



Supplementary figure S1.

The maximum likelihood (ML) phylogenies were inferred from aligned 1,372 bp (a) and 255 bp (b-d) of 16S rRNA gene sequences, derived from identified species (Supplementary table S1), stinkbug-associated strains (Supplementary table S1), and MEP-degrading strains isolated from soils. SBE, stink bug-associated beneficial and environmental group; BCC&P, *Burkholderia cepacia* complex and *B. pseudomallei* group; PBE, Plant-associated beneficial and environmental group. Two ambiguous clusters are additionally categorized, which could be different groups from the three major groups (ambiguous A and ambiguous B). **a**, A ML tree compressed based on the functional categories. **b-d**, ML trees showing detailed phylogenies of OTUs detected in this study (outlined) within each group; SBE and ambiguous A (b), BCC&P and ambiguous B (c), and PBE (d).