



Methylation-sensitive amplified polymorphism analysis of *Verticillium* wilt-stressed cotton (*Gossypium*)

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ABSTRACT. In this study, a methylation-sensitive amplification polymorphism analysis system was used to analyze DNA methylation level in three cotton accessions. Two disease-sensitive near-isogenic lines, PD94042 and IL41, and one disease-resistant *Gossypium mustelinum* accession were exposed to *Verticillium* wilt, to investigate molecular disease resistance mechanisms in cotton. We observed multiple different DNA methylation types across the three accessions following *Verticillium* wilt exposure. These included hypomethylation,

hypermethylation, and other patterns. In general, the global DNA methylation level was significantly increased in the disease-resistant accession *G. mustelinum* following disease exposure. In contrast, there was no significant difference in the disease-sensitive accession PD94042, and a significant decrease was observed in IL41. Our results suggest that disease-resistant cotton might employ a mechanism to increase methylation level in response to disease stress. The differing methylation patterns, together with the increase in global DNA methylation level, might play important roles in tolerance to *Verticillium* wilt in cotton. Through cloning and analysis of differently methylated DNA sequences, we were also able to identify several genes that may contribute to disease resistance in cotton. Our results revealed the effect of DNA methylation on cotton disease resistance, and also identified genes that played important roles, which may shed light on the future cotton disease-resistant molecular breeding.

Key words: Cotton; *Verticillium* wilt;
Methylation-sensitive amplification polymorphism