MOLECULAR BIOLOGY AND GENOMICS: OVERVIEW AND APPPLICATIONS IN WEED SCIENCE. Gregory R. Heck, Senior Molecular Biologist. Monsanto Company, 700 Chesterfield Parkway West, Chesterfield, Missouri 63017.

Unprecedented advancements in tools to understand genes, phenotypes, biological systems and environmental interactions have emerged in recent years. Collectively massed under the heading of "Genomics", these tools build on many technologies, some having their first appearance decades ago. The distinction for genomics is scale, breadth and throughput of current analyses. Rather than tracking the behavior of a single or small number of genes, entire gene networks can be assessed.

Large scale sequencing ushered in the era of genomics by providing complete organism sequences (genomes). The first finished genomes were bacterial. Although bacteria are far simpler organisms than higher plants, relevant genomes for the plant science community include photosynthetic cyanobacteria (e.g. *Synechocystis*), antecedents to the chloroplast. Both dicot (*Arabidopsis*) and monocot (rice) genomes are now accessible (www.ncbi.nlm.nih.gov/Genomes/index.html). Relatively small gaps in these genome sequences remain to be closed, but they are sufficiently complete to allow assessment of genome organization and the gene complement of higher plants. Other plant species have sequence information available in the form of Expressed Sequence Tags (ESTs) or cDNA representing segments of transcribed genes (www.ncbi.nlm.nih.gov/dbEST/dbEST_summary.html). For weed scientists, leveraging these reference genomes and EST collections can assist in gene discovery for weedy species that are unlikely to have their own genomic information. High homology has been shown to exist in closely related plant family members, enabling comparative genomics to determine the structure and orthology of genes. Approximately 80% of the *Arabidopsis* genes have recognizable homologs in rice, lending hope that weed species will be similar and that topics such as herbicide targets, resistance biology, and competitive characteristics can be studied in model species and their ecotypes.

Transcriptomics is the quantitative and qualitative comparison of the transcriptomes (the complete set of transcribed sequences in the genome at a given point in time). Synthesis of thousands of gene sequences on chips and hybridization with fluorescently labeled cDNA from comparative samples now permits the transcript profiling in response to developmental or environmental influences. Cascades of gene expression can be visualized and cohorts of gene expression changes monitored through time and can assist in response dissection. Current transcriptional profiling capability largely centers on the Arabidopsis and rice genomes. Use of these heterologous species chips for weed transcript profiling is possible, but limited due to the specificity of hybridization. Technologies that can rapidly synthesize chips from EST information or utilize emerging open platforms methodologies promise the ability of increased precision in weed transcript profiling.

Proteomics and metabolomics seek to compare the accumulated protein and small molecule profile of organisms, respectively. Since there can be a non-linear relationship extending from gene transcription to presence of an enzyme or its activity, these tools are important for a complete understanding of how genes interact to produce phenotype. Limitations include the ability to visualize all proteins by 2-D electrophoresis for proteomics and the difficulty in accommodating wide ranging chemical properties of a complete metabolite profile.

The role of a large number of genes remains to be determined. Functional genomics attempts to understand genes by creating collections of plants or microbes harboring evaluative libraries or mutant endogenous genes and screening them for altered phenotype. Insertional mutagenesis with transposons or transgenes (T-DNA) can "knock-out" (eliminate) function or be designed to activate gene expression through the use transformed enhancers and promoters. In limited situations, primarily cyanobacteria (*Synechocystis*) and the moss model systems (e.g. *Physcomitrella*), "knock-ins" are also possible where homologous recombination can be used to replace an endogenous sequence with a targeted mutation – applicable where a gene orthologous to a higher plant gene exists.

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