**Supplementary information**

**Supplementary table S1:** Selected soil properties, soil management practices, Enzymatic activities, and abundance of genes involved in the production of studied enzymes (GeoChip 4.0) of samples collected from three major grain producing regions across Australia.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sample name | Region | Soil Type | Management practices | Total C (%) | Total N (%) | pH | Enzymatic activities\* (nmol h-1 g-1 soil) | Geochip data (normalized signal intensity) |
|  NAG | CB | AG |  XYL | Acetylglucosaminidase | Exoglucanase | -amylase | Xylanase |
| N1 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, minimal till | 1.41 | 0.12 | 8.29 | 12.23 | 38.02 | 1.46 | 6.30 | 6.34 | 9.94 | 20.12 | 5.33 |
| N2 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, minimal till | 1.45 | 0.12 | 8.35 | 13.94 | 34.49 | 1.58 | 7.66 | 6.46 | 8.99 | 20.63 | 5.99 |
| N3 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, minimal till | 1.44 | 0.13 | 8.32 | 12.45 | 41.90 | 1.99 | 7.15 | 6.12 | 10.01 | 24.99 | 5.79 |
| N4 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, minimal till | 1.26 | 0.10 | 8.29 | 9.25 | 28.91 | 1.84 | 5.13 | 6.02 | 7.23 | 23.34 | 4.90 |
| N5 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, minimal till | 1.45 | 0.13 | 8.19 | 5.36 | 28.67 | 1.48 | 4.44 | 5.98 | 7.36 | 20.12 | 4.34 |
| N6 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, minimal till | 1.44 | 0.13 | 8.16 | 8.05 | 32.94 | 2.14 | 6.06 | 5.82 | 8.95 | 24.44 | 5.33 |
| N7 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, tillage | 1.38 | 0.12 | 8.11 | 8.65 | 34.42 | 2.89 | 3.71 | 5.23 | 8.66 | 28.91 | 4.02 |
| N8 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, tillage | 1.51 | 0.14 | 7.85 | 6.35 | 39.43 | 2.86 | 5.84 | 5.68 | 9.94 | 28.88 | 5.11 |
| N9 | Narrabri (NSW) | Vertisols | Monoculture, residue removed, tillage | 1.23 | 0.11 | 8.26 | 15.01 | 37.31 | 2.18 | 5.84 | 7.12 | 9.98 | 21.22 | 5.04 |
| N10 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, tillage | 1.36 | 0.11 | 8.24 | 10.28 | 35.10 | 2.65 | 7.28 | 6.23 | 8.98 | 29.02 | 5.99 |
| N11 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, tillage | 1.60 | 0.14 | 8.07 | 12.79 | 26.76 | 1.49 | 5.02 | 6.68 | 8.02 | 21.22 | 4.79 |
| N12 | Narrabri (NSW) | Vertisols | Crop rotation, residue retention, tillage | 1.12 | 0.08 | 8.12 | 12.23 | 26.40 | 1.34 | 6.40 | 6.12 | 8.01 | 19.87 | 4.79 |
| K1 | Karooonda (SA) | Kandosol | Crop rotation, residue retention, Tillage | 0.43 | 0.03 | 6.57 | 24.63 | 4.25 | 2.30 | 29.59 | 12.33 | 3.13 | 24.56 | 13.56 |
| K2 | Karooonda (SA) | Calcarosol  | Crop rotation, residue retention, Tillage | 0.58 | 0.05 | 6.49 | 36.40 | 4.30 | 2.25 | 28.90 | 17.33 | 3.46 | 23.33 | 15.46 |
| K3 | Karooonda (SA) | Kandosol | Crop rotation, residue retention, Tillage | 0.50 | 0.04 | 6.49 | 28.16 | 3.11 | 2.86 | 27.70 | 12.90 | 3.94 | 28.78 | 14.57 |
| K4 | Karooonda (SA) | Calcarosol  | Monoculture, residue removed, Tillage | 0.59 | 0.05 | 6.13 | 26.62 | 3.66 | 2.12 | 30.41 | 13.56 | 3.94 | 21.23 | 14.99 |
| K5 | Karooonda (SA) | Kandosol | Monoculture, residue removed, Tillage | 0.48 | 0.04 | 6.31 | 26.03 | 4.52 | 1.55 | 29.25 | 14.23 | 3.04 | 20.23 | 14.34 |
| K6 | Karooonda (SA) | Calcarosol  | Monoculture, residue removed, Tillage | 0.67 | 0.04 | 6.01 | 25.09 | 2.80 | 1.58 | 24.63 | 13.23 | 1.91 | 21.22 | 13.99 |
| K7 | Karooonda (SA) | Kandosol | Monoculture, residue removed, minimal till | 0.46 | 0.04 | 6.46 | 27.99 | 3.40 | 1.81 | 22.93 | 15.33 | 2.35 | 21.22 | 13.68 |
| K8 | Karooonda (SA) | Kandosol | Monoculture, residue removed, minimal till | 0.54 | 0.04 | 6.33 | 25.73 | 2.34 | 1.18 | 28.20 | 14.34 | 3.02 | 17.56 | 14.57 |
| K9 | Karooonda (SA) | Calcarosol  | Monoculture, residue removed, minimal till | 0.62 | 0.05 | 6.35 | 25.67 | 2.57 | 1.23 | 28.35 | 13.23 | 2.09 | 17.45 | 14.03 |
| K10 | Karooonda (SA) | Calcarosol  | Crop rotation, residue removed, tillage | 0.75 | 0.04 | 6.21 | 36.67 | 6.39 | 1.41 | 33.70 | 17.90 | 4.00 | 19.67 | 15.35 |
| K11 | Karooonda (SA) | Calcarosol  | Crop rotation, residue removed, tillage | 0.75 | 0.04 | 6.42 | 23.96 | 2.47 | 1.84 | 26.73 | 11.23 | 2.84 | 22.33 | 14.90 |
| K12 | Karooonda (SA) | Calcarosol  | Crop rotation, residue removed, tillage | 0.81 | 0.07 | 6.35 | 30.78 | 2.79 | 1.54 | 31.90 | 15.68 | 2.98 | 19.98 | 14.57 |
| K13 | Karooonda (SA) | Calcarosol  | Crop rotation, residue removed, minimal till | 0.62 | 0.03 | 6.99 | 30.17 | 2.22 | 1.29 | 24.08 | 15.34 | 2.71 | 18.34 | 13.44 |
| K14 | Karooonda (SA) | Calcarosol  | Crop rotation, residue removed, minimal till | 0.68 | 0.06 | 6.46 | 42.41 | 3.80 | 2.32 | 31.49 | 19.97 | 3.23 | 24.44 | 15.45 |
| K15 | Karooonda (SA) | Kandosol | Crop rotation, residue removed, minimal till | 0.48 | 0.04 | 6.79 | 26.88 | 4.30 | 2.72 | 27.70 | 14.33 | 4.00 | 28.67 | 14.33 |
| K16 | Karooonda (SA) | Kandosol | Monoculture, residue retention, Tillage | 0.55 | 0.05 | 6.92 | 29.75 | 4.38 | 1.41 | 23.69 | 15.33 | 3.81 | 20.22 | 14.34 |
| K17 | Karooonda (SA) | Kandosol | Monoculture, residue retention, Tillage | 0.47 | 0.04 | 6.57 | 29.35 | 3.46 | 1.47 | 22.35 | 16.33 | 4.33 | 19.03 | 14.23 |
| K18 | Karooonda (SA) | Kandosol | Monoculture, residue retention, Tillage | 0.55 | 0.05 | 5.95 | 29.23 | 3.57 | 1.46 | 22.35 | 16.23 | 3.91 | 19.83 | 14.23 |
| C1 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 1.52 | 0.10 | 7.71 | 19.53 | 1.90 | 2.42 | 18.77 | 9.56 | 2.09 | 28.22 | 12.03 |
| C8 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 0.74 | 0.04 | 7.56 | 17.02 | 1.90 | 1.49 | 16.62 | 9.12 | 2.09 | 20.03 | 11.22 |
| C20 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 1.11 | 0.09 | 7.32 | 13.27 | 0.81 | 2.81 | 15.11 | 7.91 | 1.56 | 29.83 | 11.03 |
| C4 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.76 | 0.12 | 7.76 | 19.43 | 1.32 | 2.61 | 14.43 | 9.79 | 1.98 | 27.09 | 11.23 |
| C9 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.01 | 0.08 | 7.12 | 19.90 | 0.40 | 2.81 | 17.04 | 10.00 | 1.94 | 28.23 | 11.23 |
| C21 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.02 | 0.08 | 7.09 | 19.22 | 0.57 | 2.24 | 16.63 | 9.68 | 1.08 | 24.46 | 11.98 |
| C10 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 1.32 | 0.10 | 7.71 | 22.81 | 1.11 | 2.54 | 13.84 | 11.22 | 1.09 | 25.34 | 10.94 |
| C13 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 1.30 | 0.09 | 7.60 | 20.44 | 1.21 | 2.21 | 17.33 | 10.46 | 1.02 | 21.03 | 11.00 |
| C18 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue retention, minimal till | 1.15 | 0.09 | 7.27 | 21.58 | 0.90 | 3.09 | 18.83 | 11.46 | 1.00 | 30.00 | 11.22 |
| C11 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.23 | 0.10 | 7.78 | 21.21 | 1.46 | 2.95 | 18.06 | 11.46 | 1.52 | 28.84 | 10.99 |
| C12 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.07 | 0.08 | 7.34 | 24.06 | 0.91 | 3.08 | 20.11 | 13.01 | 0.98 | 28.83 | 11.23 |
| C19 | Cunderdin (WA) | XanthicFerralsol | Crop rotation, residue removed, minimal till | 1.03 | 0.08 | 6.88 | 22.91 | 1.23 | 3.74 | 18.56 | 12.57 | 1.12 | 30.28 | 10.99 |
| C5 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, minimal till | 1.27 | 0.07 | 6.95 | 18.53 | 1.35 | 3.57 | 14.56 | 9.00 | 1.54 | 31.22 | 9.99 |
| C6 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, minimal till | 1.10 | 0.06 | 6.80 | 20.09 | 1.55 | 3.75 | 18.73 | 9.13 | 1.76 | 32.33 | 10.99 |
| C15 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, minimal till | 1.02 | 0.06 | 7.29 | 19.32 | 1.45 | 2.67 | 18.39 | 9.45 | 1.65 | 29.34 | 11.99 |
| C3 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, minimal till | 1.17 | 0.08 | 7.76 | 19.78 | 1.35 | 1.21 | 18.21 | 10.34 | 1.67 | 20.23 | 12.95 |
| C14 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, minimal till | 1.03 | 0.08 | 7.28 | 16.79 | 1.33 | 2.43 | 18.43 | 10.57 | 2.11 | 25.33 | 12.33 |
| C17 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, tillage | 1.15 | 0.07 | 7.98 | 18.73 | 1.34 | 1.21 | 18.21 | 10.96 | 2.84 | 19.03 | 11.25 |
| C2 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, tillage | 1.30 | 0.08 | 7.23 | 18.35 | 1.22 | 2.22 | 18.34 | 9.34 | 0.98 | 22.23 | 12.23 |
| C7 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, tillage | 1.15 | 0.08 | 6.97 | 17.79 | 1.22 | 2.35 | 16.23 | 9.46 | 0.90 | 23.23 | 11.99 |
| C16 | Cunderdin (WA) | XanthicFerralsol | Monoculture, residue removed, tillage | 1.08 | 0.08 | 7.65 | 18.35 | 1.57 | 2.56 | 15.56 | 9.57 | 0.85 | 23.35 | 10.09 |

\*Please refer to Supplementary table S2 for abbreviation.

**Supplementary Table S2:** List of enzymes, their function and genes encoding the enzymes.

|  |  |  |  |
| --- | --- | --- | --- |
| **Enzyme** | **Abbreviation** | **Function** | **Gene** |
| -Glucosidase | AG | Degrades starch | *-Amylase* |
| -D-Xylosidase | XYL | Degrades hemi-cellulose | *Xylanase* |
| N-acetyl--D-glucosaminidase | NAG | Degrades chitin | *Acetylglucosaminidase* |
| -D-cellulosidase | CB | Degrades cellulose | *Exoglucanase* |

**Supplementary Table S3:** Correlation between the relative abundance (from Pyrosequencing and qPCR data) of different microbial groups.

|  |  |  |
| --- | --- | --- |
| **Microbial Groups** | **Spearman's correlation coefficient** | **P value** |
| -Proteobacteria | 0.831 | <0.0001 |
| -Proteobacteria | 0.936 | <0.0001 |
| Acidobacteria | 0.892 | <0.0001 |
| Actinobacteria | 0.929 | <0.0001 |
| Firmicutes | 0.982 | <0.0001 |
| Basidiomycota | 0.843 | <0.0001 |

**References for a priori generic structural equation model used in this study (Supplementary Figure S1)**

**Pathway 1:**

Lebron I, McGiffen Jr ME, and Suarez DL.(2012). The effect of total carbon on microscopic soil properties and implications for crop production.*J Arid Land* **4:**251-259.

Tan K and Bartlett RJ.(1994). Principles of soil Chemistry. *Soil Science*, *157*(5), p.330.

**Pathway 2:**

Yang Y, Gao Y, Wang S, Xu D, Yu H, Wu L, Lin Q, Hu Y, Li X, He Z, Deng Y. (2014). The microbial gene diversity along an elevation gradient of the Tibetan grassland.*ISME J***8**:430-40.

Bai S, Li J, He Z, Van Nostrand JD, Tian Y, Lin G, Zhou J, Zheng T. (2013). GeoChip-based analysis of the functional gene diversity and metabolic potential of soil microbial communities of mangroves. *ApplMicrobiol Biotech***97:**7035-48.

Su JQ, Ding LJ, Xue K, Yao HY, Quensen J, Bai S. *et al*. (2015). Long-term balanced fertilization increases the soil microbial functional diversity in a phosphorus-limited paddy soil. *MolEcol***24:** 136-150.

**Pathway 3:**

Trivedi P,Rochester R, Trivedi C, Anderson IC, Singh BK. (2015). Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. *Soil BiolBiochem* **91:**169-181.

Su JQ, Ding LJ, Xue K, Yao HY, Quensen J, Bai S. *et al*. (2015). Long-term balanced fertilization increases the soil microbial functional diversity in a phosphorus-limited paddy soil. *MolEcol***24:** 136-150.

Paula FS, Rodrigues JL, Zhou J, Wu L, Mueller RC, Mirza BS, Bohannan BJ, Nüsslein K, Deng Y, Tiedje JM, Pellizari VH.(2014). Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. *MolEcol***23:**2988-2999.

**Pathway 4:**

Lauber CL, Hamady M, Knight R, Fierer N. (2009). Pyrosequencing-based assessment of soil pH as a predictor of soil bacterial community structure at the continental scale. *Appl. Environ Microbiol*, **75:**5111-5120.

Rousk J, Bååth E, Brookes PC, Lauber CL, Lozupone C, Caporaso JG, Knight R, Fierer N. (2010). Soil bacterial and fungal communities across a pH gradient in an arable soil. *ISME J* **4:**1340-1351.

**Pathway 5:**

Horn DJ, Van Horn ML, Barrett JE, Gooseff MN, Altrichter AE, Geyer KM, et al. (2013) Factors controlling soil microbial biomass and bacterial diversity and community composition in a cold desert ecosystem: role of geographic scale. *PLoS ONE* 8(6): e66103. doi:10.1371/journal.pone.0066103

You Y, Wang J, Huang X, Tang Z, Liu S, Sun OJ. (2014). Relating microbial community structure to functioning in forest soil organic carbon transformation and turnover. *EcolEvol* **4:** 633-647.

Talbot JM, Bruns TD, Taylor JW, Smith DP, Branco S, Glassman SI.*et al*. (2014). Endemism and functional convergence across the North American soil mycobiome. *Proc Natl AcadSci USA* **111:** 6341-6346.

Maestre FT, Delgado-Baquerizo M, Jeffries TC, Eldridge DJ, Ochoa V, Gozalo B. et al. (2015) Increasing aridity reduces soil microbial diversity and abundance in global drylands. *Proc Nat AcadSci USA* 112: 15684-15689.

**Pathway 6:**

Burns RG, DeForest JL, Marxsen J, Sinsabaugh RL, Stromberger ME, Wallenstein MD *et al*. (2013). Soil enzymes in a changing environment: current knowledge and future directions. *Soil BiolBiochem* **58:** 216-234.

Nannipieri PA, Giagnoni LA, Renella GI, Puglisi ED, Ceccanti BR, Masciandaro GR, Fornasier FL, Moscatelli MC, Marinari SA. (2012). Soil enzymology: classical and molecular approaches. *BiolFert Soils***48**:743-62.

**Pathway 7:**

Trivedi P,Rochester R, Trivedi C, Anderson IC, Singh BK. (2015). Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. *Soil BiolBiochem* **91:**169-181.

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Burns RG, DeForest JL, Marxsen J, Sinsabaugh RL, Stromberger ME, Wallenstein MD *et al*. (2013). Soil enzymes in a changing environment: current knowledge and future directions. *Soil BiolBiochem* **58:** 216-234.

**Pathway 8:**

Trivedi P,Rochester R, Trivedi C, Anderson IC, Singh BK. (2015). Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. *Soil BiolBiochem* **91:**169-181.

Reeve JR, Schadt CW, Carpenter-Boggs L, Kang S, Zhou J, Reganold JP. (2010). Effects of soil type and farm management on soil ecological functional genes and microbial activities.  *ISME J* **4:** 1099-1107.

Su JQ, Ding LJ, Xue K, Yao HY, Quensen J, Bai S. *et al*. (2015). Long-term balanced fertilization increases the soil microbial functional diversity in a phosphorus-limited paddy soil. *MolEcol***24:** 136-150.

Paula FS, Rodrigues JL, Zhou J, Wu L, Mueller RC, Mirza BS, Bohannan BJ, Nüsslein K, Deng Y, Tiedje JM, Pellizari VH. (2014). Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. *MolEcol***23:**2988-2999.

**Pathway 9:**

Trivedi P,Rochester R, Trivedi C, Anderson IC, Singh BK. (2015). Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. *Soil BiolBiochem* **91:**169-181.

Bailey VL, Fansler SJ, Stegen JC, McCue LA.(2013). Linking microbial community structure to β-glucosidic function in soil aggregates. *ISME J* **7:**2044-2053.

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You Y, Wang J, Huang X, Tang Z, Liu S, Sun OJ. (2014). Relating microbial community structure to functioning in forest soil organic carbon transformation and turnover. *EcolEvol* **4:** 633-647.

Talbot JM, Bruns TD, Taylor JW, Smith DP, Branco S, Glassman SI.*et al*. (2014). Endemism and functional convergence across the North American soil mycobiome. *Proc Natl AcadSci USA* **111:** 6341-6346.

Schnecker J, Wild B, Takriti M, Alves RJE, Gentsch N, Gittel A, Hofer A, Klaus K, Knoltsch A, Lashchinskiy N, Mikutta, R. (2015). Microbial community composition shapes enzyme patterns in topsoil and subsoil horizons along a latitudinal transect in Western Siberia. *Soil BiolBiochem*, **83:** 106-115.

**Pathway 10:**

Trivedi P,Rochester R, Trivedi C, Anderson IC, Singh BK. (2015). Soil aggregate size mediates the impacts of cropping regimes on soil carbon and microbial communities. *Soil BiolBiochem* **91:**169-181.

Reeve JR, Schadt CW, Carpenter-Boggs L, Kang S, Zhou J, Reganold JP. (2010). Effects of soil type and farm management on soil ecological functional genes and microbial activities.  *ISME J* **4:** 1099-1107.

Su JQ, Ding LJ, Xue K, Yao HY, Quensen J, Bai S. *et al*. (2015). Long-term balanced fertilization increases the soil microbial functional diversity in a phosphorus-limited paddy soil. *MolEcol***24:** 136-150.