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Introduction

Rice (*Oryza sativa* L.) is an important food crop in the world, being the staple food for more than half of the earth's population⁽¹⁾, including in Indonesia. Various genera and species of nematodes have been reported from upland and paddy rice in many countries^(1, 2), but the Indonesian nematofauna has not yet been well studied. Accurately identifying the phytonematodes and its damage is one of the most fundamental elements of pest management.

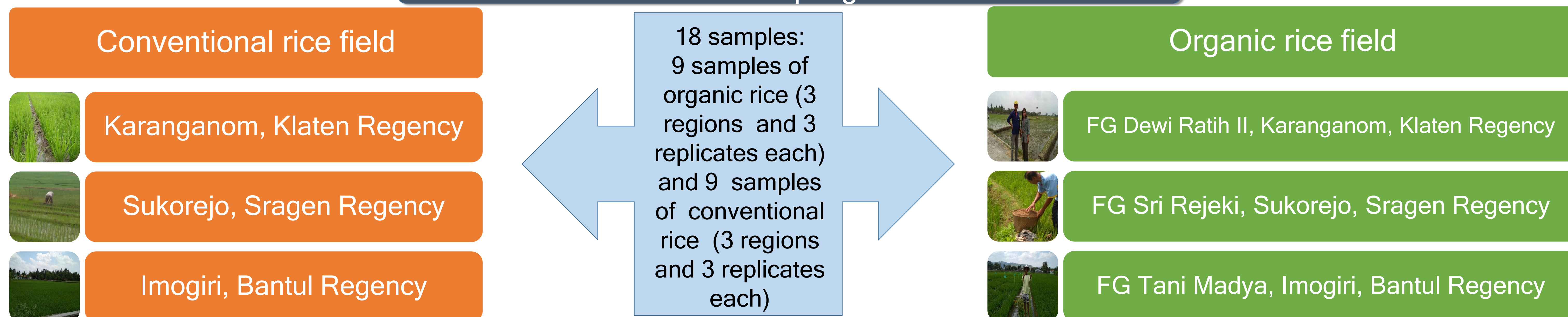
Objectives

The objectives of this project are to provide:

- A more comprehensive description of plant-parasitic nematode biodiversity from organic and conventional rice crops in three regencies of Central Java, based on the molecular, morphological and plant-pathological information,
- To analyze the effect of organic and conventional farming practices on nematode and soil microbial communities, and
- To compare metabarcoding with microscopic identification and sanger-based DNA barcoding.

Methods & Preliminary Results

A. Soil Sampling



B. Microscopic identification plant-parasitic species

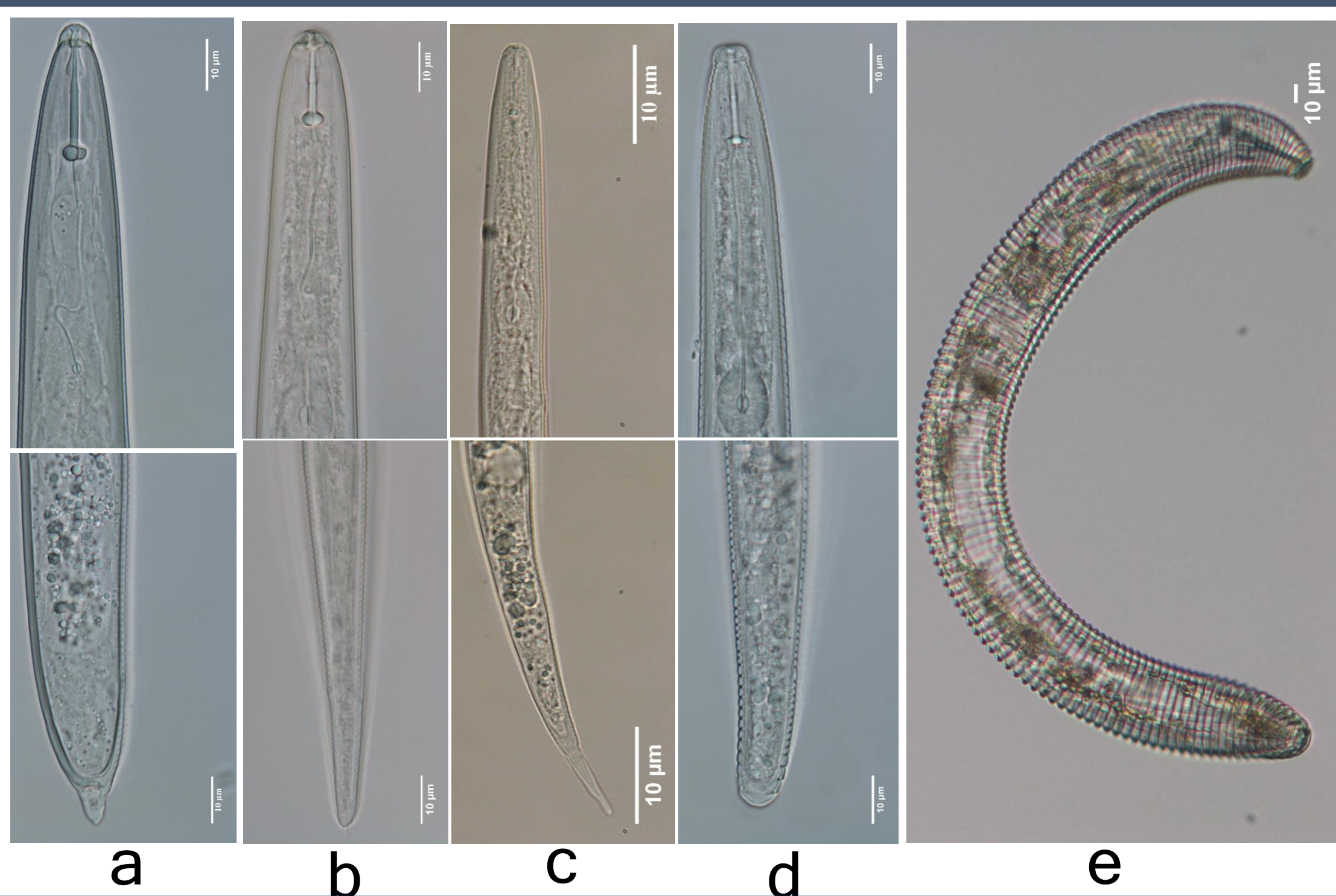


Figure 1. The five genera of plant-parasitic nematodes found to be associated with rice were; (a) *Helicotylenchus* spp., (b) *Hirschmanniella oryzae*, (c) *Meloidogyne* spp., (d) *Tylenchorhynchus* spp., and (e) *Mesocriconema* spp.



C. DNA Sanger Sequencing of PPN (D2D3 & 18S rDNA, COI mtDNA)

Analytical methods linking molecular and morphological data of plant-parasitic are explored. Well-known rice plant parasitic nematodes (e.g. *Hirschmanniella oryzae*) can be directly linked to existing barcodes. For other species, barcodes are, not yet available in GenBank. Hence, linking "traditional" identifications to useful barcodes is needed.

D. Microscopic identification nematodes, including free-living nematodes on family level (preliminary results)

The following nematode families have been found in organic and conventional fields: Alaimidae, Aphelenchoididae, Cephalobidae, Criconematidae, Dolichodoridae, Dorylaimida, Hoplolaimidae, Meloidogyidae, Mononchidae, Monhysteridae, Panagrolaimidae, Pratylenchidae, Tylenchidae. Cephalobidae, Hoplolaimidae, and Mononchidae have been identified only in organic fields.

E. Metabarcoding of nematode and microbial community (preliminary results)

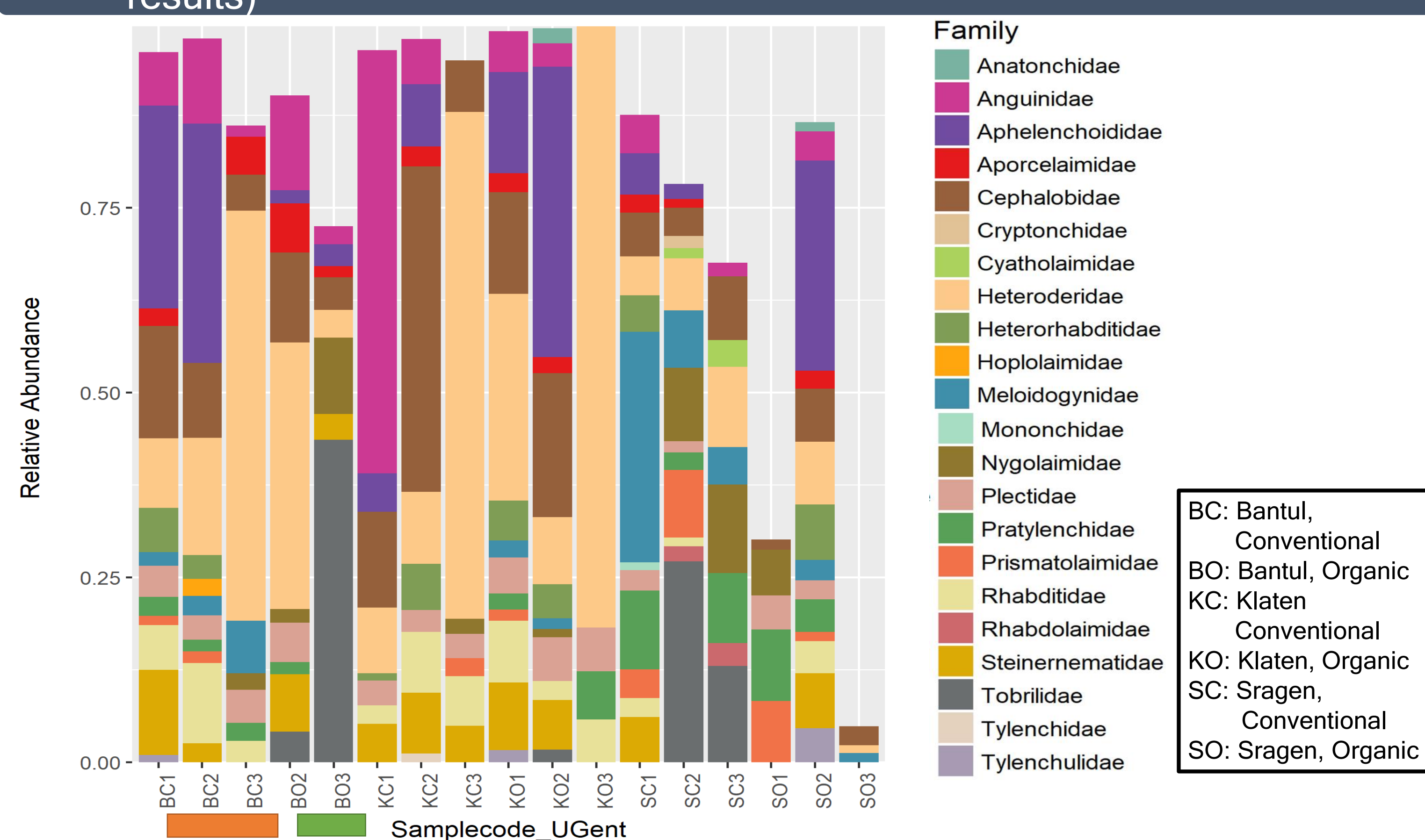


Figure 2. Relative abundance of nematode families in two cropping systems obtained via next-generation sequencing.

The nematode and microbial community of organic and conventional agriculture do not appear significantly different. Communities are preferably arranged according to the region.

Q: What next???

A: (1) Compare nematode and microbial communities of organic and conventional rice production, (2) Compare metagbarcoding community analyses with traditional identification, and (3) Compare metabarcoding community analyses with PLFA analyses (Moeskops *et al*, 2010).

Acknowledgements

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