

Fungal specific response in decomposing sugarcane leaf litter to no-tillage and bagasse mulching practices determined by Ion torrent ITS amplicon sequencing



T. Miura*, N. Kaneko, K. Fujie (Yokohama National Univ.), A. Niswati, I.G. Swibawa (Univ. Lampung), S. Haryani, H. Gunito (PT Gunung Madu Plantations), S. Shimano (Miyagi Univ. Education)

*toshikom@ynu.ac.jp

Background & study aims

- Sugarcane leaf litter is an important C and nutrient input in sugarcane plantations.
- Capturing the litter decomposition process is important to increase and maintain soil organic matter content.
- In natural ecosystems, litter is decomposed mainly by fungi and the alteration of fungal community structure due to environmental change is reflected in the decomposition process.
- Such studies are less in agroecosystems.

We determined:

- The effect of different tillage systems and bagasse (sugarcane fibers) mulching on fungal community structure
- links between fungal community and litter decomposition rate

Discussion & conclusion

No-till increase Zygomycota abundance and indicator richness.

- Zygomycota are fast-growing fungi and utilize simple soluble substrates (Kjøller & Struwe 2002).
- Glomeromycota modify physicochemical environment in litter by preferentially exporting litter N to the host plant (Nuccio et al. 2013).

Bagasse reduce OTU richness and raise Basidiomycota abundance.

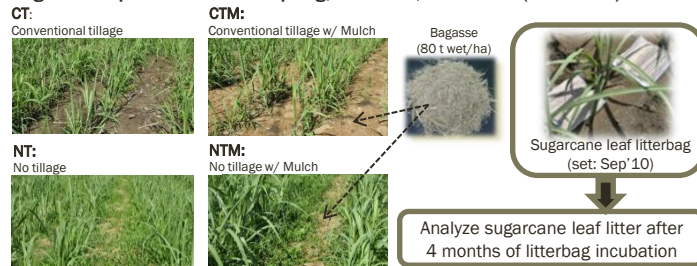
- Basidiomycota are slow-growing fungi and includes many species which can degrade lignin (Osono & Takeda 2002).

Changes in fungal community structure responding to tillage and mulching are related to litter decomposition rate

Capturing fungal community structure by deep sequencing might be able to explain the litter decomposition process under different soil managements

Study site

Sugarcane plantation in Lampung, Sumatra, Indonesia (Alisol soil)



Materials & methods

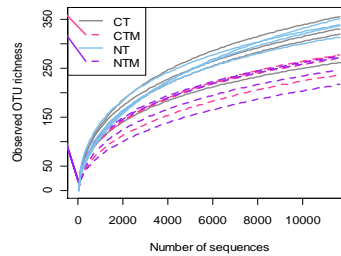
- Extract DNA from litter by ISOIL
- Amplify fungal ITS1 region (Primers: ITS1-F_KY01/ ITS2_KY01; Toju et al. 2012)
- Ligate adapters with barcode-tag and nick-repair
- emPCR by Ion OneTouch ES
- Sequence the amplicon library with 318 chip

> Data analysis by Mothur pipeline (v.1.32.1; Schloss et al. 2009)

- Clean-up of sequences**
- Chimera removal** (chimera.uchime)
- OTU clustering** (UCLUST)
- Classification** (UNITE ITS database (Abarenkov et al. 2010))

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Results



Genus-level OTU richness was not affected by tillage, but decreased by bagasse mulching ($p < 0.05^*$).

*Split-plot two-way ANOVA

Fig. 1. Rarefaction curves of OTU (85% id.) richness in each management

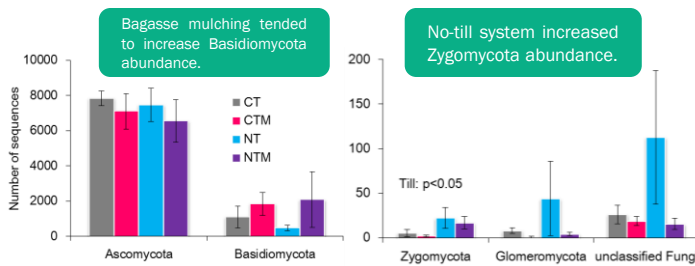


Fig. 2. Fungal community composition at phylum level

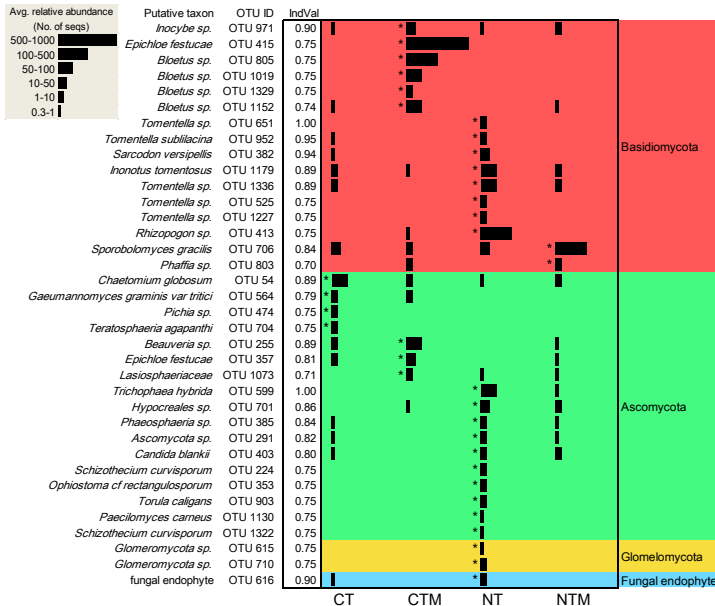
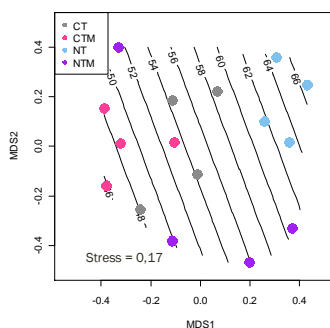


Fig. 3. Indicator OTUs (*) of each management (IndVal value ≥ 0.7)



Correlation between fungal community structure and litter decomposition rate was significant in NMDS axis1 ($p = 0.01$).

Fig. 4. NMDS of the litter fungal communities with GAM surface fits of litter decomposition rate (% mass loss)