

Figure legends

Fig. 1. Boxplot of the seasonal soil basal microbial respiration (a), nitrification rate (b) and potential nitrification rate under land use change. The statistical significance between land use types or seasons was determined based on T-test. P values of statistical results over the boxplot indicate statistical differences between winter and summer in each land use type. Significant levels between land use types were based on $*P < 0.05$; $**P < 0.01$, $***P < 0.001$, ns: non-significant.

Fig. 2. Boxplot of the seasonal the alpha diversity of soil PLFAs communities (a), AOA (c) and AOB (e) communities under land use change (LUC). Statistical significances were same as Fig. 1 and the non-significant wasn't showed. Principle coordinate analysis constrained to land use types and season dynamics showed microbial beta diversity of soil PLFAs communities (b), and weighted UniFrac distance metric of AOA (d) and AOB (f). The significant results of permutation MANOVA (LUC, season and interactive effect) were showed in each community, respectively.

Fig. 3 Relationships of soil microbial communities (a, c, e) and keystone species richness (b, d, f) with ecosystem functioning (soil microbial basal respiration, mSR; potential nitrification rate, PNR), respectively. The solid lines represent significant linear relationship across different pes, and the dark shade area shows the 95% confidence interval of the fitted models, respectively.

Fig. 4 Keystone species and environmental factors influencing the ecosystem functioning. Pairwise comparisons of environmental factors were shown with a color gradient denoting the Pearson's correlation coefficient. Keystones species, total and keystone species excluding (non-keystone) community composition of the total PLFAs (a), AOA (b), and AOB (c) were related to each environmental factor by partial mantel tests. Edge width corresponded to the Mantel's r statistic for the corresponding distance correlations, and the edge color denoted the statistical significance based on 9,999 permutations.

Fig. 5 Meta-community co-occurrence networks of total PLFAs communities (a, b, c) and functional microbial communities (AOA d, e, f; AOB g, h, i) under land use change. Only local similarity that being test with Spearman's correlation significantly (local similarity

absolute values > 0.6 and P -value < 0.01) was shown. The size of each node was proportional to the relative abundance of species. The co-occurring network colored by modularity class. The occurring species labels were considered as the keystone species based on network topological features (Z_i and P_i values) of each co-occurring network.

Fig. 6 Structural equation modeling assessing the direct and indirect effects of environmental and microbial communities' traits on the ecosystem functioning relying on different microbial community structure (PLFAs (a) and AOA (b) and NR (c), respectively.

Significant levels were based on $*P < 0.05$; $**P < 0.01$. Soil edaphic factor was the first component of the soil environmental factors (including soil pH; soil moisture, SM; soil temperature, ST) from principal components analysis; and soil substrate was the second component of the soil environmental factors (bulk density, BD; total organic carbon content, TC; total organic nitrogen content, TN; soil organic C/N ratio, C/N).

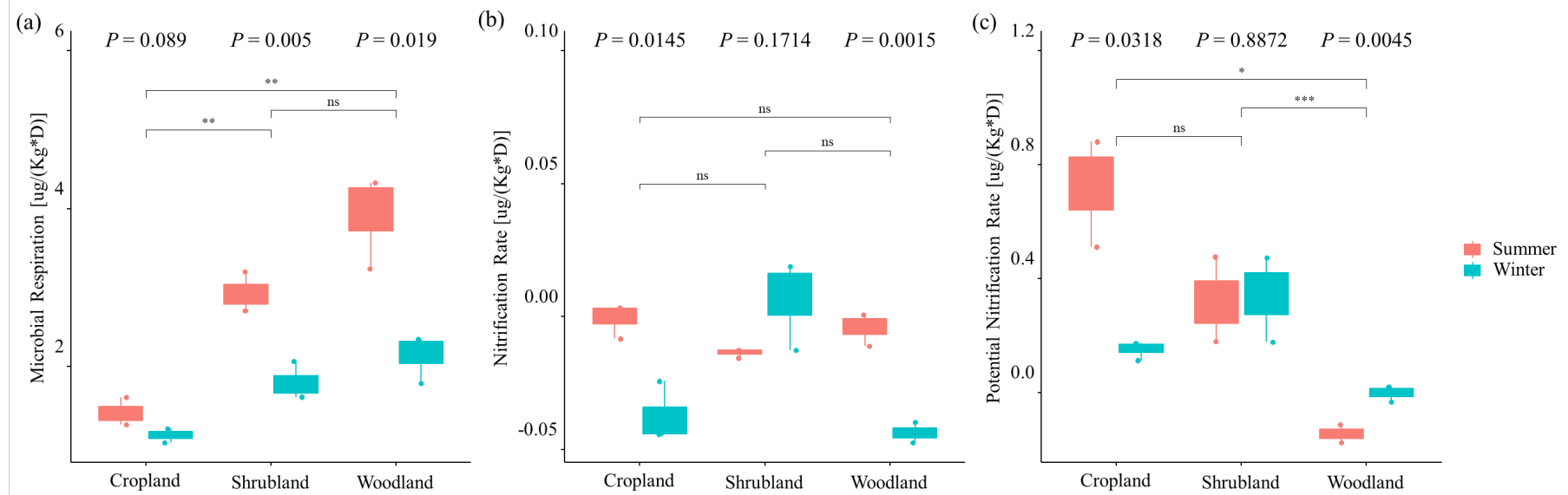


Fig. 1

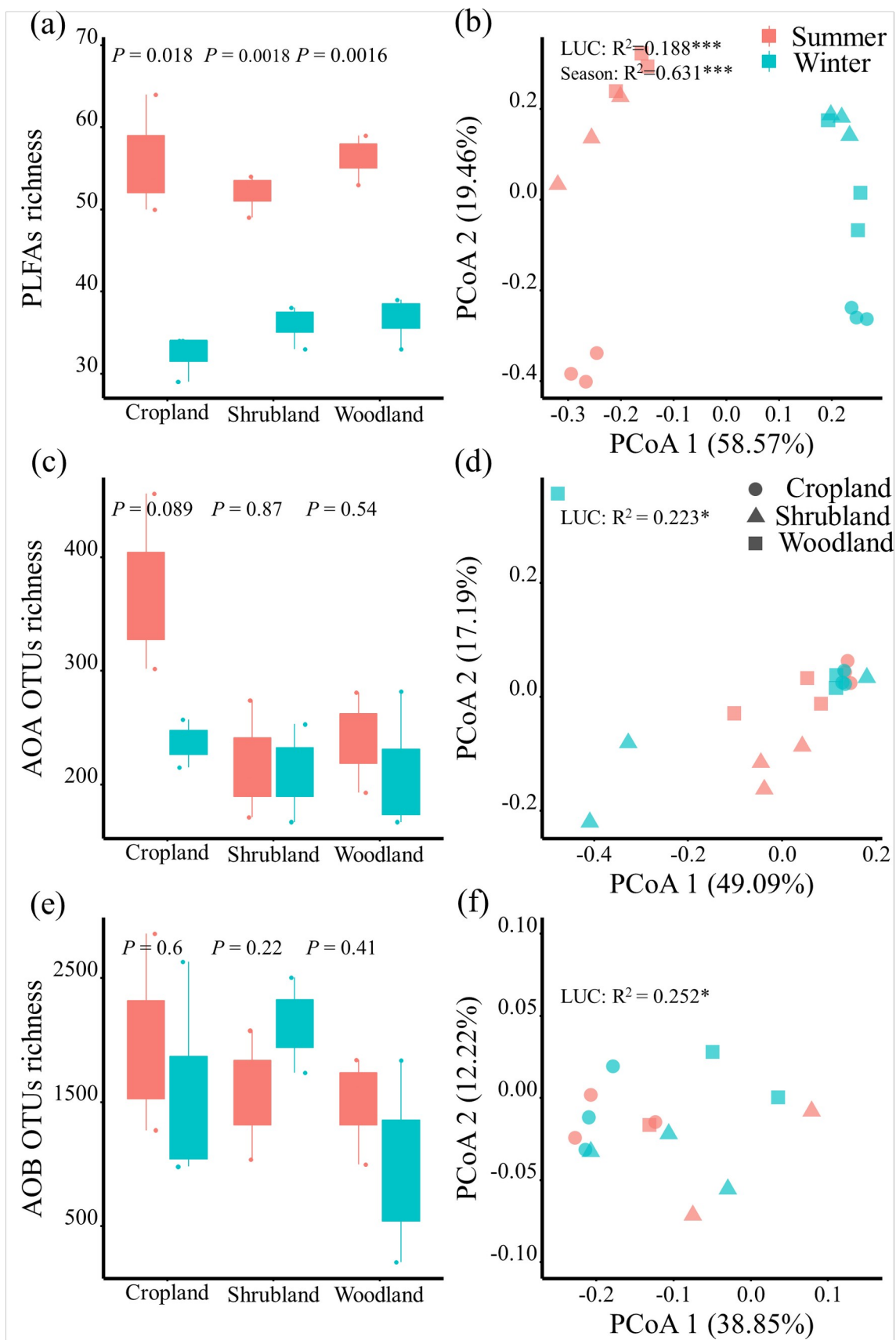


Fig. 2

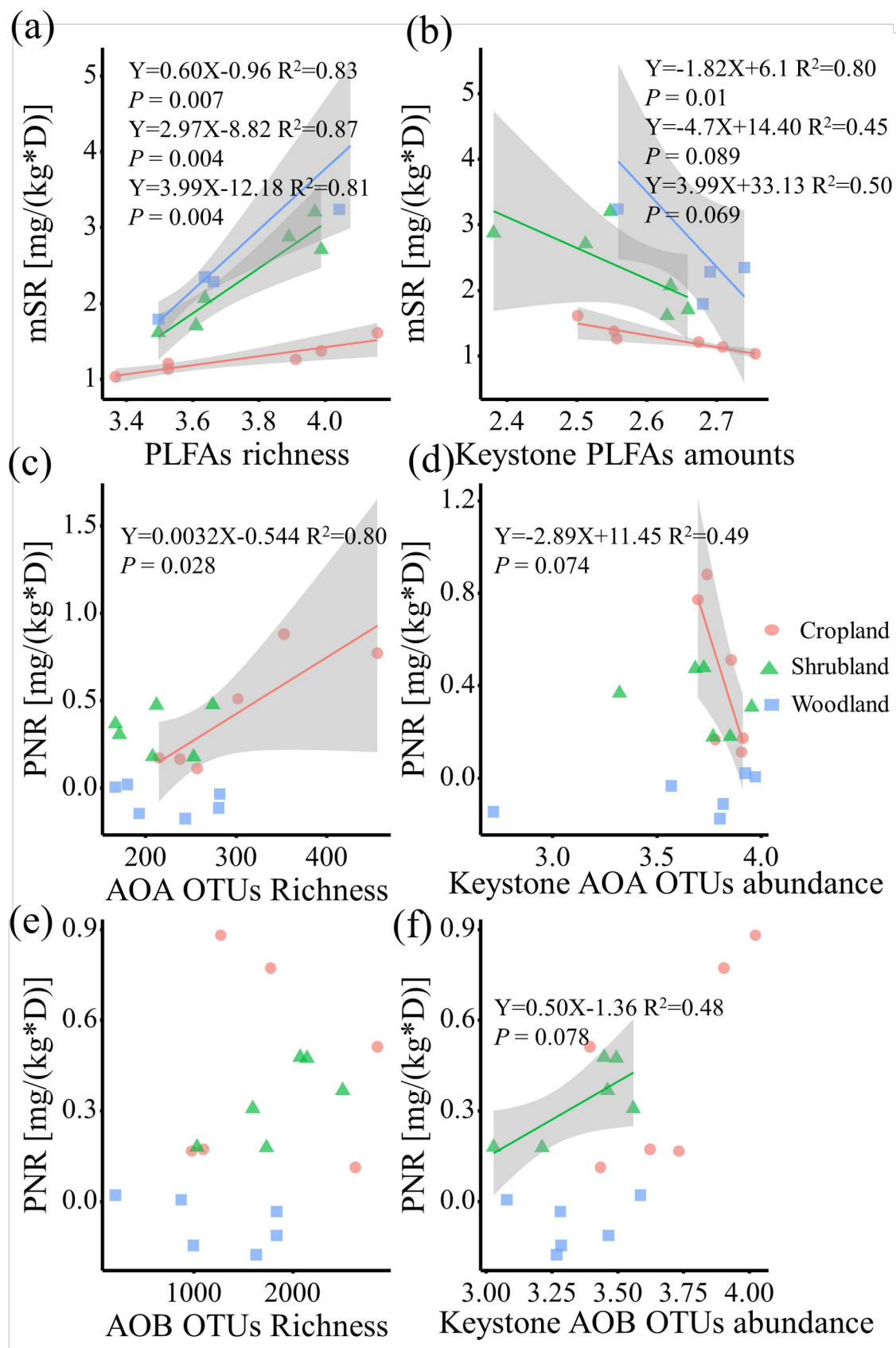


Fig. 3

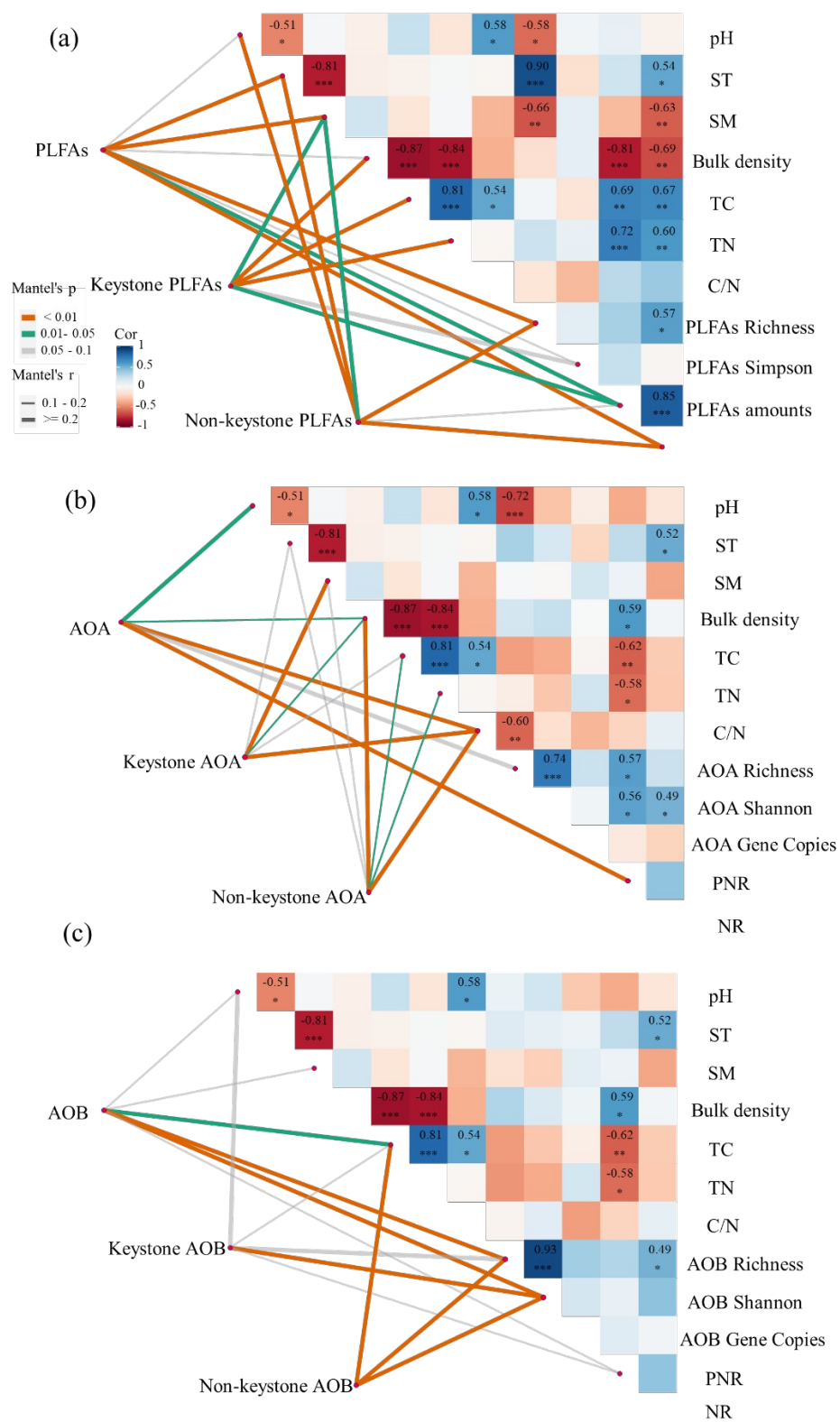


Fig. 4

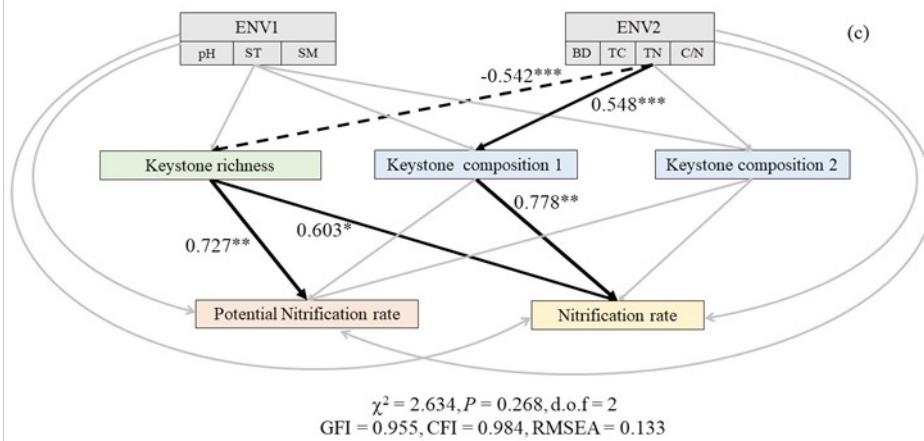
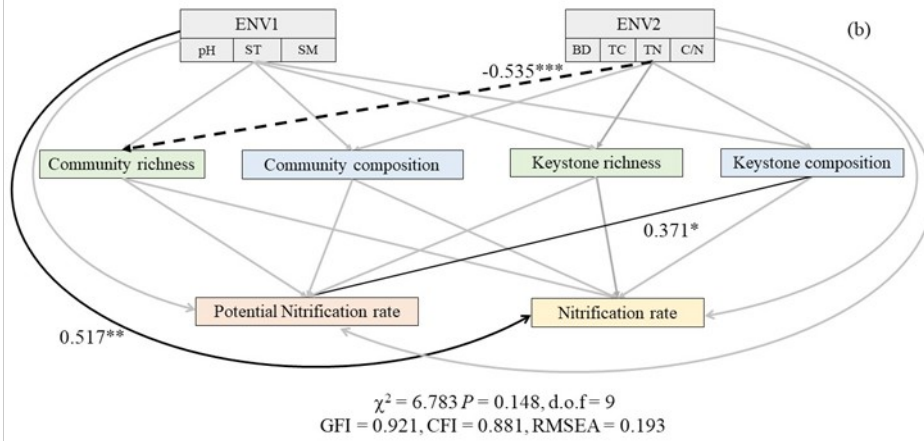
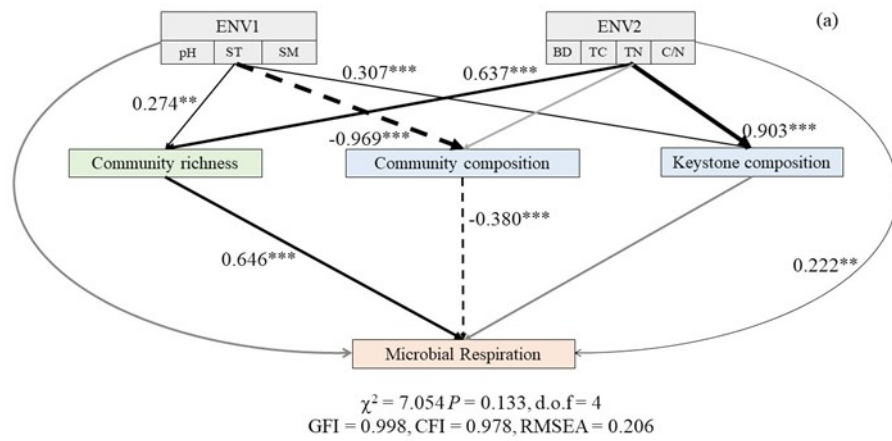


Fig. 6