

Figure S1. Assessing the genome size of *E. rostratum* LWI (A) and *B. zeicola* LWII (B).

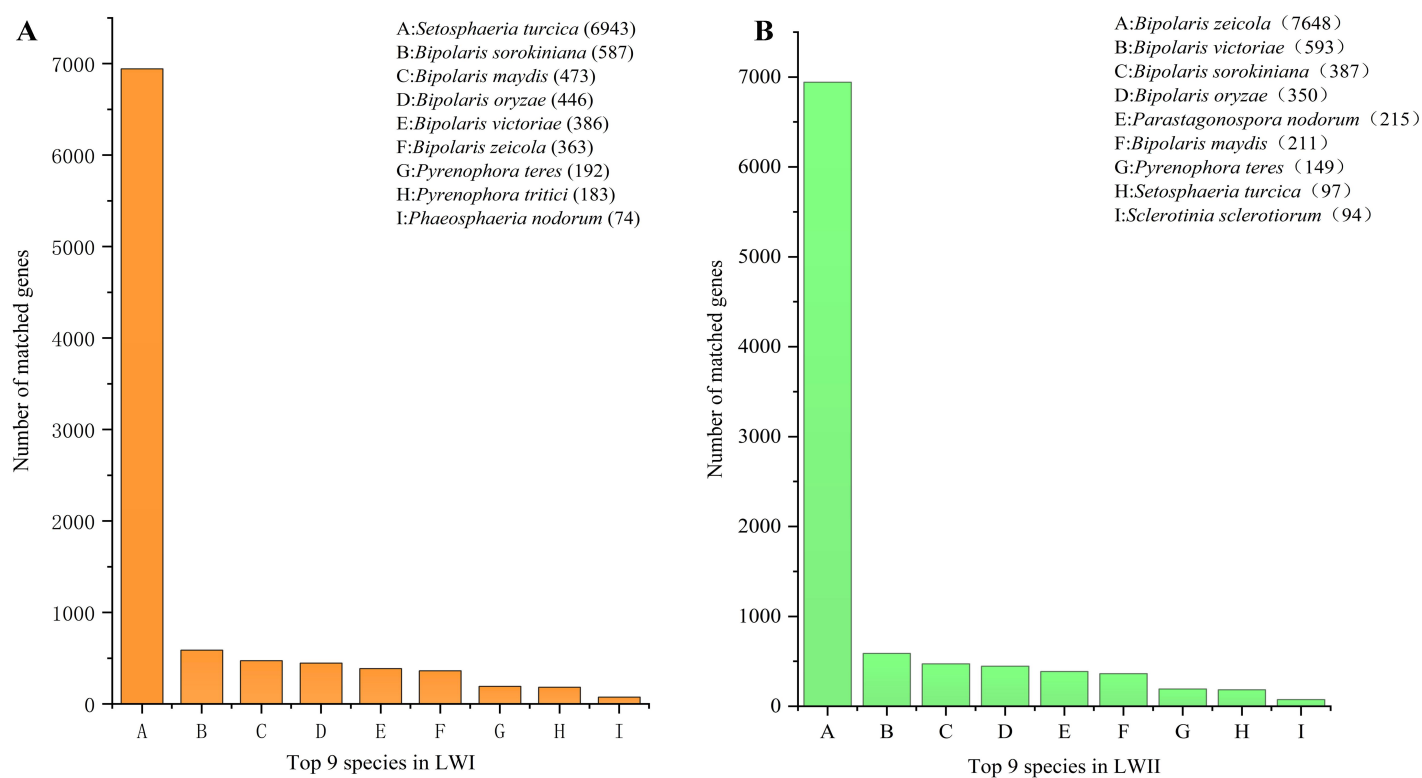


Figure S2. Predicted proteins between different fungal species using the Nr database for the *E. rostratum* LWI (A) and *B. zeicola* LWII (B) genomes.

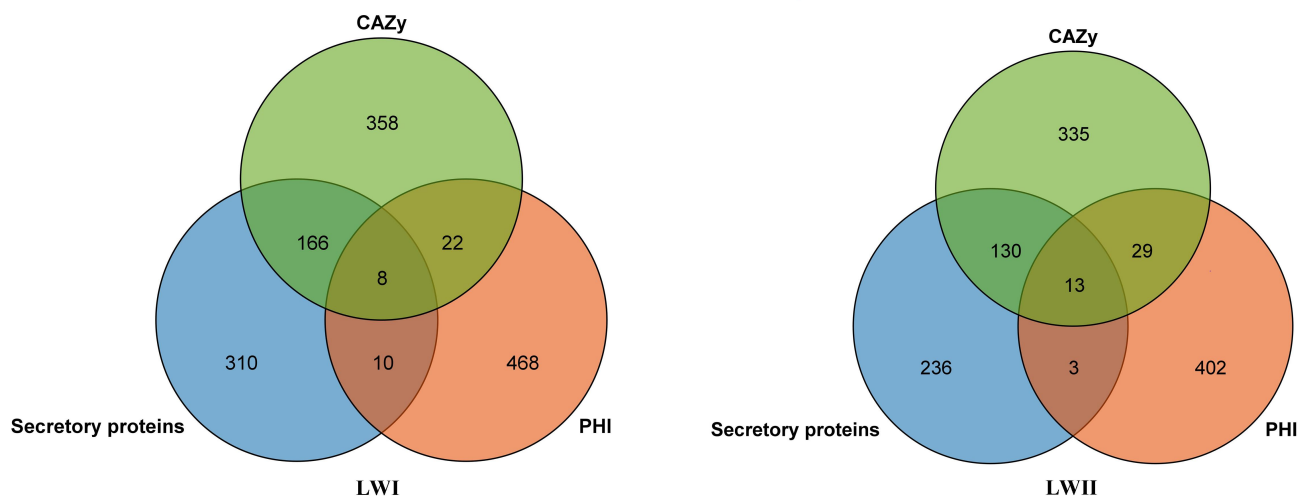


Figure S3. Intersection of annotation results of secreted protein genes, PHI genes, and CAZy genes of *E. rostratum* LWI and *B. zeicola* LWII.