Figure captions

Fig. 1 Geographical location of the study site for the three selected sub-ecosystems in the Danjiangkou Reservoir Area.

Fig. 2 Concentrations and distribution factors of aggregate-associated soil nutrients under different land types.
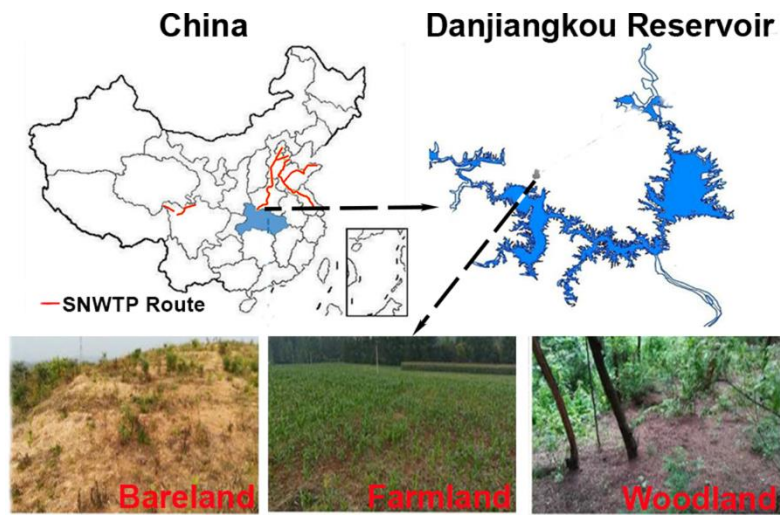
Fig. 3 Aggregate-associated soil enzymatic activities (a-d), and their geometric mean (GMea, e). And relative contributions of soil nutrition, microbial community composition and diversity on GMea by Random Forest regression model (f).

Fig. 4 Relative abundance of bacterial and fungal phylum level (higher than 1% in at least one sample) within aggregates under different land types (a and c); and Chord diagram displaying the relative abundance (%) of dominant phylum associated with land types (b and d).
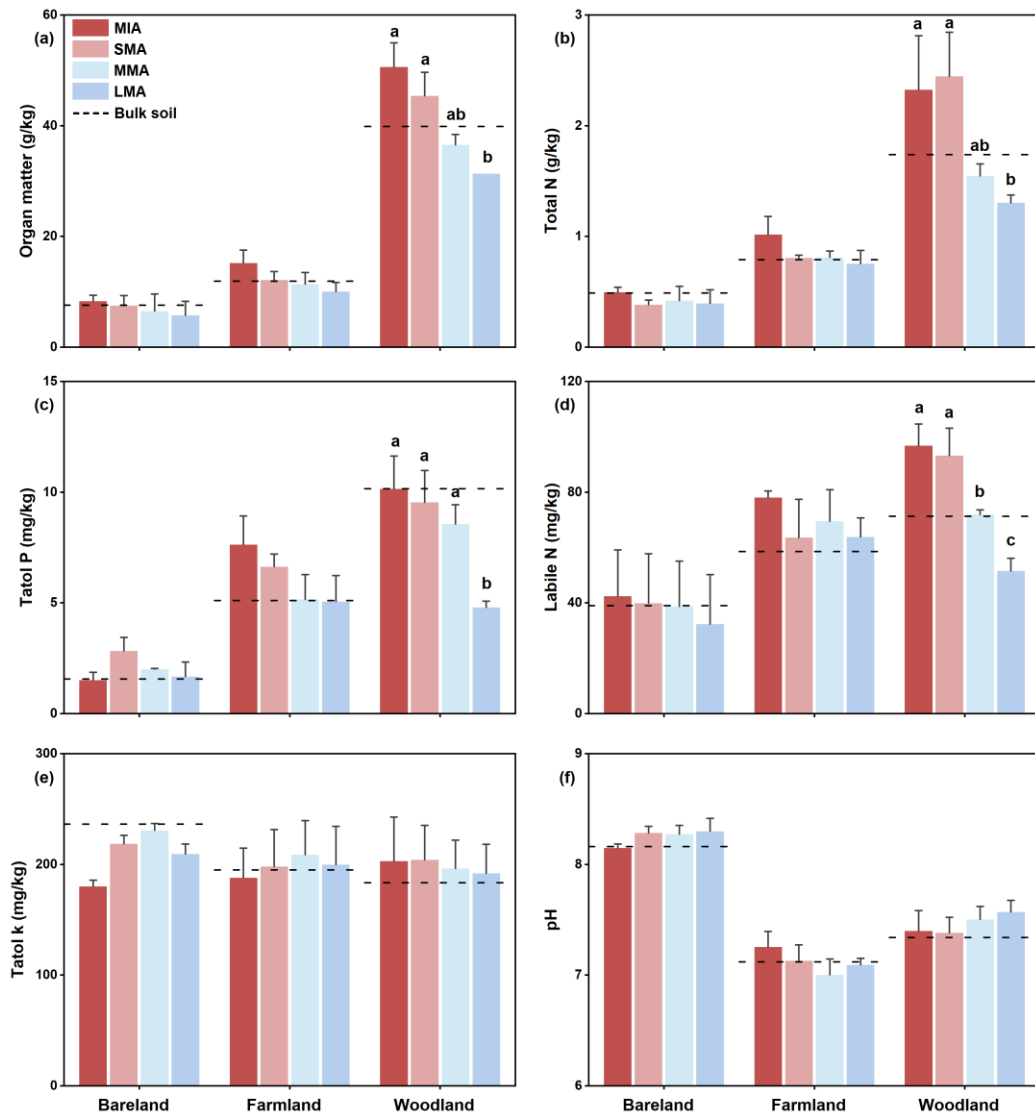
Fig. 5 LEfSe analysis identified the differentially abundant taxon (relative abundance > 0.5% in at least one sample) from phylum level to genus level among aggregates under different land-use types.

Fig. 6 Soil bacterial and fungal beta-diversity within aggregates under different land-use types.
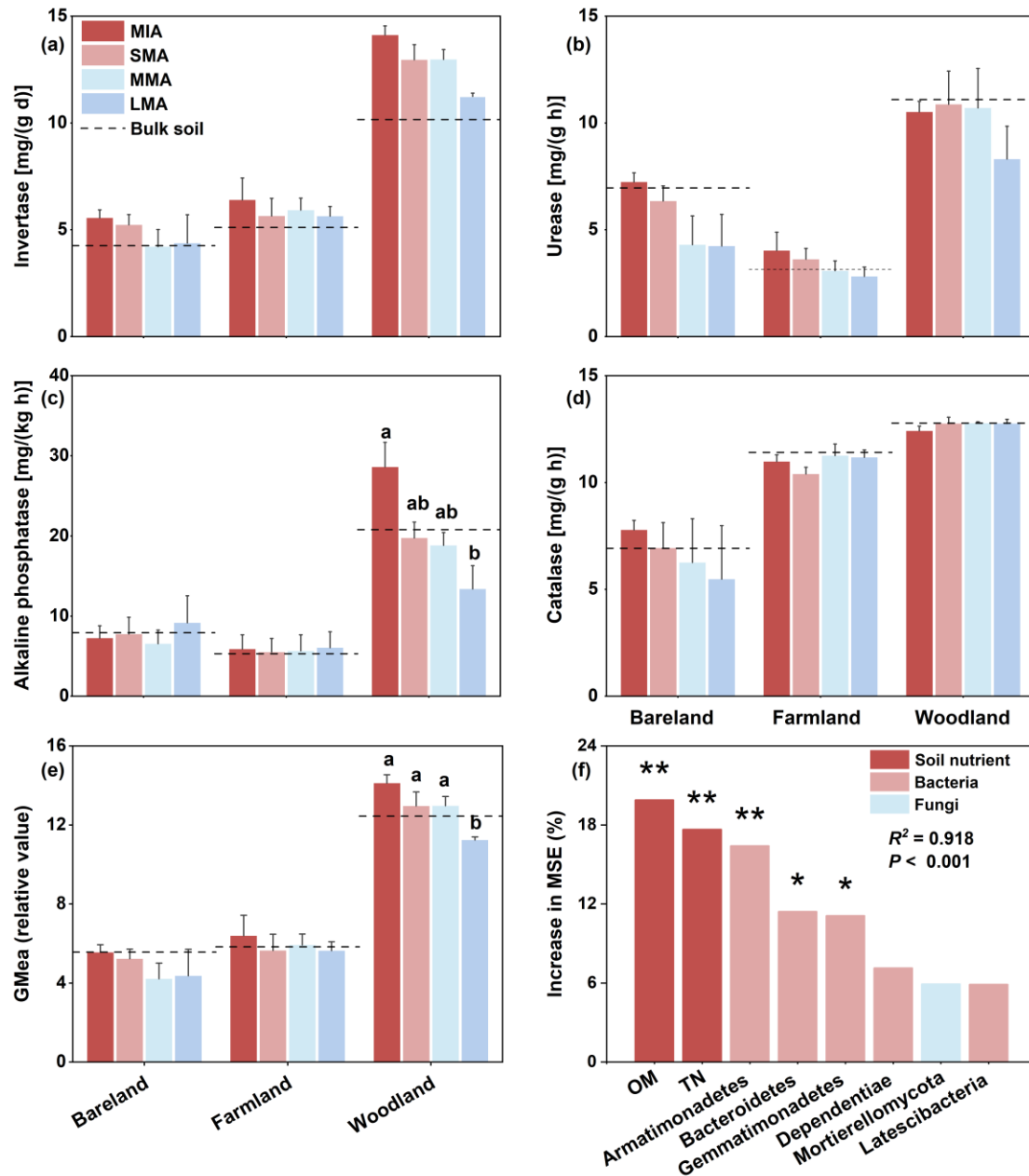
Fig. 7 Pairwise comparisons between soil properties, enzymatic activities and microbial community composition and diversity.
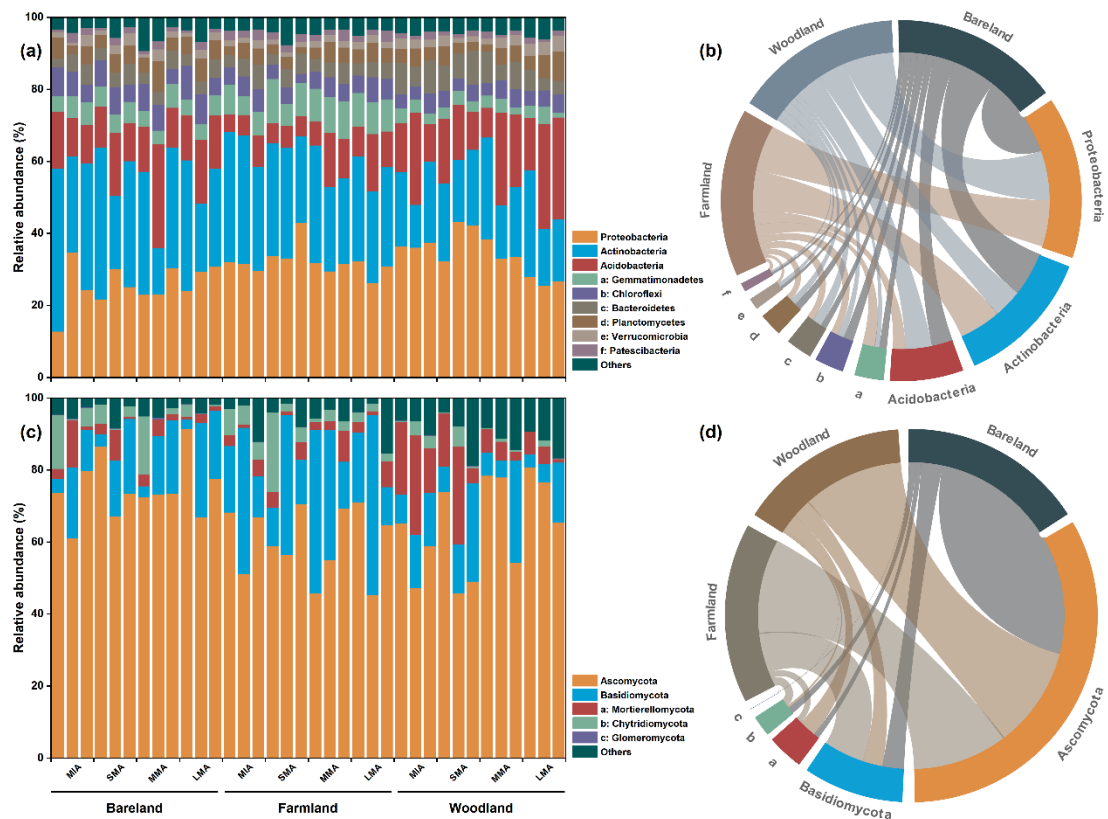
Fig. 1 Geographical location of the study site for the three selected sub-ecosystems in the Danjiangkou Reservoir Area. SNWTP Route: The South–North Water Transfer Project Central route.
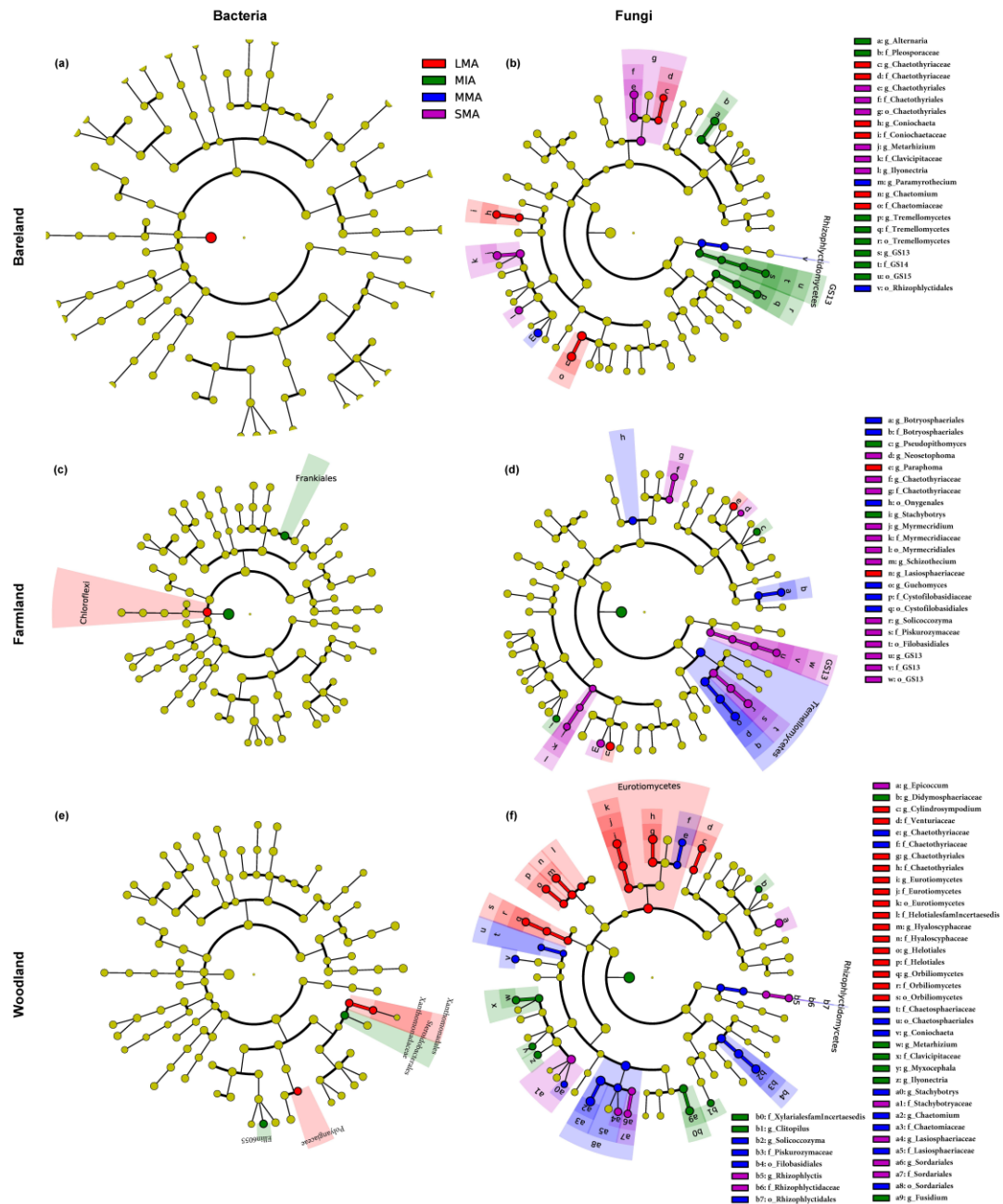
Fig. 2 Distribution factors of aggregate-associated soil nutrients and pH under different land types. Lowercase letters indicate the difference among soil aggregates in the same land type ($P < 0.05$). MIA: microaggregate (<0.25 mm); SMA: small macroaggregate (0.25-1 mm); MMA: medium macroaggregate (1-3 mm); LMA: large macroaggregate (>3 mm).
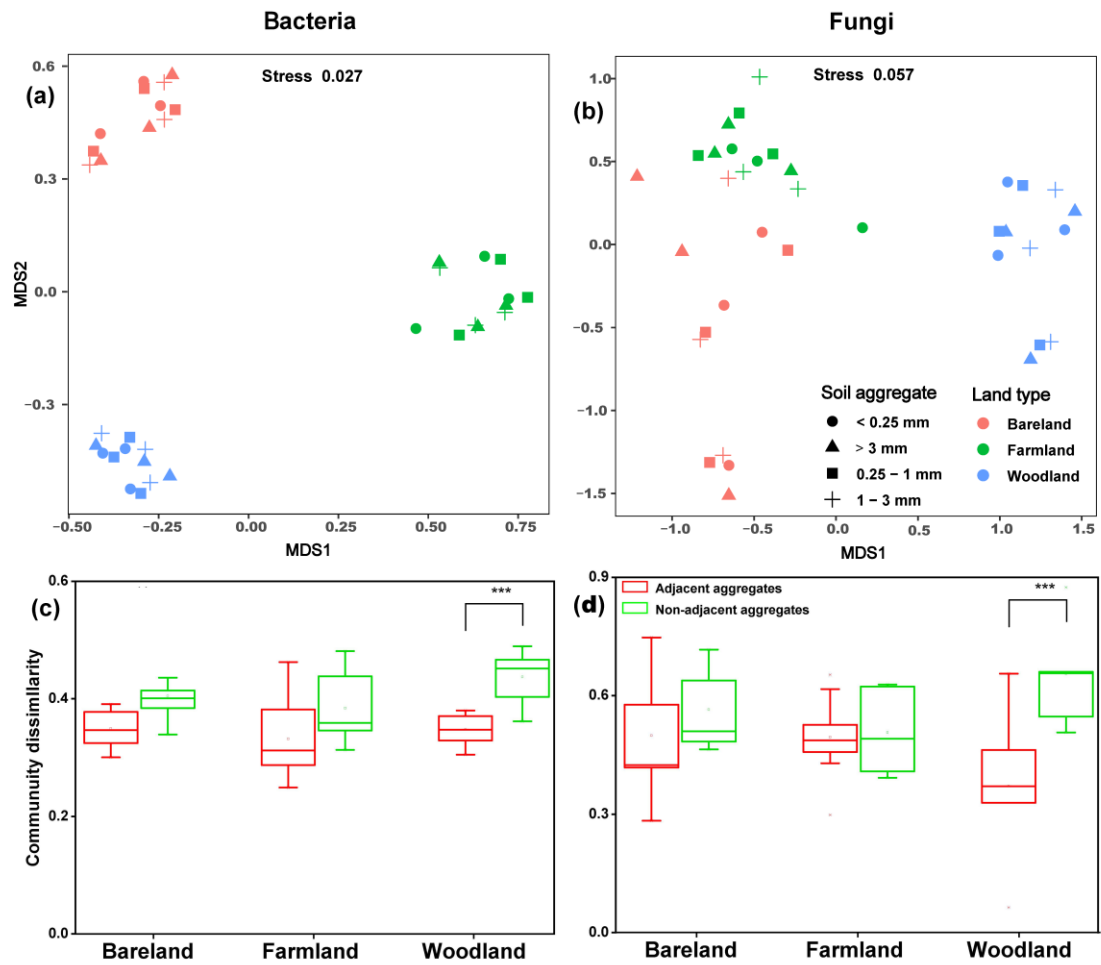
Fig. 3 Aggregate-associated soil enzymatic activities (a-d), and their geometric mean (GMea, e). And relative contributions of soil nutrition, microbial community composition and diversity on GMea by Random Forest regression model (f). Lowercase letters indicate the difference among soil aggregates in the same land type ($P < 0.05$). MIA: microaggregate (<0.25 mm); SMA: small macroaggregate (0.25-1 mm); MMA: medium macroaggregate (1-3 mm); LMA: large macroaggregate (>3 mm).
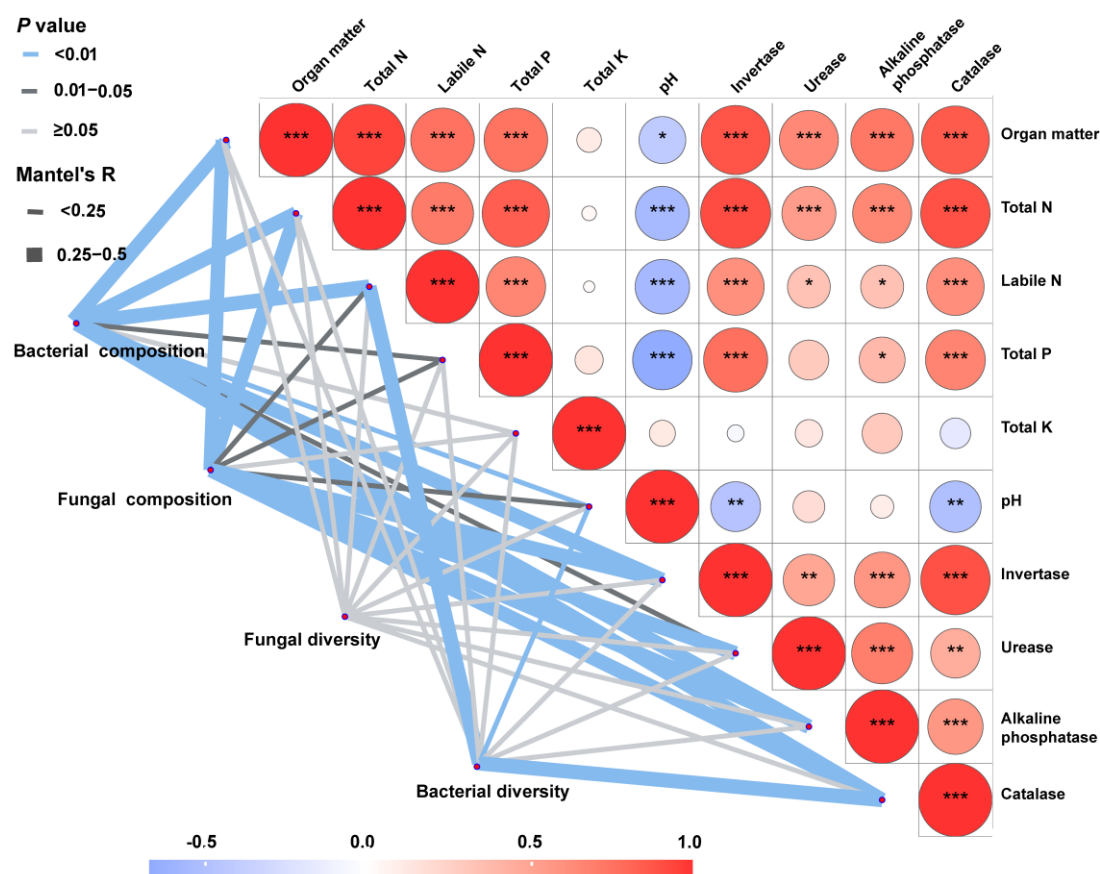
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Fig. 5 LEfSe analysis identified the differentially abundant taxon (relative abundance > 0.5% in at least one sample) from phylum level to genus level among aggregates under different land-use types. Only taxa meeting an LDA significance threshold of 3.0 are shown. Small circles with different color-coded within the cladogram represent significantly higher abundance of those taxa in a certain aggregate within each soil type.

Fig. 6 Soil bacterial and fungal beta-diversity within aggregates under different land-use types. (a) and (b) NMDS analysis for soil bacterial and fungal communities with OTUs classified at 97% sequence similarity; (c) and (d) Bray-Curtis similarity between microbial community in adjacent or non-adjacent aggregates under different land use types. MIA: microaggregate (<0.25 mm); SMA: small macroaggregate (0.25-1 mm); MMA: medium macroaggregate (1-3 mm); LMA: large macroaggregate (>3 mm). Adjacent aggregates: MIA vs SMA, SMA vs MMA, and MMA vs LMA; Non-adjacent aggregates: MIA vs MMA, MIA vs LMA, and SMA vs LMA.

Fig. 7 Pairwise comparisons between soil properties, enzymatic activities and microbial community composition and diversity. Circle and color gradient represent Pearson's correlation coefficients. Partial Mantel tests were carried out to calculate the correlation between microbial community composition or alpha-diversity and soil properties, enzymatic activities. Edge width was proportional to the Mantel's r statistic of the corresponding correlation, and edge color represented the statistical significance based on 999 permutations.