Data Article

Soil microbiome data of two apple orchards in the UK

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ABSTRACT

The microbial communities in two apple orchards were characterised using amplicon-based metabarcoding. Samples were taken from tree station locations along a linear transect and from adjacent grass aisles, at both orchards. Comparison was made between the communities occurring at tree station locations and the grass aisles, and between orchards. Further discussion of these datasets is given in https://doi.org/10.1016/j.apsoil.2018.05.015 (Deakin et al., 2018).

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Specifications table

| Subject area                      | Biology                                      |
|-----------------------------------|----------------------------------------------|
| More specific subject area        | Soil microbial ecology, metabarcoding, spatial correlation |
| Type of data                      | tab separated values (.tsv)                  |
| How data was acquired             | FASTA sequences (.fa)                        |
|                                   | Illumina MiSeq with v3 chemistry             |

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E-mail address: greg.deakin@emr.ac.uk (G. Deakin).
Data format: Raw data and analysed data
Experimental factors: Fungal and bacterial soil communities from two apple orchards from both managed and unmanaged soil
Experimental features: Operation taxonomic units quantitated using metabarcoding of ITS (fungal) and 16S (bacterial) ribosomal regions. Three samples measured for each sample point and mean used for quantification.
Data source location: Desert Orchards: UK lat. 51.210596, long. 0.601664
Cider orchard: UK lat. 52.251020, long. -2.301711
Data accessibility: The data are available with this article
Related research article: Deakin G, Tilston EL, Bennett J, Passey T, Harrison N, Fernández F, Xu X. Spatial structuring of soil microbial communities in commercial apple orchards. Applied Soil Ecology. 2018 130:1–12 [1].

Value of the data
These microbiome data include both fungal and bacterial communities from two long-standing apple orchards in the U.K. As such they offer a wealth of future opportunities to:

- Aid in identifying common microbial communities between apple orchards.
- Make comparison of microbial communities under different soil management practices, for example, long-term perennial crops vs. annual crops.
- Help identify best management practices for enhancing soil microbial communities.

1. Data

This dataset contains an abundance of and a comparative analysis of bacterial and fungal communities found in U.K. dessert apple and cider apple orchards. The data contain fungal and bacterial operational taxonomic units (OTUs) found at tree stations and adjacent (approx. 2 m) grass aisle between tree rows, further context to these data (e.g., soil description and management practice) are given in [1]. Table 1 provides a summary of the sequencing data, Table 2 a summary of the OTU taxonomic data, Table 3 and Table 4 show the top 20 by abundance fungal and bacterial OTUs, respectively, which differed significantly between tree station and grass aisle. Tables 5–8 list the numbers of OTUs aggregated at the phylum and class ranks which differed between (1) tree station and grass aisle, (2) orchards and (3) tree station, and grass aisle at each orchard. Supplementary files 1, 2, and 3 contain OTU sequence information, OTU taxonomy and raw sample abundance for the OTUs, respectively, for fungal communities and Supplementary files 4, 5, and 6 present the same for bacterial communities. The column headers in Supplementary files 3 and 6 provide sample metadata (C/D cider or dessert, Y/N tree station or grass aisle, 1–24 sample location, a/b/c sample replicate).

Table 1
The number of raw reads, reads aligned to OTUs and OTUs from each kingdom, summed for all samples and for each orchard.

|                  | Total reads per sample | Reads aligned to OTUs | Total OTUs | OTUs > 5 reads |
|------------------|------------------------|-----------------------|------------|----------------|
| **All**          |                        |                       |            |                |
| Fungi            | 12,456,087             | 7,016,415 (56.3%)     | 2,132      | 2,067          |
| Bacteria         | 13,562,736             | 9,734,624 (71.8%)     | 6,392      | 6,167          |
| **Cider**        |                        |                       |            |                |
| Fungi            | 5,357,051              | 3,069,449 (57.3%)     | 1,552      | 1,394          |
| Bacteria         | 7,000,356              | 5,069,312 (72.4%)     | 5,786      | 4,752          |
| **Dessert**      |                        |                       |            |                |
| Fungi            | 7,099,036              | 3,946,966 (55.6%)     | 1,638      | 1,371          |
| Bacteria         | 6,562,380              | 4,665,312 (71.1%)     | 4,984      | 4,472          |
2. Experimental design, materials, and methods

2.1. Study design

Soil microbial communities were profiled in soil samples taken from two geographically and agromonically distinct apple orchards. Full information on the location and history of the two orchards is given in [1]. Within each orchard, soils were sampled from two vegetation types, former tree stations and the adjacent grassed aisles; which were divided into three blocks of ca. 20 m long, each with eight consecutive. Three replicate soil cores (2.5 cm diameter, containing soil of 5 cm–20 cm depth) were taken ca. 15 cm apart for each sampling point (grass aisle and tree station).

2.2. DNA extraction and sequencing

Total genomic DNA was isolated from 0.25 g of each soil sample using the protocol as described in [1]. PCR amplification of Internal Transcribed Spacer (ITS) regions of ITS1 and ITS2 and the V4 variable region of the 16S rRNA gene was performed and samples sequenced on the Illumina MiSeq. Full PCR conditions and sequencing preparation are given in [1].

| Kingdom | Phylum | Class | Order | Family | Genus | Species |
|---------|--------|-------|-------|--------|-------|---------|
| Fungi   | 100    | 63.7  | 44.7  | 36.8   | 28.3  | 17.2    | 6.1     |
| Bacteria| 95.8   | 76.7  | 51.1  | 21.4   | 12.7  | 14.7    | NA      |

Table 2

The percentage of OTUs which could be classified at the given taxonomic rank by the UTAX algorithm at the confidence level of 0.65.

| Species/taxa | Base mean | Fold change | P value   |
|--------------|-----------|-------------|-----------|
| Eurotiomycetes(c) | 7488.35   | 20.87       | 1.55 × 10⁻⁶ |
| Eurotiomycetes(c) | 903.59    | 15.27       | 1.85 × 10⁻⁴ |
| Eurotiomycetes(c) | 797.77    | 9.48        | 4.16 × 10⁻³ |
| Mortierellaceae(f) | 664.58    | 4.74        | 4.88 × 10⁻⁷ |
| Fungi(k)       | 627.46    | 4.69        | 2.42 × 10⁻² |
| Monodictys(g)  | 328.51    | 3.07        | 1.44 × 10⁻² |
| Fungi(k)       | 371.91    | 2.88        | 1.06 × 10⁻² |
| Mortierella exigua | 1523.28  | 2.25        | 1.30 × 10⁻² |
| Cryptococcus aerius | 1048.08  | −2.37       | 4.39 × 10⁻³ |
| Ilyonectria macrodidyma | 1439.95 | −2.51       | 1.30 × 10⁻⁴ |
| Tetrachadium(g) | 668.40    | −2.74       | 2.03 × 10⁻³ |
| Trichoderma(g)  | 423.53    | −2.88       | 2.01 × 10⁻² |
| Ascomycota(p)   | 536.66    | −2.93       | 7.11 × 10⁻³ |
| Ascomycota(p)   | 2940.50   | −3.48       | 1.05 × 10⁻² |
| Ascomycota(p)   | 510.30    | −3.91       | 8.78 × 10⁻⁴ |
| Pyronemataceae(f) | 672.12    | −5.3        | 3.52 × 10⁻⁴ |
| Pichia(g)       | 406.19    | −7.23       | 1.61 × 10⁻¹¹ |
| Mrakia frigida  | 417.63    | −7.74       | 3.40 × 10⁻⁸ |
| Pyronemataceae(f) | 1418.61   | −8.03       | 2.93 × 10⁻¹⁰ |
| Dothideomycetes(o) | 378.39   | −10.38      | 3.40 × 10⁻¹⁰ |

Table 3

The top 20 (by abundance) fungal OTUs with higher abundance in grass aisles (positive fold change) or tree stations (negative fold change) and with absolute fold change > 2 and Benjamini–Hochberg corrected P ≤ 0.05.

\(^a\) The lowest assignable taxonomic rank with a UTAX confidence ≥ 0.65.
2.3. Bioinformatics analysis of sequence reads

FASTQ sequences were processed to identify operational taxonomic units (OTUs) and calculate OTU abundances using UPARSE 9.0 OTU clustering pipeline [2].

| Genus/taxa⁴ | Base mean | Fold Change | P value         |
|-------------|-----------|-------------|-----------------|
| Deltaproteobacteria(c) | 151.68    | 6.90        | $3.64 \times 10^{-29}$ |
| Acidobacteria group3(c) | 315.87    | 2.76        | $9.69 \times 10^{-8}$   |
| Myxococcales(o)       | 121.44    | 2.39        | $1.06 \times 10^{-13}$  |
| Gammaproteobacteria(c) | 421.41    | 2.16        | $4.06 \times 10^{-10}$  |
| Bacteroidetes incertae sedis(c) | 364.51    | 2.15        | $1.64 \times 10^{-6}$   |
| Acidobacteria Group5(c) | 110.04    | 2.12        | $3.97 \times 10^{-7}$   |
| Acidobacteria Group1(c) | 910.60    | 2.11        | $2.79 \times 10^{-2}$   |
| Terrimonas             | 529.47    | 2.11        | $2.00 \times 10^{-3}$   |
| Rhizobiales(c)        | 113.99    | 2.10        | $3.77 \times 10^{-9}$   |
| Betaproteobacteria     | 132.13    | 2.06        | $4.40 \times 10^{-8}$   |
| Acidobacteria Group6(c) | 105.82    | 2.05        | $8.31 \times 10^{-4}$   |
| Acidobacteria Group6 | 150.35    | 2.03        | $1.58 \times 10^{-5}$   |
| Xanthobacteraceae(f) | 146.35    | $-2.06$     | $3.95 \times 10^{-7}$   |
| Flavobacterium         | 254.87    | $-2.16$     | $4.59 \times 10^{-4}$   |
| Skermanella           | 151.03    | $-2.30$     | $6.61 \times 10^{-6}$   |
| Gemmatimonadetes(p)    | 106.09    | $-2.30$     | $6.74 \times 10^{-9}$   |
| Novosphaeraceae        | 236.82    | $-2.53$     | $2.20 \times 10^{-8}$   |
| Pseudomonas            | 899.89    | $-2.57$     | $1.44 \times 10^{-8}$   |
| Flavobacterium         | 166.80    | $-3.35$     | $3.83 \times 10^{-7}$   |
| Flavobacterium         | 130.38    | $-4.13$     | $1.50 \times 10^{-10}$  |

⁴ The lowest assignable taxonomic rank with a UTAX confidence $\geq 0.65$.

| Taxa⁵ | Vegetation type⁶ (tree station vs. grass aisle) | Orchard⁷ (cider vs. dessert) | Interaction⁸ |
|-------|-----------------------------------------------|-------------------------------|-------------|
| Ascomycota | 177; 103                                      | 447                           | 54         |
| Basidiomycota | 25; 36                                     | 117                           | 6          |
| Chytridiomycota | 6; 11                                       | 31                            | 3          |
| Fungi     | 101; 98                                       | 278                           | 17         |
| Glomeromycota | 1; 15                                      | 18                            | 1          |
| Rozellomyces | 3; 3                                       | 11                            | 3          |
| Zygomycota | 5; 8                                        | 39                            | 3          |
| Blastocladiomycota | 0; 1                                  | 1                             | 0          |
| **Total** | **318; 275**                                   | **942**                       | **87**     |

⁶ Starting from the phylum rank—the lowest level of taxon with a UTAX confidence $\geq 0.65$.
⁷ The number of OTUs in each taxon which had higher abundance in tree station (before semicolon) and higher abundance in grass aisle samples (after semicolon).
⁸ The number of OTUs in each taxon which had different abundances between the two orchards.

Table 4
The top 20 (by abundance) bacterial OTUs with higher abundance in grass aisles (positive fold change) or tree stations (negative fold change) and with absolute fold change $> 2$ and Benjamini–Hochberg corrected $P \leq 0.05$.

Table 5
The number of fungal OTUs with differential abundance (Benjamini–Hochberg corrected $P \leq 0.05$), aggregated at the phylum rank.
2.4. Assignment of taxonomic rank

The UTAX algorithm (http://drive5.com/usearch/manual/tax_conf.html) assigned each OTU representative sequence to taxonomic ranks by alignment to the reference databases ‘Unite V7’ (ITS) [3] and ‘RDP training set 15’ (16S) [4].

2.5. Statistical analyses

Statistical analyses were carried out in R 3.2.0 [5]. OTU counts were library size normalised using the DESeq. 2 median-of-ratios method [6,7]. The three samples taken from each sampling point were treated as analytical replicates and the data were pooled. OTUs with fewer than six normalised reads across all samples were excluded from further statistical analysis. All analyses were carried out separately for ITS and 16S data.

### Table 6

The number of bacterial OTUs with differential abundance (Benjamini–Hochberg corrected \( P \leq 0.05 \)), aggregated at the phylum rank.

| Taxa\(^a\) | Vegetation type\(^b\) (tree station vs. grass aisle) | Orchard\(^c\) (cider vs. dessert) | Interaction\(^d\) |
|------------|-----------------------------------------------|---------------------------------|----------------|
| Acidobacteria | 54; 61 | 445 | 82 |
| Actinobacteria | 19; 38 | 219 | 28 |
| Armatimonadetes | 3; 0 | 12 | 2 |
| Bacteria | 76; 73 | 603 | 63 |
| Bacteroidetes | 63; 40 | 248 | 45 |
| candidate division WPS-1 | 1; 7 | 34 | 1 |
| candidate division WPS-2 | 1; 8 | 20 | 2 |
| Candidatus Saccharibacteria | 11; 8 | 47 | 8 |
| Chlamydiae | 23; 2 | 54 | 11 |
| Chloroflexi | 7; 3 | 77 | 7 |
| Cyanobacteria/Chloroplast | 8; 0 | 3 | 4 |
| Euryarchaeota | 1; 0 | 3 | 0 |
| Firmicutes | 26; 5 | 68 | 19 |
| Gemmatimonadetes | 17; 1 | 61 | 11 |
| Hydrogenedentates | 1; 0 | 2 | 1 |
| Latescibacteria | 8; 5 | 35 | 7 |
| Nitrospirae | 5; 0 | 10 | 3 |
| Parcubacteria | 11; 2 | 62 | 13 |
| Planctomycetes | 10; 55 | 288 | 17 |
| Proteobacteria | 233; 130 | 911 | 177 |
| Verrucomicrobia | 22; 51 | 196 | 43 |
| Elusimicrobia | 0; 2 | 8 | 1 |
| Fibrobacteres | 0; 5 | 5 | 2 |
| Spirochaetes | 0; 3 | 5 | 2 |
| Tenericutes | 0; 3 | 3 | 2 |
| Aminicenantes | 0; 0 | 1 | 1 |
| BRC1 | 0; 0 | 6 | 0 |
| Ignavibacteria | 0; 0 | 1 | 0 |
| Pacearchaeota | 0; 0 | 1 | 0 |
| Poribacteria | 0; 0 | 2 | 0 |
| Thaumarchaeota | 0; 0 | 1 | 1 |
| Woesearchaeota | 0; 0 | 3 | 0 |
| Total | 600; 502 | 3434 | 553 |

\(^a\) Starting from the phylum rank—the lowest level of taxon with a UTAX confidence \( Z \geq 0.65 \).

\(^b\) The number of OTUs in each taxon which had higher abundance in tree station (semicolon) and higher abundance in grass aisle samples (after semicolon).

\(^c\) The number of OTUs in each taxon which had different abundances between the two orchards.

\(^d\) The number of OTUs in each taxon which had different abundances between tree station compared to grass aisle samples at each orchard.
2.6. Differential OTU abundance

DESeq. 2 was used to detect OTUs with differential relative abundances in relation to vegetation type, orchards and their interactions. The fitted model was: Spatial location within each orchard, vegetation type (grass vs. tree), orchard (cider vs. dessert), and the interaction between vegetation type and orchard. Statistical significance was determined at the 5% level (Benjamini–Hochberg adjusted [8]).

| Taxa               | Vegetation type (tree station vs. grass aisle) | Orchard (cider vs. dessert) | Interaction |
|--------------------|-----------------------------------------------|-----------------------------|-------------|
| Agaricomycetes     | 10; 26                                        | 72                          | 1           |
| Agaricostilbomycetes | 1; 0                                      | 0                           | 0           |
| Ascomycota         | 35; 32                                       | 120                         | 8           |
| Basidiomycota      | 4; 5                                         | 19                          | 0           |
| Chytridiomycetes   | 4; 3                                         | 12                          | 0           |
| Chytridiomycota    | 1; 8                                         | 18                          | 3           |
| Dothideomycetes    | 33; 13                                       | 56                          | 10          |
| Eurotiomycetes     | 21; 8                                        | 39                          | 4           |
| Exobasidiomycetes  | 2; 0                                         | 1                           | 0           |
| Fungi              | 101; 98                                      | 278                         | 17          |
| Glomeromycota      | 1; 7                                         | 9                           | 0           |
| Lecanoromycetes    | 2; 1                                         | 3                           | 0           |
| Leotiomycetes      | 26; 9                                        | 52                          | 3           |
| Microbotryomycetes | 2; 4                                         | 8                           | 2           |
| Monoblepharidomycetes | 1; 0                                   | 1                           | 0           |
| Mortierellomycota  | 1; 6                                         | 27                          | 3           |
| Murcoromycolina Incertae sedis | 1; 1                           | 1                           | 0           |
| Orbiliomycetes     | 7; 1                                         | 5                           | 1           |
| Pezizomycetes      | 14; 4                                        | 29                          | 6           |
| Rozellomycota      | 3; 3                                         | 11                          | 3           |
| Saccharomycetes    | 1; 3                                         | 4                           | 1           |
| Sordariomycetes    | 38; 31                                       | 130                         | 19          |
| Tremellomycetes    | 6; 1                                         | 15                          | 3           |
| Zygomycota         | 1; 1                                         | 10                          | 0           |
| Blastocladiomycota | 0; 1                                         | 1                           | 0           |
| Glomeromycetes     | 0; 8                                         | 9                           | 1           |
| Pezizomycolina Incertae sedis | 0; 1                           | 6                           | 1           |
| Geoglossomycetes   | 0; 0                                         | 3                           | 1           |
| Pucciniomycolina Incertae sedis | 0; 0                           | 1                           | 0           |
| Ustilaginomycetes  | 0; 0                                         | 1                           | 0           |
| Zygomycota Incertae sedis | 0; 0                           | 1                           | 0           |
| **Total**          | **318; 275**                                 | **942**                     | **87**      |

* Starting from the phylum rank—the lowest level of taxon with a UTAX confidence ≥ 0.65.
* The number of OTUs in each taxon which had higher abundance in tree station (before semicolon) and higher abundance in grass aisle samples (after semicolon).
* The number of OTUs in each taxon which had different abundances between the two orchards.
* The number of OTUs in each taxon which had different abundances between tree station compared to grass aisle samples at each orchard.
Table 8

The number of bacterial OTUs with differential abundance (Benjamini–Hochberg corrected $P \leq 0.05$), aggregated at the class rank.

| Taxa                          | Vegetation type$^b$ (tree station vs grass aisle) | Orchard$^c$ (cider vs dessert) | Interaction$^d$ |
|-------------------------------|-----------------------------------------------|--------------------------------|-----------------|
| Acidobacteria                 | 15; 5                                         | 65                             | 9               |
| Acidobacteria Group1          | 2; 1                                          | 30                             | 3               |
| Acidobacteria Group10         | 1; 6                                          | 27                             | 3               |
| Acidobacteria Group13         | 2; 0                                          | 4                              | 2               |
| Acidobacteria Group15         | 2; 0                                          | 5                              | 1               |
| Acidobacteria Group16         | 4; 4                                          | 33                             | 3               |
| Acidobacteria Group17         | 3; 4                                          | 20                             | 4               |
| Acidobacteria Group18         | 1; 0                                          | 2                              | 0               |
| Acidobacteria Group2          | 4; 0                                          | 8                              | 2               |
| Acidobacteria Group20         | 1; 0                                          | 1                              | 1               |
| Acidobacteria Group22         | 1; 3                                          | 20                             | 4               |
| Acidobacteria Group3          | 6; 7                                          | 39                             | 12              |
| Acidobacteria Group4          | 2; 5                                          | 39                             | 6               |
| Acidobacteria Group5          | 2; 2                                          | 10                             | 1               |
| Acidobacteria Group6          | 5; 19                                         | 94                             | 23              |
| Acidobacteria Group7          | 1; 4                                          | 19                             | 5               |
| Acidobacteria Group8          | 19; 37                                        | 218                            | 28              |
| Alphaproteobacteria           | 50; 18                                        | 164                            | 36              |
| Anaerolineae                  | 2; 0                                          | 14                             | 3               |
| Armatimonadetes               | 1; 0                                          | 10                             | 1               |
| Armatimonadia                 | 2; 0                                          | 2                              | 1               |
| Bacilli                       | 2; 0                                          | 25                             | 1               |
| Bacteroidetes                 | 76; 73                                        | 603                            | 63              |
| Bacteroidetes incertae sedis  | 5; 4                                          | 25                             | 10              |
| Bacteroidia                   | 5; 0                                          | 7                              | 2               |
| Betaproteobacteria            | 33; 18                                        | 102                            | 33              |
| candidate division WPS-1      | 1; 5                                          | 30                             | 1               |
| candidate division WPS-2      | 1; 8                                          | 20                             | 2               |
| Candidatus Saccharibacteria    | 11; 8                                         | 47                             | 8               |
| Chlamydiae                    | 6; 0                                          | 14                             | 4               |
| Chlamydia                     | 17; 2                                         | 40                             | 7               |
| Chloroflexi                   | 5; 1                                          | 38                             | 2               |
| Chloroplasm                    | 8; 0                                          | 2                              | 3               |
| Clostridia                    | 20; 1                                         | 27                             | 14              |
| Cytophagia                    | 10; 2                                         | 18                             | 5               |
| Deltaproteobacteria           | 34; 48                                        | 220                            | 34              |
| Epsilonproteobacteria         | 1; 0                                          | 1                              | 0               |
| Euryarchaeota                 | 1; 0                                          | 2                              | 0               |
| Firmicutes                    | 2; 2                                          | 12                             | 2               |
| Flavobacteriia                | 8; 1                                          | 16                             | 4               |
| Gammaproteobacteria           | 92; 16                                        | 238                            | 50              |
| Gemmatimonadetes              | 17; 1                                         | 61                             | 11              |
| Holophagae                    | 2; 1                                          | 5                              | 2               |
| Hydrogenedentates             | 1; 0                                          | 2                              | 1               |
| Latecibacteria                | 8; 5                                          | 35                             | 7               |
| Negativicutes                 | 2; 0                                          | 2                              | 1               |
| Nitrosira                     | 5; 0                                          | 8                              | 2               |
| Opitutae                      | 2; 1                                          | 8                              | 1               |
| Parcubacteria                 | 7; 1                                          | 49                             | 9               |
| Parcubacteria(p)              | 4; 1                                          | 13                             | 4               |
| Planctomycetes                | 1; 14                                         | 51                             | 2               |
| Planctomycetia                | 9; 38                                         | 223                            | 15              |
| Proteobacteria                | 23; 30                                        | 184                            | 24              |
| Spartobacteria                | 6; 18                                         | 61                             | 14              |
| Sphingobacteria               | 21; 11                                        | 88                             | 10              |
| Subdivision3                  | 4; 24                                         | 83                             | 22              |
| Verrucomicrobia               | 3; 6                                          | 26                             | 4               |
| Verrucomicrobiae              | 7; 2                                          | 18                             | 2               |
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**Transparency document. Supporting information**

Transparency data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.11.067.

**Appendix A. Supporting information**

Supplementary data associated with this article can be found in the online version at https://doi.org/10.1016/j.dib.2018.11.067.

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### Table 8 (continued)

| Taxa\(^a\)          | Vegetation type\(^b\) (tree station vs grass aisle) | Orchard\(^c\) (cider vs dessert) | Interaction\(^d\) |
|----------------------|-----------------------------------------------|----------------------------------|-------------------|
| Caldilineae          | 0; 1                                         | 10                               | 1                 |
| candidate division WPS-1(p) | 0; 2                                      | 4                                | 0                 |
| Elusimicrobia        | 0; 2                                         | 7                                | 1                 |
| Erysipelotrichia     | 0; 2                                         | 2                                | 1                 |
| Fibrobacteres        | 0; 5                                         | 5                                | 2                 |
| Ktedonobacteria      | 0; 1                                         | 13                               | 1                 |
| Mollicutes           | 0; 3                                         | 3                                | 2                 |
| Phycisphaerae        | 0; 3                                         | 14                               | 0                 |
| Spirochaetia         | 0; 3                                         | 4                                | 2                 |
| Thermoleophilia      | 0; 1                                         | 1                                | 0                 |
| Acidobacteria Group11| 0; 0                                         | 3                                | 0                 |
| Acidobacteria Group12| 0; 0                                         | 1                                | 0                 |
| Acidobacteria Group23| 0; 0                                         | 1                                | 0                 |
| Acidobacteria Group25| 0; 0                                         | 18                               | 1                 |
| Acidobacteria Group9 | 0; 0                                         | 1                                | 0                 |
| Aminicenantes(p)     | 0; 0                                         | 1                                | 1                 |
| BRC1                 | 0; 0                                         | 6                                | 0                 |
| Chloroflexia         | 0; 0                                         | 2                                | 0                 |
| Cyanobacteria        | 0; 0                                         | 1                                | 1                 |
| Endomicrobia         | 0; 0                                         | 1                                | 0                 |
| Ignavibacteria       | 0; 0                                         | 1                                | 0                 |
| Nitrospirae          | 0; 0                                         | 2                                | 1                 |
| Oligoflexa           | 0; 0                                         | 2                                | 0                 |
| Pacearchaeota(p)     | 0; 0                                         | 1                                | 0                 |
| Poribacteria         | 0; 0                                         | 2                                | 0                 |
| Spirochaetes         | 0; 0                                         | 1                                | 0                 |
| Thaumarchaeota       | 0; 0                                         | 1                                | 1                 |
| Thermoplasmata       | 0; 0                                         | 1                                | 0                 |
| Woesearchaeota(p)    | 0; 0                                         | 3                                | 0                 |
| **Total**            | **600; 502**                                 | **3,434**                        | **553**           |

\(^a\) Starting from the phylum rank—the lowest level of taxon with a UTAX confidence ≥ 0.65.

\(^b\) The number of OTUs in each taxon which had higher abundance in tree station (before semicolon) and higher abundance in grass aisle samples (after semicolon).

\(^c\) The number of OTUs in each taxon which had different abundances between the two orchards.

\(^d\) The number of OTUs in each taxon which had different abundances between tree station compared to grass aisle samples at each orchard.
References

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