Table S1. Information of selected forward (F) and reverse (R) primers targeting different type of genes for qPCR.

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| --- | --- | --- |
| Target gene | Primer | Primer sequence |
| Bacterial 16S rDNA | Eub338F | 5′-ACTCCTACGGGAGGCAGCAG-3′ |
| Eub806R | 5′-GGACTACHVGGGTWTCTAAT-3′ |
| Fungal ITS | ITS1F | 5′-CTTGGTCATTTAGAGGAAGTAA-3′ |
| ITS2R | 5′-TGCGTTCTTCATCGATGC-3′ |
| Archaeal 16S rDNA | Arch344F | 5′-ACGGGGYGCAGCAGGCGCGA-3′ |
| Arch915R | 5′-GTGCTCCCCCGCCAATTCCT-3′ |

Table S2. Vegetation and soil edaphic properties of different revegetation sites. The mean and standard error in parentheses are shown. Different letters represent significant differences among sites. MS, 5Y, 28Y, 36Y, 53Y and 61Y indicate mobile sand (control), 5-, 28-, 36-, 53- and 61-year-old revegetation sites, respectively.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Item (unit) | MS | 5Y | 28Y | 36Y | 53Y | 61Y |
| BSCs Coverage (%) | 0 c | 78.3 (4.4) b | 94.3 (1.2) a | 96.0 (0.6) a | 97.0 (1.5) a | 100.0 (0.0) a |
| BSCs Thickness (cm) | 0 b | 0.6 (0.1) b | 0.8 (0.03) ab | 0.8 (0.03) ab | 1.0 (0.03) a | 1.2 (0.08) a |
| BSCs mass (g cm2) | 0 b | 0.4 (0.02) b | 0.6 (0.03) b | 0.9 (0.1) ab | 1.0 (0.02) ab | 1.2 (0.1) a |
| Shrub coverage (%) | 5.7 (1.2) c | 27.7 (1.5) b | 47.7 (1.5) a | 42.3 (1.5) ab | 36.0 (1.0) ab | 31.7 (1.7) b |
| Silt content (%) | 0.7 (0.03) c | 4.2 (0.5) c | 16.1 (1.3) b | 17.3 (0.4) b | 32.1 (2.6) a | 32.7 (2.6) a |
| Clay content (%) | 0.3 (0.2) c | 1.5 (0.1) c | 3.4 (0.1) b | 3.2 (0.1) b | 6.3 (0.5) a | 5.7 (0.3) a |
| pH | 8.5 (0.1) ab | 8.7 (0.04) a | 8.4 (0.06) ab | 8.5 (0.06) ab | 8.2 (0.07) b | 8.4 (0.03) ab |
| EC (us/cm) | 45.8 (5.2) b | 92.5 (9.8) b | 179.9 (14.2) ab | 184.6 (13.5) ab | 379.7(68.7) a | 303.7(89.2) a |
| TC (g kg-1) | 0.2 (0.02) b | 1.7 (0.2) b | 5.6 (0.6) ab | 5.9 (0.4) ab | 13.9 (1.4) a | 15.1 (0.8) a |
| TN (g kg-1) | 0.1 (0.02) b | 0.2 (0.03) b | 0.4 (0.05) ab | 0.4 (0.03) ab | 1.0 (0.1) a | 1.0 (0.04) a |
| TP (g kg-1) | 0.3 (0.01) b | 0.4 (0.01) b | 0.6 (0.02) ab | 0.6 (0.02) ab | 0.9 (0.04) a | 0.9 (0.03) a |
| Ammonia (mg kg-1) | 0.1 (0.02) b | 0.2 (0.07) b | 0.6 (0.2) a | 0.3 (0.1) ab | 0.3 (0.09) a | 0.2 (0.02) a |
| Nitrate (mg kg-1) | 0.2 (0.01) b | 0.3 (0.04) ab | 0.5 (0.1) ab | 0.4 (0.08) ab | 0.5 (0.03) ab | 0.7 (0.3) a |
| C/N | 1.8 (0.2) b | 8.5 (0.3) b | 13.0 (0.5) ab | 14.1 (0.5) a | 14.5 (0.01) a | 15.8 (0.1) a |
| C/P | 0.8 (0.04) e | 4.6 (0.2) d | 9.0 (0.3) c | 9.4 (0.3)c | 16.1 (0.5) b | 17.8 (0.2) a |
| N/P | 0.5 (0.05) b | 0.6 (0.04) b | 0.7 (0.04) b | 0.7 (0.04) b | 1.1 (0.03) a | 1.1 (0.01) a |

Table S3. Differences of soil microbial communities among revegetation sites examined by the dissimilarity test of *adonis*. MS, 5Y, 28Y, 36Y, 53Y and 61Y indicate mobile sand (the control), 5-, 28-, 36-, 53- and 61-year-old revegetation sites, respectively.

|  |  |  |
| --- | --- | --- |
| Compared sites | R2 | *P-*value |
| MS – 5Y | 0.87 | 0.1 |
| MS – 28Y | 0.92 | 0.1 |
| MS – 36Y | 0.91 | 0.1 |
| MS – 53Y | 0.92 | 0.1 |
| MS – 61Y | 0.88 | 0.1 |
| 5Y – 28Y | 0.71 | 0.1 |
| 5Y – 36Y | 0.71 | 0.1 |
| 5Y – 53Y | 0.71 | 0.1 |
| 5Y – 61Y | 0.71 | 0.1 |
| 28Y – 36Y | 0.39 | 0.1 |
| 28Y – 53Y | 0.43 | 0.1 |
| 28Y – 61Y | 0.73 | 0.1 |
| 36Y – 53Y | 0.39 | 0.1 |
| 36Y – 61Y | 0.74 | 0.1 |
| 53Y – 61Y | 0.74 | 0.1 |

Table S4. The numbers and percentages of shared and unique genes between revegetation sites. The values in normal font are the number of overlapping genes between different sites, and values in bold font are unique genes to each site. MS, 5Y, 28Y, 36Y, 53Y and 61Y indicate mobile sand, 5-, 28-, 36-, 53- and 61-year-old revegetation sites, respectively.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Sites | MS | 5Y | 28Y | 36Y | 53Y | 61Y |
| MS | **109(0.001)** | 23083(0.244) | 23728(0.250) | 23749(0.251) | 23688(0.250) | 23461(0.248) |
| 5Y |  | **140(0.001)** | 54768(0.579) | 54963(0.581) | 54689(0.578) | 49846(0.527) |
| 28Y |  |  | **1782(0.018)** | 75914(0.802) | 73067(0.772) | 54847(0.580) |
| 36Y |  |  |  | **8069(0.085)** | 76426(0.808) | 54921(0.580) |
| 53Y |  |  |  |  | **1810(0.019)** | 54775(0.579) |
| 61Y |  |  |  |  |  | **63(0.000)** |

Fig. S1Relationships between α-diversity (Shannon index) of overall functional genes (A), normalized signal densities of C- (B), N- (C), P-(D) cycling related genes and revegetation year.

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