Improvement of Sorghum through Transgenic Technology

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Sorghum is the fifth most important cereal crop in the world. It is largely grown on marginal soils with residual moisture where other major cereals cannot be grown due to inadequate water. Sorghum is a multipurpose crop and the species shows great diversity. For a large part of Asia and Africa, sorghum’s grain is used as food and its stalk as fodder and feed. In rest of the world, sorghum is considered as forage crop and also as stock for ethanol production.

Sorghum yield has been substantially increased through conventional breeding in India. However, resistance to abiotic stresses and biotic stresses such as shoot fly, stem borer, grain mold, and charcoal rot is limited due to inadequate genetic resources that can be readily used in crop improvement programs. Therefore, genetic engineering technology can assist the production of agronomically desirable crops that exhibit increased resistance to pests, pathogens, and environmental stress and enhancement of nutritional qualities.

Sorghum research has received less attention compared to other cereals for adoption of modern molecular tools, and very few laboratories in the world are addressing sorghum crop improvement programs through novel methods. Extensive research has been focused on other cereal crops, and a number of genes conferring agronomic advantages have been introduced through Agrobacterium and particle bombardment. In this article, we present the current status, progress, and prospects in transgenic sorghum technology and future approaches to increase its economic value, thereby providing monetary benefits to sorghum farmers.

Sorghum Transformation

The first report of the successful transformation of sorghum appeared as early as the 1990s. Yet, sorghum is considered to be the most recalcitrant crop for tissue culture and plant regeneration, thereby for genetic transformation. Recalcitrance in sorghum tissue culture is reportedly due to the release of phenolics, lack of regeneration in long term in vitro cultures, and a high degree of genotype dependence. The release of phenolics into the culturing medium can be overcome by frequent subculture and by the addition of polyvinyl pyrrolidone phosphate (PVPP) in the medium. However, transformation followed by regeneration remains extremely complicated in sorghum transgenic technology.

Genetic transformation of sorghum has picked up momentum in recent years, with a greater number of reports published in the last couple of years. Though different explant sources such as immature inflorescence, immature embryo, and shoot meristem are reported in sorghum...
Crop improvement traits

Sorghum is chiefly grown in low input conditions; therefore, development of host plant resistance to biotic and abiotic stresses is a viable option. Demand for sorghum as a health food is gaining importance, and thus, incorporation of certain value added traits is advantageous to the food industry.

Worldwide, sorghum producers face a major threat to their crops from insect pests, and the most destructive pests are the lepidopteran stem borer (Chilo partellus) and the dipterans, midge (Stenodiplosis sorghicola) and shoot fly (Atherigona soccata). Building resistance through conventional breeding is limited due to a lack of reliable resistance sources. Insecticidal crystal proteins (CRY) from Bacillus thuringiensis are very effective against the lepidopterans and dipterans. Bt and other genes with insecticidal activities are being evaluated for eventual use in transforming crops and reducing losses due to these pests.

Girijashankar et al. (2005) produced transgenic sorghum plants carrying a synthetic gene, Bt cry1Ac, under the control of a wound inducible promoter from a maize protease inhibitor gene (mni). They reported low levels of Bt protein of 1 – 8 ng per gram of fresh leaf tissue. A moderate level of tolerance was reported, which in turn conferred partial protection against neonate larvae of the spotted stem borer (Chilo partellus).

Padmaja produced transgenic plants carrying a synthetic gene Bt cry1B under the control of the constitutive promoter maize ubiquitin (ubi) in the parental lines of Indian hybrids via particle bombardment. Some of the events are promising in insect bioassays with 80% larval mortality compared to non-transformed control plants (Padmaja, personal communication).

The agronomically important gene chi II, encoding rice chitinase under the constitutive CaMV 35S promoter, has been transferred to sorghum for resistance to stalk rot (Fusarium thapsinum) by Zhu et al. (1998) and Krishnaveni et al. (2001).

Trials are also underway to engineer sorghum to withstand abiotic stress conditions, such as drought and salinity. Efforts are in progress to transfer genes mtlD, p5CSF129A, and codI to Indian sorghum genotypes for biosynthesis of osmoprotectants. Expression of
these genes leads to accumulation of osmolytes, resulting in tolerance to various abiotic stresses (Maheshwari et al., personal communication). Overexpression of the gene for mannitol-1-phosphate dehydrogenase (*mtld*) for biosynthesis of mannitol enhances tolerance to water deficit stress, primarily through an osmotic adjustment that improves growth of transgenic plants under water stress and salinity. The *pSCSf129A* gene codes for pyrroline-5-carboxylate synthase, which catalyses the first two steps of proline biosynthesis in plants. *codA* codes for choline oxidase, which converts choline into glycine betaine.

Sorghum grain is loaded with starch and is relatively poor in protein and lipid. Tadesse and Jacob (2003) introduced the *dhdp-rapecl* mutated gene, which encodes an insensitive form of dihydricinolate synthase, the key regulatory enzyme of the lysine pathway. Overexpression of the gene produces sorghum lines with elevated lysine content. Enrichment of the essential amino acid lysine in sorghum grain improves nutritional quality. Efforts are also underway to transfer the high molecular weight (HMW) wheat glutenin gene *1Ax1* into sorghum to alter dough quality to meet demands from the bakery industry (SV Rao, personal communication).

**Biosafety concerns**

There are no transgenic sorghum crops under commercial cultivation to date. The most important issue related to biosafety concerns in sorghum is pollen-mediated gene flow to the wild species *Sorghum halepense* (Johnsongrass), a wild weedy relative, reported to occur naturally at frequencies of 2.5% at a distance of 13m (Schmidt and Bothma, 2006). The concern is that transfer of the herbicide tolerance gene to *S. halepense* through gene flow would make control of the weed unattainable. Godwin (2005) reported that hybridization of *S. halepense* (2n=40) and cultivated sorghum, *S. bicolor* (2n=20), would produce unviable triploids. Transgenic technology in sorghum is at a juvenile stage. Recently Gao et al. (2005) established transgenic technology using the positive selectable marker gene *pmi* (phosphate mannose isomerase), which is biosafe and found widely in other crops.

**Future prospects**

Despite the use of other monocot promoters such as rice actin (*act-1*) and maize ubiquitin (*ubi1*), use of native promoters in sorghum may be explored if it helps to increase the levels of transgene expression. In the eukaryotic genome, DNA elements called scaffold/matrix attachment regions (MARs) are primarily involved in structural and functional organization. They are thought to influence gene expression, and evidence from other transgenic crops reveals that these sequences, when flanking the transgene, result in enhanced expression of the integrated gene(s). Research in making potentially well-defined synthetic MARs and improving stable transgene expression in sorghum are areas of immediate attention. Construction of a detailed genetic map of sorghum is underway, and it offers a wealth of genomic tools to the sorghum scientific community with great potential to improve sorghum (Bedell et al., 2005). Financial assistance from non-governmental organizations like the Bill and Melinda Gates Foundation, Andhra Pradesh-Netherlands Biotechnology Programme (APNLBL), and CGIAR grants, in addition to public sector support, to improve sorghum nutritional quality with enhanced levels of vitamins, minerals, and protein, and also to withstand biotic and abiotic stresses will improve sorghum transgenic technology and lead to increased quality and productivity in the coming years.

**References**

“No unintended effects in composition or nutritional assessment of feeds from first generation GE crops were registered in any of the more than 100 studies with food producing animals”

The cultivation of genetically engineered plants (GEP) increased worldwide during the last 10 years, up to about 100 million ha yearly. Soybean, maize, rapeseed, and cotton are the predominant crops. These plants, the so-called first generation GEP, are characterized by input traits such as tolerance to pesticides or herbicides, or resistance against insects. They are considered substantially equivalent to their isogenic counterparts because they do not exhibit substantial differences in their composition or their nutritional value.

Second generation GEP are characterized by their output traits, such as an increase in valuable compounds (nutrient precursors, amino acids, fatty acids, vitamins, enzymes, etc.), an improved availability of nutrients, or a decreased concentration of undesirable substances (e.g., phytate, lignin, allergenic substances, etc.).

Nutritional and safety assessment of second generation GEP presents a formidable challenge for animal nutritionists. This article reviews the nutritional and safety assessment of feeds from first generation GEP, and comments on the parameters for assessing second generation GEP.

Feeds from GEP with input traits (first generation)

Most GEP currently under cultivation are first generation, i.e., varieties without substantial changes in composition or nutritive value. Numerous scientific associations and expert panels have proposed guidelines for the nutritional and safety assessment of feeds from first generation GEP (e.g., EFSA 2004, ILSI 2003). Based on these recommendations, nutritional studies with first generation GEP feeds have been undertaken worldwide.

Since 1997, 16 studies were performed at the Institute of Animal Nutrition of the German Federal Agricultural Research Centre (FAL) in Braunschweig to determine the effect of first generation GEP feeds on the nutrition of dairy cows, growing bulls, growing and finishing pigs, laying hens, and chickens for finishing, as well as on the growth and laying characteristics of quail. This research was recently summarized by Flachowsky et al. (2007).

The majority of feeds tested in the studies (e.g., Bt-maize, Pat-maize, and Pat-sugar beet) were grown under conditions similar to their isogenic counterparts in fields at FAL. The composition of feeds was analysed, and animal studies were used to assess nutritional qualities, including parameters such as digestibility, feed intake, health and performance of target animal species, and effects on food quality derived from the animals. Reproduction was also considered in generation studies with quail (20 generations are now completed) and laying hens (4 generations).

Both chemical analyses and the animal studies reveal no significant differences between GEP feeds and their isogenic counterparts (reviewed in Table 1) and hence strongly support their substantial equivalence. Our results agree with more than 100 studies published in the literature and reviewed recently (Table 2).

Mycotoxin contamination of some GE crops is lower than non-GE, which may be one exception to their substantial equivalence. For example, Bt maize is less severely attacked and weakened by the corn borer and hence might have a greater resistance to field infections, particularly by Fusarium fungi, which produce mycotoxins. Evidence of reduced mycotoxin contamination in GE crops has been demonstrated in some but not all cases, as summarized by Flachowsky et al. (2005). In long-term studies, numerous researchers investigated the influence of levels of corn borer infestation of isogenic and Bt hybrids on mycotoxin contamination. Most researchers concluded that a lower level of mycotoxin contamination was observed in the transgenic hybrids, despite the considerable geographical and temporal variation observed.
Table 1: Analyses of feeds from first generation GE crops (Federal Agricultural Research Centre; Flachowsky et al. 2007)

<table>
<thead>
<tr>
<th>GMP</th>
<th>Analytical measurements</th>
<th>Animal Species/categories</th>
<th>Type of Study</th>
<th>Animal number (isogen/ transgene)</th>
<th>Duration (days)</th>
<th>Composition of GM-feeds</th>
<th>Digestibility</th>
<th>Zootechnical parameters</th>
<th>Further measurements</th>
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</thead>
<tbody>
<tr>
<td>Bt-maize Grain</td>
<td>Crude nutrients, Amino acids, Fatty acids, NSP, Minerals</td>
<td>Growing and fattening pigs</td>
<td>Digestibility</td>
<td>3 times: 6/6</td>
<td>14</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>Mycotoxins</td>
<td>Growing/ fattening</td>
<td>Digestibility</td>
<td>12/36</td>
<td>91</td>
<td>NS</td>
<td>-</td>
<td>NS</td>
<td>Slaughtering data, Fate of DNA</td>
</tr>
<tr>
<td>Crude nutrients</td>
<td>Growing pigs</td>
<td>Digestibility</td>
<td>5/5</td>
<td>14</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Crude nutrients, Starch, NSP, Amino acids, Fatty acids, Minerals</td>
<td>Laying hens</td>
<td>Digestibility, measuring of performance</td>
<td>6/6</td>
<td>10</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td>Fate of DNA</td>
<td></td>
</tr>
<tr>
<td>Crude nutrients</td>
<td>Broilers</td>
<td>Digestibility</td>
<td>6/6</td>
<td>5</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Crude nutrients</td>
<td>Broilers</td>
<td>Growing</td>
<td>9/27</td>
<td>35</td>
<td>NS</td>
<td>-</td>
<td>NS</td>
<td>Fate of DNA</td>
<td></td>
</tr>
<tr>
<td>Crude nutrients, Starch, Amino acids, Fatty acids</td>
<td>Growing and laying hens</td>
<td>10 generations (growing, laying)</td>
<td>Layers presently 20th generation</td>
<td>42</td>
<td>-</td>
<td>NS</td>
<td>-</td>
<td></td>
<td></td>
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<tr>
<td>Crude nutrients, Starch, Amino acids, Fatty acids</td>
<td>Growing and laying hens</td>
<td>4 generations (growing, laying)</td>
<td>Layers</td>
<td>32/32</td>
<td>91</td>
<td>NS</td>
<td>-</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bt-maize Silage</td>
<td>Crude nutrients</td>
<td>Growing and fattening bulls</td>
<td>Growing/ fattening</td>
<td>20/20</td>
<td>246</td>
<td>NS</td>
<td>-</td>
<td>NS</td>
<td>Slaughtering data, Fate of DNA</td>
</tr>
<tr>
<td>Crude nutrients</td>
<td>Sheep</td>
<td>Digestibility</td>
<td>4/4</td>
<td>24</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
<td></td>
</tr>
<tr>
<td>Bt-potatoes</td>
<td>Crude nutrients</td>
<td>Broilers</td>
<td>Growing</td>
<td>9/18</td>
<td>21</td>
<td>NS</td>
<td>-</td>
<td>NS</td>
<td>Fate of DNA</td>
</tr>
<tr>
<td>Pat-maize</td>
<td>Crude nutrients, Starch, Sugar, NSP, Amino acids, Fatty acid</td>
<td>Pigs</td>
<td>Digestibility</td>
<td>5/5</td>
<td>14</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Pat Sugar beets</td>
<td>Crude nutrients, Sugar</td>
<td>Sheep</td>
<td>Digestibility</td>
<td>4/4</td>
<td>24</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Roots</td>
<td>Crude nutrients, Sugar</td>
<td>Pigs</td>
<td>Digestibility</td>
<td>5/5</td>
<td>14</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Top Silage</td>
<td>Crude nutrients</td>
<td>Sheep</td>
<td>Digestibility</td>
<td>4/4</td>
<td>24</td>
<td>NS</td>
<td>NS</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Roundup Ready soybeans</td>
<td>Crude nutrients, Starch, Amino acid Fatty acids, Minerals</td>
<td>Pigs</td>
<td>Growing/ fattening</td>
<td>12/36</td>
<td>40</td>
<td>NS</td>
<td>-</td>
<td>NS</td>
<td>Slaughtering data, Fate of DNA</td>
</tr>
</tbody>
</table>
Feeds from GEP with output traits (second generation)

Second generation GEP are characterized by either:

- An increased content of desirable/valuable traits, such as:
  - Nutrient precursors (e.g., β-carotene)
  - Nutrients (amino acids, fatty acids, vitamins, minerals, etc.)
  - Substances which may improve nutrient digestibility (e.g., enzymes)
  - Substances with surplus effects (e.g., prebiotics)
  - Improved sensory properties/palatability (e.g., essential oils, aromas)

- Or a decreased content of undesirable substances, such as:
  - Inhibiting substances (e.g., lignin, phytate)
  - Toxic substances (e.g., alkaloids, glucosinolates, mycotoxins).

At present, detailed standardized test procedures are not generally available to analyze feeds from second generation GEP. Possible approaches for testing those feeds were recently reviewed by Flachowsky and Böhme (2005). Recommendations for nutritional and safety assessment of feeds from second generation GEP are being developed by EFSA and ILSI.

The following points should be considered when making a nutritional assessment of second generation GEP feeds. Feeds with intended beneficial physiological properties relating to amino acids, fatty acids, minerals, vitamins, and other substances may contribute to higher feed intake of animals and/or improved conversion of feed/nutrients into food of animal origin. Furthermore, the excretion of nitrogen, phosphorus, and other nutrients may be reduced. Consequently, depending on the claimed difference due to the genetic modification, the experiment must be designed to demonstrate these effects. Specific, targeted experimental designs are necessary to show the efficiency of the following altered nutrient constituents:

- Bioavailability or conversion of nutrient precursors into nutrients (e.g., β-carotene).
- Digestibility/bioavailability of nutrients (e.g., amino acids, fatty acids, vitamins).
- Efficiency of substances which may improve digestibility/availability (e.g., enzymes, reduced phytate).
- Utilization of substances with surplus effects (e.g., prebiotics).
- Improvement of sensory properties/palatability of feed (e.g., essential oils, aromas).
- Lower content of undesirable substances should be demonstrated in animal health and/or performance.

Genetic modifications may be associated with side effects (Cellini et al. 2004), and the larger the modification, the greater the chance of inducing secondary changes. As the basis for comparative approaches, special animal studies seem to be necessary to examine these questions. Therefore the nutritional and safety assessment of feeds from second generation GEP is a significant challenge for animal nutritionists.
The fate of transgenic DNA and transgenic proteins

The consumption of feeds from GEP results in the intake of transgenic DNA and proteins; therefore, studies were conducted on their fate within the gastrointestinal tract of animals, and the potential to which extent transgenes or their products may be incorporated into animal tissues. Studies in this area were excellently reviewed recently by Alexander et al. (2007).

Results on the fate of transgenic DNA in feeds can be summarized as followed:

– DNA is a permanent part of food/feed (daily intake: human: 0.1 – 1 g; pig: 0.5-4 g; cow: 40-60 g).
– Transgenic (t) DNA intake amounted to ≈ 0.005 % of total DNA-intake, if 50 % of the diet comes from GE crops.
– DNA is mostly degraded during conservation (silage making) and industrial processing, as well as in the digestive tract (pH, enzymes).
– Small fragments of DNA may pass through the mucosa and may be detected in some body tissues (especially leucocytes, liver, and spleen).
– Fragments of high-copy number genes from plants have been detected in animal tissues to a higher extent than from low-copy numbers.
– No data exists showing that tDNA is characterized by unique behavior compared to native plant-DNA during feed treatment and in animals.

The fate of novel proteins in feed from GEP consumed by animals has also generated interest arising from consumers questions. Results from studies can be summarized as follows (see also Alexander et al., 2007):

– In ruminant feed, proteins are mostly degraded in the rumen, and microbial and by-pass proteins are degraded by enzymes in the smaller intestine, similar to non-ruminants.
– The chemical and physiological properties (including microbial and enzymatic degradation) of novel proteins have been intensively tested.
– Intact novel proteins have not been detected outside of the digestive tract in target animals (also not in animal tissues and products).
– There is no evidence that novel proteins are characterized by unusual chemical/physical properties distinct from native protein.

Conclusions

From the data presented above, the following conclusions can be drawn:

– Presently, over 500 million hectares of GE crops have been cultivated worldwide.
– Most animal studies have been done using first generation GE crops.
– No unintended effects in composition (except lower mycotoxins) or nutritional assessment of feeds from first generation GE crops were registered in any of the more than 100 studies with food producing animals.
– Novel experimental designs are necessary for the nutritional and safety assessment of feeds from second generation GE crops.
– Transgenic DNA and novel protein do not demonstrate unique properties during feed treatment or in animals.
– Case by case studies are necessary to answer open questions.

References

EFSA (European Food Safety Authority) (2004): Guidance document of the scientific panel on genetically modified organisms for the risk assessment of genetically modified plants and derived food and feed. EFSA J. 99, 1-93
The Incredible, Pharmaceutical Egg

Eric Wong

Transgenic animals have been developed as bioreactors for the production of human pharmaceuticals. In mammals, high levels of recombinant protein have been produced in the milk of transgenic animals. Milk serves as an ideal fluid for foreign protein production because it can be collected non-invasively, animals such as dairy cattle have been selected for high milk production, and the industry for collection and processing of milk is already established. Similarly the chicken egg has also been considered an ideal system for the production of foreign proteins. The egg is laid as a sterile container, it can be collected non-invasively, and an industry is also already in place for the collection and processing of eggs. The lack of efficient methods for generating transgenic chickens, however, has hampered the development of transgenic chickens as bioreactors.

Retroviral vectors have been successfully employed as gene transfer vectors in both mammalian and avian systems. Retroviruses are considered to be excellent gene transfer vectors because they infect cells with high efficiency, and the natural lifecycle of the retrovirus involves the conversion of its RNA genome into DNA, which is then inserted into the host genome. In this way a transgene inserted into the retroviral genome can be stably integrated into the host chromosome. Previous studies that used avian leukemia virus as a gene transfer vector in poultry have resulted in low levels of transgene expression, efficiency of transgenesis, and germ line transmission. Other disadvantages of retroviruses are their small genome size and thus limited space for insertion of a transgene, silencing of transgene expression following integration into the host genome, and negative public perception of retroviruses. A well known example of a retrovirus is HIV.

In the current online issue of the Proceedings of the National Academy of Sciences, Helen Sang’s group at the Roslin Institute report the development of an efficient method for generating transgenic chickens using a lentiviral vector (Lillico et al., 2007). Lentiviruses are retroviruses that have been previously utilized to generate transgenic quail (Scott and Lois, 2005). Sang’s group used lentiviral vectors derived from equine infectious anemia virus (EIAV), which were rendered replication-defective by deletion of all viral coding sequences. They constructed two lentiviral vectors for the expression of human proteins under the control of regulatory elements of the chicken ovalbumin gene. One construct contained a gene for a humanized miniantibody, which was derived from a mouse monoclonal antibody that showed potential for the treatment of malignant melanomas. The second construct contained a human interferon beta-1a gene, which is a cytokine with antiviral, antiproliferative, and immunomodulating activity. These vectors were constructed with or without the well-characterized estrogen responsive element (ERE) present in the ovalbumin gene. The ERE is required for steroid-responsive and tissue-specific expression of the ovalbumin gene.

A chicken egg contains approximately 6 grams of protein, 3.6 grams in the egg white and 2.7 grams in the egg yolk, of which ovalbumin makes up more than 50% of the egg white protein. The ovalbumin gene is exclusively expressed in the oviduct of the hen, and thus the ovalbumin promoter has been a favorite target for the expression of foreign proteins into eggs. In this study Sang’s group injected recombinant lentiviral vectors into embryos from newly laid eggs to generate Go transgenic birds. Transgenic cockerels were generated from all three constructs tested. In one Go cockerel, the transgene was transmitted to 4% (19/463) of its progeny. Southern blot analysis confirmed the presence of the lentiviral vector inserted into the host genome.

Transgenic chickens from the G1 and G2 generations were examined for transgene expression in eggs and other tissues. Expression was restricted to the magnum portion of the oviduct and was not detected in pancreas, brain, intestine, liver, heart, and breast muscle. Recombinant proteins were secreted into the egg white of eggs from transgenic G1 and G2 hens. Protein levels remained consistent in the first to the 150th egg collected, which demonstrated that there was no silencing of the transgene. Mean values for recombinant proteins ranged between 3.5 to 426 μg/ml of egg white. Recombinant human interferon beta-1a in egg white was functional based on a standard antiviral/cytopathic effect assay, which assessed the ability of egg white protein to protect cells from infection and subsequent lysis by Semliki Forest virus. The level of protection correlated with the assayed concentration of the
recombinant protein. Interestingly, inclusion of the ERE in the constructs did not enhance the quantity of recombinant protein synthesized by transgenic hens. Because there was a limited sample size, however, no firm conclusions can be drawn; but addition of ERE does not appear to dramatically help protein production.

In conclusion, the Roslin group has generated transgenic hens that synthesize functional recombinant therapeutic proteins specifically in the oviduct of laying hens, which becomes a component of egg white. This use of lentiviral vectors is an efficient method of transgenesis, which shows high frequency of germline incorporation and does not show evidence of transgene silencing throughout the laying cycle. It remains to be seen if the transgene remains active in subsequent generations. This method overcomes a major hurdle for the development of transgenic chickens as bioreactors. In the future, the repertoire of eggs will be expanded from white and brown eggs to eggs with different pharmaceutical proteins.

References

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Industry News

ISAAA Releases Annual Global Status Report of Biotech Crops

Tracy Sayler

In 2006, the first year of the second decade of commercialization of biotech crops (2006-2015), the global area of biotech crops continued to climb for the tenth consecutive year, at a sustained double-digit growth rate of 13% or 30 million acres per year, reaching 252 million acres. That is according to the International Service for the Acquisition of Agri-Biotech Applications (ISAAA), a non-profit organization whose mission is directed toward advancing the benefits of agricultural biotechnologies to developing countries.

The U.S. continues to drive growth in North America and globally, accounting for the greatest absolute acreage increase in 2006, with the addition of about 11.8 million acres. Brazil leads growth in South America, with an increase of 22% for a total of 28.4 million acres, of primarily soybeans and biotech cotton, the latter commercialized in Brazil for the first time in 2006.

India is emerging as a key leader in the adoption of biotech crops, according to the ISAAA. The country tallied the most substantial percentage increase at 192% or 6.17 million acres to 9.38 million acres, jumping two spots in the world ranking to become the fifth largest producer of biotech crops in the world, surpassing China for the first time.

South Africa made significant strides in the past year to lead the African continent forward by almost tripling its biotech crop area. Notably, the gain came from Bt white maize, primarily used for food, and Bt yellow maize, used for livestock feed.

Growth also continues in the countries of the EU, where Slovakia became the sixth EU country out of 25 to plant biotech crops. Spain continues to lead the continent, planting 148,000 acres in 2006; however, the other five EU countries reported a five-fold increase in plantings, from 3,700 acres in 2005 to about 21,000 acres in 2006.

Future Growth: Biofuels, Rice, Drought Tolerance

ISAAA predicts growth to continue in the second decade of commercialization. “The commercialization of biotech rice alone could drive adoption of biotech crops well beyond the conservative estimate of 20 million farmers up to 80 million farmers,” says Clive James, chairman and founder of ISAAA and author of the report. This estimate is based on an adoption rate of one third by the world’s 250 million rice farmers, most of whom are small resource-poor farmers, 90% of whom are in Asia. Biotech rice with insect resistance to enhance yields could make a substantial impact on the UN Millennium Development goal of reducing poverty by half by 2015, says James, and golden rice with enhanced vitamin A could improve nutrition significantly.

Biofuels will also be a major growth driver. Biotech crops will be used to increase the efficiency of and meet added demand for alternative energy, as well as exploring biotech options to bring cellulose-based ethanol from energy crops to market. Another
driver will be biotech crops with drought-tolerant traits, expected to reach the market within the next five years, unlocking substantial production opportunities in drier climates, while increasing yield potential and decreasing irrigation needs (thus conserving water) in other areas.

While the Americas led the first decade of biotech crop adoption, James predicts that the second decade will likely feature significant growth in Asia and its developing countries of India, China, and the Philippines, as well as new biotech countries like Pakistan and Vietnam. In Africa, the experiences of South Africa will likely lead other countries to begin planting biotech crops, including Egypt, Burkina Faso, and Kenya, where promising field trials have already been conducted. Finally, the consistent global increase in adoption of biotech crops will likely prove to be a trend that merits increased recognition by the EU. France, as a leading member state, is a key example, increasing its area of Bt maize multi-fold to about 12,000 acres in 2006.

<table>
<thead>
<tr>
<th>Rank</th>
<th>Country</th>
<th>Area (million hectares)</th>
<th>Biotech Crops</th>
</tr>
</thead>
<tbody>
<tr>
<td>1*</td>
<td>USA</td>
<td>54.6</td>
<td>Soybean, maize, cotton, canola, squash, papaya, alfalfa</td>
</tr>
<tr>
<td>2*</td>
<td>Argentina</td>
<td>18.0</td>
<td>Soybean, maize, cotton</td>
</tr>
<tr>
<td>3*</td>
<td>Brazil</td>
<td>11.5</td>
<td>Soybean, cotton</td>
</tr>
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<td>4*</td>
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<td>6.1</td>
<td>Canola, maize, soybean</td>
</tr>
<tr>
<td>5*</td>
<td>India</td>
<td>3.8</td>
<td>Cotton</td>
</tr>
<tr>
<td>6*</td>
<td>China</td>
<td>3.5</td>
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</tr>
<tr>
<td>7*</td>
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<td>2.0</td>
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</tr>
<tr>
<td>8*</td>
<td>South Africa</td>
<td>1.4</td>
<td>Maize, soybean, cotton</td>
</tr>
<tr>
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<td>Soybean, maize</td>
</tr>
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</tr>
<tr>
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</tr>
<tr>
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</tr>
<tr>
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<tr>
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</tr>
<tr>
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<td>Maize</td>
</tr>
<tr>
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<td>Iran</td>
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<td>Slovakia</td>
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<td>Maize</td>
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* 14 biotech mega-countries growing 50,000 hectares, or more, of biotech crops
“As we look into the future at the second decade of commercialization, many factors are poised to drive substantial growth of biotech crops well beyond the early adopters,” says James. “It is in this decade that biotech crops can make a significant contribution and impact on the world’s 1.3 billion poor.”

While 22 countries planted commercialized biotech crops in 2006, since 1996 an additional 29 countries, totaling 51, have granted regulatory approvals for biotech crops for import for food and feed use and for release into the environment. A total of 539 approvals have been granted for 107 events for 21 crops. Thus, biotech crops are accepted for import for food and feed use and for release into the environment in 29 countries, including major food importing countries like Japan, which do not plant biotech crops.

Of the 51 countries that have granted approvals for biotech crops, the U.S. tops the list followed by Japan, Canada, South Korea, Australia, the Philippines, Mexico, New Zealand, the European Union, and China. Maize has the most events approved (35) followed by cotton (19), canola (14), and soybean (7).

Adherence to good farming practices with biotech crops, such as rotations and resistance management, will remain critical as it has been during the first decade, the ISAAA notes. Continued responsible stewardship must be practiced, particularly by the countries of the South, which will be the major new deployers of biotech crops in the second decade of commercialization of biotech crops, 2006 to 2015.

The complete report can be found online: www.isaaa.org.

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Conference News

FAO E-mail Conference Invitation: Water scarcity and agricultural biotechnologies

The FAO Biotechnology Forum is devoting its next e-mail conference to the role that biotechnologies can play in helping developing countries cope with water scarcity. Organised in collaboration with our colleagues in FAO’s water programme (http://www.fao.org/ag/agi/aglw/), it is one of the many activities planned to coincide with the World Water Day, which is celebrated each year on 22 March. This year its theme is “Coping with water scarcity” and FAO is the coordinating agency within the UN system for the theme. The primary focus of the conference will be on the use of biotechnology to increase the efficiency of water use in agriculture, while a secondary focus will be on two specific water-related applications of micro-organisms, in wastewater treatment and in inoculation of crops and forest trees with mycorrhizal fungi. To discuss and exchange experiences on this subject, we invite you to join the conference. The background document for the conference is available at http://www.fao.org/biotech/C14doc.htm. The conference is open to everyone, is free and will be moderated. It begins on 5 March and finishes on 1 April 2007. All e-mail messages posted during the conference will also be placed on the Forum website (http://www.fao.org/biotech/forum.asp). To join the Forum (and also register for the conference), send an e-mail to mailserv@mailserv.fao.org leaving the subject blank and entering the following text on two lines: subscribe BIOTECH-L
subscribe biotech-room2

Those who are already Forum members should leave out the first line of the above message, to register for the conference. For more information, contact biotech-mod2@fao.org.