**Supplementary Table 2. Taxonomic assignments and functional inference based on phylogenetic placement** **for** **aggregating** **(cyanosphere) OTUs in the cold desert (HSN)**.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Phylum** | **Deepest Taxonomic Assignment** | **OTU ID** | **Nutritional type / typical habitat** | **Reference** | **Diazotrophywithin genus** | **Reference** |
| Firmicutes | *Staphylococcus* | 1084865 | Copiotrophs/ saprophytic fermentative | [1] | no |  |
| Firmicutes | *Streptoccoccus gordonii* | 1083194 | Copiotrophs/ saprophytic fermentative (largely animal, but also rhizospheres, manure) | [2] | no |  |
| Alphaproteobacteria | *Methylobacterium aerolaum* | 4323871 | Strict aerobe/ mostly copiotrophs and C1 facultative | [3] | yes | [4] |
| Betaproteobacteria | *Pelomonas saccharophila* | 1108275 | Copiotrophs/ saprophytic, aerobic, facultative lithoautotroph | [5] | yes | [5] |
| Betaproteobacteria | *Snodgrassella* | 933546 | Copiotrophs/ saprophytic microaerophillic | [6] | no | genome |
| Deltaproteobacteria | Myxobacteria (Chondromyces?) | 565046 | Aerobic copiotrophs/ saprophytic/ dung |  |  |  |
| Deltaproteobacteria | Myxobacteria | New.ReferenceOTU69 | Aerobic copiotrophs/ saprophytic/ dung | [7] | no | Kegg Pathways |
| Deltaproteobacteria | Myxobacteria | New.CleanUp.ReferenceOTU14037 | Aerobic copiotrophs/ saprophytic/ dung |  |  |  |
| Gammaproteobacteria | *Escherichia/Sighella* | 1111294 | Copiotrophs/ saprophytic facultative anaerobe | [8] | yes | 15 |
| Gammaproteobacteria | *Haemophilus parinfluenzae* | 865469 | Aerobic copiotrophs/animal commensal | [9] | no | KEGG Pathways |
| Gammaproteobacteria | *Acinetobacter johsnonii* | 988314 | Copiotrophs/ saprophytic obligate aerobe | [10] | yes | [11] |
| Gammaproteobacteria | *Stenotrophomonas maltophila* | 1083508 | Copiotrophs/ saprophytic/nosocomial | [12] | yes | [11] |
| Gammaproteobacteria | *Stenotrophomonas maltophila* | 1834768 | Copiotrophs/ saprophytic/nosocomial | yes |
| Gammaproteobacteria | *Moraxella* | 990864 | Aerobic copiotrophs/animal commensal | [13] |  |  |
| Bacteriodetes | *Bacteriodes vulgatus* | 589277 | Copiotrophs/ saprophytic/anaerobes, rare in soil | [14] | no | KEGG Pathways |
| Bacteriodetes | Cytophagaceae | New.CleanUp.ReferenceOTU1843 | Found in terrestrial, marine and freshwater environments | [15] |  |  |
| Bacteriodetes | Cytophagaceae | New.CleanUp.ReferenceOTU7233 |  |  |  |  |
| Actinobacteria | Actinomycetales | 937735 |  |  |  |  |
| (Cyanobacteria) | higher plant plastid | 153978 | NA (from plant roots or pollen) |  |  |  |
| (Cyanobacteria) | higher plant plastid | 1126072 | NA (from plant roots or pollen) |  |  |  |
| Unassigned |  | New.ReferenceOTU31 |  |  |  |  |
| Unassigned |  | New.CleanUp.ReferenceOTU8675 |  |  |  |  |

**Supplementary Table 3. Taxonomic assignments and functional inference based on phylogenetic placement** **for** **aggregating** **(cyanosphere) OTUs in the hot desert (FB)**.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Phylum** | **Deepest Taxonomic Assignment** | **OTU ID** | **Nutritional type/typical habitat** | **Reference** | **Diazotrophy within genus** | **Reference** |
| Gammaproteobacteria | *Stenotrophomonas maltophila* | 1834768 | copiotrophs/ saprophytic/nosocomial | [12] | yes | [11] |
| Bacteriodetes | Sphingobacteriales | 1087471 |  |  |  |  |
| (Cyanobacteria) | higher plant plastid | 153978 | NA (from plant roots or pollen) |  |  |  |

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