

# Microbial Community Response to Different Biochar Amendments in Sugarcane and Rice Soils

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## Introduction

Biochar, a product of biomass thermal carbonation under limited oxygen condition, has been used as a soil amendment to improve soil fertility, enhance carbon sequestration, and remediate contaminants. Recent research studies have reported contradicting observations about the effects of biochar applications on soil microbial community structure. While some found that biochar shifts soil microbial community structure through changing soil physicochemical properties and facilitating labile carbon for microorganisms to utilize, others observed that microbes can hardly use carbon source from biochar due to its resistance to biodegradation. In addition, biochars derived from certain feedstocks such pine wood increase the populations of fungi but not bacteria. Clearly, the exact nature of biochar influence on soil microbial communities is still unclear, and additional studies are needed to elucidate the impact of biochar amendment in different soils, especially under different agroecosystems.

## Objective

In this research, we investigated biochar applications in two representative production agroecosystems in Louisiana, rice and sugarcane, respectively, with the aim to evaluate and compare the effects of different biochar applications on soil microbial community changes using phospholipid fatty acid analysis (PLFA).

## Methods and Material

### Site Experiments

Two experimental sites with one sugarcane in Duson, LA and the other one rice in Crowley, LA were established. The sugarcane field was applied with sugarcane biochar and wood biochar, while the rice field was applied rice biochar and wood biochar, respectively. At the end of growth season, surface soil (0-15 cm) samples were collected, freeze-dried and grounded to pass through 2 mm sieve before analysis. Samples include two field replications and two lab replications.

### PLFA Analysis

Soil samples of 3 grams from each field treatment were extracted using a solvent mixture of ethanol:chloroform:phosphate buffer (2:1:0.8) and the supernatants were separated by separation funnel overnight. Organic phase of the supernatants was collected and concentrated using N<sub>2</sub>, followed by dissolving in 0.5 mL chloroform. The sample was then transferred into a preconditioned silicon column and washed with chloroform and acetone, respectively, to remove nonpolar lipid and glycolipid. The polar lipids were collected by eluting the silicon column with methanol, dried under N<sub>2</sub>, and methylated with KOH-methanol solution. The collected FAMES were analyzed using a Shimadzu gas chromatograph with C19:0 as internal standard (White, 2012). The quantified FAMES were categorized into 7 groups: general biomarkers for all microorganisms (14:0, 16:0, 18:0); saturated fatty acid (SFAs) (15:0, 17:0, 19:0); cyclopropyl fatty acids (cy17:0, cy19:0); monounsaturated fatty acids (MUFAs) (16:1w9 cis, 18:1w9 trans, 18:1w9cis), and hydroxyl fatty acids (HFAs) (2OH 12:0, 3OH12:0, 2OH14:0, 3OH 14:0 and 2OH 16:0) for Gram negative bacteria (G-), terminal branched PLFA (i15:0, a15:0, i16:0 and i17:0) for Gram positive bacteria (G+), polyunsaturated fatty acid (PUFAs) 18:2w9,12 for fungi. Two-way ANOVA (SAS 9.4) along with principle component analysis (PCA) and factor analysis (SPSS 24) were performed for statistical analysis.

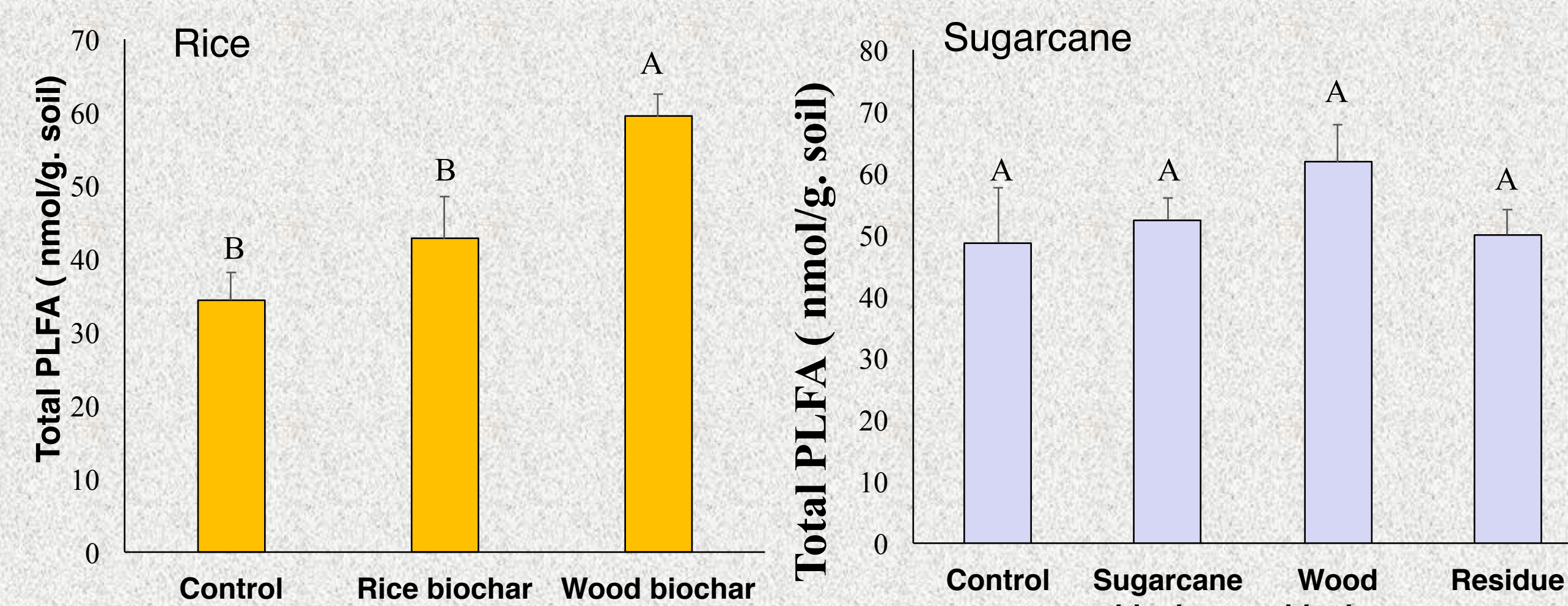


Fig.1. Effect of field treatments on total PLFA in rice and sugarcane soils. Letters above bars indicate statistically difference among treatments at  $\alpha=0.05$

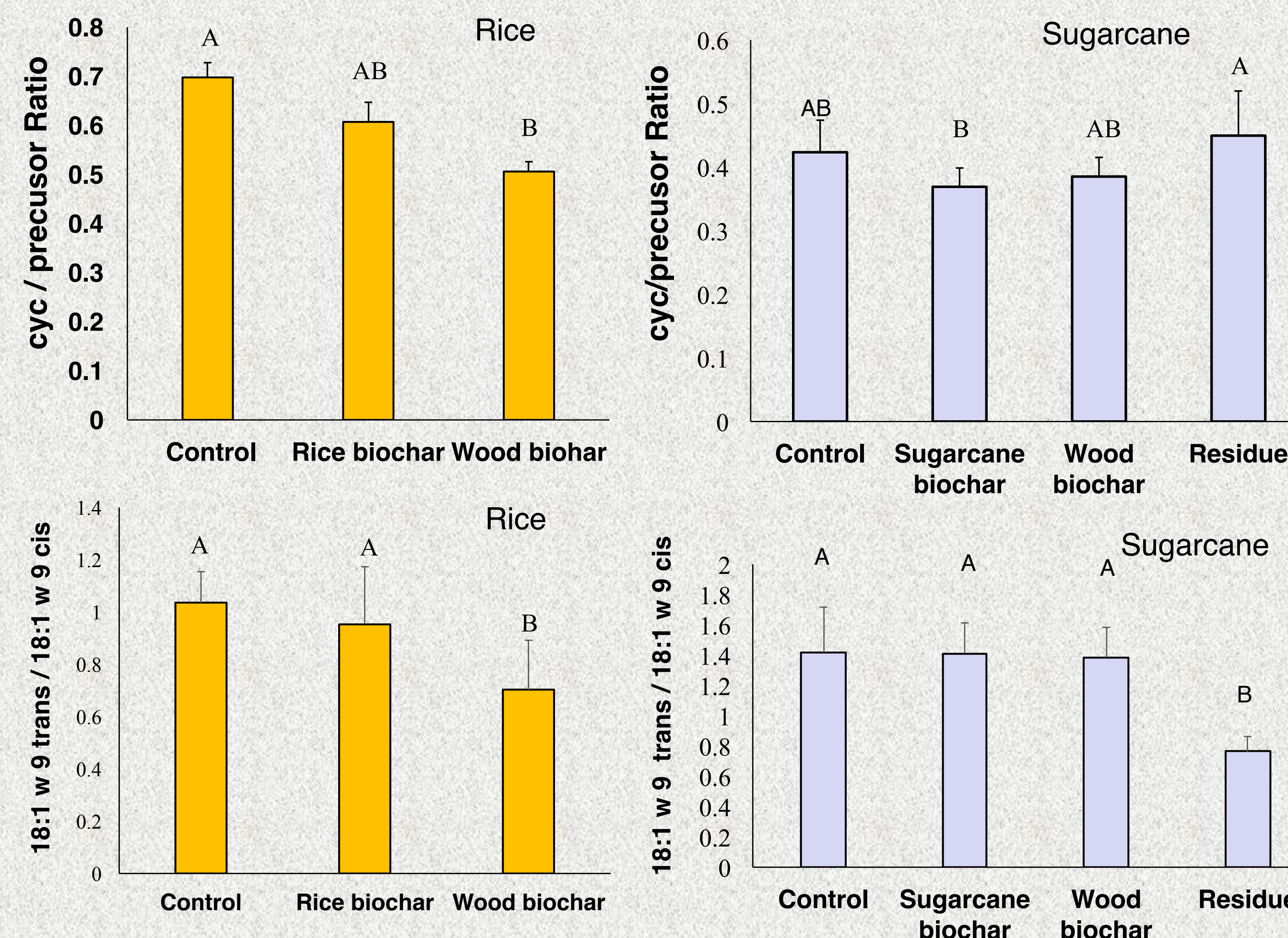


Fig. 2 Effect of field treatments on the ratio of cyclopropyl PLFA (cy17:0+cy19:0) /monounsaturated precursor (16:1cis+18:1cis), and the ratio of 18:1w9 cis/ 18:1w9 trans.

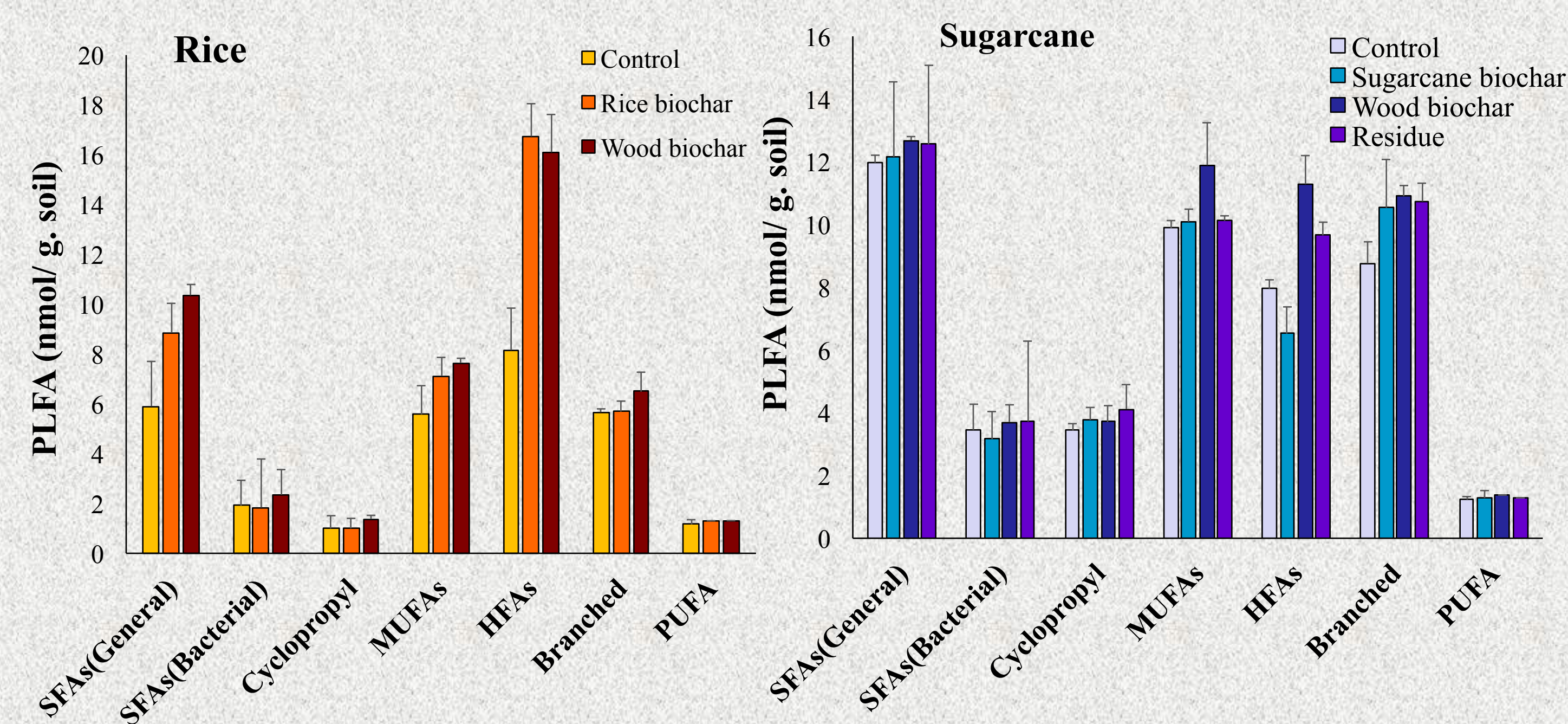


Fig. 3 Effect of field treatments on specific PLFA groups in rice and sugarcane soils.

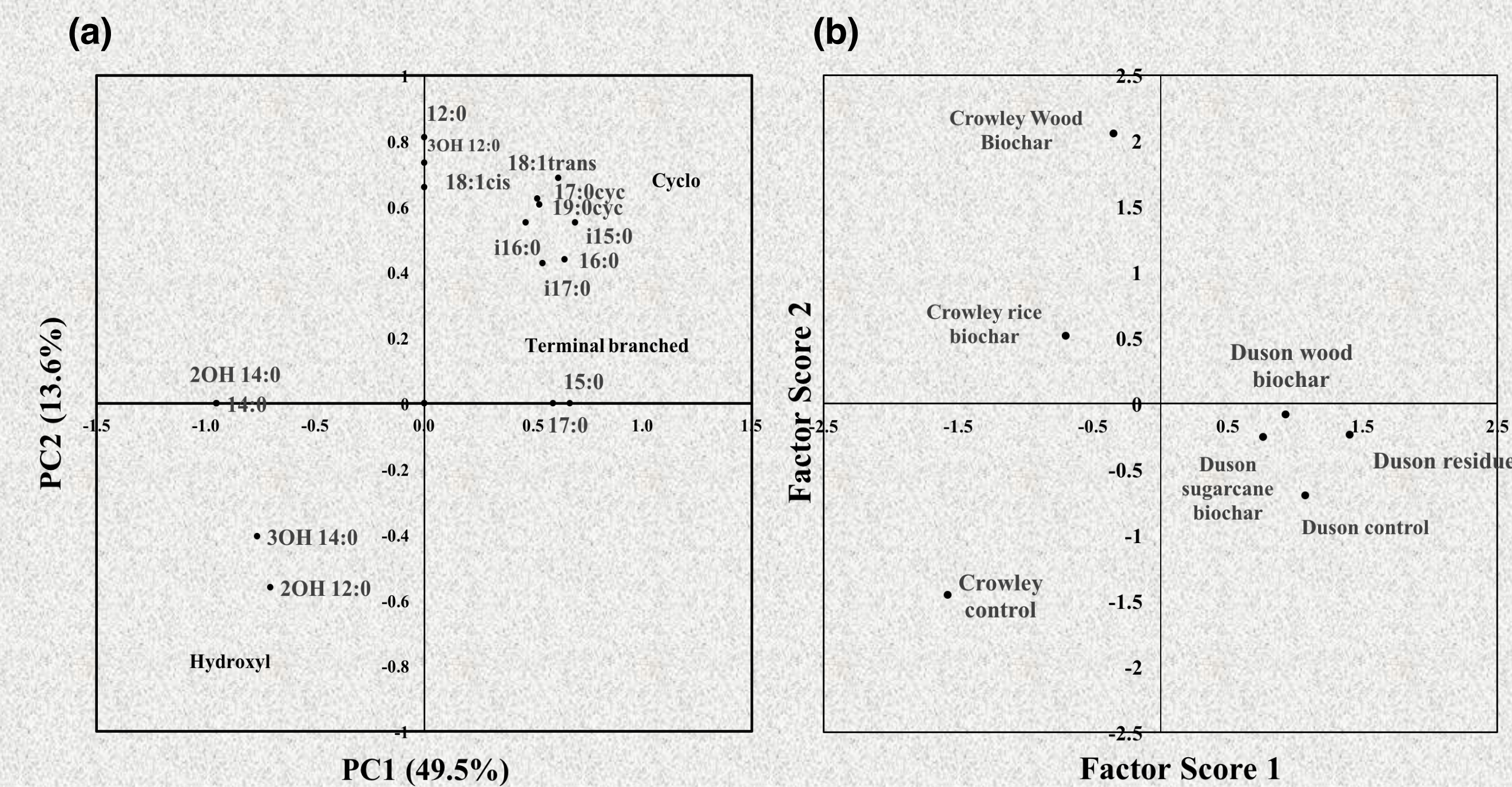


Fig. 4. PCA analysis of individual PLFA variance of both rice and sugarcane soils (a), and factor analysis of principal components (b).

## Results

- Biochar applications generally increased total microbial biomass in both rice and sugarcane soils (Fig.1). Biochar amendment tends to greatly increase HFAs group followed by SFAs, MUFAs in rice soil, whereas it only elevated HFAs and branched FAs in sugarcane soil (Fig. 2). This indicates that biochar enhances particularly G- besides the positive impact on the activity of the most microorganisms in rice soil, whereas it affects positively on both G+ and G+ bacteria in sugarcane soil. Biochar application affects little on fungal biomarker polyunsaturated fatty acid 18:2w9,12.
- Wood biochar decreased stress indicators, ratios of cyc/precursor from 0.7 to 0.5 and trans/cis from 1.0 to 0.7, respectively, in rice soil, but had little effect in sugarcane soil. This suggests that biochar tend to improve soil quality that help to reduce stress level microorganisms in rice soil. In addition, for both fields, biochar increased terminal branched FAs, which indicates the improvement in nutrient sufficiency and low pollution environment.
- PCA analysis showed that cyclopropyl fatty acids (cy17:0, cy19:0), monounsaturated fatty acids (MUFAs)(16:1w9 cis, 18:1w9 trans,18:1w9cis), and terminal branched PLFA groups were more influenced by biochar treatments. Factor analysis clearly showed the separation of two soil systems of rice and sugarcane, and biochar amendment influenced soil microbial community structure more significantly in rice than sugarcane agroecosystem.

## Conclusion

PLFA results show biochar applications significantly affect soil microbial community structure. Wood biochar tends to have greater effect than rice and sugarcane residue biochars. An integrated difference of both soil type and production system likely contributed to the differential effect of biochar amendments on soil microbial activity and community structure between rice and sugarcane agroecosystems.