The 21st Century Frontier R&D Program was developed in 2000 by the Ministry of Science and Technology of Korea 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 the development of better crops are dependent on cooperative works in genomics, transformation, molecular breeding, and should eventually make a significant contribution to global food security.

CFGC is a virtual institution supporting research projects that are carried out in universities, research institutes, and industries throughout the nation. During the 10 years of the program 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 maximize the novelties of the final outcome, over 500 novel genes for crop transformation will be identified and characterized via genomic approaches. At least 10 new crop varieties with desirable traits will be developed using transformation and marker-assisted selection technologies. 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.
Program Summary

- Final goal: to characterize 500 novel genes through functional genomic approaches
- Period: 10 years (2001/7/1 – 2011/6/30)
- Funds: US$113 mln (government US$100 mln, private sector US$13 mln)
- Granted institutes: 27 (university 18, research institute 4, industry 5)
- Research scientists: 637 (PhD 172, MS 221, etc. 244)

During the first 5 years of the program, development of the infrastructural research tools and resources has been emphasized, and will be shared and utilized with other scientists throughout the program period to identify genes and transform major crops essential for genetic improvement. Insertion mutant pools of rice tagged with T-DNA (led by G. An of POSTECH) or Ac/Ds (led by M.Y. Eun of NIAB) have been built up. Tagged mutants exhibiting phenotypes with altered agronomic traits are being characterized. Flanking sequences on tag insertion sites of over 31,730 mutants have been characterized and released to the public through http://www.cfgc.snu.ac.kr and the FST database at Salk Institute (http://signal.salk.edu/cgi-bin/RiceGE). G. An’s T-DNA insertion lines hit more than 50% of the rice genes. Mutant seeds are available upon request.

Marker Insertion Mutant Pools of Rice

- Goal:
  1. to develop a large scale of insertional mutagenized population
  2. to obtain molecular information on tagged insertion sites
  3. to share resources for functional analysis of rice genes
- Systems:
  1. T-DNA insertion mutant pool
  2. Ac/Dc-tagged pool
- Significance:
  1. Mutant phenotype offers a direct way to relate a gene to its function
  2. Insertion tag offers a direct way to locate the mutated gene
- Publications:

The rice 60,000 genome-wide oligomeric DNA microarrays have been printed, and are being distributed by B.H. Nahm of Green Gene Biotech (http://www.ggbio.com) and M.K. Kim of Seoul National University. Recently, they have upgraded the microarray by in situ synthesis of 300,000 oligonucleotide probes of exon sequences on a slide. Experimental results obtained with these chips have also been released to the public through the web. The activities are being continued to build up more resources and information in the second phase. These tools and resources make high-throughput screening more efficient.
Rice Whole Genome Exon Microarray (env2.0)

- 355,168 probes/slide
- 1 probe/300 bp exon, 5.5 probes/gene
- Genes with defined direction and ORF: 37,398
- Genes with defined direction and no ORF: 15,102
- Genes with inconclusive direction: 4,449
- Predicted genes: 17,537
- Mitochondrial genes (123), chloroplast genes (74)
- Markers (5): Gus, GFP, Bar, Kan, Hyg

Advantages of exon microarray:
- samples as low as 5 µg of total RNA
- to test alternative splicing
- to test cross-hybridization
- markers confirm the transformation

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 various functional genomic tools and resources, such target genes are screened out and their functions are being studied in detail. Most of them are related to the developmental processes, pathogen and stress responses, signal transduction, metabolism, etc. A variety of novel genes, including PAPP5, NDPK2, ABF2, ABF3, BOP1, GmEXP1, OsHDAc, HpaG, Ore14, Ore15, and Ore17, have been studied. PAPP5 is a phytochrome-specific type 5 protein phosphatase that 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 transducer, NDPK2, were both enhanced.

In addition, a functional pathogenomics study to identify the genes important for pathogenicity, including toxin production, disease-related enzyme biosynthesis, and symptom development, showed significant progress. Genome sequencing, generation of transposon-tagged mutant pools, and screening for nonpathogenic mutants and toxin nonproducers have been carried out with Burkholderia glumae, a causal agent of bacterial grain rot of rice. Genetic loci for the biosynthesis of toxoflavin, its transporter, and the Hrp pathogenicity island have been identified and characterized by I.G. Hwang of Seoul National University.

International cooperative activity is also being supported. The International Solanaceae Genome Project, supported by 19 countries, was launched in 2004. Chromosome 2 of tomato has been assigned to the Korean delegate, Doil Choi of Seoul National University, and 12% of the genome will be thereby sequenced in the next 4 years. In parallel, massive EST sequencing of pepper is being carried out to make a link to the tomato genome.

As an effort to coordinate and expedite the collaborative research, the CFGC database Kropbase (http://kropbase.snu.ac.kr) has been constructed by M.K. Kim of Seoul National University. We have also established a seed and genetic resource stock center that maintains such information as well as the tools and resources needed to support the program. These resources are freely available, even to the public.
Massive transformation of major crops will accelerate functional characterization of useful genes and commercialization of transgenic varieties. Collaborative research activities between gene cloners and plant transformers to generate transgenic crops are highly encouraged. Environmental stress-resistant rice has been produced through transformation with genes encoding trehalose synthesis enzymes by Jukon Kim of Myongji University. Transgenic rice resistant to rice leaffolder has been also developed by transformation with the modified cry1Ac gene. Soybean and pepper are notorious for their recalcitrance to genetic transformation. Efficient transformation protocols for inbred lines have been developed, and disease-resistant pepper has been subsequently obtained by transformation with the PepEST gene and CP gene of CMVPO by C.H. Harn of Nongwoo Bio Co. The processes to evaluate the food and environmental safety of developed transgenic crops are underway.

Marker-assisted selection (MAS) is a useful molecular breeding tool to improve the efficiency of conventional breeding. Molecular markers are being developed to construct molecular linkage maps of QTLs, hybrid vigor, and other agronomically useful traits. MAS is also being exploited to incorporate the desirable traits of indica (or Tongil) varieties into japonica ones, or to utilize the useful traits from wild and weedy rices.

Science and technology have made extraordinary progress in the last century, contributing tremendously to the improvement of human life. We are among those responsible for leading 21st-century science and technology, being convinced that all our goals can be achieved by establishing continuous and new horizons for global collaboration.