

Construction of Primer Database using Gene Coding Regions of *Arabidopsis*

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Objectives

We have constructed primer database using entire gene sequences on *Arabidopsis* genome to prepare a scaffold for comparative mapping between *Arabidopsis* and *Brassica rapa*.

Materials and Methods

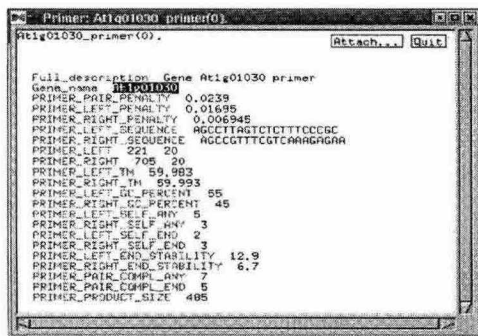
1. Materials: full sequences of *Arabidopsis* genome, composed of five chromosomes, obtained from GenBank.
2. Methods
 - parse of sequences of entire gene coding region (26,828 genes) on *Arabidopsis* genome
 - design of primer for entire gene coding regions using high-throughput method (3) saving of information of genes and primers into ACEDB.

Results and Discussion

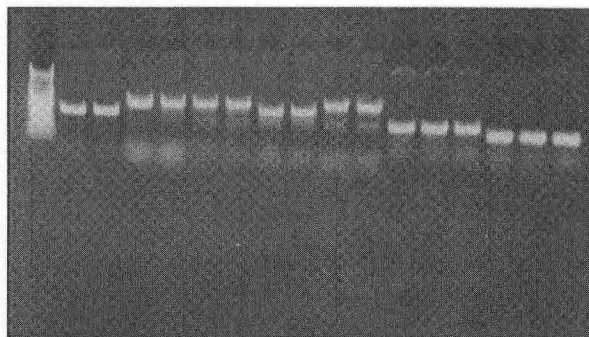
We constructed *Atgene* primer database (www.brassicagenome.org) based on ACEDB, having objected-oriented model and cross-referencing among genomic data. The result generated the design for 129,885 primers against 26,828 genes. *Atgene* primer database has the 6 classes containing chromosome, sequenceMap, locus, gene name, primer, sequence. Now we have designed the primers for the partial mRNA, approximately 300-500bp, of *Arabidopsis* to use as the high-sensitivity probe as well as the universal primers for the conserved region among genes at a level of protein. This database may have the advantage of identifying genes, determining their functions, and especially, comparing for gene structure between *Arabidopsis* and *Brassica*.

Acknowledgement

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AtGene primer database



PCR experiment using AtGene primer database