Transcriptional responses of the bacterium *Burkholderia terrae* BS001 to the fungal host *Lyophyllum* sp. strain Karsten under soil-mimicking conditions

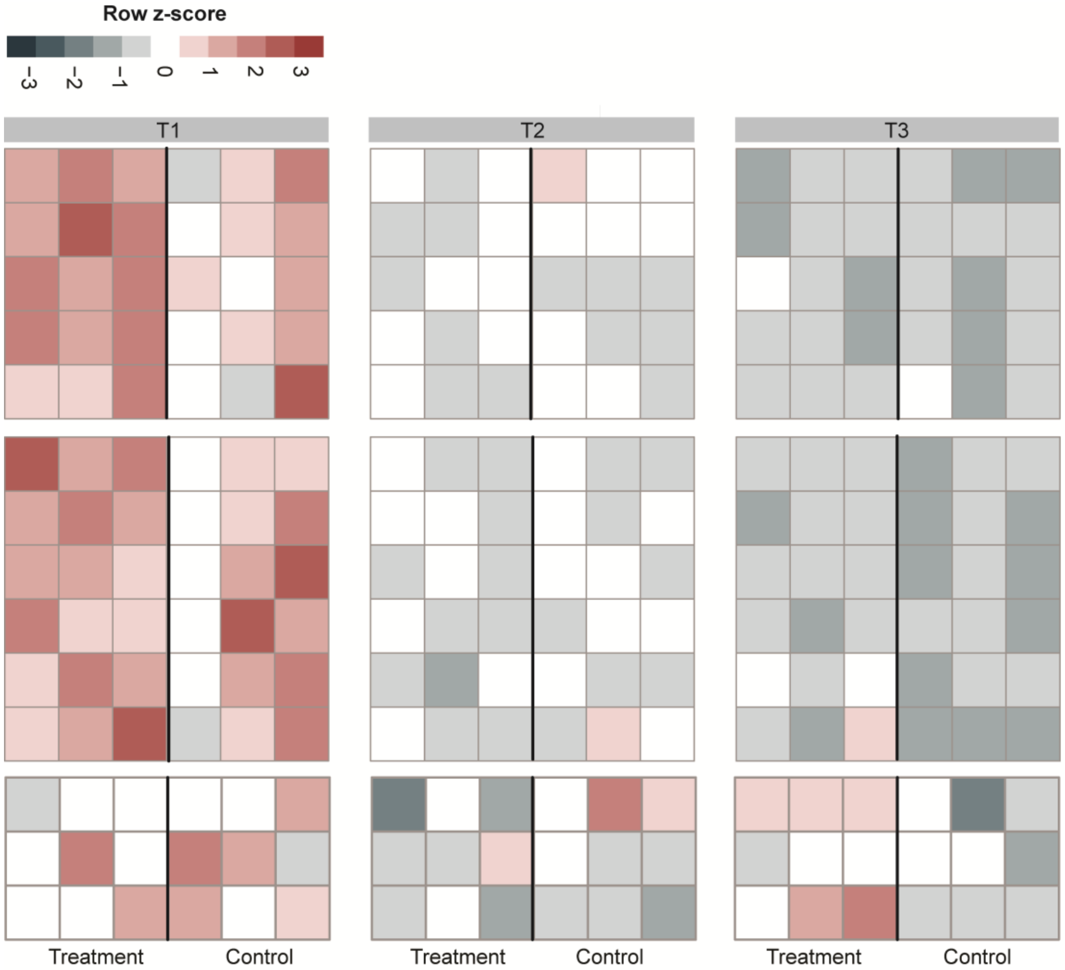
Irshad Ul Haq* Francisco Dini-Andreote and Jan Dirk van Elsas
Microbial Ecology Group, Groningen Institute of Evolutionary Life Sciences (GELIFES), Nijenborgh 7, 9747 AG, University of Groningen, The Netherlands.

*Corresponding author: Irshad Ul Haq, Microbial Ecology, Groningen Institute of Evolutionary Life Sciences (GELIFES), Nijenborgh 7, 9747 AG, University of Groningen, The Netherlands.
E–mail address: i.u.haq@rug.nl

Microbial Ecology

Figure S3 Three gene clusters potentially involved in the metabolism of oxalate. Heat map showing the expression pattern of genes belonging to different clusters presumed to be involved in the degradation and uptake of oxalate at three different time points (T1, T2 and T3) The heat map was constructed based on normalized read counts. The standardized normalized read counts, denoted as the row Z–score, is plotted in color scale (red indicates higher expression and blue indicates lower expression). The names of the putative gene products are given in front of each gene with their respective locus tags.

Gene clusters potentially involved in oxalate metabolism



GntR family transcriptional regulator	AKAUv1_1160009
Oxalate/formate antiporter	AKAUv1_1160010
Putative oxalyl-CoA decarboxylase	AKAUv1_1160013
Formyl-CoA transferase, NAD(P)-binding	AKAUv1_1160014
Formyl-CoA transferase, NAD(P)-binding	AKAUv1_1160019
Formyl-CoA transferase, NAD(P)-binding	AKAUv1_2660028
Conserved membrane protein of unknown function	AKAUv1_2660029
Conserved membrane protein of unknown function	AKAUv1_2660030
RuBisCO operon transcriptional regulator	AKAUv1_2660031
Oxalate/formate antiporter	AKAUv1_2660032
Putative aldehyde dehydrogenase DhaS	AKAUv1_2390002
Tartronate semialdehyde reductase, NADH-dependent	AKAUv1_2390002
Hydroxypyruvate isomerase	AKAUv1_2390003
Glyoxylate carboligase	AKAUv1_2390004