

1868 Impacts of Domestication, Breeding and Polyploidization on Plant Genome Evolution Revealed in *Gossypium*: The NBS-LRR Encoding Gene Family

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Domestication, breeding and polyploidization represent three major forces of crop plant genome evolution. However, little is known about how these activities influence the evolution of crop plant genomes at the genomic level. The nucleotide-binding site (NBS)-leucine-rich repeat (LRR) encoding gene family, probably consisting of >1,000 gene members in the cotton genome, represents a large multigene family in plants. It not only contributes to plants at least 80% of the genes conferring resistance to various pathogens, but also is a desirable model system to address this question. We have investigated the variation and fate of the gene family in the course of the evolution of 35 species representing all eight basic genome groups of the genus *Gossypium*, with special emphasis on domestication, breeding and polyploidization. The results provide the first insights into how crop plant domestication, breeding and polyploidization affect the fate and evolution of a multigene family that is subjected to both natural and artificial selection. The knowledge will provide novel basis for plant genetic improvement and breeding, especially breeding for biotic stress resistance.