

## **Progress Report for Crop Functional Genomics Program in Korea**

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The 21st Century Frontier R&D Program has been developed by the Ministry of Science and Technology to boost national competitiveness in science and technology, improve the quality of life, and benefit humanity. The Crop Functional Genomics Center (CFGC), which belongs to the program, focuses on the functional genomic study for crop improvement. Unraveling the complex relationship between genes and phenotypes and applying this information to developing better crops are dependent on co-operative works in genomics, transformation, and molecular breeding, and should eventually make a significant contribution to global food security. For the 10 years of period, the CFGC will run target-oriented basic research and their application projects in the fields of plant functional genomics, crop transformation, and plant molecular breeding. To overcome the limits of novelties in outcome, over 500 novel genes for crop transformation will be identified and characterized using genomic information. To demonstrate the usefulness, at least 10 new crop varieties with desirable traits will be developed using transformation or marker-assisted selection technology. Since we believe that promoting basic science is the best way to improve scientific competitiveness in the world market, this program places a strong emphasis on original and creative ideas. Science and technology have made extraordinary progresses in the last century and have contributed tremendously to improving human life. We are among those responsible for leading 21st century science, and we are convinced that all our goals can be achieved by establishing a new paradigm for global collaboration.

During the first 3 years of the program, projects developing research tools and resources have been emphasized, which can be shared and utilized with other scientists throughout the program duration to identify genes and transform major crops essential for genetic improvement. Insertion mutant pools of rice tagged with T-DNA or Ac/Ds have been built up. Tagged mutants exhibiting phenotypes with altered agronomic traits are being characterized. Flanking sequences on tag insertion sites of over 30,000 mutants are being characterized and released to the public through <http://www.cfgc.snu.ac.kr>. Mutant seeds are available upon request. A rice 60K genome-wide oligomeric DNA microarray had been developed. A DNA chip containing 10K pepper genes was printed and is being distributed. Experimental

results obtained with those chips are released to the public through the web. Those activities are being continued to build up more resources and information in the 2nd phase. These tools and resources make high through-put screening more efficient.

Although conventional plant-breeding programs have improved yields for crops grown in stressful environments, there is a growing belief that further gains can only be achieved through targeted manipulation of genes involved in stress resistance. By using those various functional genomics tools and resources, such target genes are screened out and their functional is being studied in detail. Most of them are related to the developmental processes, pathogen and/or stress responses, signal transduction, metabolism etc. Efforts to understand function of genes affecting agronomic traits are carried out also by individual scientist and a variety of novel genes such as *PAPP5*, *NDPK2*, *ABF2 & 3*, *BOP1*, *GmEXP1*, *OsHDAc*, *HpaG*, *Ore14*, *15 & 17*, etc have been discovered. *PAPP5* is a phytochrome specific type 5 protein phosphatase specifically dephosphorylates biologically active Pfr-phytochromes and enhances phytochrome-mediated photoresponses. Depending on the specific serine residues dephosphorylated by *PAPP5* at high light, phytochrome stability and affinity for a downstream signal trans-downducer, *NDPK2*, were enhanced. Functional pathogenomics to identify the genes important for pathogenicity including toxin production, disease-related enzyme biosynthesis, and symptom development also showed tremendous progress. Genome sequencing, generation of transposon-tagged mutants pools, and screening for non-pathogenic mutants and toxin non-producers has been carried out with *Burkholderia glumae*, a causal agent of bacterial grain rot of rice. Gene locuses for biosynthesis of toxoflavin, its transporter, and Hrp pathogenicity island has been identified and characterized.

International cooperative activity is also being supported. The International Solanaceae Genome Project supported by 19 countries launched 2004. Chromosome 2 of tomato is assigned to Korean delegate and 12% of genome will be sequenced in next 4 years. Massive cDNA sequencing of pepper is also being carried out in parallel to make a link to tomato genome.

To coordinate collaborative research, a database, Kropbase, has been constructed. We have also established a seed and genetic resource stock center that maintains such information, tools and resources to support the program. These resources are freely available even to the public through the web.

Massive transformation of major crops will accelerate functional annotation of useful genes and commercialization of transgenic varieties. Collaborative research activities between gene cloner and plant transformer to generate transgenic crops are highly encouraged. Environmental stress resistant rice was obtained through

transformation with genes encoding trehalose synthesis enzymes. Transgenic rice resistant to rice leaffolder was developed by transformation with *cry1Ac* gene. Soybean and pepper is notorious for its recalcitrance to genetic transformation. Efficient transformation protocols for inbred lines have been developed and disease resistant pepper was obtained by transformation with PepEST gene. Currently those events are under the process to evaluate food and environmental safety of the transgenic crops.

Marker assisted selection is a useful molecular breeding tool to improve the efficiency of conventional breeding. Molecular marker is being developed to construct molecular linkage maps of QTLs, hybrid vigor and other agronomically useful traits. MAS is also being utilized to combine the desirable traits of *indica* (or Tongil) varieties into *japonica* ones and to incorporate useful traits from wild and weedy rice by using subspecies-specific markers .

Since we believe that promoting basic science is the best way to improve scientific competitiveness in the world market, this program places a strong emphasis on original and creative ideas. Science and technology have made extraordinary progresses in the last century and have contributed tremendously to improving human life. We are among those responsible for leading 21st century science, and we are convinced that all our goals can be achieved by establishing a new paradigm for global collaboration.

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### **Education**

B.S. in Agricultural Chemistry, Seoul National University (1972-1976)

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### **Professional Experience**

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