AEIC Fall Meeting

September 13-14, 2006

Portland, Maine

The AEIC Meeting was held in Portland, Maine on September 13-14 and was hosted by EnviroLogix, Inc. The group was welcomed to Portland by Bruce Ferguson of EnviroLogix.

AEIC Business Meeting

Secretary's Minutes of 2006 Spring Meeting: A motion was made, seconded and approved to accept the minutes.

Treasurer's Report:

Currently:

Beginning Balance	$19958	
Member dues	7950	
Interest on account	33	
Total	27941	
Expenditures		
Expenses		4139
Certificate of Deposit		10000
		14139
New Balance	$13802 (actual total reserves are $23802 due to the $10000 CD)	

A motion was made, seconded and approved to accept the Treasurer's report.

Membership Update:

The AEIC membership is currently comprised of 14 large companies, 12 small companies, 2 associate members and 1 individual member. Possible new members who will be invited to subsequent meetings are Silliker Labs, Ventria, Biolex and food companies such as Kraft, Nestle, Unilever, etc. Omics (Portland, OR) has indicated that they will be joining AEIC.

2007 AEIC Spring Meeting: BASF/Syngenta will host the Spring Meeting in April, 2007 in Research Triangle Park, North Carolina. There may also be an ISO TAG Meeting either before or after the Spring Meeting.

Possible agenda topics:

- Focus on cotton for at least ½ day
- New testing platforms: Eppendorf (GMO chip); ABI or Roche
- SDI (genomic antibodies)
- Methods to express proteins
- DNA quality documents from the EU: new requirement for submitting DNA Samples
- Measurement techniques for output traits not expressing novel proteins
- Allergen detection/regulatory changes: new allergen database that is available; sera banks; ILSI PATC>what is it and what projects is it engaged in

2007 AEIC Fall Meeting: It was proposed that the meeting would focus on canola/oils testing. Bayer CropScience Canada has offered to host the meeting in Saskatoon.

AEIC Board Nominations/Election: The 2006 election will again be held via e-mail and will occur in mid-October. Member companies have one vote/company. Nominations will be accepted for the office of Vice President through September 26. Several nominations were made at the meeting but due to the absence of the nominees, confirmation of their willingness to accept their nomination will be made the AEIC Secretary. Doris Dixon (Monsanto), currently the AEIC Vice President, will succeed Ray Shillito (Bayer) as the President for 2007.

New Business:

Collaborative study on known samples by PCR and ELISA to compare the methods:

--It was suggested that AEIC ask ISTA for access to their data to compare the methods. Doris will approach ISTA and if they say no, AEIC will then come up with our experiment.

UPDATES:

USDA GIPSA (R. Jenkins): GIPSA runs a rapid test performance evaluation program, proficiency program, an intra-lab method validation program and an inter-lab method validation (with JRC and AACC). The proficiency program is still voluntary and free of charge. The next round of samples will be sent out in October, 2006. GIPSA currently has 145 labs participating, with 32 of the labs from the US. The majority of the participating labs use DNA-based testing. Approximately 25% of the participating labs have the capability to test for all events that are provided. In 2006, there were 56 participating labs—15 labs provided qualitative responses only, 6 provided quantitative responses only, and 35 labs provided a combination of both qualitative and quantitative responses. GIPSA recently performed the sensitivity and specificity testing of LLRICE601/62 using both the construct and event-specific tests. A discussion

concerning GIPSA's proficiency samples, i.e., the concentrations are too low for protein tests, was held. D. Layton (EnviroLogix), D. Grothaus (EnviroLogix) and F. Spiegelhalter (GeneScan) will draft a letter to GIPSA management expressing the need to change the samples.

Protein Paper (D. Grothaus): The AEIC Protein Paper will be published in the July/August issue of the Journal of AOAC International. AEIC will investigate whether we can purchase a PDF version that can be distributed as a reprint. Dave will speak with VIP Consulting (V. Pantella) about their proposal to write one pagers for technical publications which will more or less advertise the publication of the paper.

Certified Reference Material (CRM) Request from Japan (D. Dixon/R. Shillito): There has been an ongoing request from the Japanese government to the tech providers for certified reference materials. The Japanese agencies make their own methods for the GM traits and then license the methods to private companies to sell. They now want to add certified reference materials to the kits to calibrate their plasmid material. The CropLife International (CLI) Detection Group is working on a response to the Japanese government. The CLI Group also wants to eventually have a face-to-face meeting with the government.

CropLife International Detection Group (R. Shillito): The Detection Group members include Bayer, Monsanto, Syngenta, Dow and DuPont. The group has discussed certified reference materials (CRMs) and the fact that IRMM CRMs are expensive and the samples are not large. It was mentioned that the EU requires that CRMs for traits be publicly available, however, this does not mean that a company must supply the CRMs to IRMM. AOCS provides a CRM for LibertyLink T25 event. For stacks, the EU JRC does not require CRMs if the individual parental traits have accepted CRMs available. Monsanto supplies CRMs for stacks that are unique, i.e., one of the traits is not approved as a single trait.

USDA AMS (M. Sussman): A proposal has been submitted to the Plant Variety Protection Office (PVPO) to submit biomarker data to fast track a plant variety patent. However, ASTA will not consider anything but phenotypic traits. Therefore, biomarker data will be supplemental. AMS is currently straddling the fence on the use of biomarker data. AMS is providing molecular biology lab services for USDA APHIS, PPQ and BRS. AMS also provides quality assurance for the agricultural sector and variety identification for fruits and vegetables such as ugly ripe tomatoes and avocado market order enforcement. AMS also participates in the Food Emergency Response Network (FERN) and has recently been conducting proficiency testing for ricin in baby food. AMS also participates in Codex and ISO committees.

ASTA/ISTA (D. Dixon): ISTA held their annual meeting in Zurich, Switzerland. ISTA has changed their membership structure in order to attract more members. ISTA is also conducting accreditation/training for lab analysts. ISTA also has a GMO Taskforce which is asking companies to provide a source of certified reference material for proficiency program.

Codex Committee on Methods and Sampling (CCMAS) (M. Sussman): A criterial paper was introduced as a proposal. The UK and Germany wrote the document for biotech testing which was essentially paraphrased from the AEIC papers. The concept of GMO testing is still opposite of the US's. The paper was not a work item therefore, it could not be adopted as a standard. A number of comments were provided on the paper and these were sent back to the authors. A suggestion was made that the paper be sent to FAO to be published as a technical document.

ISO/TAG 34 (R. Shillito): TC 34 has set up a subcommittee to address technical issues. This subcommittee would include WG 7 which has done biotech testing standards. There is a need for $50,000 to fund the subcommittee for 3 years. The US government is willing to chip in, however, they cannot supply the full amount. Therefore, there is a need for companies to chip in $10,000 from each company. It was suggested that AEIC continue to fund WG 7. ISO held a forum on sampling. A number of the standards are now out of date for sampling and there is a need to bring together experts to establish new guidelines. There is a need of $20,000 to fund this activity. ILSI has been asked to organize a session on biotech for an Asian conference on nutrition. It would also be advantageous to have AEIC speakers and a workshop on detection methods. The conference is scheduled for September 9-13, 2007 in Taipei. The WG 7 Meeting may also occur at the same time in Taipei.

Members to convene to discuss the review by experts: Frank S., Doris D., Dave G., Ray S. and Mike S.

INVITED TALKS

Introduction to "Omics" (S. Martino-Catt, Monsanto): The central dogma of molecular biology is that DNA is transcribed to RNA which is in turn translated to protein which results in a trait in the organism. "Super-sized" technologies such as going from genes to genomes, occurred about 10 years ago. This allowed scientists to get rid of bias for just a few genes, i.e., instead of concentrating on 1-3 genes being responsible, more genes are considered as contributing to the trait. This super-sizing caused a shift in the paradigm about basic biology.

For DNA, technology development has occurred which includes more automation, better chemistry (i.e., fluorescent dyes and nucleotide derivatives), alternative platforms (beads rather dyes) and improvements in data analysis such as quality control metrics, automation of analysis and data warehouses. There are over 100 billion gene sequences publicly available currently. To date several plant genomes have been sequenced (*Arabidopsis*, rice, poplar, *Medicago*, loblolly pine, etc.). Sequenced genomes allows the annotation of genes by molecular function, biological process, etc. Annotation allows applications such as molecular markers for marker-assisted breeding and DNA-based diagnostics. Another application is comparative genomics which allows positional cloning and physical mapping.

For RNA, there are "open systems" and "closed systems". Open systems refer to no prior knowledge of genes/sequences is needed. Profiles of all transcripts are available. Some of the techniques of open systems include SAGE, MPSS, cDNA-AFLP. In "closed systems", the researchers must have prior knowledge of genes/sequences. Applications included are oligonucleotides or cDNAs arrayed onto a solid surface. Open and closed systems are utilized for gene discovery, mechanism of action, biochemical processes, promoter discovery and annotation of "unknowns", i.e., guilt by association via similar patterns of behavior.

Proteins have a higher order of complexity as compared to DNA and RNA. One gene yields multiple proteins. Proteins experience post-translational modifications and their dynamic range spans orders of magnitude. There are a diversity of protein types such as soluble, membrane-bound, etc. The gold standard methods for protein analysis is 2-D gels and mass spectrometry. These methods have been made easier via robotics and computer analysis. Amino acid sequencing helps to identify genes. Protein methods still have the limitation of sensitivity in order to identify individual proteins. New techniques such as fractionation without gels are being developed. The Beckman-Coulter Proteome Lab unit fractionates proteins in a liquid state (2-D). The samples are then placed in a 96-well plate for mass spectrometry analysis. Fractionation without gels also allows serum proteomics since serum albumin can be sequestered. However, making sense of the data is still a challenge. Protein detection/characterization has applications for gene discovery, mechanism of action studies, networks/interactions, signal transduction pathways, diagnostics (protein biomarkers), etc.

Metabolomics refers to the identification of metabolites within an organism. The analytical approaches for metabolomics are primarily based around gas chromatography and mass spectrometry. Metabolites have a higher order of complexity than proteins due to the number of compounds, diversity of compounds, dynamic range spans an order of magnitude, instability of compounds and no extensive databse of knowns for comparison. Metabolomics is the most immature of the "omics". There are two types of analyses—targeted and non-targeted. Targeted is restricted to one to few metabolites of interest. Non-targeted analysis is the analysis of all metabolites. The mass spectrometry spectra are translated to chemical structure, however, there is a definite need for more extensive libraries of compound structures. The applications for metabolomics includes pathway discovery, mechanism of action, regulatory network discovery, flux/kinetic studies and diagnostics.

The trend in molecular biology is toward a systems biology approach. This means putting together all "omics" technologies to get an all around view. It is much more powerful to integrate data from all sources. The challenges include data generation, data management (uniformity, accessibility, metadata), data analysis (statistical approaches, appropriate algorithms), validation (biological approaches. The "omics" technologies allow "smarter" plant breeding in that the researcher has a better idea of what they are selecting for and thus, the process is accelerated.

NIST: Taking the Measure of Measurements (M. Holden, NIST): NIST management is discussing a greater commitment to supporting agricultural biotechnology. Therefore, NIST is asking for input of ideas from the stakeholder community as to what their involvement could be. Ideas should be sent to M. Holden (Marcia.Holden@nist.gov).

NIST has been conducting a project on the quantitation of total plant genomic DNA. The questions that have investigated included a) are commonly used methods comparable; b) how do these methods compare to independent measurements; c) is there a need for total genomic DNA reference materials? This project is important due to the need for accurate detection of traces of biotech crops in conventional crop material. The amount of total DNA added to an assay is important for the limits of detection and limits of quantitation of the assay.

Comparisons were made between tissue types and extraction methods. The preparations of DNA were scanned at 260nm and 230/280nm to determine the quality of DNA extracted. The DNA preparation concentrations were adjusted to a standard concentration based on the 260nm reading. There was a lot of variability between extractions of different tissues (leaf vs. seed vs. crop, etc.). The DNA preparations from corn flour were then compared using picogreen or the Hoeschst dye which both bind differently to DNA. Picogreen values differed between the three DNA extraction methods. There was also an absence of dye binding in some of the DNA preparations due to the interference molecules. SDS and triton are acknowledged by the dye manufacturers as interference molecules. However, no mention is made of CTAB, however, this seemed to be the interference molecule from the extraction methods. It was found that it requires 100 times more SDS than CTAB to interfere with the dye binding. If the DNA preparation is washed well, the CTAB will not interfere with the dye binding. There also seemed to be a physical structure issue with plant DNA that also interferes with picogreen. Supercoiled plasmid preparations will bind more picogreen when linearized. An experiment revealed that physical disruption (vortexing, syringe shearing, sonication) and enzyme digestion (EcoRI) had no effect on the dye binding. Treating the DNA with proteases had little or no effect on the dye binding.

Methods for DNA concentration estimation were also investigated. These included a) digesting the DNA with enzymes and using isotope dilution LC mass spectrometry and GC mass spectrometry; b) ICP-OES (inductively-coupled plasma optical emission spectrometry; c) HPLC determination of the phosphate anion. It was found that HPLC lacks the precision of ICP-OES so it was felt that ICP-OES may be a useful independent and traceable methodology for DNA quantitation.

Update on the Biosafety Protocol (R. Krueger, Monsanto): The Biosafety Protocol (BSP) is an international environmental treaty. The treaty was completed in 2000 and took effect in 2003 with 134 signatory countries. The US is not a signatory. The scope of the treaty is transboundary movement of LMOs (living modified organisms) to promote conservation and sustainable use of biodiversity. Very few of the LMO exporting countries (such as the US) are signatories. Issues around implementation of the BSP are debated at Meetings of the Parties (MOPs). The most recent MOP was held in

Brazil and the next MOP will be in Germany in the Fall of 2008. The US chose not to be a signatory since it felt it was not necessary since it thought the whole treat would de-rail before it was signed. US as a signatory has not been brought back before Congress since the initial decision under Jesse Helms. The BSP is important since it is the first global agreement dealing with the regulation of biotechnology. It focuses on the effects of biotechnology on biodiversity and mandates science-based risk assessments. It also establishes a global database of laws, regulations, decisions and risk assessment summaries. The success of the treaty depends on sound implementation decisions and the global approach offers an opportunity for harmonization of regulations. The Global Industry Coalition (GIC) coordinates input to the BSP from private sector developers and users of biotechnology. The GIC represents thousands of companies and supports implementation of a fair and effective BSP based on science-based decision making.

MOP-3 which was held in Curitiba, Brazil in 2006 reached a final decision on Article 18(2)(a) which deals with the documentation for LMO food/feed/processing products, had general agreement on adequacy of risk assessment methodology, set risk assessment capacity building as a priority, agreed on schedule of expert meetings on liability leading to MOP-4 consideration, agreed to create criteria to improve the quality of the roster of experts, agreed on the need for a comprehensive Biosafety Clearinghouse (BCH), made no changes in the voting rules on compliance matter and changed the approach of capacity building funding decisions. There are 5 key implementation issues: liability and redress; handling, transport, packaging and identification requirements (Article 18(2)(a)); risk assessment/risk management; operation of the BCH; and socio-economic considerations. The MOP-3 decision for Article 18 (2)(a) is workable and should be implemented. For risk assessment, exisiting procedures and guidance materials are effective and should be shared. Liability and redress is best handled through laws at the national level of each country. Guidance should be created to allow Parties to develop systems to cover damage to biodiversity.

Update on LLRICE601 (R. Shillito, Bayer): US FDA has concluded that the LLRICE601 poses no safety concerns. USDA has conducted a preliminary risk assessment which indicates that LLRICE601 is safe in the environment. LLRICE601 contains a 35S bar cassette. Field trials were conducted with the event in 1998-2001. The event was discontinued in 2001 and was never commercialized. A deregulation extension has been filed with the USDA. The PAT protein expression in rough rice is 117 ng/g. Lateral flow devices (LFD; test strips) are available from both EnviroLogix and SDI and have been verified by USDA GIPSA to detect 1 kernel in 50 kernels. The sample size is according to the tolerance limits. Three 50 seed samples provide 95% confidence of less than 2% LLRICE601 in the sample. The LFDs work on brown rice at 1 in 50 seeds. A real-time PCR based on the 35S-bar (oligos in the 35S and bar gene) is available which detects LLRICE601, LLRICE62 and LLRICE06. Based on three 30g samples of rough rice (each sample contains approximately 1050-1250 long grain rice grains), the limit of detection is <0.1% (95% certainty). Since LLRICE601 was a backup line and was discontinued in 2001, Bayer has limited amounts of old seed available, thus there are limited amounts of calibration/control materials for assays. USDA is currently

conducting an inquiry to figure out how the event got into the 2003 foundation seed. It was not found in the 2005 foundation seed.

Identity Preservation System for Rice Varieties (J. Wells, Horizon Ag.): Horizon Ag is a joint venture of 5 rice companies. Rice varieties are public. Foundation and registered seed increases are done in Puerto Rico and Horizon Ag has a web-based system for tracking. Clearfield rice (ALS tolerance) is now marketed and this rice variety is free of LLRICE601. The ePedigree system was developed using seed producers as a model. The system tracks the seed through the entire life cycle, starting with breeder seed and ending at the mill door. The web site integrates all production, harvesting, processing, storage and sales. The system is capable of accommodating vast amounts of information but can be structured to deliver information defined by the user. There is a lot of interest in the system now but it is not currently in use. The use must be mill driven.

Verification of Performance for NK603/Mon810 Event Specific Methods Using Real-Time PCR (R. Jenkins, USDA GIPSA): Method validation verifies that an analytical method is acceptable for the purpose. Validation is an essential component of a comprehensive system of quality assurance in analytical chemistry as applied to food safety. GIPSA conducted a study to establish a preeminent method for quantification of transgenic traits in grains using real-time PCR. The acceptance criteria for the assay were : a) positive target DNA control—demonstrates that the test samples perform as predicted; b) amplification reagent control—contains all reagents except the test sample; c) relative standard deviation (RSD)—less than 33% RSD at all target concentrations within the dynamic range; and d) trueness--+/- 25% throughout the dynamic range of fortified samples. The fortified samples for Mon810 and NK603 were ground and the DNA was isolated via the CTAB method. The DNA was quantified using the picogreen reagent kit. Samples were diluted to 20ng/ul and then gel electrophoresis was performed. The PCR reactions were set up in triplicate for each sample including the standard curve of the endogene and the transgene. The IRMM endogene samples were treated as unknowns. The PCR method was well below 25% for truness and had good accuracy. The IRMM material was used as a calibrator for the fortified NK603 samples. The method had low bias and no longer met trueness criteria. Two endogenous control genes were looked at. The SSIIb gene did not meet the trueness criteria. With the HMGa gene, the PHI corn and BMV samples had high RSD values. In summary, the PCR variability met trueness criteria. For the BMV vs. IRMM calibrants, the method had low bias but was outside the trueness criteria. For the BMV vs TSD Mon810 calibrants, trueness was met. For the endogenes, SSIIb had some borderline for trueness, HMGa met trueness and invertase and ADH did not meet trueness. The conclusions were: a) the scope of the method with IRMM reference material is limited; b) BMV samples showed low bias for NK603; c) BMV samples showed low bias for Mon810; d) ISO/DIS 21570 procedure does not take into account zygosity and amplification efficiency differences between maize cultivars; and e) there is a need for an empirically determined correction factor.

Strip Reader Technology (D. Grothaus, EnviroLogix): The challenge for the grain handlers is that there is an increased presence of GM grain due to more GM crops being planted, admixtures in stored grain at the farm and elevator, decreased grower premiums paid for low-level GM grain, grower dissatisfaction—fewer opting to plant non-GM crops, decreased ability to satisfy non-GM contracts, difficult to analyze failures and

track contract fulfillment, grain handlers getting excessive positives, etc. Solutions to handle these challenges included a less sensitive strip test which became a subjective "vision test" for the grain handler. Another solution put forth was reflex testing—a grain handler gets an initial positive result, dilutes the extract/repeats test. This added significant time/expense. The next solution is the optical reading of the test strips. The advantages of this method is that the test line on the strip increases with the increase of antigen in the extract, the line intensity increase with %GM and data can be collected as a readout. The readout is a distribution which takes into account different source materials, different lot of test strips, etc. The distribution allowed the establishment of cutoffs which employed -2 standard deviations. This ensures 97.5% of the samples are called positive. Independent validations were conducted with grain customers in the field and the reader performance was compared with PCR via a certified PCR lab in Hong Kong. The goals accomplished with the development of the reader included non-subjective determination of the test strip line, allows acceptance of minimally contaminated loads of grain, commodity barges can be filled, less rejects, paper printout for documentation. The challenges for using a reader include keeping up with new grain varieties, multiple traits in new varieties lead to multiple positives, customers need to adhere to protocols and requires a tighter manufacturing and quality control specifications of test strips.

Lateral Flow Devices Kit Inserts Discussion (D. Grothaus, EnviroLogix): Kit insert information was reviewed by the AEIC paper published in 2000. The information should include matrix interferences—need to be clear on what events are detected and at what level. The insert should also have an "intended use" section and specify what tissue/material can be used. The insert should also be clear about limit of detection for multiple events. The sample sizes should be clearly stated and recommended testing protocols should be included.

MEMBER PRESENTATIONS:

BASF (L. Privalle, BASF): BASF Plant Science is a wholly-owned subsidiary of BASF. BASF was founded in 1865—the age of dyes. In 1965, the company expanded globally and uses a policy of "verbund"—nothing is wasted—in everything that it does. Agricultural biotechnology fits well into the specialty chemistry and agricultural product areas. Ludwigshafen, Germany is located across the Rhine River from Mannheim and is the main manufacturing site for BASF. The Specialty Chemicals area produces vitamins, enzymes, amino acids and intermediates. The Agricultural Products area produces herbicides, fungicides, insecticides and specialty products. It is located in Limbergerhof, Germany. BASF Plant Science is a start-up company with the backing of a large parent company. The BASF parent company has a commitment of 10 million euros over 10 years to Plant Science. BASF Plant Science focuses on soybean, corn, wheat and canola. The company consists not only of the site in Research Triangle Park, NC but also includes Exseed Genetics (Iowa), DNA Landmarks, Plant Science Sweden (focusing on potatoes), Metanomics (metabolomics company), SunGene (canola), Crop Design (stress genes from rice). The projects for Plant Science include crop protection, yield, drought tolerance, enhanced corn, PUFA (omega-3 canola oil), transgenic potatoes (fungal resistance) for EU. Drought tolerance is a multiple prong approach which is aimed at

increasing yield in corn and canola. There are also working on nematode resistance and PUFA (omega-3 fatty acids in canola). BASF is also using plants as factories to produce carotenoids in marigolds. The carotenoids are used in fish and poultry food. They are also working on amylopectin potato. These potatoes are only used for starch production and are not used for food since they virtually turn to glue when cooked. The pulp from these potatoes after the starch is extracted is used for animal feed. The amylopectin is used in the paper, textile and adhesive industry.

Syngenta (G. Aux, Syngenta): For Syngenta, research & development is the engine for profitable growth. It supports technology and leadership efficiency, core business growth and new business. Syngenta has 5000 employees globally. Ten percent of sales goes to research and development ($822 million in 2005; $100 million to the seed development). Syngenta is uniquely positioned to deliver on promises due to its platform technologies which include genomics, bioinformatics, crop transformation, marker-assisted breeding, advanced formulation, etc. R&D sites are located in Basel, Switzerland (fungicides, insecticides), Alderley Park (toxicology) and Jealott's Hill (chemical discover, weed control, formulation, bioscience, environmental science), UK, Greensboro, NC (formulation, environmental science) and Research Triangle Park, NC (biotechnology). Syngenta Biotechnology (SBI) was formed in 1984 and has 260 employees, 190 of which are scientists. SBI unites two powerful tools—transgenic crops and precision breeding. Projects are aimed at input traits (for agribusiness and the grower) and output traits (processor, retailer, consumer). The current biotech pipeline is as follows:

Agrisure GT (glyphosate tolerance)	Launched
Agrisure CB/LL (ECB + Liberty tolerance)	Launched
Agrisure GT/CB/LL	Launched
Agrisure RW (corn rootworm)	Launch 2007 season
Agrisure GT/RW	Launch 2007
Agrisure CB/LL/RW	Launch 2007
Agrisure GT/CB/LL/RW	Launch 2008
VIP/Broad lepidopteran	Launch 2009
Optimum GAT (corn)	
Optimum GAT (soybean)	Launch 2009
Output Traits	
Corn amylase (biofuels)	Launch 2008
Microbial Quantum (biofuels; animal feed)	First sales in Latin America; US reg. pending
Corn phytase (animal feed)	US FDA dossiers; target launch is 2010

Agrisure RW contains event MIR604 which is a modified *cry*3Aa gene.
It is effective against Northern, Western and Mexican corn rootworm. The target launch date is 2007 via Garst, Golden Harvest, Northrup King, Greenleaf Genetics and other brands via licensing agreements.

Optimum GAT is licensed from Pioneer Hi-Bred and combines glyphosate tolerance and ALS tolerance in corn and soybeans. This provides more weed control options for the grower as well as providing a weed resistance tool. The target launch date is 2009.

VIP (vegetative insecticidal protein) is a new technology with a novel mode of action. The protein is derived from *Bacillus thuringiensis* and is effective against black cutworm, corn earworm, Western bean cutworm and fall armyworm. It can be stacked with other B.t. Cry proteins to enhance resistance management. The target launch date is 2009.

The following are early R&D biotech traits and precision breeding projects:

	Stage
Nitrogen efficiency	Early R&D
Yield enhancement	Early R&D
Drought tolerant corn	Early R&D
Drought tolerant soybeans	Early R&D
Nematode resistance (soybean)	Early R&D
Asian rust resistance (soybean)	Elite breeding
Ultra-low linolenic soybean	Elite breeding
Aphid resistance (soybean)	Early R&D
Broad lepidopteran (cotton)	Late Development
Soybean specialty oils	Early R&D

Syngenta research possesses powerful tools to analyze crop genomes which has resulted in >11,200 genes being mapped in corn. This has applications in marker-assisted breeding and for native traits such as yield enhancement and nitrogen efficient corn, improved tomato fruit quality. For nitrogen efficient corn, utilizing candidate genes from rice. A novel product from plant breeding that has been introduced onto the market this year is the PureHeart "personal" watermelon which is a small watermelon sufficient for one person. For drought tolerance, native trait and functional genomics approaches have been used. Multiple new trait constructs are currently under evaluation in field trials.