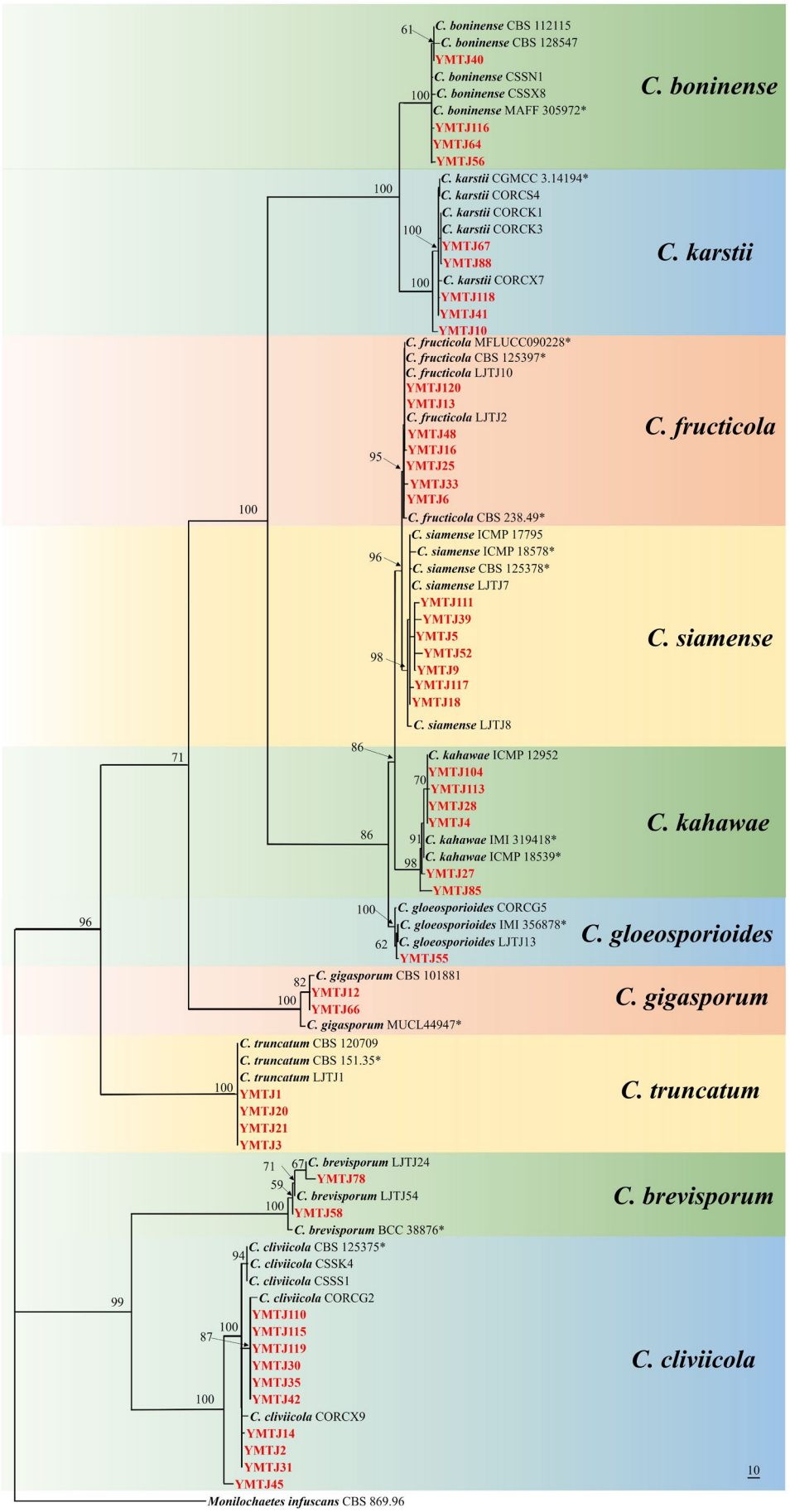

Figure. S3 Maximum parsimony phylogenetic analysis of the 48 representative strains associated with maize leaves from Sichuan Province, China. The tree conducted with the concatenated sequences of *ACT*, *TUB2*, *CAL*, *GAPDH*, and ITS. Parsimony bootstrap values of more than 60% are shown at the nodes. The tree is rooted with *Monilochaetes infuscans*.