

# Identification of soil factors associated with root-knot nematode density in green manure-applied fields

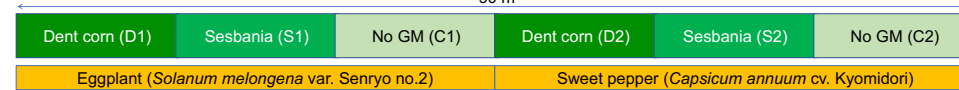
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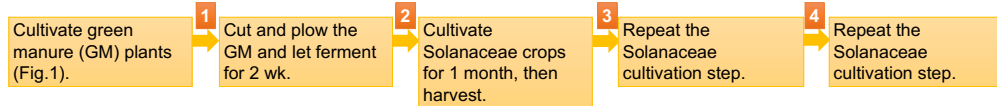
Fig.1 Growth of green manure plants in field. (A) Dent corn (*Zea mays* cv. 'Gold dent KD850') and (B) Sesbania (*Sesbania cannabica* 'Densuke')

**Aims of this study**  
 To explore the effects of green manure in terms of inorganic soil elements (pH, EC, nitrate nitrogen, available phosphate, exchangeable K, Mg and Ca), microbiome and autotrophic nematodes in the field soil, and examine how these factors interact with the plant-parasitic nematode density.

## Field design



## Field soil sampling



## Changes of inorganic soil elements

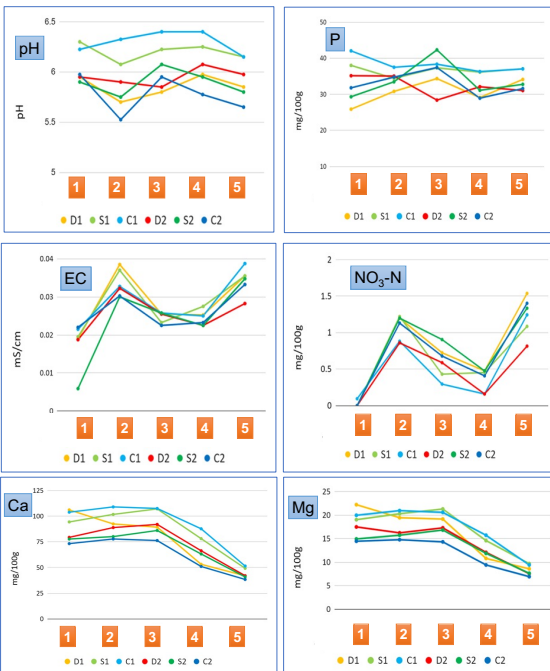


Fig.2 pH turned acidic after the GM fermentation in S2 and C2. P remained at relatively constant level. EC and NO<sub>3</sub>-NO showed similar movements, both increased significantly by the GM fermentation and decreased until after the second Solanaceae cultivation, then increased again. Ca, Mg and K did not change by the GM fermentation, but continuously decreased in the repeated Solanaceae cultivations.

## Root-knot nematode (RKN, *Meloidogyne incognita*) infection

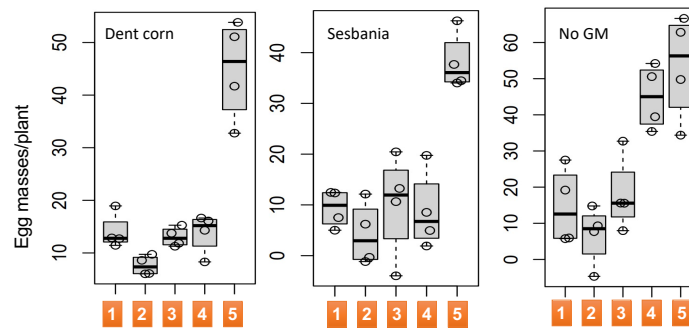


Fig.3 Collected soil was used in pot inoculation tests using susceptible tomato cultivar seedlings. Each seedling was inoculated with 300 second-stage *M. incognita* juveniles, and egg mass number was counted 5 weeks after the inoculation. Parasitic nematode-suppressing effect was continuously observed until after the first Solanaceae cultivation in all soil types. This suppression effect continued until after the second Solanaceae cultivation in GM-applied soils, but not in soils without the application of GM.

## Conclusion and Perspective

- Cultivation and fermentation of green manure (GM) plants, followed by repeated cultivations of Solanaceae crops affected the level of inorganic elements in the soil.
- GM-applied soil showed prolonged suppression effect against the RKN infection.
- Field tests were done in 2021, being repeated in 2022.

## Microbiome profiles by taxonomy bar plot

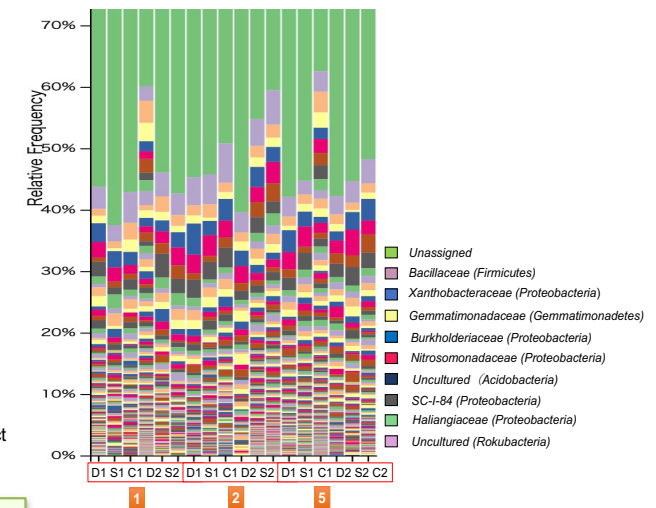


Fig.4 DNA was extracted from each soil sample and amplicon sequencing of 16S rRNA genes was performed by the Nanopore technology. Based on the RKN infection results (Fig.3), we are now inspecting the differentially detected bacterial species in sample no.4 (in progress).

**Acknowledgement**  
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