

US-EC Task Force on Biotechnology Research
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— ABSTRACTS —

INTRODUCTION

The Need for a Global Long Term Strategy in Plant Biotechnology

MARC ZABEAU

Department of Plant Systems Biology
Ghent University – VIB
Belgium

While the genomics revolution has considerably expanded our understanding of plant biology, and will continue at an ever increasing pace, we are only now starting to fully appreciate the complexity of the challenges ahead, namely translating this knowledge into added value in agriculture. The apparent paradox of plant biotechnology is that the resources currently available for research – both public and private - amount to only a fraction of that of medical/ pharmaceutical research, while its scientific challenges are comparable if not greater. Not only is the field dealing with a broad diversity of plant species, the more rapid evolution of their genomes complicates the translation of molecular knowledge across species.

Despite the apparent diversity of applications of plant biotechnology around the world, the “grand” objectives of global agriculture – improved yield and quality, sustainability and diversification of products – are strikingly universal. The resources required for genomics and large scale biology programmes often exceed the budgets of national funding agencies, including those of the wealthier developed countries. Consequently, there is a rational and economic basis to start reflecting on coordinating plant biotechnology research on a global scale, and for setting the stage for a global long term strategy. The potential benefits of coordinating research internationally are clearly illustrated by recent successful examples. For instance, the International Solanaceous Genome Initiative – a grass roots academic initiative – secured the funding for sequencing the tomato genome and for jump starting a global solanaceous genome programme. Another example is the European Technology Platform “Plants for the Future” – a joint academia-industry initiative. This initiative recently articulated a 20-year vision and a strategic research agenda for plant biotechnology reflecting a consensus between the different stakeholders, and is positively influencing the climate and the financial conditions for plant science research in Europe.

What could be achieved with a global long term strategy? First and foremost, a constructive dialogue between scientists across all fields – model and crop species, disciplines, areas of biology and fundamental and applied science – should result in a consensus on global research priorities and goals. Second and equally important, a global strategy will undoubtedly contribute to improve the perception of the importance and the impact of plant biotechnology a *conditio sine qua non* to secure the funding necessary to realize the ambitious goals. Finally, a global strategy developed in truly participative manner offers the best guarantee for the effective translation of the immense scientific knowledge that will be accumulated in the coming decades across different plant species, between the developed and the developing countries as well as into the agricultural practice.

In conclusion, the present workshop presents a unique opportunity to start articulating a global long term strategy in Plant Biotechnology.

HIGH THROUGHPUT FUNCTIONAL GENOMICS**Exploring Chemical Space in the Plant World**

NATASHA RAIKHEL

Center for Plant Cell Biology and Botany and Plant Sciences Department
University of California, Riverside
Riverside, CA 92521

Bioactive chemicals have a long history of helping plant physiologists unravel mechanisms, including those involving: inhibitors of GA biosynthesis, inhibitors of ethylene action, inhibitors of auxin transport, cytoskeleton-disrupting drugs, and inhibitors of GDP-GTP exchange proteins, just to name a few. However, this approach has also met with strong criticism due to the complexities associated with understanding the action mode of compounds at the molecular level. This is one reason why drug companies must advertise the side effects of the drugs they sell. What has motivated biologists to revisit their interest in small molecules? While a little more than ten million pure compounds are known in chemical literature, the potential chemical diversity (defined as the number of unique chemical structures) of compounds composed of carbon, hydrogen, nitrogen, oxygen, sulfur, phosphorous, and the halogens (the organic chemists periodic table) of molecular weight <1000 likely exceeds 10^{60} . The compounds that have thus far been tested for effects on plants are therefore only a minute fraction of the structural possibilities. The development of combinatorial and automated techniques for synthesizing novel compounds brought forth significant enhancement in the productivity of chemists and makes the likelihood of synthesizing molecular libraries that are representative of chemical space much greater. These advances allow for the identification of chemicals that specifically disrupt a process or the function of a protein. Once these chemicals are identified, we can combine their use with genetic screens to identify genes involved in the same process. The use of unbiased libraries of diverse small molecules will allow plant biologists to discover numerous new bioactive molecules valuable for studying the function of uncharacterized plant genes. Importantly, when combined with Arabidopsis functional genomics, chemical genomics is powerful for the effective and efficient analysis of regulatory networks underlying a specific process. The chemical genomics approach can address loss-of-function lethality and gene redundancy and allow instantaneous, reversible, tunable, and conditional control of a phenotype. Well-characterized bioactive chemicals and their targets identified in Arabidopsis can be used in non-model species to improve agronomic traits and increase crop value.

HIGH THROUGHPUT FUNCTIONAL GENOMICS**Interactome Networks**

MARC VIDAL

Associate Professor, Department of Cancer Biology
Director, Center for Cancer Systems Biology
Dana-Farber Cancer Institute
Associate Professor of Genetics, Harvard Medical School
Boston, MA

Despite the considerable success of molecular biology to understand diseases such as cancer, many fundamental questions remain unanswered. Most importantly, since the majority of gene products in the cell mediate their function together with other gene products, biological processes should be considered as complex networks of interconnected components. In other words, for any normal biological process, or any disease mechanism, such as cancer, one might consider a “systems approach” in which the behavior and function of such networks are studied as a whole, in addition to studying some of its components individually. The draft of the human genome sequence is likely to help such a transition from molecular biology to systems biology.

Our laboratory uses a model organism, the nematode *C. elegans*, to study the role of protein networks in development and, doing so, develop the concepts and technologies needed for a transition to systems biology. Our goals are to:

- i) generate protein-protein interaction, or 'interactome', maps for *C. elegans* networks involved in development,
- ii) develop new concepts to integrate such interactome maps with other functional maps such as expression profiles (transcriptome), global phenotypic analysis (phenome), localization of expression projects (localizome), etc.... and
- iii) use such integrated information to discover novel network properties.

HIGH THROUGHPUT FUNCTIONAL GENOMICS**Sequences and Experiments**

MARK STITT

Max Planck Institute of Molecular Plant Physiology (Golm)

14476 Potsdam-Golm, Germany

Plant research is funded at a lower level than human or animal research, but has to tackle a wide range of species including crops but also species and life forms that play an important role in diverse ecosystems. The chemistry of nucleic acids is relatively simple and generic, major advances have already been made and more can be expected. As sequencing becomes cheaper and cheaper and more sequencers want work to do, technology will deliver sequences much faster than it is possible to collect even rudimentary experimental information about the roles of genes. There is an urgent need for further experimental strategies to analyse gene function, alone and in interactions with other genes. Transcript profiling is important, but has its obvious limits, as do the other 'omics. These need to be extended by new strategies to analyse post-transcriptional, translational and post-translational regulation, and the impact of the latter on the biological activities of proteins. We require multiple phenotyping platforms at all levels of plant function from molecules through to whole plants and from them to small-scale ecosystems. These will need to be linked together via bioinformatics, whereby different strategies will be needed to link different sorts of parameters.

HIGH THROUGHPUT FUNCTIONAL GENOMICS**Understanding Natural Genetic Variation**

DETLEF WEIGEL

Max Planck Institute for Developmental Biology
Tübingen, Germany
and Salk Institute
La Jolla, CA

During crop domestication, humans have selected many alleles that positively influence traits such as plant architecture, yield, disease resistance etc. In plants such as maize, it is commonly thought that current gains in yield are mostly achieved by selecting new mutations, rather than making use of standing variation present in wild populations. Recent studies, such as those that Dani Zamir will discuss, clearly indicate that wild germplasm may contain alleles with considerable impact on modern varieties. A barrier to fully exploiting this fact is our poor understanding of the extent of genetic variation in any species, be it domesticated or wild species. I will discuss our efforts to understand sequence variation in the reference plant *Arabidopsis thaliana* on a whole-genome level. Ultimately, we would like to understand which genes that are known from laboratory studies to impact a certain trait are being used by nature to modulate that trait, and whether the spectrum of genes being used in different species is similar. This will give important insights into which genes one should focus on during conventional breeding programs or in transgenic approaches.

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY**Achieving the Virtual Plant**

GLORIA CORUZZI
Department of Biology
New York University
100 Washington Sq. East
New York, N.Y. 10003

At the core of all plant species there is a finite digital code: the genome. The challenge for the next 10 years will be to discover all the genes, determine their function, and their regulatory and physical interactions. A transforming 20 year goal will be to build an *in-silico* model of the plant, encompassing all these levels of organization that can be used to predict responses of all systems and to rationally engineer plants for agronomic benefit. To achieve this goal, we need to foster and fund the collection of high-throughput experimental data. On a first order level (next 5 years) we need to catalog and collect quantitative data on DNA, RNA and protein interaction networks. A second level (10 years), we need to collect metabolic data, protein modification states, and enzyme levels at the cellular/organellar resolution level. On the bioinformatics end, we must develop tools and databases that combine heterogeneous genomic datatypes, and develop of new software that depicts physical and regulatory relationships among gene products in a dynamic fashion. Because the experimental treatment space is infinite, we need to foster community efforts to collectively cover large experimental spaces so as to predict network states under untested conditions. Finally, the plant community must coordinate our genomic and bioinformatic activities with other model organism genome efforts, to enable the development of approaches that are agnostic to the source of the genomic data- between plant species, and across phyla.

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY**Bioinformatics: Current Limitations and Insights for the Future**

SEUNG YON RHEE

Carnegie Institution, Department of Plant Biology
260 Panama St.
Stanford, CA 94305

Biology has undergone several rounds of transformation in terms of the research paradigms it has operated, ranging from theoretical to experimental, in the pursuit of discovering new molecular mechanisms that regulate biological form and function. In the decades to come, it will take on another transformation to understand the modes of action of biological processes at the organism level, where computational models of systems-wide properties could serve as the basis for prediction of biological behavior, leading to new experimentation and discovery. In order for this transformation to occur, it is essential to standardize and improve the description, curation, processing, integration and interpretation of the massive amounts of biological data, both high and low-throughput data, by the life science research community. Databases have been a standard way of managing and processing large amounts of information in diverse arenas including academic disciplines, industry, and government sectors for many years. The use of database technologies has drawn the attention of a subset of the biological community, but its use has been limited to a small sector of the community - mainly those involved in the organization and distribution of data resources. While these resources are perused by a great number of the research community, the majority of these users are relatively unaware of the initiatives undertaken to acquire, curate and enhance the content of these databases in service to the wider research community. This can both limit the uses of these data to its maximal capacity as well as lead to misuses of the data. In addition, more and more experimental biologists are generating data on a large scale and are in need of developing and managing databases of their own.

BIOINFORMATICS AND COMPUTATIONAL BIOLOGY**Comparative and Evolutionary Analysis of Plant Genomes**

YVES VAN DE PEER

Department of Plant Systems Biology
Ghent University
Belgium

The transfer of structural and functional information from one organism to another is one of the main applications of comparative genomics. However, such transfer between species is often a difficult task, one reason being the presence of a large number of duplicated genes in genomes and the fact that most genes are members of large gene families. Recent analysis of eukaryotic genome sequences has indeed revealed that gene duplication, and subsequent functional divergence, has been rampant. Furthermore, many eukaryotic organisms – including plants - had their whole genome duplicated, sometimes more than once. Apart from developing mathematical models to simulate the birth and death of genes in plant genomes to unveiling the importance of such events for plant evolution and plant complexity, we are interested in identifying the ‘real’ or ‘closest’ functional homologs between different species. These homologs can potentially be identified as genes showing conservation of co-expression (correlation of expression profiles), conservation of interaction, conservation of gene order, and similarity in promoter sequences.

Regarding transcriptional regulation, we are interested in studying organisms with simpler transcriptional networks, such as green algae that contain fewer duplicated genes. For instance, we are involved in the genome annotation of different strains of the unicellular green alga *Ostreococcus tauri*, which has about 8000 genes. By comparative approaches, and using functional genomics data, we hope to be able to make faster progress unraveling transcriptional networks. Unraveling pathways can be important for metabolic engineering but is expected to be easier in algae than in more complex higher plants because functional redundancy and subfunctionalisation is expected to be limited.

AGRICULTURAL BIOTECHNOLOGY PERSPECTIVE**Traits for Plant Biotechnology****STEVEN P. BRIGGS**

Division of Biological Sciences, Cell and Development Biology
University of California, San Diego
9500 Gilman Drive
La Jolla, CA 92093

Plant biotechnology is the application of scientific knowledge to the improvement of plant traits. Improvements are in quantity or quality. Nearly all commercial improvements have been in productivity. Increased productivity conserves land and water, lowers the cost of production, and can increase the available supply of food, feed, fiber, or medicine. The biggest opportunity to improve productivity is by increasing disease resistance. Disease resistance is fully under genetic control and routinely causes significant yield loss even under ideal environmental conditions. Post-harvest rot caused by disease organisms and poisoning from mycotoxin contamination contribute to the problem. Stress tolerance is the second largest opportunity even though the range of tolerance is limited by physical factors and, therefore, is only partially under genetic control. Scientific innovations are anticipated to provide solutions for both of these traits in the coming two decades. We're limited in plant biotechnology primarily by a lack of understanding of which traits to improve and which genetic changes in the plant will cause the improvement, especially for improving quality. Nevertheless, progress has been made in creating crops with enhanced nutrition; self-processing grain for wet milling; and feed grain that digests anti-nutritional factors like phytic acid. More research is needed to define quality traits and to discover genes that improve these traits. The emerging reservoir of microbial genes will contribute disproportionately to the improvement and creation of quality traits.

AGRICULTURAL BIOTECHNOLOGY PERSPECTIVE

Re-domestication of Wild Tomato Species

DANI ZAMIR
Faculty of Agriculture
The Hebrew University of Jerusalem
P.O. Box 12
Rehovot 76100, Israel

Natural biodiversity is an under-exploited sustainable resource that can enrich the genetic basis of cultivated plants with novel alleles that improve productivity and adaptation. We evaluated the progress in breeding for increased tomato (*Solanum lycopersicum*) yield using genotypes carrying a pyramid of three independent yield promoting genomic regions introduced from the drought tolerant green-fruited wild species *S. pennellii*. Yield of hybrids parented by the pyramided genotypes was more than 50% higher than a control market leader variety both under wet and dry fields conditions that received 10% of the irrigation water. This demonstration of the breaking of agricultural yield barriers provides the rationale for implementing similar strategies for other agricultural organisms that are important for global food security.

AGRICULTURAL BIOTECHNOLOGY PERSPECTIVE**Public Good Crop Germplasm Improvement: Delivering the Fruits of the Golden Age of Plant Biology**

CHRIS LAMB
John Innes Centre
Norwich, UK

Plant biology is entering a golden age. We have the parts list from an ever increasing number of model and reference species and ongoing efforts like the Arabidopsis 2010 programme will establish the blueprint from which we can understand natural genetic variation, how plants are adapted to specific environments and how breeders have modified the blueprints for agricultural production. Systems oriented approaches, such as the development of the virtual plant are rapidly complementing powerful reductionist approaches to provide major insights into complex biological processes such as flowering time and disease resistance of major agronomic significance. Furthermore, insights from the study of plants are once again having an impact and relevance right across biology, RNAi being an excellent current example.

Although our science is fantastically exciting and hugely relevant to issues such as global climate change, sustainability and international development, we face a number of challenges that will require creative solutions. One challenge is to re-connect with an urbanised society about the importance of plants in our world and hence of the importance of plant science. A related challenge is to attract first-rate young scientists into our field against strong competition from the larger and better resourced biomedical sector and the inadequate teaching of plant biology in our schools.

There is also a major challenge in the delivery of useful outputs from our science. The research now under way has the potential to change plant breeding from an empirical art to a precise targeted and ultimately predictive science lead enterprise for accelerated improvement of current crops, the domestication of new crops and the development of novel plant-based green industries as well as sustainable production of high quality nutritious food.

However, in the UK the pipeline from scientific advance to improved crop varieties is broken because of the demise of public good breeding for major crops. One of the founding components of the John Innes Centre was the Plant Breeding Institute, which was founded in 1912 to apply Mendel's rediscovered laws to the improvement of wheat. The PBI, which was hugely successful, perhaps too successful, in producing new varieties, with 80% of the wheat seed market at its zenith, brought together fundamental researchers with plant breeders. In the political Zeitgeist of the 1980's and in response to concerns from the seed companies that they were competing with government-subsidised breeders, the breeding operation was sold off to Unilever, with the fundamental plant researchers moving to Norwich to help create the modern JIC. The adverse impact of this fracture is becoming ever more apparent as we see the potential opportunities for genome-based crop improvement emerge and the fall out from the global restructuring and consolidation of the ag biotech industry works through. Much of the application of biotech and genome based approaches is now focused on a small group of increasingly high tech crops like maize, soy and cotton, with wheat almost relegated to the status of an orphan crop in the UK. The structure of the wheat seed market means that it is impossible to support genome-based improvement from the seed royalties even though this is the apex of a multibillion value added chain and affects a substantial proportion of the landscape of SE England.

We are exploring ways of mending the pipeline through creation of a virtual centre for public good germplasm improvement for broad acre UK crops in partnership with the National Institute of Agricultural Botany. NIAB bring to the table the capacity for genotyping phenotyping and systematic trialling at multiple sites to sit alongside JIC's expertise in cytogenetics, genomics and molecular genetics. Examples of the type of work we envisage are:

- * Systematic identification, evaluation and characterisation of new genetic variation from JIC's extensive germplasm collections and the CIMMYT synthetics
- * Adapting genotypes by incorporation of traits from exotics,
- * Identification of novel traits in the field for genetic characterisation in model, reference and crop species
- * Allele mining and phenotypic evaluation,
- * Association genetics
- * Breeding strategies designed to create novel, genome based ideotypes.

The overall aim is to develop a long-term pre-competitive programme to provide novel germplasm that the commercial breeders can exploit rather than to produce finished varieties ourselves. We hope that this new initiative will include a substantial training component bringing together lab and field-based aspects to bring through a new generation of breeders equipped to work in the new era of genome based targeted breeding.

The need to establish a public good germplasm improvement effort is mirrored by some of the challenges facing the development of improved varieties for developing country farmers, including the need to realise the potential for genome based breeding and to build capacity through training programmes. An interesting illustration of how this might work comes from a project funded by the Kirkhouse Trust (patron Ed Southern), which has supported high level training workshops in Bangalore and a PhD studentship at JIC to develop molecular markers and genetics maps for the Indian legume *Dolichos lablab* using tools, resources and skills from JIC's programmes on *Medicago truncatula* and pea. We hope this type of programme, which builds capacity and fast-tracks development of resources exploiting syntenic relationships and ultimately genomics, can be a prototype for international interactions paralleling a public good germplasm improvement effort on UK broad acre crops like wheat, rape and pea.

AGRICULTURAL BIOTECHNOLOGY PERSPECTIVE**Monitoring Genomic Diversity in Contrasted Plant Populations and Diverse Species**

JEAN CHRISTOPHE GLASZMANN

Cirad, UMR Pia 1096

Plant genomics opens unprecedented avenues for exploring applications of biotechnology in making the best use of plants. Recent achievements suggest that genetic engineering will make it possible to install new traits or improve conventional agronomic traits by genetic engineering, provided that benefit is equitable, biosafety is ensured and socioeconomic progress is sustainable. Scientists' imagination will be a major source of innovation, difficult to predict. What is undoubtedly going to remain a priority is the increase of food production and food quality with less chemical input and water consumption. Various programmes are targeted to this objective, involving comparative biology and transfers of knowledge from model or advanced crops to crops so far orphan.

Concentration of integrated research on model crops is relevant, and deployment of genetic diversity assessment on the "second circle" crops is essential. I wish to advocate for two lines of progress: (1) high throughput genotyping should make it possible to quickly type thousands of plants with thousands of markers; in this condition, proper agroecological and phenotypic characterization of key plant populations should enable identification of essential genes or chromosome segments, whose accelerated deployment will allow quick response to emerging agronomic threats. (2) the extension of this approach to a wider circle of crops, be they cultivated in fields or gardens, or to plants which are simply harvested or sampled in their spontaneous stands; this attention to large numbers of species has numerous potential biological and socioeconomic virtues. Genotyping and model-assisted phenotyping deserve particular efforts.

AGRICULTURAL BIOTECHNOLOGY FOR DEVELOPING COUNTRIES**Capturing the Value of Bioscience Innovations in Holistic Solutions to Complex Problems in Resource-poor Cropping Systems**

JONATHAN CROUCH^{1*}, ALESSANDRO PELLEGRINESCHI¹, HEI LEUNG^{2*} AND RACHID SERRAJ³

¹CIMMYT – International Maize and Wheat Improvement Center, Mexico

²IRRI – International Rice Research Institute, Philippines

³IAEA – International Atomic Energy Agency, Austria

*Generation Challenge Program – www.generationcp.org

The genomics revolution has greatly accelerated our ability to generate new knowledge across the plant sciences. However, there has been only limited translation of that knowledge into new skills for tropical plant breeding programs. This is partly due to the unexpected levels of complexity that have been unveiled as we have delved more deeply into the genetic basis of complex traits, their phenotypic expressions and interactions in complex target environments.

Equally significant, is the constraint we impose on effective product development through the way we structure public sector agricultural research. The Generation Challenge Program (GCP) attempts to foster a new architecture of innovation that creates an effective pathway from fundamental genomics research, through field-based agro-physiology to knowledge-led plant breeding. In particular, the GCP seeks to create holistic solutions for more efficient use of water in tropical agro-ecosystems, generating increased crop value with lower inputs and thereby providing direct impacts on the livelihoods of those dependent on resource-poor cropping systems.

There is clearly an urgent need for modern tropical crop breeding programs capable of integrating advances from a diverse array of disciplines. Contributions to most plant breeding goals are still to be found in the largely untapped global germplasm collections. The absence of efficient large-scale mechanisms for targeted allele and gene mining is a fundamental constraint to the molecularization of plant breeding. In addition, the role of whole plant physiology modeling is going to become a critical tool for combining new insights from our reductionist genomics approaches into valuable understanding at the field level. Finally, molecular breeding simulation technologies will become pivotal tools for translating this knowledge into skills that can directly impact plant breeding programs.

AGRICULTURAL BIOTECHNOLOGY FOR DEVELOPING COUNTRIES**Harnessing the New Sciences In Support of Agriculture in the Developing World**

DEBORAH DELMER

Associate Director, Food Security

The Rockefeller Foundation

New York, NY 10018-2702

With strong research capacity and a full array of genomics information available, Asia is poised to reap great benefits for rice improvement from the genomics revolution. The challenge now is to address key constraints for other key crops throughout the developing world. It is relatively easy to make a list of worthy targets: increased investment in genomics for orphan crops; a better understanding of the power (and the limits) of use of information about synteny; much better understanding of hybrid vigor and clarification of the value of hybrid crops beyond just maize; creation of many more locally-adapted inbred lines for breeding of all crops, especially for crops like cassava and other root crops; clear new strategies for durable control of fungal and bacterial diseases that do not seriously compromise yield or resistance to pests; better control of geminiviruses; imaginative use of the new findings about small RNAs, including their various functions, potential movement between host and symbionts/pathogens/ parasites, and development of strategies for their employment in aid of crop improvement; very cheap but accurate diagnostic kits and/or sentinel plants for detection of both abiotic and biotic factors in the environment; identifying Bt genes to control storage pests and nematodes; better understanding of plant-mycorrhizal interactions; create enhanced tolerance to drought at critical growth stages; enhance nutrient use efficiency and nutritional quality; use of specific genes to control flowering seed size, seed shattering, stem, leaf, flower, or root architecture; develop imaginative ways to control gene flow and to monitor the movement of GM crops in small-farm environments; develop a broad suite of promoters for use in fine-tuning the expression of genes for the above traits.

Many of the goals listed above are already achievable in principle using the current tools of genomics; others will require considerably more innovation at the basic level to achieve. We surely need continued innovative discoveries, but I would argue that, in the next ten years, what is most critical for the developing world is to design a much more effective path that connects current knowledge to downstream applications for the public good. Scientists and policy makers need to understand more clearly the myriad of constraints faced by poor farmers, and to find more innovative ways to educate and mentor young scientists that will favor their return and empower them to be serious scientists at home and to provide them adequate infrastructure and stable sources of funding for R&D when they return home. We also need to understand how to better assess performance of crops under conditions of small-farm Africa as opposed to large-farm Iowa. Imaginative public-private partnerships that are structured to be “win-win” for both sectors should be encouraged. Keeping new discoveries available for use in development of crops for the poor, and finding faster, cheaper, but responsible, means to regulate GM crops in poor countries are also critical issues.

AGRICULTURAL BIOTECHNOLOGY FOR DEVELOPING COUNTRIES**Engaging Developing Countries in Biotech Development: Experiences from ABSPII**

DESIREE M. HAUTEA

IPB Director and ABSP II Regional Coordinator for Southeast Asia

Institute of Plant Breeding, College of Agriculture

University of the Philippines Los Baños

4031 College, Laguna

The Philippines

Plant biotechnology is at an expansion phase. New advances in genomics are poised to revolutionize applications in agriculture, health and nutrition, energy and the environment. Genetic engineering will continue to be a key process in the innovation chain. Bioengineered crops will remain as one of the most cost-effective technologies for delivery of adequate, high quality and diverse products of importance to both developed and developing world. Technological success and public acceptance will continuously underpin the wider diffusion of bioengineered products. There is growing concern that biotech solutions to the most pressing problems of developing countries will be beyond their reach and the consequences will have implications in food security and flow of global products and services. It is therefore imperative to engage developing countries in its development.

In most developing countries, public research institutions have remained the driving force for translating usable knowledge into products and services to meet national goals. A multi-stakeholder and multi-disciplinary collaborative research tied to a problem in which the developing country has a major interest, relevant knowledge and local capacity will ensure maximum and sustained participation. By way of illustration, an overview of ABSPII, a collaborative project being implemented in a number of developing countries worldwide to develop and deliver public bio-engineered crops will be presented. ABSPII's product strategy addresses and integrates all elements of the commercialization process including technology development, regulatory and intellectual property (IP) processes, marketing and distribution, and outreach and communications. The presentation will explain ABSPII's product strategy and how it is being implemented, and present updates and insights from the most advanced products under development

CONCLUDING REMARKS**Can Plant Biotechnology Become a Truly Social Science?**

LAWRENCE BUSCH
Department of Sociology
Institute for Food and Agricultural Standards
Michigan State University
East Lansing, MI 48824-1111

The last several decades have witnessed major advances in plant genetics and genomics. Doubtless, we are poised to see even greater advances in the coming decades. But the future of the field is clouded by a variety of issues that have yet to be satisfactorily addressed: (1) The choice of research trajectories is too narrowly defined. Private sector goals, based largely on profitability, limit too greatly what products can be delivered by either the public or private sector. (2) Much of the public remains highly skeptical about plant biotechnology, especially as applied to food and agriculture. We have yet to develop means for satisfactorily involving the public in determining directions for plant biotechnology research. (3) The regulatory environment is simultaneously too cumbersome and inadequate. On the one hand, only large companies can bring products to market easily. On the other hand, a 'normal accident' is likely without regulatory change. If an accident occurs, it will stifle research for several decades. (4) The expansion of intellectual property rights to plants and plant parts is creating what has been called an 'anticommons' in which projects are blocked by competing patent claims. (5) The major problems facing most small farmers in developing nations cannot be resolved by focusing exclusively on productivity. Increased productivity is likely to drive prices down even further, pushing those farmers into even deeper poverty. Plant biotechnologists can either dismiss these problems as outside the field and watch support for research wither, or they can directly address them. If they do the latter, then plant biotechnology will have to become a truly social science.

CONCLUDING REMARKS

Priorities for Plant Biotechnology

EM. PROF. MARC VAN MONTAGU
Department of Molecular Genetics
Ghent University – VIB
Belgium

It might be important that the EU-US meeting for Plant Biotechnology focus on a global effort for: - Value increase for agriculture – Creation of a Plant Derived Industry – Development of a sustainable agriculture – Indiscriminate access to Plant Biotechnology for all developing countries.

The actions to promote these priorities pass through: - a better support, worldwide, for fundamental research in Plant Sciences – a better interaction between fundamental and applied plant research – rebuilding the Plant Breeding capacity of Europe and the emerging economies by promoting molecular tools for breeding and an attention for neglected crops – stimulate molecular ecology – the creation of a social awareness of the importance of Science and Technology in agriculture.

Some specific research points to consider: - molecular base of hybrid vigor and apomixis – yield increase for crops of arid areas such as sorghum, barley, millets – biosynthetic pathways of secondary metabolites as this will be essential in identifying and capturing the value of the biodiversity in remaining natural areas.

Knowledge on these points can be obtained with the technologies of functional genomics and metabolomics coming available in a limited number of specialized research centers.