Supplementary information:

Developing conversed microsatellite markers and their implications in evolutionary analysis of the *Bemisia tabaci* complex

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Table S1 Microsatellites predicted from the transcriptomes of the three species. Microsatellite motifs, sizes and relative microsatellite-containing sequences were listed.

Table S2 The location of microsatellites in 3'UTR, 5'UTR and CDS regions. The location, microsatellites motif and nr annotation of each microsatellite-containing sequences in MEAM1, MED and Asia II 3 were shown.

Table S3 Number of microsatellite-containing genes mapped to KEGG pathway among the three species.

Table S4 Microsatellite-containing genes in 'Lysosome', 'Drug metabolism-other enzymes' and 'MAPK' pathways.

Table S5 Characteristics of the identified microsatellites. Microsatellite primer sequences, PCR annealing temperature, repeat motifs, allele size ranges, numbers of alleles and functional annotations were shown.

Table S6 Cross-species amplification of microsatellites from the three species. No amplification products are shown by "_".

Table S7 The gene diversity of each marker revealed in the six species of the *B. tabaci* complex.