

Genomic Resequencing Unravels the Genetic Basis of Domestication, Expansion, and Trait Improvement in *Morus Atropurpurea*

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Mulberry is an economically important plant in the sericulture industry and traditional medicine. However, the genetic and evolutionary history of mulberry remains largely unknown. Here, we this work presents the chromosome-level genome assembly of *Morus atropurpurea* (*M. atropurpurea*), originating from south China. Population genomic analysis using 425 mulberry accessions revealed that cultivated mulberry is classified into two species, *M. atropurpurea* and *Morus. alba*, which may have originated from two different mulberry progenitors and have independent and parallel domestication in north and south China, respectively. Extensive gene flow is revealed between different mulberry populations, contributing to genetic diversity in modern hybrid cultivars. This work also identifies the genetic architecture of the flowering time and leaf size. In addition, the genomic structure and evolution of sex-determining regions are identified. This study significantly advances the understanding of the genetic basis and domestication history of mulberry in the north and south, and provides valuable molecular markers of desirable traits for mulberry breeding.