**Supplementary Material**

**Method S1: PCR protocol for microbiome analysis**

From the DNA samples, the variable regions V6-V8 of bacterial 16S rRNA genes were amplified by nested PCR approach. We performed first round of PCR reactions with 30 ng DNA, 1X PCR buffer, 0.2 mM dNTPs, 0.3 μM each of primers 799F (AACMGGATTAGATACCCKG) [57] and 1492R (GGYTACCTTGTTACGACTT) (modified from [58]) and 2000 U/ml GoTaq DNA Polymerase (Promega, WI, USA) in a 30 μl reaction volume. This was followed by a second round of PCR with 1:10 diluted PCR product from round 1, 1X PCR buffer, 0.2 mM dNTPs, 0.3 μM and M13-1062F (TGTAAACGACGGCCAGTGTCAGCTCGTGYYGTGA, [59, 60] and 1390R (ACGGGCGGTGTGTRCAA) [61] primers. A third round of PCR was done with 1:1 dilution of second PCR product, IonA-barcode-M13 primers [60] for sample tagging and1390R-P1 for IonTorrent PGM sequencing. The PCR profile: 3 min initial denaturation at 95°C, denaturing at 95°C for 45 s, annealing at 54°C for 45 s, and extension at 72°C for 1 min, and final extension at 72°C for 5 min was set on thermocycler (BIORAD). The same protocol was followed with 35 cycles for first round, 25 and 8 cycles, for second and third rounds, respectively.

The Internal Transcribed Sequence (ITS) regions were amplified using primers M13-ITS7F (TGTAAAACGACGGCCAGTGTGARTCATCGAATCTTTG) and ITS4R (TCC TCC GCT TAT TGA TAT GC) [62]. The 30 µl reaction mixture contained 30 ng of sample DNA, 1x PCR buffer, 0.2 mM dNTPs, 0.3 μM of each primer and 1250 U/ml GoTaq DNA Polymerase (Promega, WI, USA). We performed the second round of PCR using 1:10 dilution of first PCR product as template, 1x PCR buffer, 0.2 mM dNTPs, 0.3 μM of each primer and 1250 U/ml GoTaq DNA Polymerase, barcode-M13 forward primer and ITS4-P1 (CCTCTCTATGGGCAGTCGGTGATTCCTCGCTTATTGATATGC) as reverse primer. The amplification profile was 5 mins initial denaturation at 95 °C followed by denaturing, annealing, and extension at 95 °C for 30 s, 55 °C for 30 s and 72 °C for 1 min, repeated at 35 cycles for first round and 8 cycles for the second round. Final extension was carried out at 72 °C for 7 mins.

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| **Table S1**: SIMPER (Similarity Percentages) analysis in leaves of E+ and E- plants in total and *Epichloë*-depleted fungal communities(VE- ‘Valtteri’ plants without *Epichloë,* VE+ - ‘Valtteri’ with *Epichloë,* KE- ‘Kasper’ without *Epichloë* and KE+ ‘Kasper’ with *Epichloë*) showing micobial taxa with difference in average relative abundances. OTUs – Operational Taxonomic Units, Av.Abund – Average Abundance, Av.Diss. – Average Dissimilarity, Diss/SD – Dissimilarity/ Standard Deviation, Contrib% - Contibution percentage, Cum% - Cumulative percentage  **Total communities** | | | | | | | |
| **Groups VE- & VE+**  **Average dissimilarity = 77.97** | | | | | | | |
|  | **Group VE-** | **Group VE+** |  |  |  |  |  |
| **OTUs** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** | **Cum.%** | **Taxa** |
| otu2 | 0.02 | 59.43 | 29.7 | 4.12 | 38.1 | 38.1 | *Epichloë* |
| otu1 | 28.53 | 8.75 | 11.24 | 1.4 | 14.42 | 52.52 | *Mycosphaerella\_tassiana* |
| **Groups KE- & KE+**  **Average dissimilarity = 81.97** | | | | | | | |
|  | **Group KE-** | **Group KE+** |  |  |  |  |  |
| **OTUs** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** | **Cum.%** |  |
| otu2 | 0.03 | 36.83 | 18.4 | 2.88 | 22.45 | 22.45 | *Epichloë* |
| otu1 | 30.87 | 7.06 | 11.94 | 2.24 | 14.57 | 37.02 | *Mycosphaerella\_tassiana* |
| otu3 | 0.03 | 18.91 | 9.45 | 1.8 | 11.52 | 48.55 | *Cadophora* |
| otu4 | 0.01 | 7.82 | 3.91 | 1.89 | 4.77 | 53.31 | Heliotales\_unidentified |
|  |  |  |  |  |  |  |  |
| ***Epichloë*-depleted communities** | | | | | | | |
| **Groups VE- & VE+**  **Average dissimilarity = 55.99** | | | | | | | |
|  | **Group VE-** | **Group VE+** |  |  |  |  |  |
| **OTUs** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** | **Cum.%** | **Taxa** |
| otu1 | 28.60 | 19.39 | 10.02 | 1.38 | 18.49 | 18.49 | *Mycosphaerella\_tassiana* |
| otu3 | 12.11 | 7.81 | 7.16 | 1.14 | 13.22 | 31.71 | *Cadophora* |
| otu4 | 5.27 | 3.08 | 3.09 | 1.12 | 5.70 | 37.42 | Heliotales\_sps. |
| otu5 | 5.93 | 7.75 | 2.89 | 1.33 | 5.34 | 42.75 | Pleosporales\_sps. |
| otu12 | 4.25 | 0.72 | 1.97 | 0.66 | 3.65 | 46.40 | *Phaeosphaeria triglochinicola* |
| otu11 | 4.70 | 2.01 | 1.96 | 0.97 | 3.61 | 50.01 | Capnodiales sps. |
|  |  |  |  |  |  |  |  |
| **Groups KE- & KE+**  **Average dissimilarity = 72.32** | | | | | | | |
|  | **Group KE-** | **Group KE+** |  |  |  |  |  |
| **OTUs** | **Av.Abund** | **Av.Abund** | **Av.Diss** | **Diss/SD** | **Contrib%** | **Cum.%** |  |
| otu3 | 0.03 | 29.32 | 14.65 | 1.73 | 20.26 | 20.26 | *Cadophora* |
| otu1 | 31.6 | 11.49 | 10.33 | 1.96 | 14.28 | 34.54 | *Mycosphaerella\_tassiana* |
| otu4 | 0.01 | 12.1 | 6.04 | 1.84 | 8.36 | 42.9 | Heliotales\_sps. |
| otu5 | 6.48 | 4.06 | 3.21 | 1.55 | 4.44 | 47.34 | Pleosporales\_sps. |
| otu6 | 7.36 | 1.83 | 2.81 | 1.05 | 3.89 | 51.23 | *Vishniacozyma victoriae* |