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Advances in genome sequencing and annotation have eased the difficulty of identifying new gene sequences. Predicting the functions of these newly identified genes remains challenging. Genes descended from a common ancestral sequence are likely to have common functions. As a result, homology is widely used for gene function prediction.

Non-homology-based prediction of gene functions in maize ...

Genome synthesis potentially allows the researchers to gain a much greater degree of control of an organism, and it also leads to a completely new way to understand the biology of genomes. In 2008, the first mega-size bacteria genome was built from oligonucleotides . Next, the 4-Mb genome of E. coli was redesigned and engineered [2, 3].

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To make the pan-genome represent the full range of genetic diversity of soybean, we sequenced a total of 2,898 soybean accessions (871 from our previous studies [Fang et al., 2017, Zhou et al., 2015] and 2,027 from this study) by Illumina technology with an average coverage depth of more than 13× for each accession (Figure 1A; Table S1).These accessions included 103 wild soybeans, 1,048 ...