

# The Recognition and Utilization of Natural Genetic Resources for Advances in Plant Biology through Genomics and Biotechnology

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## 1. Introduction

Biological diversity is the most essential gift from nature, and many elite or superior genes that confer favorable traits remain to be discovered and utilized. With the advancement of “omics” development, plant genetic resources and biodiversity have become more attractive for future agricultural and horticultural advancements. The data mining of these genetic resources to advance domestication has great potential for enhancing the crop yield and quality through molecular breeding and genetic engineering. A better knowledge of accumulated genomic plant resources would help us to provide a fundamental understanding of the underlying genetics, physiology, biochemistry, and metabolism fields, with the aim of developing improved breeding technology for future agriculture and horticulture.

The introduction of newly identified germplasms for major crops allows us to improve their valuable traits, such as oil, fiber, and bioproduct production, and enables us to grow the understanding of the genetic background, genome information, proteome, and metabolome of plants. Second- and third-generation sequencing, GWAS, transcriptomics, proteomics, metabolomics, and the genetic basis of quality and production have been widely developed.

## 2. Results

A total of 25 manuscripts were submitted to this Special Issue, and 14 manuscripts were accepted and published. The contents of these manuscripts include genetic resources, genomics, biotechnology, genetic transformation, and tissue culture ([https://www.mdpi.com/journal/agronomy/special\\_issues/genetic\\_resources\\_biotechnology#keywords](https://www.mdpi.com/journal/agronomy/special_issues/genetic_resources_biotechnology#keywords), accessed on 25 April 2024).

With regard to genetic resources, Fu et al. identified an important lobed-leaf phenotype candidate gene (*BjLM11*) of *Brassica juncea* L., which was found by an F<sub>2</sub> population derived from ‘MN001’ and ‘MU056’ that was constructed using GradedPool-Seq [1]. Luo et al. reviewed and summarized the studies on the phyto-physiological chemistry, cytology, molecular biology, and genomics of *Houttuynia cordata* Thunb., an important medicinal and vegetable plant in China [2]. Road deicing salts are widely used during the winter in northern China, and Columbine (*Aquilegia*), a herb with ornamental and commercial values, has been considered and evaluated for salt tolerance by monitoring their germination state with three *Aquilegia* species (*A. oxysepala*, *A. parviflora*, and *A. viridiflora*). The results showed that *A. oxysepala* is suitable for being planted as a ground cover in urban areas based on salt tolerance [3]. Genetic diversity and population structure in Türkiye bread wheat germplasm were analyzed by Haliloglu et al. using iPBS-Retrotransposons-based markers for carrying out improved nutrition evaluations [4].



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In genomics (including other omics), the complete chloroplast genome of *Brasenia schreberi* has been reported by Sun et al. [5]. In a study on the genome-wide analysis ABCB genes for secondary cell wall (SCW) development in Moso bamboo (*Phyllostachys edulis*), the results showed that eight *PhABCB* genes, *PhABCB7*, *PhABCB11*, *PhABCB14*, and *PhABCB21* may be involved in the SCW biogenesis [6]. Moreover, the *FaMAX1* gene related to drought tolerance and the regulation of *Festuca arundinacea* Schred plant tillering was identified by Yang et al. [7].

In biotechnology, GradedPool-seq was used for a lobed-leaf phenotype study in *B. juncea* [1]. iPBS-Retrotransposons-based markers were used for analyzing genetic diversity and population structure in Türkiye bread wheat germplasm [4], a genome sequence was used for *B. schreberi* chloroplasts [5], and de novo transcriptome was used for drought tolerance and the regulation of the plant tillering analysis of *F. arundinacea* Schred [7]; CRISPR/Cas9 was also used for the construction and functional evaluation of multiple knockout vectors of the *FAD2* gene family of soybeans, and the results showed that the knockout expression of multiple *FAD2* genes increased soybean oleic acid content and decreased linoleic acid content [8].

Tissue culture (vitro culture) is an important experiment technique widely used for plant reproduction, transformation, and functional verification of biological genes, etc. Wang et al. used an in vitro culture for modified gene expression, DNA methylation, and small RNA expression in rice [9]. Miroshnichenko et al. evaluated the morphogenic response of a donor of an A<sup>u</sup> genome of modern wheat in vitro [10].

Red *Toona sinensis* (A. Juss) Roem is a woody and spring seasonal vegetable in China, and its buds exhibit rapid dehydration, wilting, vigorous breathing, and transpiration after picking. Its stem sections are prone to browning, with Zhao et al. reporting a comparative physiological analysis of the lignification, anthocyanin metabolism, and correlated gene expression in red *T. sinensis* buds during cold storage [11]. The lignin biosynthesis gene 4CL (4-coumarate: coenzyme A ligase) of *Apium graveolens* L. was also identified by Zhong et al. using gene cloning, bioinformatics analysis, and transgenic *Arabidopsis thaliana* [12]. The effect of bee pollination efficiency on the quality and yield of strawberries was investigated by Liu et al., who analyzed the composition of strawberry flower volatiles and their effects on the behavior of strawberry pollinators, *Bombus terrestris* and *Apis mellifera*. Their study provided a reference for formulating more reasonable bee pollination practices to improve strawberry fruit quality [13]. Soil microbes have important roles in soil ecosystems and Cyanobacteria, which are widely regarded as important soil microorganisms for agricultural production. With regard to this topic, the community composition specificities in paddy soil under different ecological conditions were researched by Song et al. [14].

### 3. Future Perspectives

This Special Issue, titled “The Recognition and Utilization of Natural Genetic Resources for Advances in Plant Biology through Genomics and Biotechnology”, has come to a closure. We are very grateful for the efforts made by journal editors, peer reviewers, and relevant authors. Without their help, this research topic would not be presented to the readers of *Agronomy*. We also would like to thank all colleagues who contributed to this Special Issue. Moreover, the subsequent Special Issue, “Recognition and Utilization of Natural Genetic Resources for Advances in Plant Biology through Genomics and Biotechnology Volume II”, is currently online and accepting applications ([https://www.mdpi.com/journal/agronomy/special\\_issues/2F8G6PNGS0](https://www.mdpi.com/journal/agronomy/special_issues/2F8G6PNGS0), accessed on 25 April 2024), for which we hope to obtain novel research results and the latest research manuscript submissions in this field.

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