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Progress of soybean germplasm collection, creation, evaluation and utilization in China  
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China has the most abundant soybean germplasm in the world, but there still has gaps for collection, creation, evaluation and utilization of the germplasm. Since 1999, a number of wild soybean accessions and newly developed cultivars has been collected, and the total number of accessions in the collection has reached 40,000 including 30,000 *Glycine max* and 10,000 for *Glycine soja*. In order to increase the genetic diversity, new EMS mutagenized lines with various seed composition, seed shape, plant morphology, and maturity were developed and preserved in the collection. The mutation rate of the EMS mutagenized population was approximately  $\sim 1/12.5$  kb based on whole-genome resequencing analysis. We created and evaluated core collections and identified accessions with one or more favorite traits including resistance to frogeye spot, soybean mosaic virus, or soybean rust, tolerance of salinity or drought, high protein or high oil etc. Association analyses of various populations identified molecular markers related to favorite traits, some of these markers were used to screen the germplasm for novel genes. Compared to the traditional nature variation in the accessions, mutants can accelerate the process to determine genes controlling quantitative traits, such as plant height and branching. The markers identified from resequencing 25 cultivated soybean, 7 wild soybean and association mapping were included in DNA chip and to facilitate gene discovery. The availability of the phenotypes and genotypes of the accessions has promoted usage of Chinese germplasm for functional genomics research and genetic improvement in soybean.