New Biotech Initiatives at Texas A&M University, USA

Only insect resistant and herbicide tolerant biotech traits have been commercialized in cotton, though they were grown on about 70% of the world cotton area in 2013/14. In the twenty years since these traits were deregulated, no new trait has reached the commercial stage. Thus, the pace and the range of the introduction of new events can be regarded as slower and narrower. A great deal of effort has gone into developing new biotech traits such as colored cotton, technology protection systems, resistance to leaf curl virus, resistance to whitefly, resistance to boll weevil. The most recent and prominent traits under investigation are drought tolerance and nitrogen use efficiency. There may be many other areas that are equally important, but they have not been reported so far. The big question is then: when will the next biotech trait be commercialized in cotton?

The development of new biotech traits was originally expected to be a rather fast process. Scientists believed that the steps involved, i.e., extraction of DNA from an organism known to have the trait of interest, cloning, mass production of the modified gene inducts and other processes, would be faster than in conventional breeding this process resembled searching for something in the dark. It became evident that it was very important to be familiar with the biochemical and physiological action mechanisms and the regulation of gene expression, as well as to ensure the safety of the gene and the gene product to be utilized. Long before a genetically engineered crop is made available for commercial use, it is subjected to rigorous safety and risk assessment procedures. At first glance, the process seems to be cumbersome, but that is not the factor delaying the introduction of new traits. There is strong evidence linking the delay to many factors, but identification of a suitable gene, one with the desired action, seems to play a decisive role in delaying the induction of new traits. The following paragraphs look at some new areas of research currently being explored at Texas A&M University, USA. The original material was published in the January 2015 issue of the Texas A&M Plant Breeding Bulletin.

The University conducted a study to identify which, in their opinion, should be the top research and educational priorities for the future in Texas and around the world. The highest priorities identified were: feeding the world, protecting the environment, improving health, enriching youth with newer technologies, and growing the economy. These grand challenges called for proposals that would provide the basic collaborative structure to encourage interdisciplinary action designed to reach the desired goals. The Plant Improvement Group at the University identified four research areas where transformational breakthroughs are needed to develop a breeding technology that will drive improvements in productivity capable of meeting the challenges of feeding, clothing, and sheltering nine billion people by 2050 and 11 billion by 2100.The following are the four basic technology targets.

Gamete Cycling

Traditional breeding for genetic improvement of plants and animals has increased agricultural productivity dramatically, but is slower than engineering cycles because it is dependent on the biological duration of the life cycle (plants going from seed to seed, and animals reaching sexual maturity). It is theoretically possible, as has recently been demonstrated in mice, to develop fertile offspring from gametes (sperm and egg) produced from cells grown in culture media, thereby eliminating the step of sexual maturation. Combined with genomic technology, selection can then be done at the cell or gamete level, dramatically increasing the speed of the breeding process. This will likely make it possible to attain a turnover rate of five generations per year, as compared to the current three generations/year for maize, 1/year for cotton, 0.5/year for cattle, and 0.1/year for some tree species. It will also allow large population sizes to be maintained and selected, further increasing the rate of genetic gain, and at a fraction of the cost of maintaining plants and animals in the field.

Genome-wide Breeding

Genomic Selection (GS), or Whole Genome Selection, aims at simultaneously estimating multiple marker effects throughout the whole genome in order to establish their value in breeding for quantitative traits. Whole genome genotyping may provide new tools allowing plant breeders and geneticists to predict the best environments for selection nurseries, identify parents that can be used to create genetic variation for selection of improved genotypes, and provide genomic information for genetic selections that are highly associated with desirable phenotypes. Genome-Wide Selection considers allelic replication a potentially more effective way to deal with unbalanced phenotypic data than by replication of strains or phenotypes, which is common in applied breeding programs.

Genome Editing

One of the most promising potentially transformative areas that is complementary to Whole Genome Selection and High Throughput Phenotyping involves new technologies referred to as Genome Editing. This technology could provide breeders and genomicists with the ability to introduce or "knock in" precise alterations to a DNA sequence or expel or "knock out" specific genes from the sequence. Recent advances in mammalian genetics involve the use of "knock-out" or "knock-in" technologies that use engineered nucleases to cut the double-stranded DNA at a precise location. Then the technician either allows the strands to repair themselves (thus knocking out that gene) or inserts a modified DNA sequence from the same species, from other organisms or some other man-made DNA (a detectable signal, e.g.) into the chromosome, thereby producing a functional knock-in. Thus, with precise DNA alterations involving as few as one or two nucleotide changes or the introduction of a copy of a gene from the same species, this technology can enable genomic modifications in plants that would be indistinguishable from those produced by conventional breeding and induced mutagenesis.

High Throughput Phenotyping

A major challenge is to develop technologies that will allow plant improvement teams to apply genomics for improving quantitative traits such as yield, drought resistance, heat resistance, adaptation to the spatial variability of soil properties, nutritional components, etc. The current bottleneck in phenotyping technology is being addressed at several research centers through technologies collectively referred to as High Throughput Phenotyping. Plant improvement teams record a plethora of data types that require relatively large amounts of time per data point. High Throughput Phenotyping technologies would be coupled with genomic technologies, such as Whole Genome Selection, to associate quantitative trait loci or quantitative markers with a multitude of phenotypic measurements to identify the breeding value of potential parents or the genotypic/phenotypic value of individual plants and strains.

Application of these transformational technologies will lead to the development of improved crop cultivars with much needed traits such as biotic and abiotic stress resistance and nutritional enrichment. It is an accepted fact that the training of future plant improvement scientists is a major component in the drive toward fulfilling future expectations. The University is working on educating and training a diverse pool of innovative human capital. The Texas A&M University has been offering a distance learning degree course in plant breeding since 2013. With the exception of physical presence on campus at Texas A&M, all courses and requirements are the same for the off-campus students; all courses are the same as those taken by on-campus students, and they are all taught by the same professors, except that they are delivered via the Internet. Dr. Wayne Smith, a renowned cotton researcher, has been at the forefront of this program. This is an excellent opportunity for cotton researchers to improve their qualifications. Additional information is available at https://scsdistance.tamu.edu/purchase/.