CAPSMaker: A streamlined SNP-based high-throughput marker design system for realizing digital breeding in soybean

Joo-Seok Park[1,2], Yo-Ram Choi[1], Jin-Hyun Kim[3], Chae-Young Lee[3], Min-Gyun Jeong[1], Yeong-Il Jeong[1], Yang Jae Kang[4*], Hong-Kyu Choi[5*]

[1]Department of Applied Bioscience, Dong-A University, Busan, Korea;

[2]Research Institute of Molecular Alchemy, Gyeongsang National University, Jinju, Korea.

[3]Department of Medical Bioscience, Dong-A University, Busan, Korea;

[4]Division of Life Science Department, Gyeongsang National University, Jinju, Korea;

5Department of Molecular Genetics, Dong-A University, Busan, Korea;

The development of next-generation sequencing (NGS) and bioinformatics tools has revolutionized the study of genetic markers, which are crucial for breeding crops with desirable agronomic traits. These technological advances have allowed scientists to explore genetic variations on an unprecedented scale, leading to more efficient and precise breeding programs. Despite the creation of numerous tools to enhance the convenience, accuracy, and efficiency of molecular breeding, they often focus on genetic variants in short user-input sequences, neglecting the vast potential of omics data for genomic variants. This limitation has created a significant gap in effectively utilizing large-scale genomic data. To address this gap and facilitate the design of molecular markers across the entire genome in soybean, we developed CAPS Maker, an automated web-based platform for designing cleaved amplified polymorphic sequence (CAPS) and derived CAPS (dCAPS) markers. CAPS Maker features a user-friendly graphical interface, including a 'SNP Browser' and a 'Primer Table,' along with internal programs that design uniquely activated primer pairs. This ensures high specificity and efficiency in marker creation. CAPS Maker enables researchers to automatically design CAPS/dCAPS markers for developing new soybean cultivars with valuable traits, leveraging its capability to manage highly duplicated genomes.

*Corresponding author: Yang Jae Kang (Tel. 055-772-1352, E-mail: kangyangjae@gnu.ac.kr), Hong-Kyu Choi (Tel. 051-200-7508, E-mail: hkchoi@dau.ac.kr)