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| **Table S1** Data obtained from sequencing data of V3-V4 and ITS1-5f variable regions of 16S and ITS rRNA of bacteria and fungi, respectively |
| **Sample Id** | **Raw reads** **(#)** | **Clean reads** **(#)** | **Average (bP)** | **Q20** **(%)** | **Q30** **(%)** |
| **Bacteria (16S; V3-V4)** |
| KMHS | 82683±5896.88 | 56828±5279.14 | 414±0.35 | 98.53 | 95.03 |
| KMDS | 78496±1221.47 | 53440±1695.85 | 415±1.35 | 98.49 | 94.95 |
| KMHR | 89360±2068.77 | 85206±2173.38 | 412±4.17 | 98.52 | 94.91 |
| KMDR | 87776±1118.32 | 82087±1320.08 | 418±8.66 | 98.54 | 94.97 |
| QJHS | 83394±3034.12 | 57511±3461.80 | 417±0.11 | 98.55 | 95.12 |
| QJDS | 87785±843.12 | 61060±1326.42 | 417±0.49 | 98.53 | 95.06 |
| QJHR | 90055±4791.24 | 84522±5262.63 | 408±0.97 | 98.42 | 94.66 |
| QJDR | 87272±1047.99 | 82447±1010.24 | 407±0.52 | 98.43 | 94.68 |
| ZTHS | 86069±3369.16 | 60739±2423.73 | 416±0.40 | 98.59 | 95.22 |
| ZTDS | 81226±4054.05 | 55098±5018.95 | 420±2.68 | 98.50 | 94.91 |
| ZTHR | 89645±3092.62 | 84158±2709.50 | 420±2.71 | 98.48 | 94.81 |
| ZTDR | 88343±2632.49 | 80832±1724.36 | 413±2.87 | 98.37 | 94.54 |
| **Fungi (ITS; 1-5f)** |
| KMHS | 90,065±10890.45 | 75,146± 8191.67 | 261± 10.42 | 97.04 | 91.54 |
| KMDS | 98,885±4429.65 | 87,804± 2342.49 | 248± 28.58 | 99.32 | 94.47 |
| KMHR | 90,041±3836.71 | 75,631± 3783.71 | 285± 0.13 | 94.64 | 85.39 |
| KMDR | 88,754±4983.62 | 76,233± 6738.24 | 275± 15.55 | 95.22 | 86.90 |
| QJHS | 86,939±24611.14 | 74,661± 21402.28 | 257± 2.82 | 97.79 | 93.37 |
| QJDS | 96,700±343.92 | 77,352± 2240.57 | 246± 10.66 | 98.90 | 96.35 |
| QJHR | 85,890±673.91 | 73,783± 365.71 | 284± 1.19 | 94.67 | 85.44 |
| QJDR | 91,019±2976.83 | 77,443± 2710.93 | 281± 3.60 | 94.73 | 85.65 |
| ZTHS | 99,472±4488.53 | 84,713± 5857.42 | 238± 13.43 | 98.98 | 96.58 |
| ZTDS | 97,328±2171.44 | 69,526± 10316.32 | 239± 19.36 | 99.13 | 96.86 |
| ZTHR | 92,148±2214.13 | 77701± 2497.13 | 285± 0.51 | 94.62 | 85.37 |
| ZTDR | 89,914±3593.84 | 76,902± 3990.70 | 285± 1.07 | 94.71 | 85.68 |
| Here; Q20 and Q30 are the percentages of bases with base quality values greater than 20 (sequencing error rate less than 1%) and 30 (sequencing error rate less than 0.1%). Data is represented as standard error of means (±SEM, n=3).  |

**Table S2** Relative abundance of top 10 dominant bacterial and fungal phyla in different sample

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Taxonomy** | **KMHS** | **QJHS** | **ZTHS** | **KMDS** | **QJDS** | **ZTDS** |
| **Bacteria (16S; V3-V4)** |
| Proteobacteria | 0.4397±0.0501 | 0.3825±0.0321 | 0.4318±0.0135 | 0.4233±0.0120 | 0.3994±0.0564 | 0.5105±0.1790 |
| Cyanobacteria | 0.0008±0.0008 | 0.0028±0.0030 | 0.0003±0.0001 | 0.0013±0.0014 | 0.0016±0.0012 | 0.0030±0.0025 |
| Firmicutes | 0.0015±0.0025 | 0.0115±0.0058 | 0.0010±0.0006 | 0.0025±0.0026 | 0.0175±0.0043 | 0.1527±0.2383 |
| Actinobacteriota | 0.3271±0.0488 | 0.0665±0.0088 | 0.2809±0.0322 | 0.2848±0.0193 | 0.0840±0.0194 | 0.1348±0.0734 |
| Chloroflexi | 0.0237±0.0043 | 0.0988±0.0202 | 0.0261±0.0027 | 0.0363±0.0088 | 0.1152±0.0624 | 0.0166±0.0094 |
| Acidobacteriota | 0.0902±0.0063 | 0.1355±0.0222 | 0.1099±0.0228 | 0.0975±0.0057 | 0.1231±0.0137 | 0..0651±0..0344 |
| Gemmatimonadota | 0.0265±0.0084 | 0.1301±0.0211 | 0.0387±0.0057 | 0.0318±0.0055 | 0.0889±0.0124 | 0.0209±0.0063 |
| Bacteroidota | 0.0408±0.0140 | 0.0850±0.0177 | 0.0602±0.0094 | 0.0500±0.0151 | 0.0709±0.0116 | 0.0656±0.0128 |
| Myxococcota | 0.0111±0.0032 | 0.0329±0.0032 | 0.0078±0.0007 | 0.0252±0.0110 | 0.0427±0.0041 | 0.0082±0.0048 |
| Crenarchaeota | 0.0150±0.0085 | 0.0020±0.0007 | 0.0149±0.0059 | 0.0218±0.0149 | 0.0012±0.0009 | 0.0038±0.0009 |
| **Taxonomy** | **KMHR** | **QJHR** | **ZTHR** | **KMDR** | **QJDR** | **ZTDR** |
| **Bacteria (16S; V3-V4)** |
| Proteobacteria | 0.4562±0.1317 | 0.2556±0.0168 | 0.7105±0.0550 | 0.5971±0.3361 | 0.2531±0.0438 | 0.5197±0.0660 |
| Cyanobacteria | 0.4891±0.0983 | 0.6625±0.0565 | 0.2187±0.0806 | 0.3224±0.3373 | 0.6865±0.0677 | 0.3611±0.0993 |
| Firmicutes | 0.0011±0.0012 | 0.0087±0.0124 | 0.0019±0.0014 | 0.0035±0.0049 | 0.0029±0.0011 | 0.0099±0.0032 |
| Actinobacteriota | 0.0326±0.0228 | 0.0199±0.0096 | 0.0140±0.0111 | 0.0269±0.0219 | 0.0182±0.0081 | 0.0384±0.0354 |
| Chloroflexi | 0.0012±0.0006 | 0.0098±0.0079 | 0.0014±0.0010 | 0.0025±0.0029 | 0.0066±0.0032 | 0.0106±0.0113 |
| Acidobacteriota | 0.0005±0.0003 | 0.0025±0.0029 | 0.0002±0.0003 | 0.0006±0.0007 | 0.0016±0.0010 | 0.0018±0.0015 |
| Gemmatimonadota | 0.00007±0.00007 | 0.0003±0.0001 | 0.0002±0.0002 | 0.0000±0.0000 | 0.0004±0.0005 | 0.0001±0.0002 |
| Bacteroidota | 0.0166±0.0126 | 0.0154±0.0089 | 0.0479±0.0569 | 0.0405±0.0486 | 0.0116±0.0049 | 0.0337±0.0182 |
| Myxococcota | 0.0005±0.0006 | 0.0110±0.0006 | 0.0110±0.0054 | 0.0014±0.0020 | 0.0003±0.0004 | 0.0079±0.0066 |
| Crenarchaeota | 0.0002±0.00005 | 0.0001±0.0001 | 0.0001±0.00004 | 0.0001±0.0001 | 0.0004±0.0002 | 0.0005±0.0005 |
| **Taxonomy** | **KMHS** | **QJHS** | **ZTHS** | **KMDS** | **QJDS** | **ZTDS** |
| **Fungi (ITS; 1-5f)** |
| Ascomycota | 0.7581±0.0330 | 0.6677±0.1272 | 0.6141±0.0908 | 0.5565±0.3854 | 0.6953±0.0122 | 0.5989±0.0863 |
| Basidiomycota | 0.1162±0.0414 | 0.0048±0.0039 | 0.2394±0.1216 | 0.3677±0.3425 | 0.0826±0.0407 | 0.1091±0.0552 |
| Mortierellomycota | 0.0172±0.0054 | 0.2164±0.1264 | 0.0271±0.0041 | 0.0127±0.0146 | 0.0504±0.0117 | 0.0172±0.0051 |
| Mucoromycota | 0.0004±0.0001 | 0.0125±0.0127 | 0.0003±0.0001 | 0.0052±0.0084 | 0.0520±0.0356 | 0.1322±0.0966 |
| Rozellomycota | 0.0142±0.0110 | 0.0007±0.0002 | 0.0351±0.0194 | 0.0049±0.0036 | 0.0015±0.0007 | 0.0712±0.0912 |
| Fungi\_phy\_Incertae\_sedis | 0.0049±0.0036 | 0.0073±0.0016 | 0.0054±0.0014 | 0.0058±0.0066 | 0.0461±0.0246 | 0.0039±0.0001 |
| Chytridiomycota | 0.0337±0.0116 | 0.0063±0.0069 | 0.0257±0.0034 | 0.0087±0.0126 | 0.0028±0.0019 | 0.0120±0.0101 |
| Aphelidiomycota | 0.0002±0.0002 | 0.0063±0.0055 | 0.0003±0.0003 | 0.0105±0.0147 | 0.0067±0.0049 | 0.0087±0.0061 |
| Basidiobolomycota | 0.0000±0.0000 | 0.0003±0.0004 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0009±0.0010 | 0.0000±0.0000 |
| Olpidiomycota | 0.0005±0.0005 | 0.0000±0.0000 | 0.0002±0.0001 | 0.0004±0.0003 | 0.0000±0.0000 | 0.0010±0.0001 |
| **Taxonomy** | **KMHR** | **QJHR** | **ZTHR** | **KMDR** | **QJDR** | **ZTDR** |
| **Fungi (ITS; 1-5f)** |
| Ascomycota | 0.8852±0.0546 | 0.9095±0.0858 | 0.9059±0.0732 | 0.8597±0.1470 | 0.8701±0.0284 | 0.8030±0.0866 |
| Basidiomycota | 0.0025±0.0023 | 0.0026±0.0038 | 0.0024±0.0028 | 0.0093±0.0135 | 0.0074±0.0101 | 0.0043±0.0033 |
| Mortierellomycota | 0.0001±0.0001 | 0.0000±0.0000 | 0.00003±0.00006 | 0.0286±0.0494 | 0.0001±0.0001 | 0.0000±0.0000 |
| Mucoromycota | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 |
| Rozellomycota | 0.0001±0.0001 | 0.0000±0.0000 | 0.0000±0.0001 | 0.0048±0.0084 | 0.0000±0.0000 | 0.0001±0.0001 |
| Fungi\_phy\_Incertae\_sedis | 0.0001±0.0002 | 0.0001±0.0001 | 0.0020±0.0034 | 0.0047±0.0053 | 0.0000±0.0000 | 0.0003±0.0004 |
| Chytridiomycota | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0002±0.0004 | 0.0000±0.0000 | 0.0002±0.0002 |
| Aphelidiomycota | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0004±0.0007 |
| Basidiobolomycota | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0000±0.0000 |
| Olpidiomycota | 0.0002±0.0002 | 0.0000±0.0000 | 0.0010±0.0002 | 0.0000±0.0000 | 0.0000±0.0000 | 0.0006±0.0010 |

Relative abundance in bacterial and fungal communities of the top 10 species with highest abundance at phylum level. Data is represented as standard error of means (±SEM, n=3).