



Development of EST-SSR markers related to disease resistance and their application in genetic diversity and evolution analysis in *Gossypium*

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ABSTRACT. Cotton (*Gossypium* spp) is one of the most economically important crops that provide the world's most widely used natural fiber. Diseases such as Fusarium wilt and particularly Verticillium wilt seriously affect cotton production, and thus breeding for disease resistance is one of the most important goals of cotton breeding programs. Currently, potential exists to improve disease resistance in cultivated cotton. Increasing the understanding of the distribution, structure, and organization of genes or quantitative trait loci for disease resistance will help the breeders improve crop yield even in the event of disease. To facilitate the mapping of disease-resistance quantitative

trait loci to achieve disease-resistant molecular breeding in cotton, it is necessary to develop polymorphic molecular markers. The objective of this study was to develop simple sequence repeat markers based on cotton expressed sequence tags for disease resistance. The efficacy of these simple sequence repeat markers, their polymorphisms, and cross-species transferability were evaluated. Their value was further investigated based on genetic diversity and evolution analysis. In this study, the unique sequences used to develop markers were compared with the *G. arboreum* and *G. raimondii* genome sequences to investigate their position, homology, and collinearity between *G. arboreum* and *G. raimondii*.

Key words: Disease resistance; Evolution; *Gossypium*; Expressed sequence tag-simple sequence repeat; Genetic diversity