breeding technologies to increase crop production in a changing world. Science **327:** 818-822 (invited review)

Berger, B., Parent. B. & **Tester**, M. (2010) High throughput imaging to study drought responses. Journal of Experimental Botany **61:** 3519-3528

Plett, D., Safwat, G., Shirley, N., Møller, I.S., Gilliham, M., Roy, S.J., Jacobs, A., Johnson A. & **Tester**, M. (2010) Improved salinity tolerance of rice through cell type-specific expression of AtHKT1;1. PLoS ONE **5**(9): e12571

Møller, I.S., Gilliham, M., Jha, D., Mayo, G.M., Roy, S.J., Coates, J.C., Haseloff, J. & **Tester**, M. (2009) Shoot Na^+ exclusion and increased salinity tolerance engineered by cell type-specific manipulation of Na^+ transport in Arabidopsis. Plant Cell **21:** 2163–2178

Munns, R. & **Tester**, M. (2008) Salinity tolerance in higher plants. Annual Reviews of Plant Biology **59:** 651-681

Abstract

Understand and engineering salinity tolerance in crop plants

Genetics and genomics are powerful tools for gene discovery, and increasingly efficient transgenic technologies are generating large numbers of GM crop plants. However, gene expression often needs to be manipulated in more targeted ways by, for example, activating genes in only specific cells or at specific times. Using salinity as an example, it will be shown how gene over-expression in specific cells in the root can increase salinity tolerance, including in rice.

The genotyping of mapping and mutant populations is now highly efficient. However, the ability to quantitatively phenotype these populations are now commonly limiting forward progress in plant science. The increasing power of digital imaging and computational technologies offers the opportunity to relieve this phenotyping bottleneck. The Plant Accelerator™ is a 4500 m^2 growth facility that opened this year and which provides -omic-scale phenotyping of large populations of plants. New genetic loci for components of salinity tolerance discovered using this exciting new approach will be presented.

The application of these technologies provides opportunities to significantly increase abiotic stress tolerance of crops, and thus contribute to increasing agricultural production in many regions.