

Figure S1. Monitoring framework of ecological community (as in Ushio 2022). (a) Locations of the five rice plots in 2017. (b) Research framework to generate quantitative environmental DNA time series and network reconstruction. (c) Ecological community network reconstructed by nonlinear time series. These figures were reproduced from Ushio (2022) *Proceedings of the Royal Society B*.

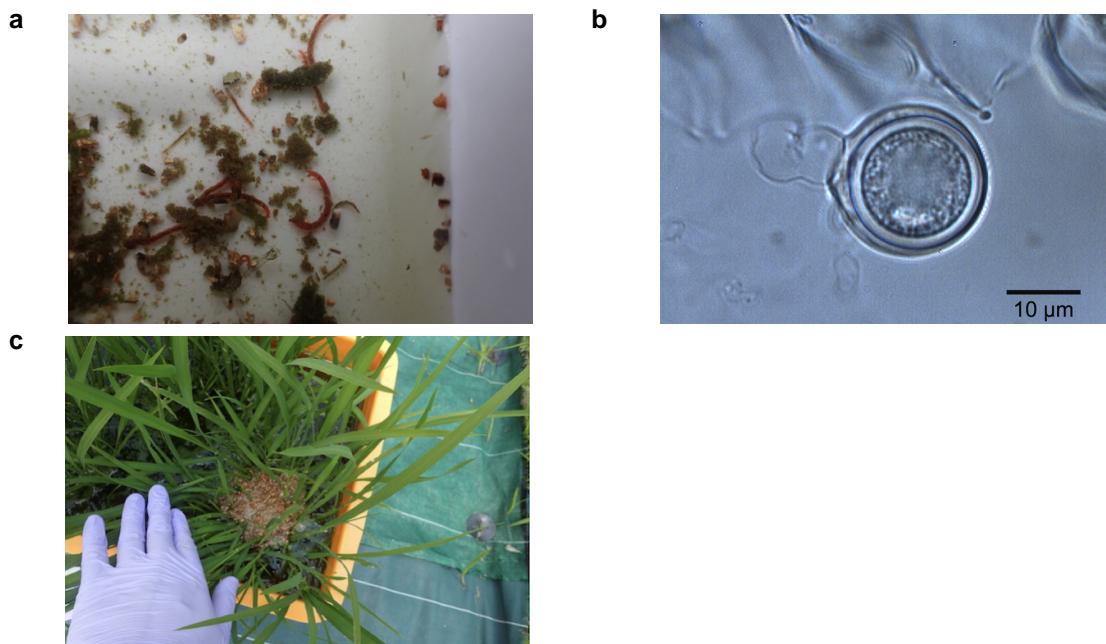


Figure S2. Midge (*Chironomus kiiensis*) and *Globisporangium nunn* used in the manipulation experiment in 2019. (a) Larvae of midge (*Chironomus kiiensis*) naturally colonized in the rice plots. The larvae were manually removed by a commercial net with ϕ 1 mm mesh. **(b)** Microscopic image of *Globisporangium nunn* (photo by M. Tojo). **(c)** *Globisporangium nunn* was incubated in vermiculite and added to the rice plots. For the control and midge-removed treatments, vermiculite without *Globisporangium nunn* was added.

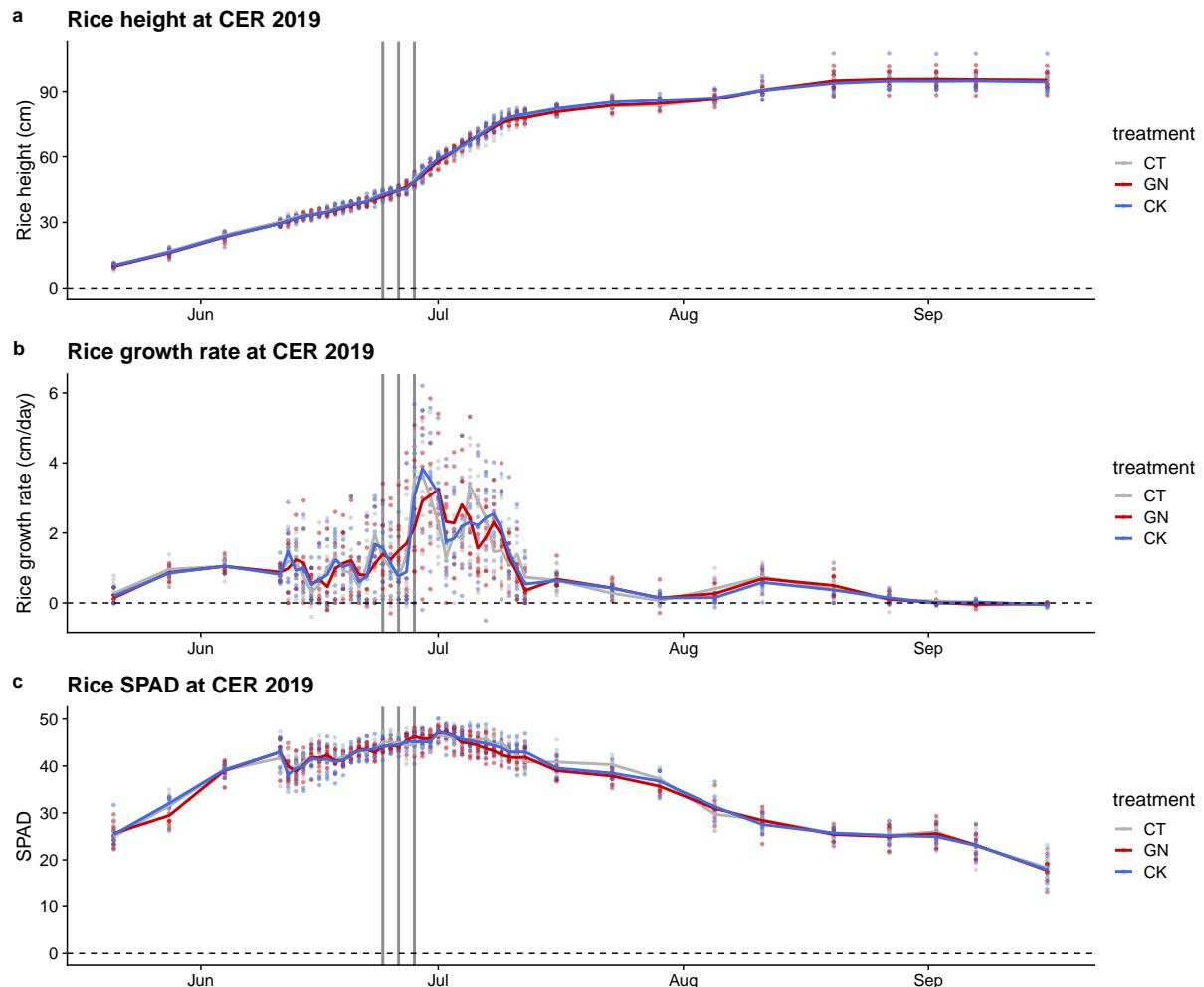


Figure S3. Rice growth trajectory in 2019. (a) Rice height, (b) growth rate, and (c) SPAD values of the rice during the growing season in 2019. Points indicate observed values, lines indicate mean trends, and gray lines indicate the field manipulation experiments. Colors indicate the treatments.

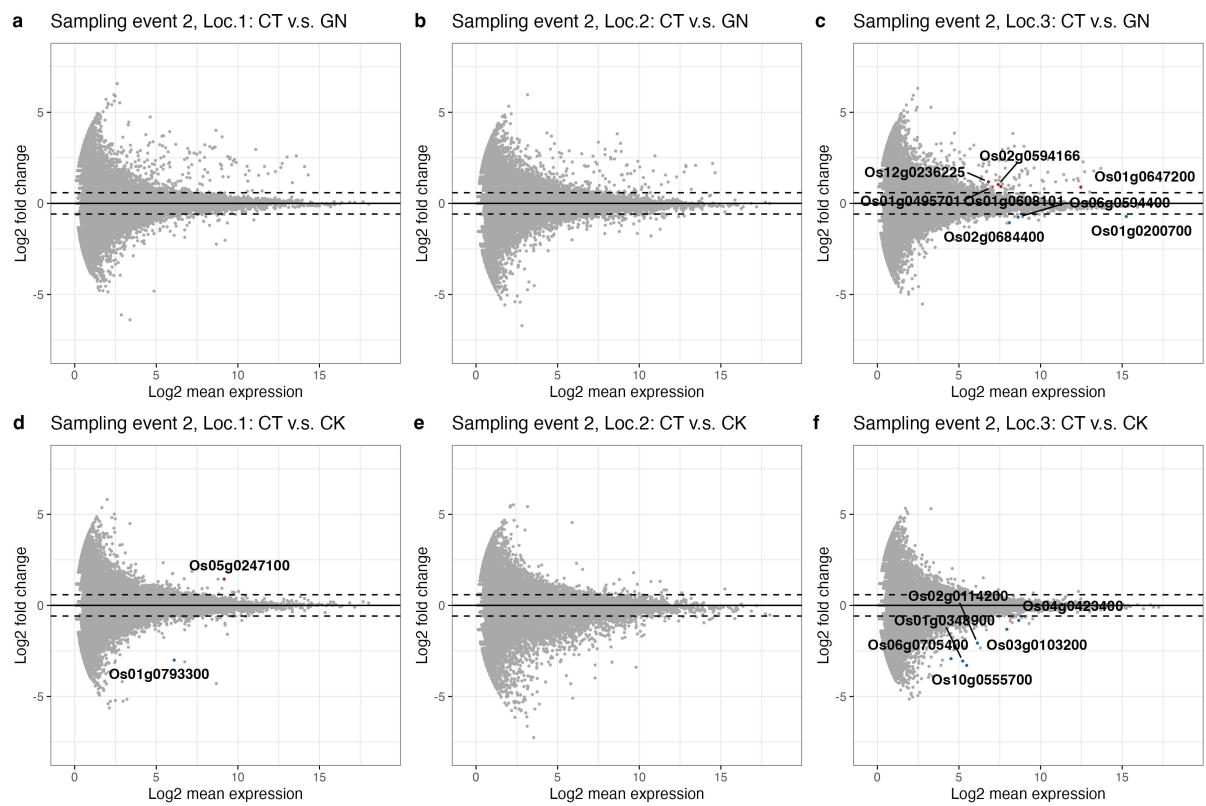


Figure S4. Differential expression gene (DEG) patterns for each Wagner pot (Pot location-specific analysis). DEG for (a) location 1, (b) location 2, and (c) location 3 for the control (CT) versus *Globisporangium nunn*-added (GN) treatments. (d-f) DEG analysis for the control versus *Chironomus kiiensis*-removed (CK) treatments for rice grown at locations 1-3. Red and blue points indicate significant up- and down-regulated genes, respectively. Upper and lower dashed lines indicate $\log_2(1.5)$ and $-\log_2(1.5)$, respectively.