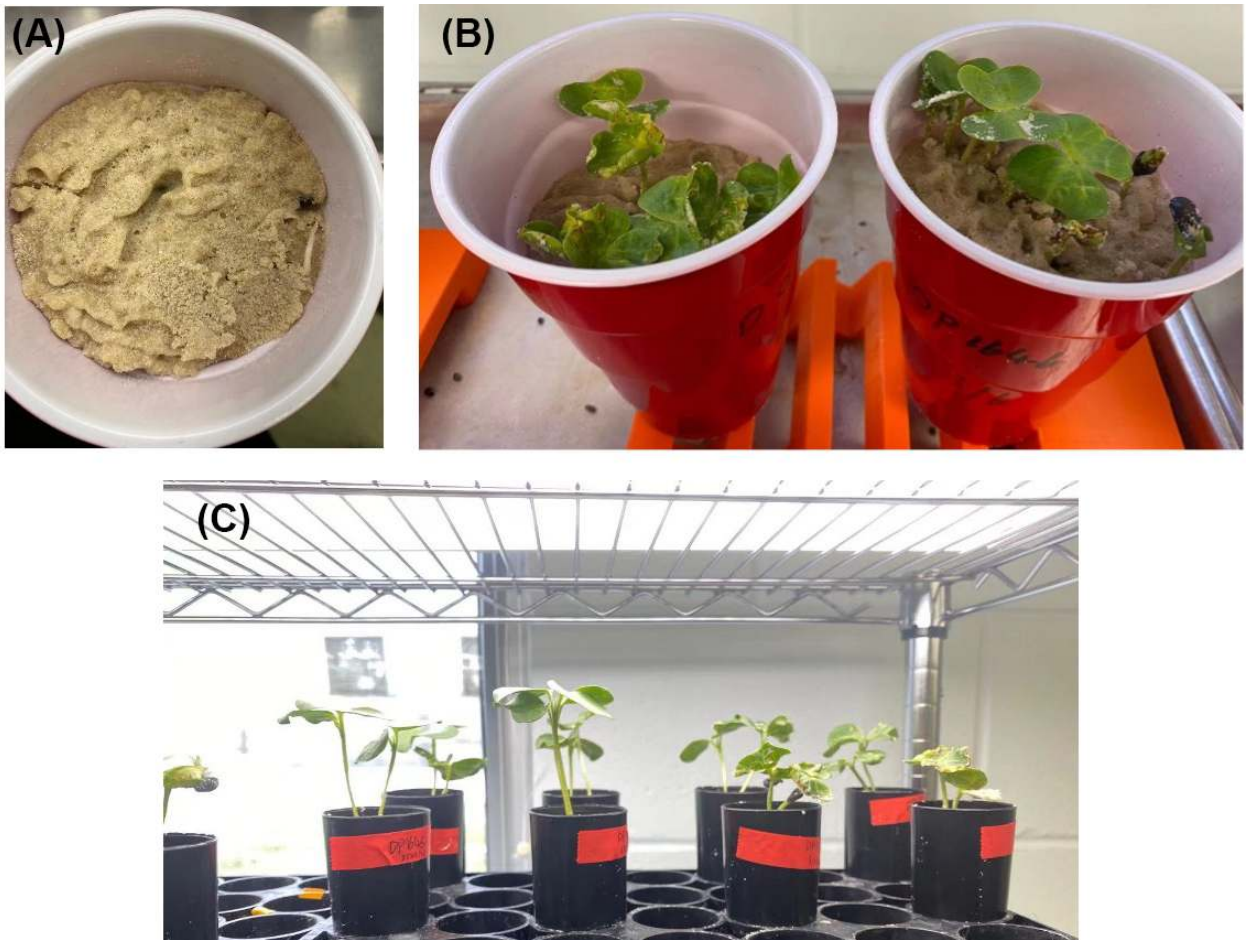

Fig. 1 Cotton seed germination and growth. (A and B) Cotton seed germination and seedling growth in plastic pots containing autoclaved sand. The germination rate of cultivars Deltapine® 1646B2XF and PHY400 W3FE was around 70% and 50%, respectively. (C) A pilot study was performed to test if cotton seedlings were tolerant to transplant. This step was important to help us determine the protocol to use for the bioassay. Result showed that all transferred seedlings were in good growth condition.

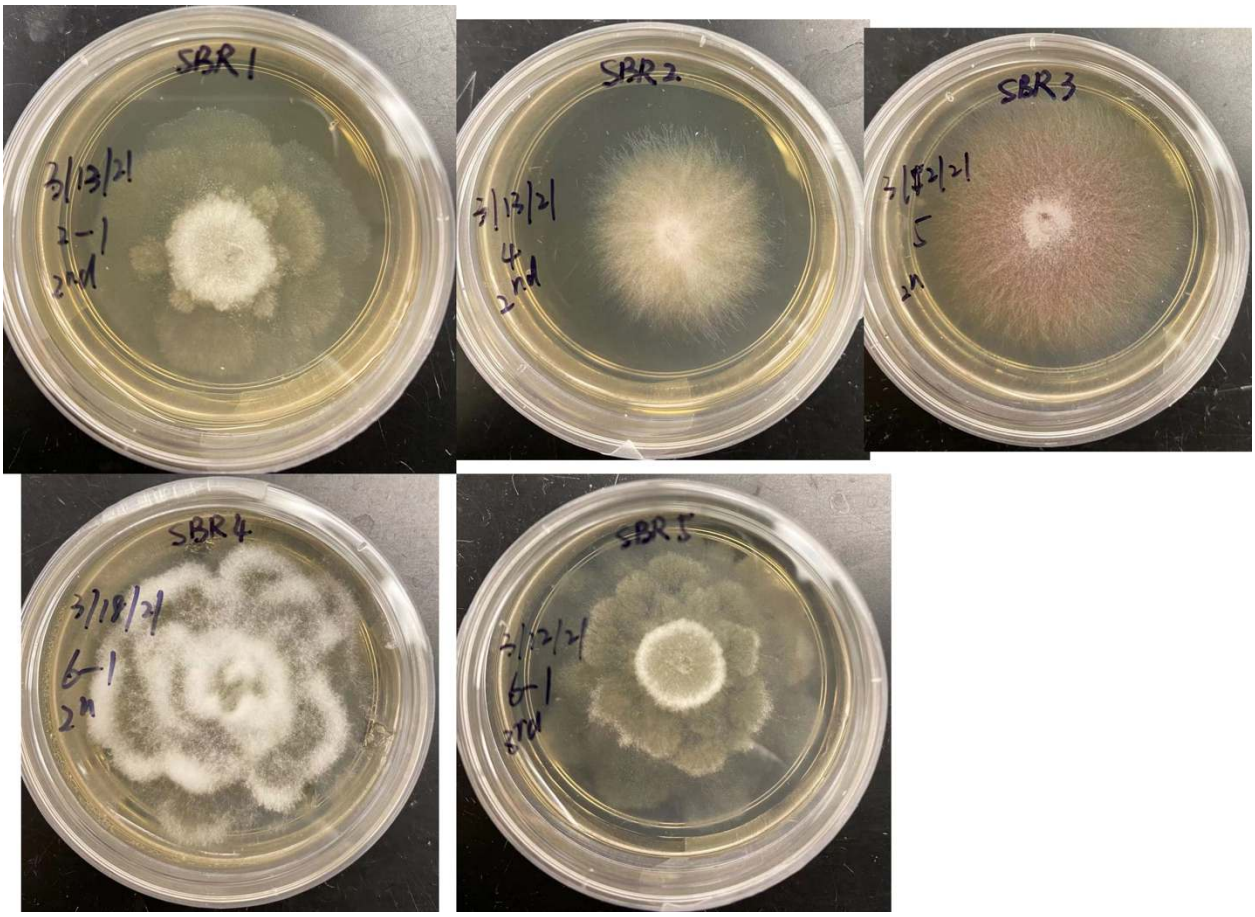

Fig. 2 Candidates of chitin-consuming fungi isolated from soil under cotton plots in the sod-based rotation. Fungal strains were isolated using the crab/lobster shell approach, followed by culturing them on MMN media.

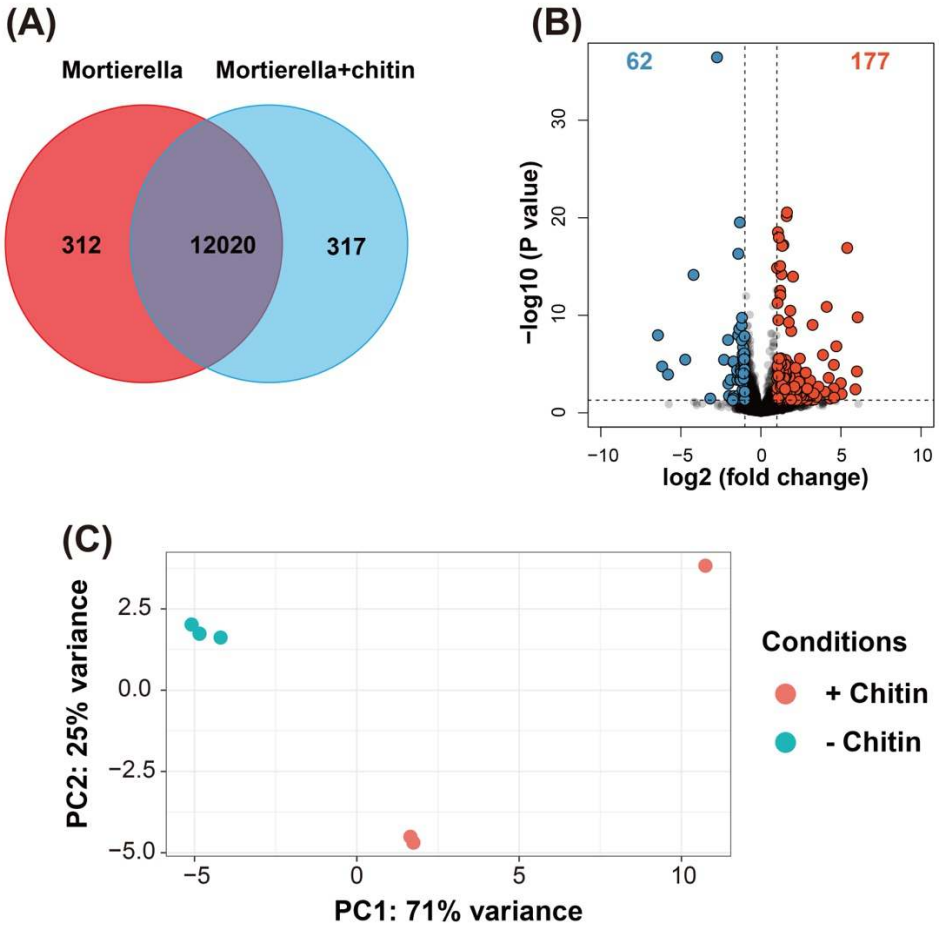

Fig. 3 Comparison of *Mortierella* gene expression with and without the chitin substrate. (A) Venn diagram showing unique and shared *Mortierella* genes. (B) Volcano plots showing upregulated (red dots) and downregulated (blue dots) *Mortierella* genes in response to chitin substrate (with cutoff values of |log2FoldChange| >1 and *P* value < 0.05). (C) PCA displaying the overall expression pattern of *Mortierella* genes with and without the chitin substrate.

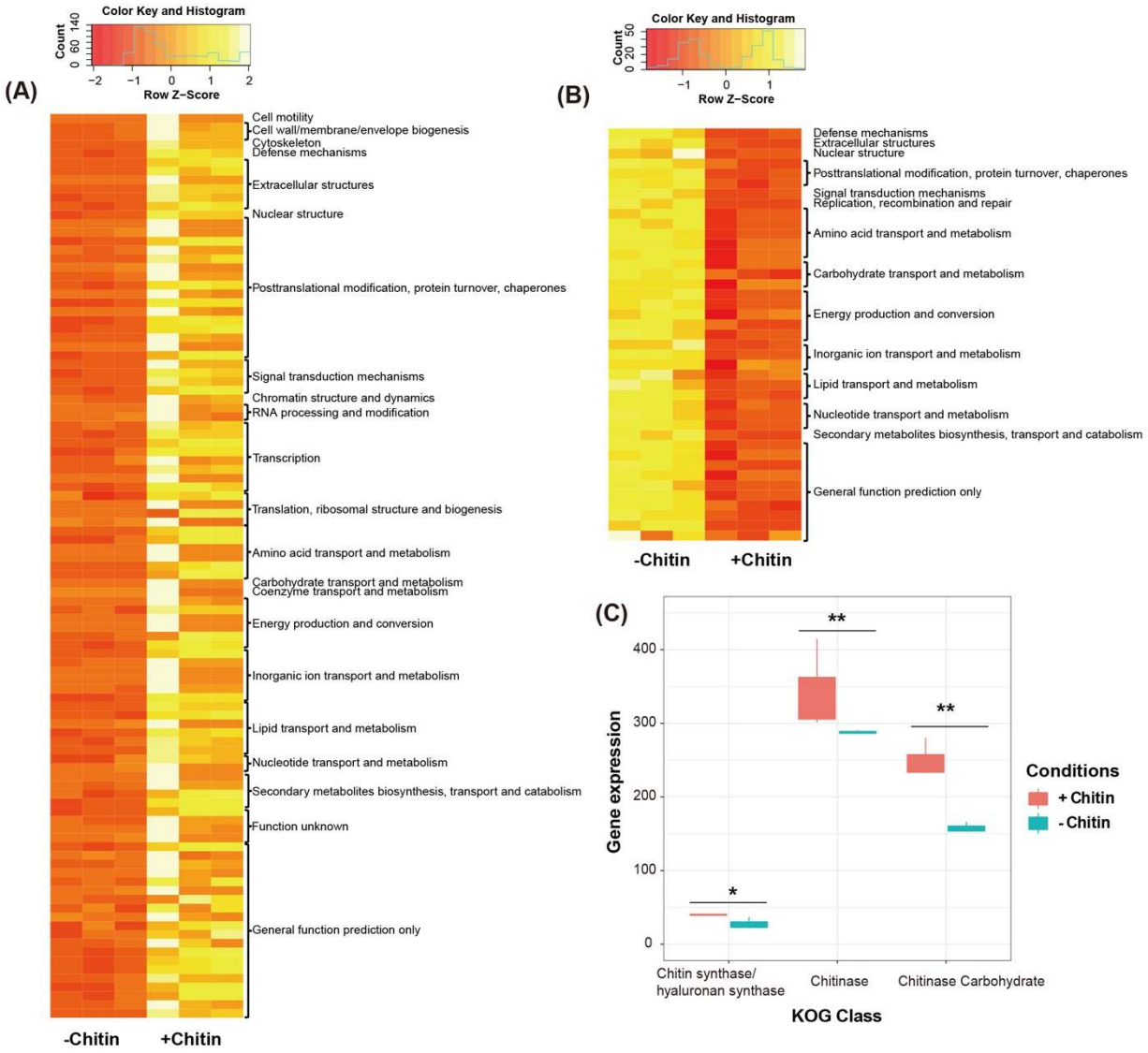

Fig. 4 Heatmap of EuKaryotic Orthologous Groups of up-regulated (A) and down-regulated (B) *Mortierella* genes in response to the chitin substrate (only genes with annotations are shown). (C) Comparison of genes related to chitin-related functions with and without chitin substrate. Asterisks represent significant differences between treatments with and without chitin substrate, determined by a *t*-test. "*" and "**" indicate significance at $P < 0.05$ and 0.01, respectively.

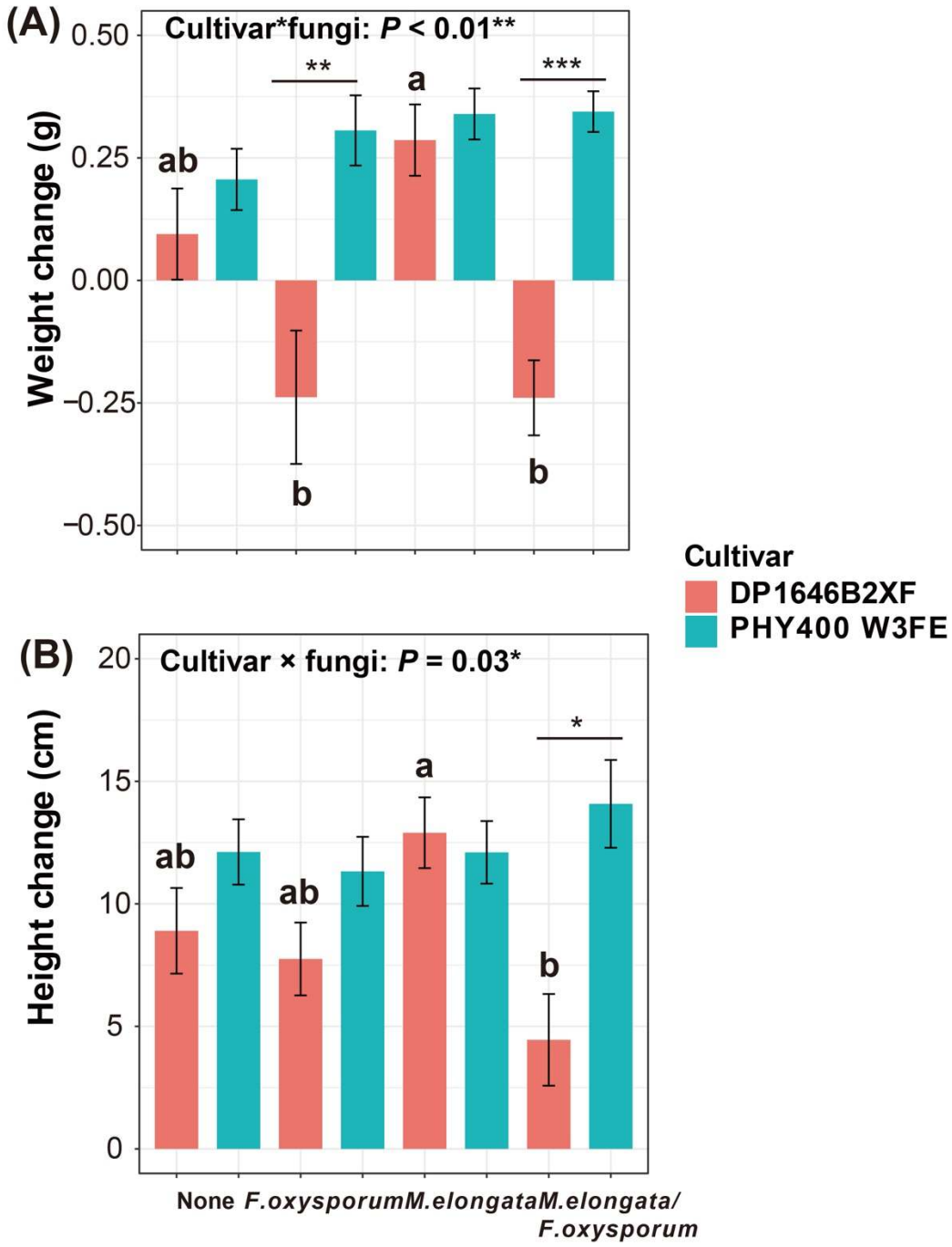

Fig. 5 The effect of *M. elongate* and *F. oxysporum* on cotton performance. A two-way ANOVA showed that there were interactions of fungal treatment by cultivars in changes in weight and height. Significant differences (shown by lowercase letters) among fungal treatment in DP1646B2XF were determined using a Tukey's HSD test, and cultivar effects (shown by asterisks) for each fungal treatment were determined with a *t*-test. *, **, and *** indicate significance at $P < 0.05$, 0.01, and 0.001, respectively.

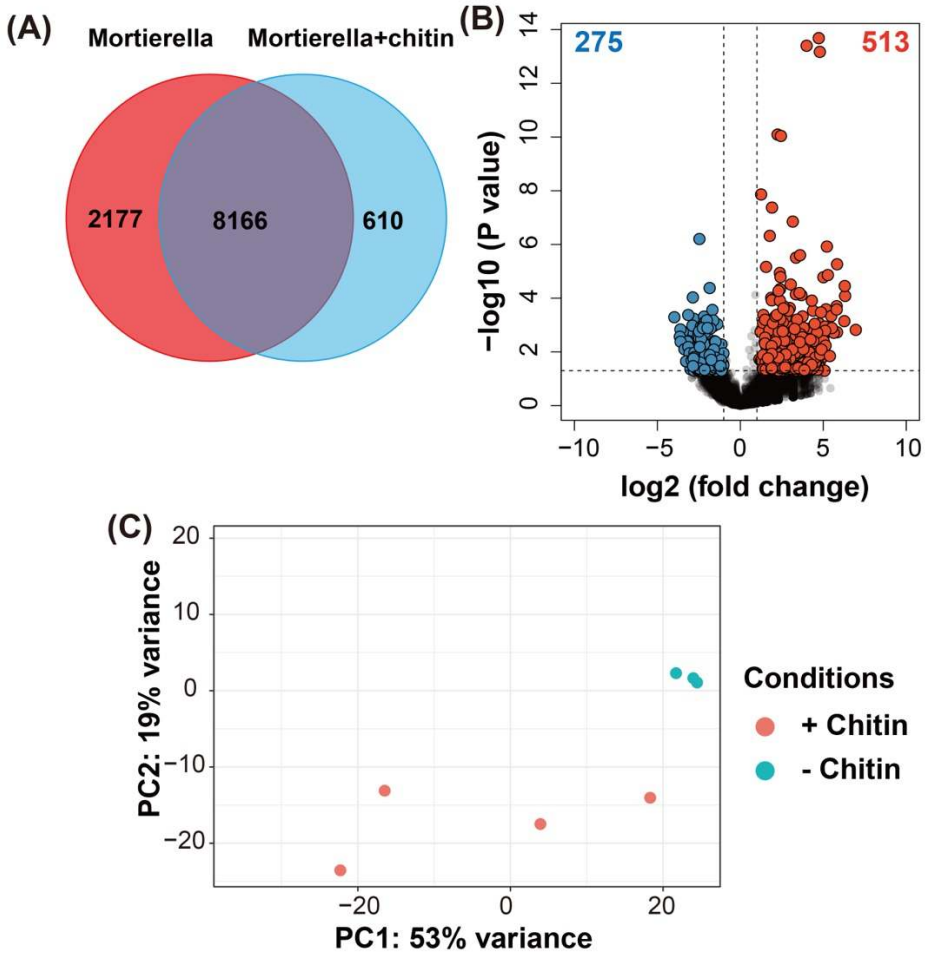

Fig. 6 Comparison of *Mortierella* gene expression in roots with and without chitin substrate. (A) Venn diagram showing unique and shared *Mortierella* genes. (B) Volcano plots showing upregulated (red dots) and downregulated (blue dots) *Mortierella* genes in response to chitin substrate (with cutoff values of | log2FoldChange| >1 and *P* value < 0.05). (C) PCA displaying the overall expression pattern of *Mortierella* genes with and without chitin substrate in roots.

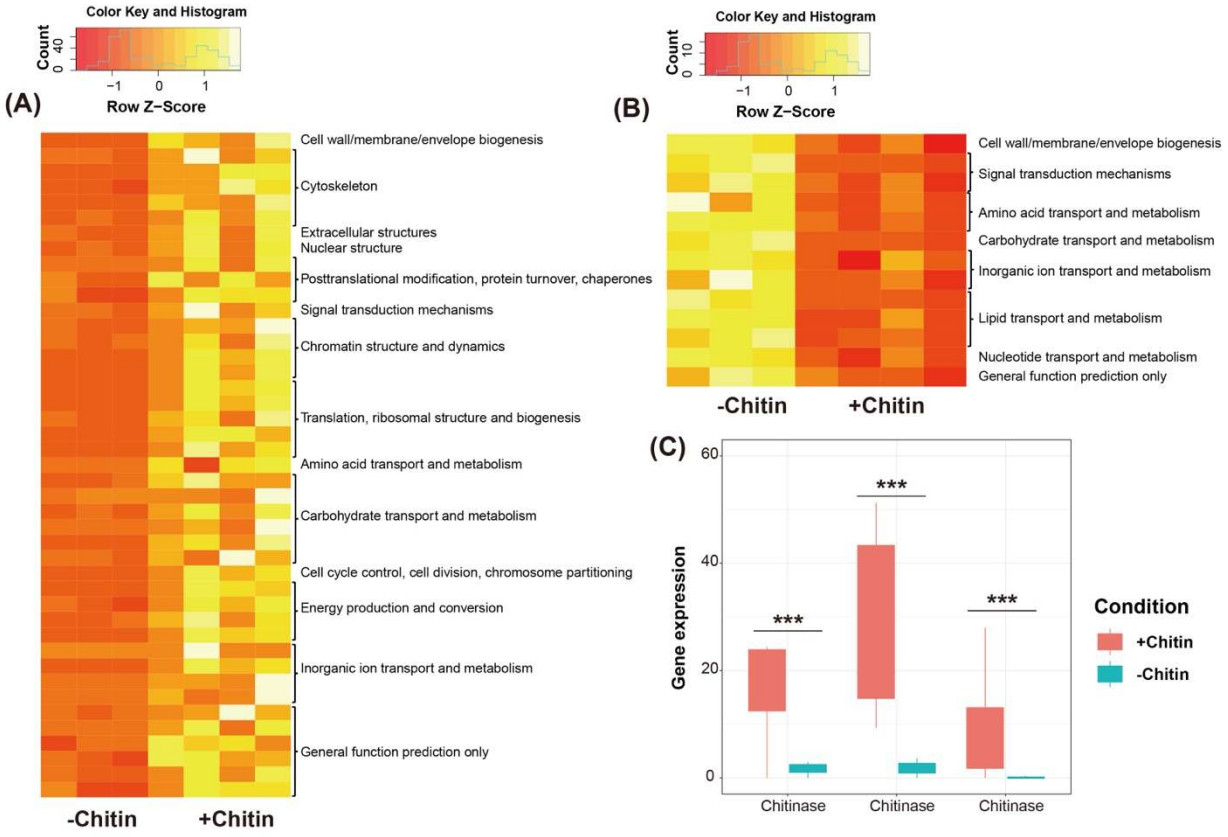

Fig. 7 Heatmap of EuKaryotic Orthologous Groups of highly up-regulated (A) and down-regulated (B) *Mortierella* genes in response to chitin substrate in plant roots (only genes with annotations are shown). (C) Comparison of genes related to chitin-related functions with and without chitin addition in plant roots. Asterisks represent significant differences between treatments with and without chitin substrate, determined by a *t*-test. "***" indicates significance at $P < 0.001$.

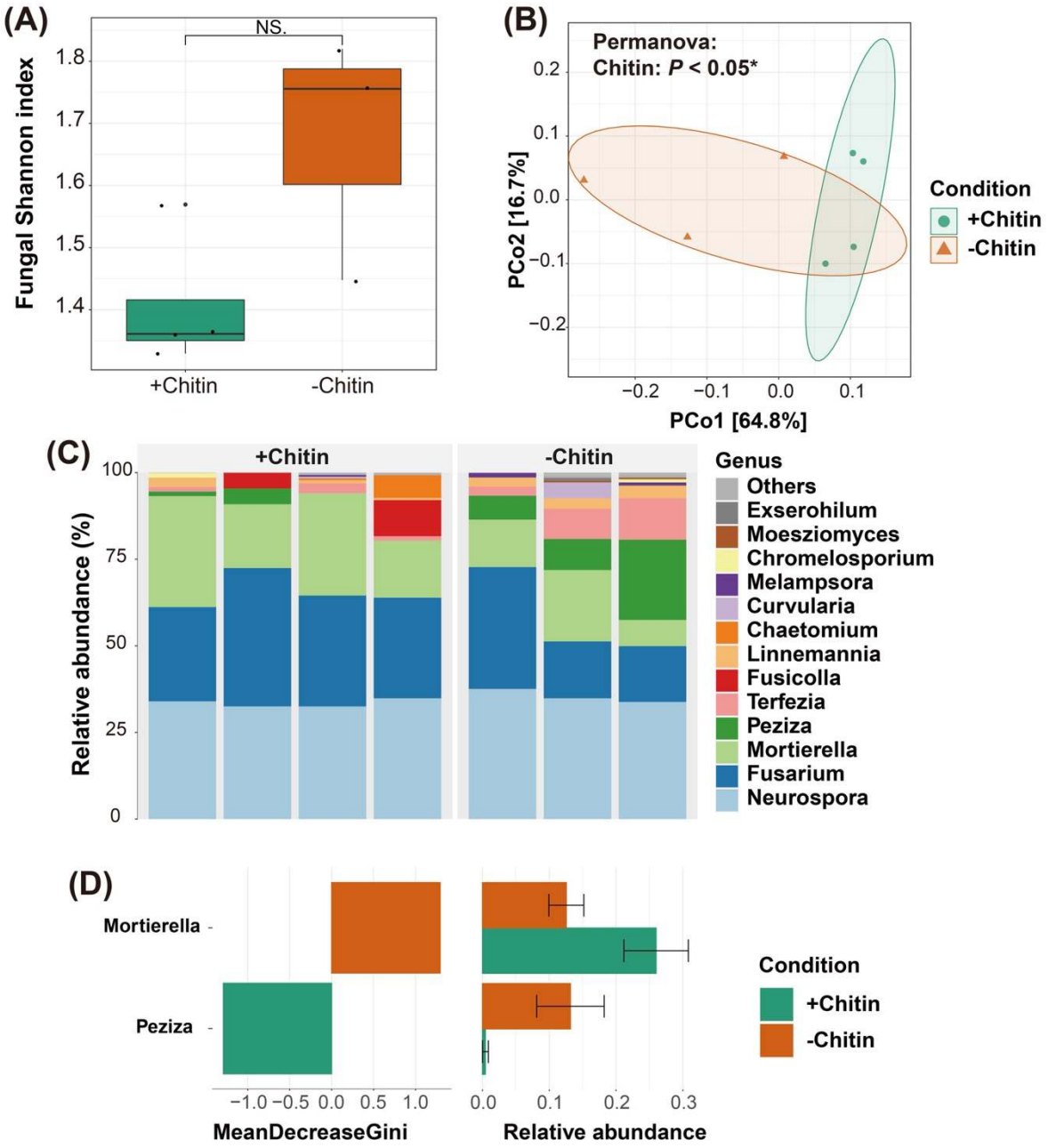

Fig. 8 Diversity and composition of fungal communities in plant roots in response to chitin addition. (A) Alpha diversity is represented by the Shannon index. Significant difference was determined by a *t-test*. (B) Beta diversity is visualized using a principal coordinate analysis (PCoA) with Bray-Curtis dissimilarity distances. (C) Dominant fungal genera with and without chitin addition. (D). Random Forest models detecting fungal biomarkers that were significantly affected by chitin addition.