

Web interface for breeding design based on phenotype-mapped pedigree information in soybean cultivars

Min-Gyun Jeong¹, Chaeyoung Lee^{2,3}, Jin Hyun Kim^{2,4}, Yoram Choi¹, Hye Jeong Kim⁵, Young-Soo Chung⁵ and Hong Kyu Choi^{5*}

¹*Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea*

²*Department of Applied Bioscience, Dong-A University, Busan, Republic of Korea*

³*Dongnam Institute of Radiological & Medical Sciences, Busan, Republic of Korea*

⁴*Genomics Division, Department of Agriculture Biotechnology, National Institute of Agriculture Sciences, Rural Development Administration, Jeonju, Republic of Korea*

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

*Corresponding author: hkchoi@dau.ac.kr

For breeding design, parental information of any domesticated species is an important source because it's an indicator of the genetic relationship among bred lines. As the accumulation of genome and phenome data on cultivars rapidly increases, well-structured pedigree and system to utilize it have played a key role. For this reason, we intended to construct a pedigree-based web interface to link the phenotypic information and genealogical relationship of soybean cultivars. A well-structured pedigree of 178 korean soybean cultivars and its phenotype information were used as key data for database construction. Three submodules consisting of pedigree-, tabular- and single cultivar-based search pages constitute the web interface. Furthermore, comparison of the parental information and a SNP-based phylogeny from cultivars in its pedigree presented that there is a certain degree of correlation between them. Our web page is developed as an intuitive auxiliary system for breeding design in the future and plans to expand itself to a global database by integrating international soybean data. This web interface is available at <https://tgil.donga.ac.kr/SoyPedi/index.html>