

Supplementary figures

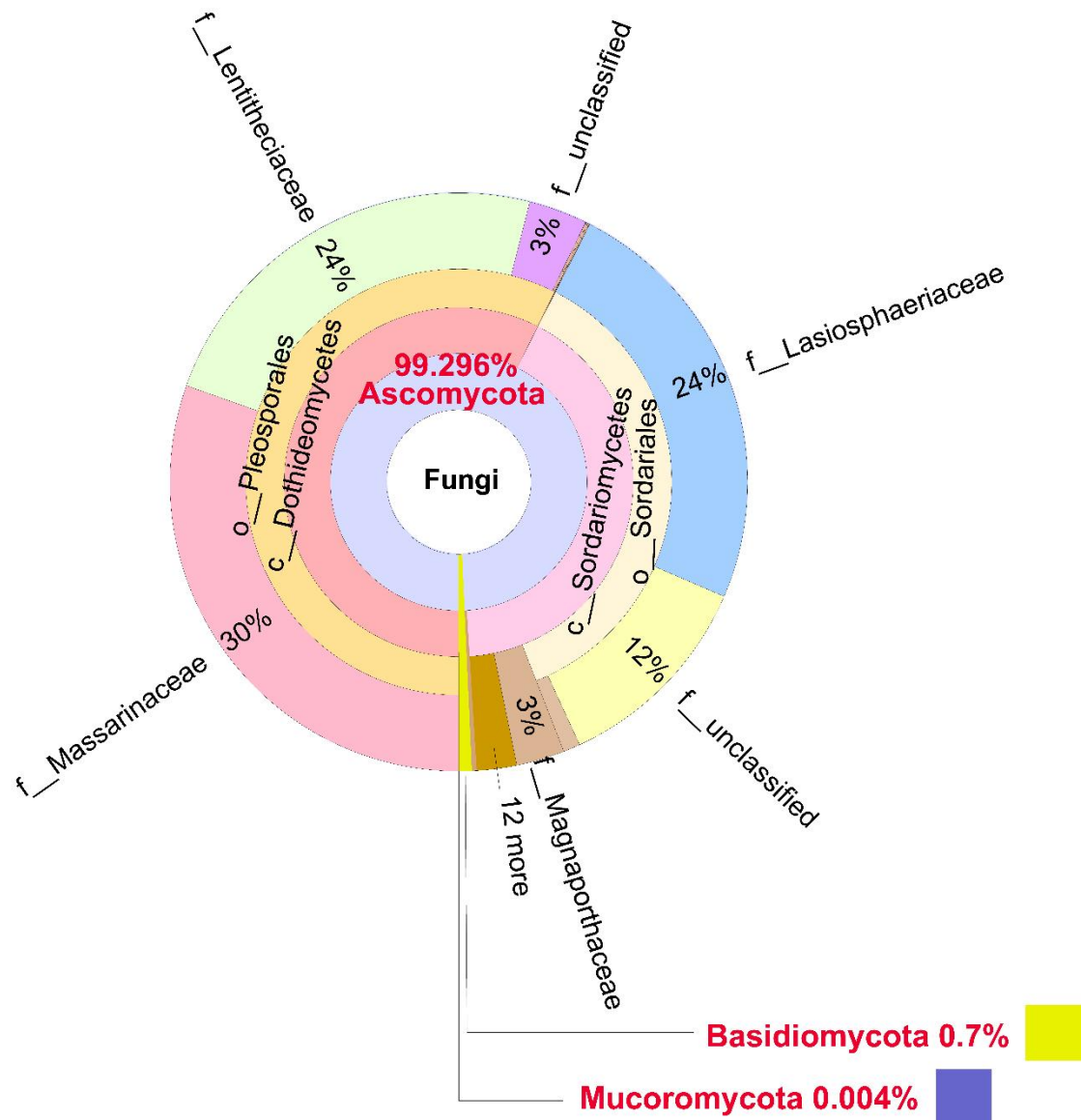


Fig. S1. Krona-based taxonomic classification of fungal ASVs (FASVs) in wild rice.

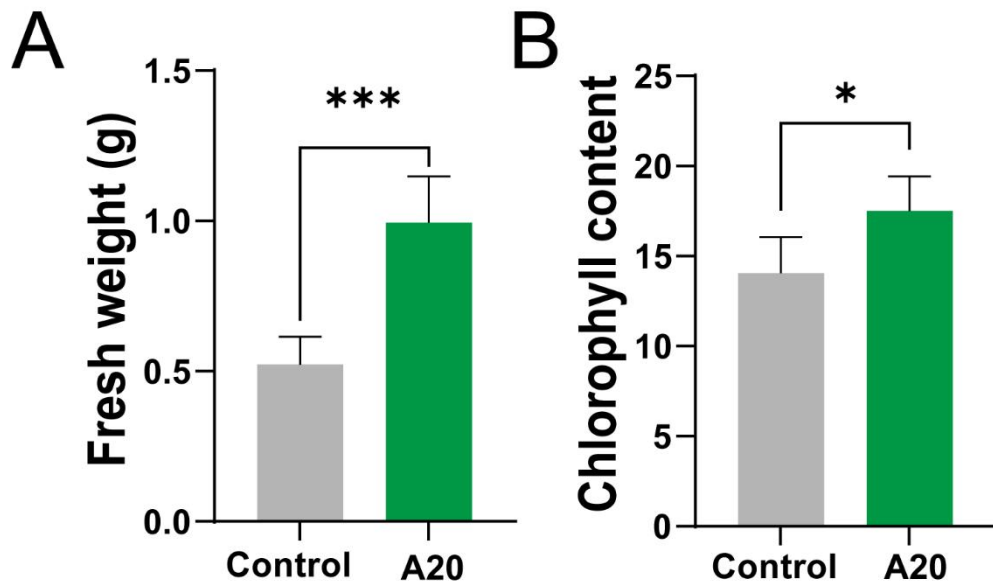


Fig. S2. Growth indexes of *F. oryzae*-fertilized rice. (A) Fresh weight. (B) Chlorophyll content. Bars show the means \pm SDs.

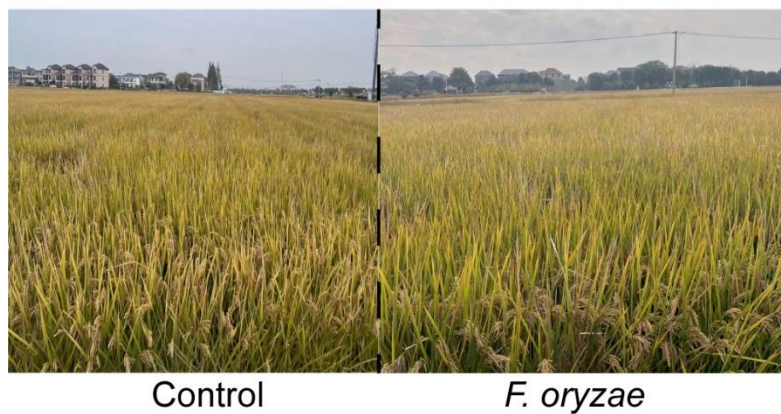


Fig. S3. A field experiment of the impact of *F. oryzae* on rice was conducted in Hangzhou, China.

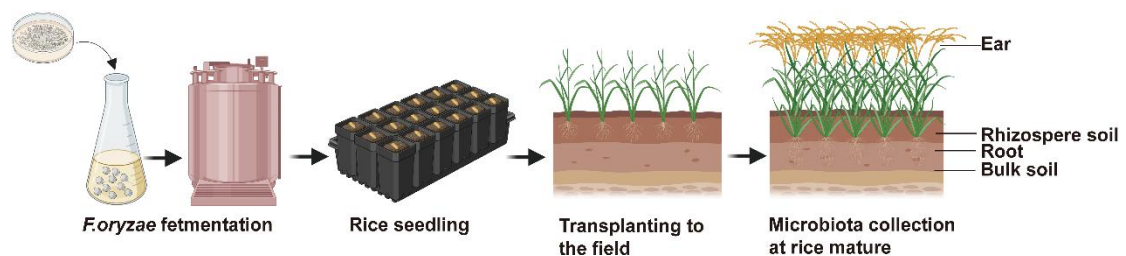


Fig. S4. Schematic illustration for investigation on the impact of *F. oryzae* on rice microbiota.

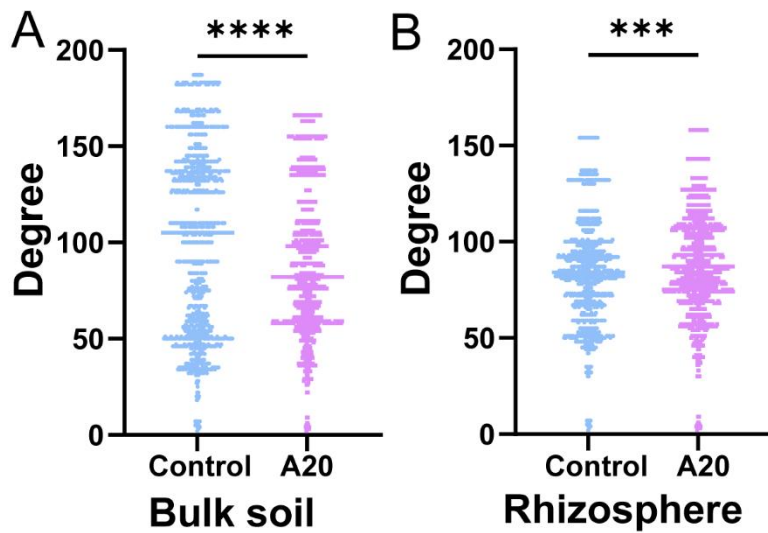


Fig. S5. Node degree comparison in bulk soil and rhizosphere. (A) In the bulk soil, the control network has higher complexity than the fertilized network. (B) In the rhizosphere, the fertilized network exhibited higher complexity than the control network. Significant difference (t-test): ***, p -value < 0.001, ****, p -value < 0.0001.

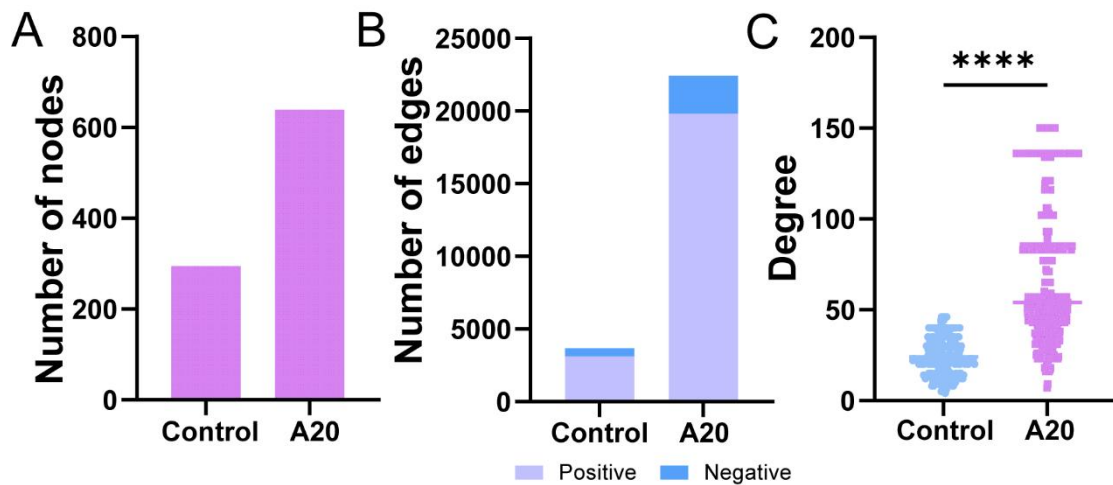
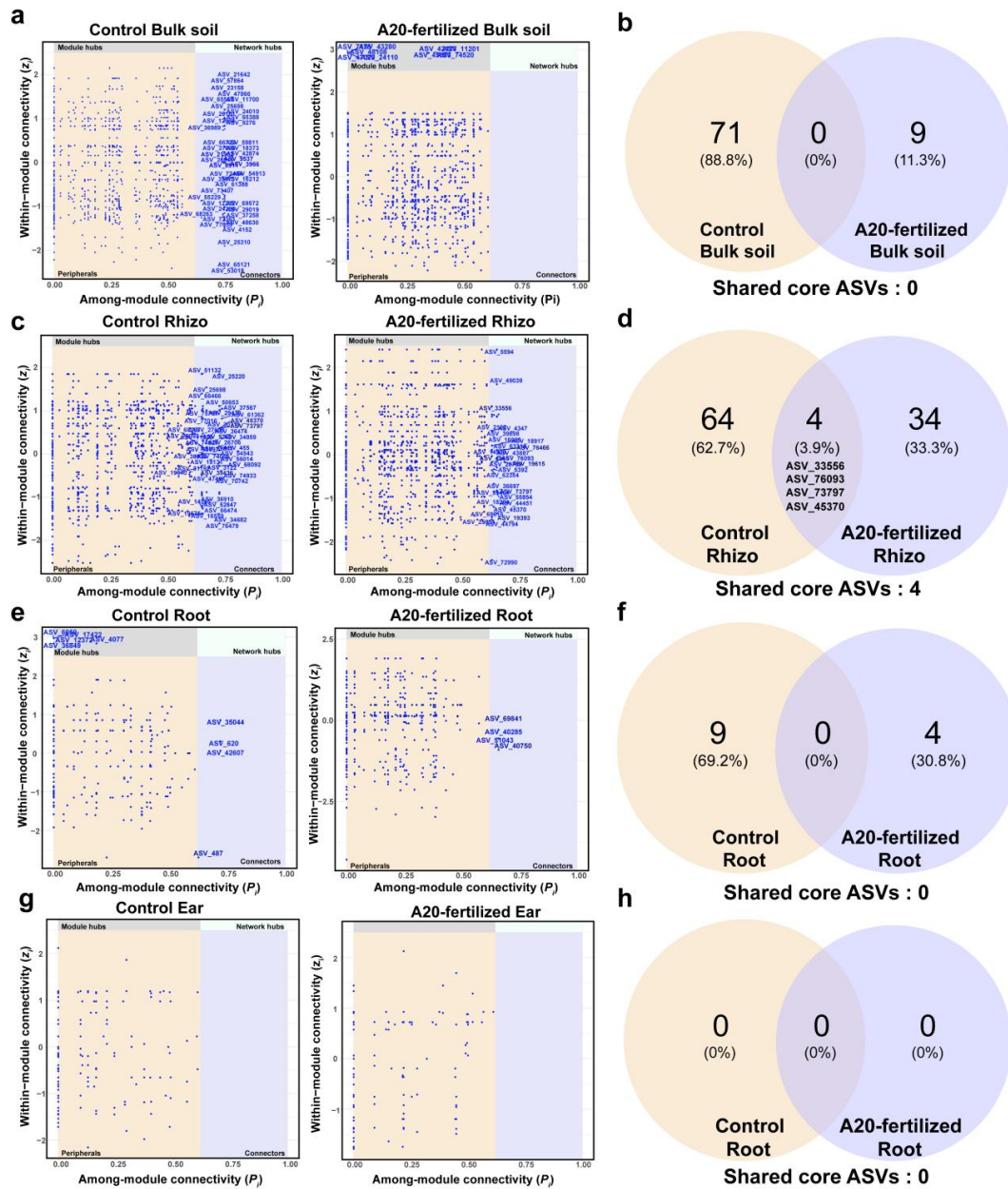


Fig. S6. The number of nodes, edges, and the node degree in the root microbiota. (A-C) The fertilized root network has higher complexity than the control network. Significant difference (t-test): ****, p -value < 0.0001.



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g. S7. Z_i - P_i plot of OTUs on different rice compartments variation (bulk soil, rhizosphere soil, root, and ear). The Z_i (within-module connectivity) and P_i (among-module connectivity) of each OTU were calculated to identify key OTUs in the co-occurrence network. Nodes were ultimately divided into four categories: module hubs ($Z_i > 2.5$), network hubs ($Z_i > 2.5$ and $P_i > 0.62$), connectors ($P_i > 0.62$), and peripherals ($Z_i < 2.5$ and $P_i < 0.62$).

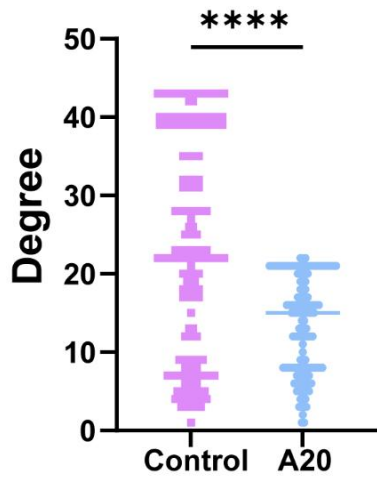


Fig. S8. Node degree comparison in ears. The control network has higher complexity than the fertilized network. Significant difference (*t*-test): ****, p -value < 0.0001.

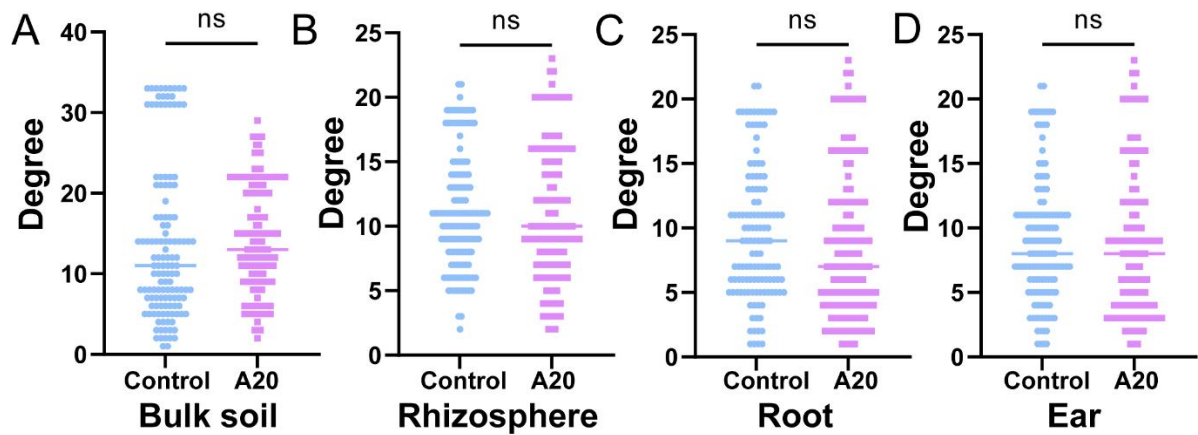


Fig. S9. Node degree analysis of fungi. (A-D) No significant differences in network connectivity among bulk soil, rhizosphere, root, and ear compartments between fertilized and control.

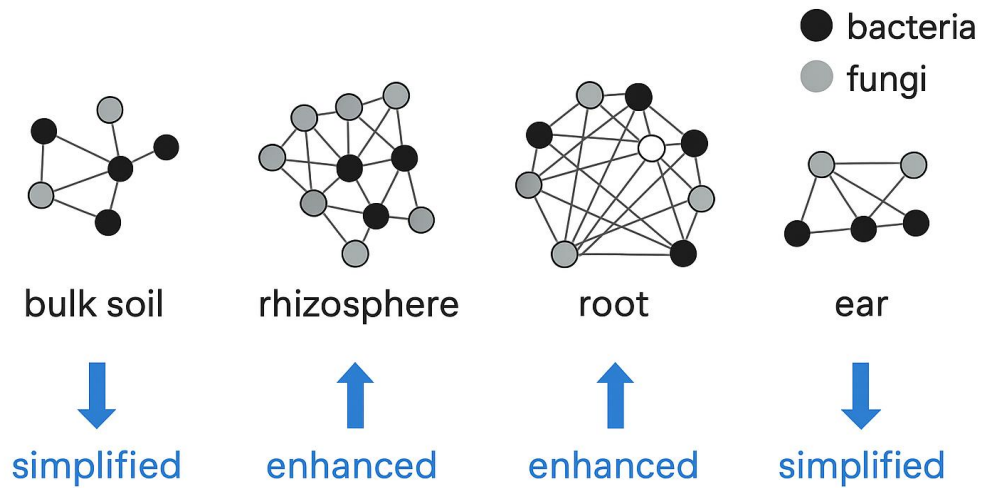


Fig. S10. *F. oryzae* modulates rice microbiota in a compartment-specific manner.

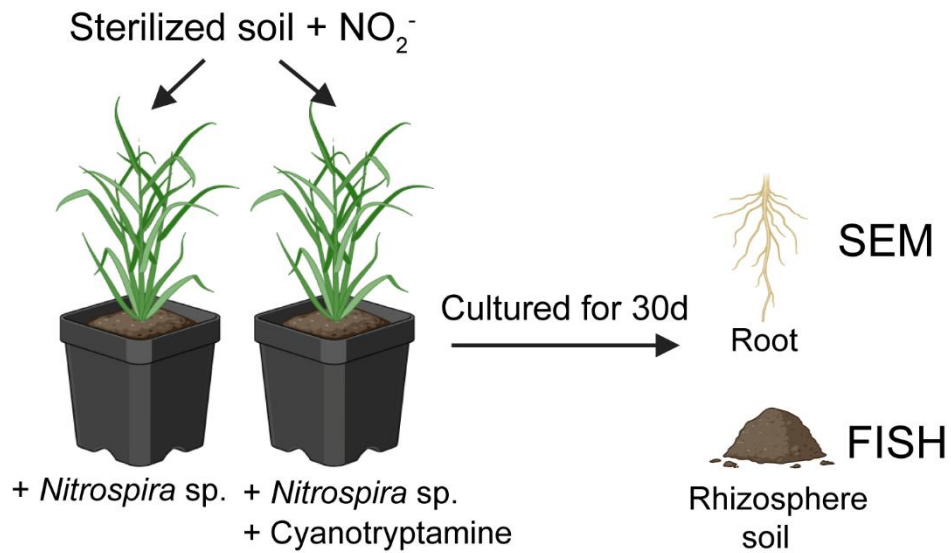


Fig. S11. Schematic illustration for investigation on the impact of Cyanotryptamine on rice microbiota.

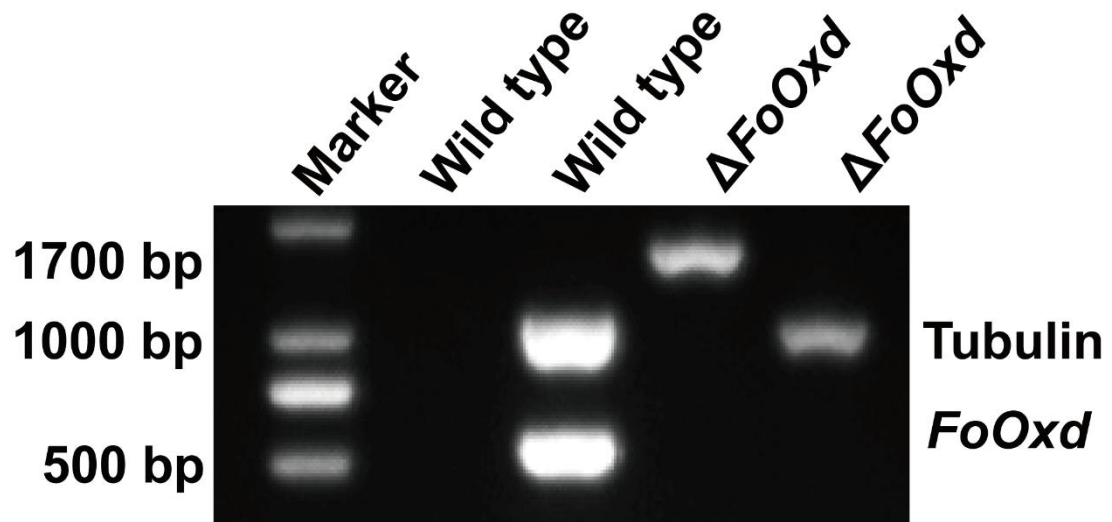


Fig. S12. PCR test the fragment *FoOxd*.