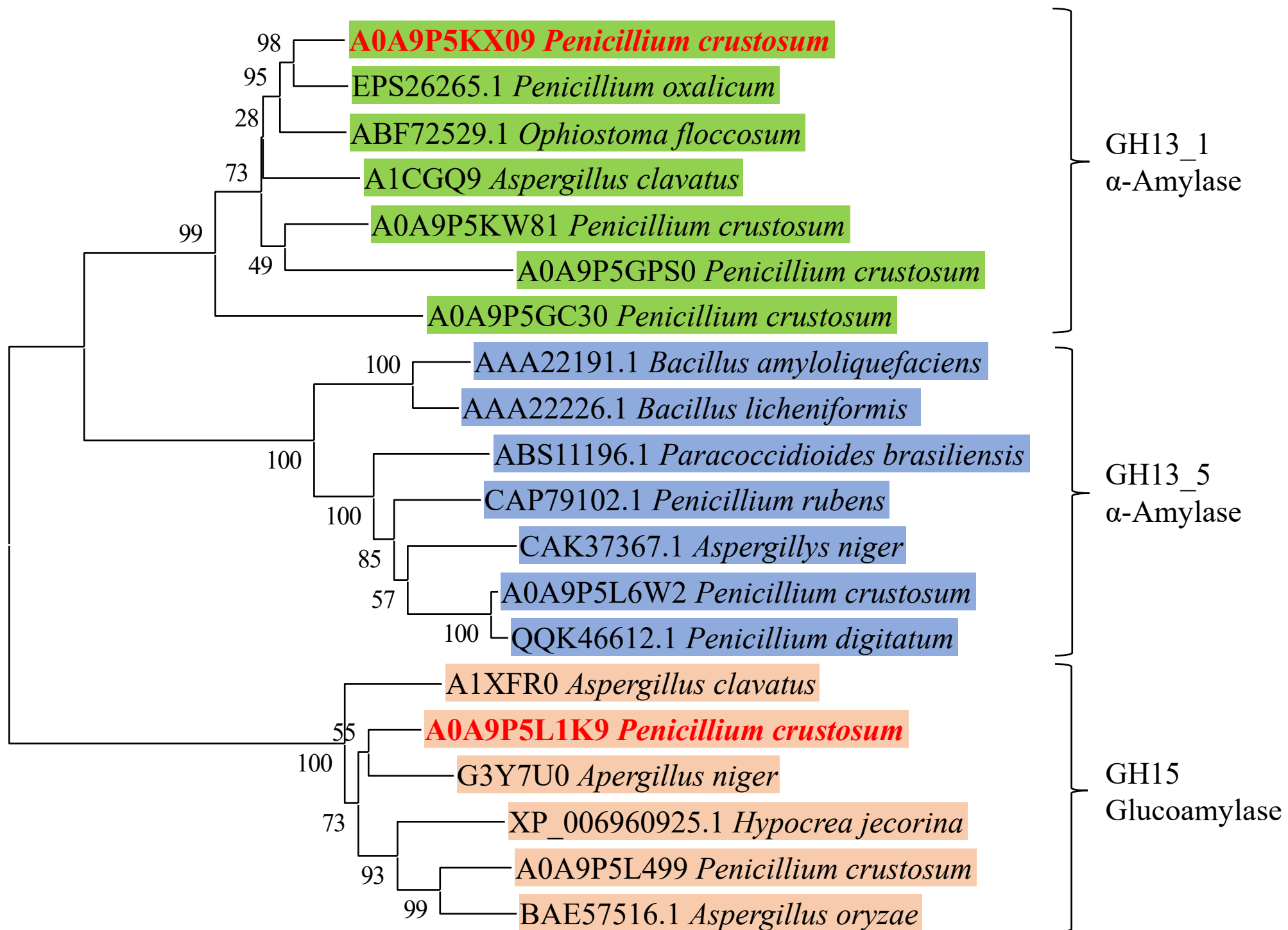




0.20

Supplementary Figure 6. Phylogenetic analysis. Bootstrap values (%) are shown next to the branches. The phylogenetic tree is drawn to scale, with branch lengths measured in the same units as the evolutionary distances used to infer the tree. This analysis included 20 amino acid sequences. All ambiguous positions were removed for each sequence pair using the pairwise deletion option. The final dataset comprised 717 positions. The *P. crustosum* G10 proteins analyzed in this study are highlighted in bold red. CAZy families and subfamilies are indicated by different colors. Evolutionary analyses were conducted using MEGA11 (Tamura et al. 2021).