

Collection, Evaluation, and Utilization of Cotton Germplasm in China

DU Xiong-ming, ZHOU Zhong-li, SUN Jun-Ling, PAN Zhao-e, JIA Yin-hua

(Cotton Research Institute, Chinese Academy of Agricultural Sciences; Key Laboratory of Cotton Genetic Improvement, Ministry of Agriculture, Anyang, Henan 455000, China)

A total of 8193 accessions, including 6822 *Gossypium hirsutum*, 350 *G. hirsutum* race (sub-species), 385 of *G. barbadense*, 378 of *G. arboreum*, 17 of *G. herbaceum* and 41 wild species, of cotton germplasm are now maintained in China. This germplasm is kept in Beijing National Long-term Genebank and Anyang Cotton Medium-term Genebank. Live plants of the wild species are kept in Cotton garden at Hainan Island. A total of 2222 accessions including 2013 *G. hirsutum* and 209 *G. barbadense* cotton germplasms were introduced from 53 foreign countries during past 100 years. The top five countries with large numbers of introduced germplasm were America, Russia, Australia, Pakistan, and Egypt. A cotton germplasm database system was also established. Total 14580 accessions of cotton germplasm were distributed to 9 countries and 23 provinces or cities in China in 1984–2007, averaging 634 accessions per year. 1756 accessions of superior germplasm were distributed to China in the past. Some of them have been distributed for more than 20 times such as PD lines. 206 new cotton varieties/lines have been bred and released in 1984–1998 through the utilization of 281 accessions of germplasm, which are 3.4% of total maintained accessions. A series of transformation techniques have been used in the process of developing germplasm. Variant lines were derived from progenies of upland cotton, and showed significant differences from the wild-type recipient in terms of fiber quality, lint percentage, boll weight and other agronomic traits. The genetic diversity of main sources germplasm of upland cotton with different parental origins, breeding periods, and ecological growing areas, and cotton introgressed lines from interspecific hybridization were studied on the basis of simple sequence repeat (SSR) markers. Meanwhile, SSR fingerprinting analysis on distinct mutants of fiber development in *G. hirsutum* was set up. These studies give an overview of the genetic diversity of the cotton germplasm in China, and provide a guide for breeders to develop new cultivars efficiently.