Project Title

Soil Health and Green Pea Yield in Ontario: Insights from Microbiome Research

Research Agency/location

Lab work: McMaster University, Hamilton, Ontario; Field work: commercial field sampling around Ontario

Lead and Key Investigators

- Lead: Rebecca Doyle (Assistant Professor, Biology, McMaster University)
- Elaine Roddy (Vegetable Crops Specialist, OMAFA)
- Dan Oliver (Agronomy, Seed & Compliance Manager, Nortera Foods)
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Summary

This project explored how soil health, including fertility and microbial communities, relates to green pea yield in Ontario. We found that soil chemistry (especially pH and calcium) strongly influences microbial communities, but these microbes did not directly predict yield. While we have begun analyzing soil microbiomes, the number of samples is still limited. This means we cannot yet determine whether microbial communities will be equally or more predictive of yield compared to traditional soil measures. Continued sampling and analysis will help clarify whether microbiomes can become a useful predictor for growers.

Background

Green pea yields in Ontario vary widely within and between fields. While soil fertility is known to influence crop performance, the role of soil biology—particularly microbial communities—is less understood. This project explores how soil health indicators, including microbiomes, relate to pea yield.

Objective

To identify soil factors (both chemical and biological) that may explain differences in pea yield across Ontario fields.

Materials and Methodology

Field Sampling:

- 2024: Three commercial fields sampled at 20 subsites each.

- 2025: One main field (McEE) sampled extensively; three additional fields sampled at bloom stage.

Data Collected:

- Soil fertility (pH, nutrients like Ca, Fe, Al).
- Plant tissue nutrients at key growth stages.
- Pea yield at selected subsites.
- Soil microbiomes (bacterial communities) using DNA sequencing.

Key Findings

Soil Fertility Matters

- Fields with balanced calcium and pH had distinct microbial communities.

Microbiomes Respond to Soil Conditions

- Microbial composition varied by site and was linked to soil properties like pH and calcium.
- **Important:** Microbiome differences did **not** directly predict yield
- These findings are based on a small number of microbiome samples, so conclusions about their role in yield prediction are preliminary

Yield Drivers

- Traditional soil fertility measures (e.g., potassium and magnesium balance) remain strong predictors of yield.

Weather Challenges

- 2025 sampling was limited by adverse conditions, highlighting the need for multi-year data.

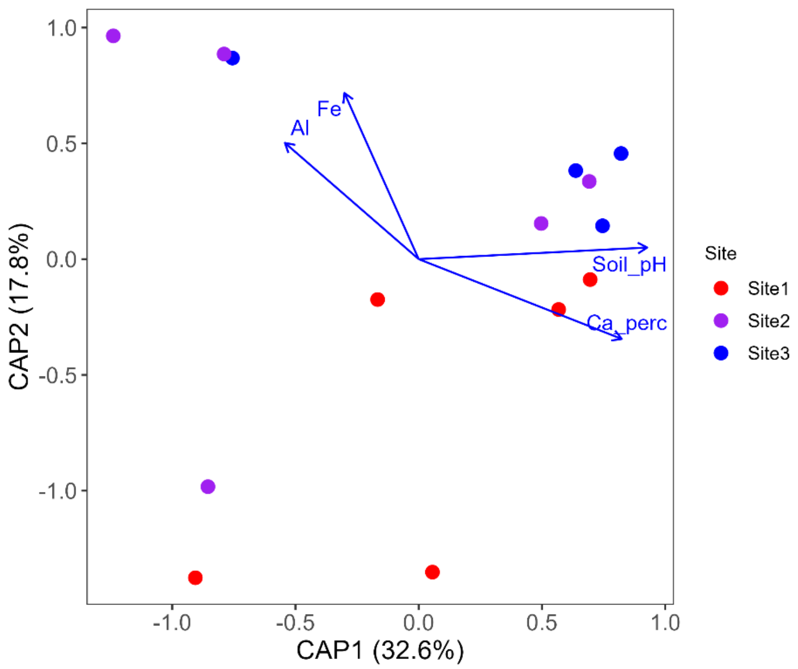


Figure 1: Microbial communities differ between fields and are influenced by soil factors like pH and calcium.

Table 1: Soil pH and calcium had the strongest link to microbial patterns; iron and aluminum also played a role.

Predictor	**Stat summary**
Site	**F[2, 5] = 1.817, p = 0.015**
Al	**F[1, 5] = 2.434, R2 = 0.547, p = 0.019**
K_perc	F[1, 5] = 1.106, R2 = 0.231, p = 0.225
Ca_perc	**F[1, 5] = 2.507, R2 = 0.798, p = 0.001**
Soil_pH	**F[1, 5] = 1.894, R2 = 0.862, p = 0.001**
Fe	**F[1, 5] = 0.930, R2 = 0.606, p = 0.008**
Adj_Yield_ton_per_ac	F[1, 5] = 1.086, R2 = 0.122, p = 0.484

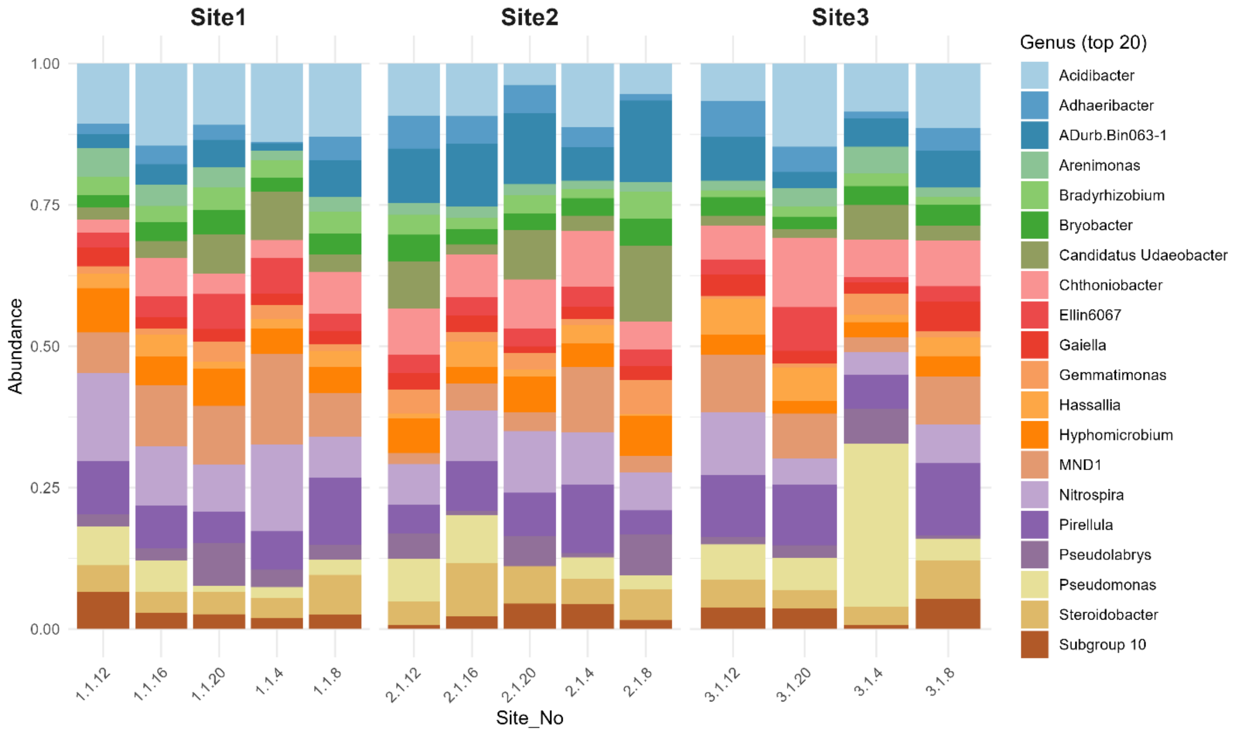
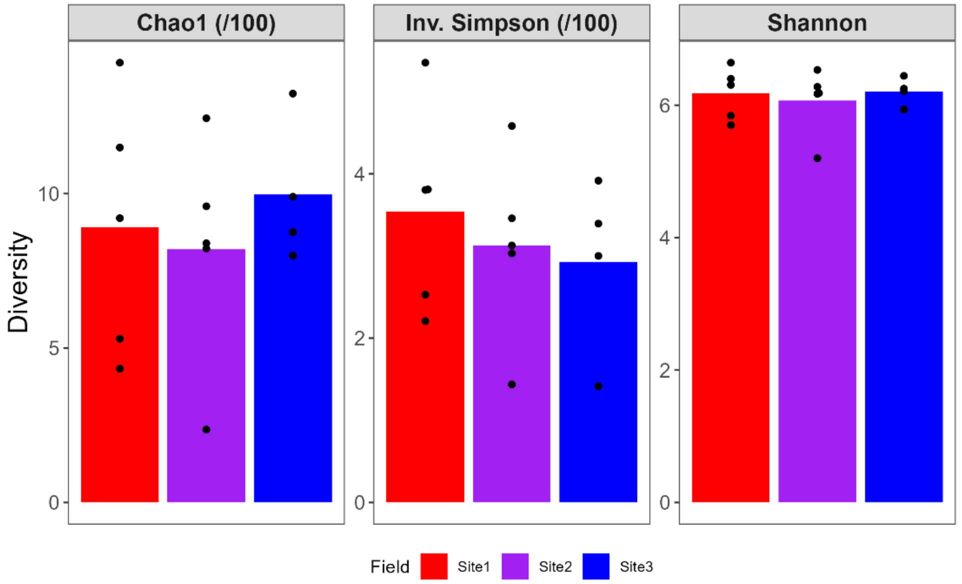


Figure 2: Some microbes (e.g., *Pseudomonas*) were more common in certain subsites, but this didn't translate to yield differences.



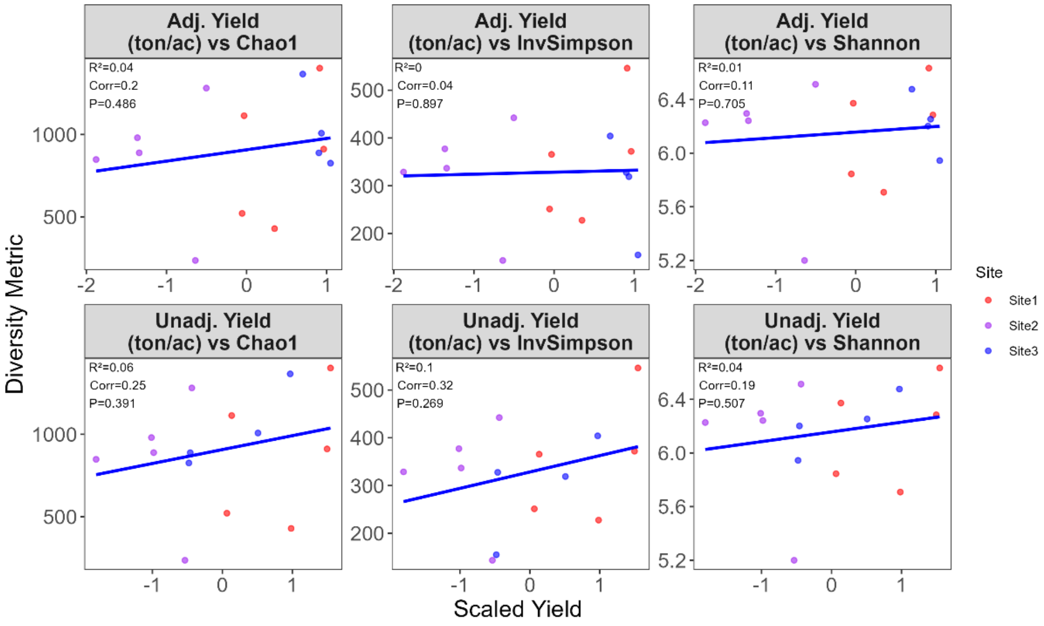


Figure 3: Microbial diversity (number of species) was similar across sites and unrelated to yield.

What This Means for Growers

- Microbiome research is promising but not yet a direct tool for yield prediction.
- Continued monitoring across seasons will help clarify links between soil biology and crop performance.
- Balanced soil fertility, especially potassium, remains the most actionable factor for improving yield.

Next Steps

- Complete microbiome sequencing for 2025 samples.
- Optimizing sequencing output by adding an inhibitor removal step prior to PCR.
- Expand sampling to more fields and seasons.
- Develop practical soil health indicators for growers.

Supplemental results

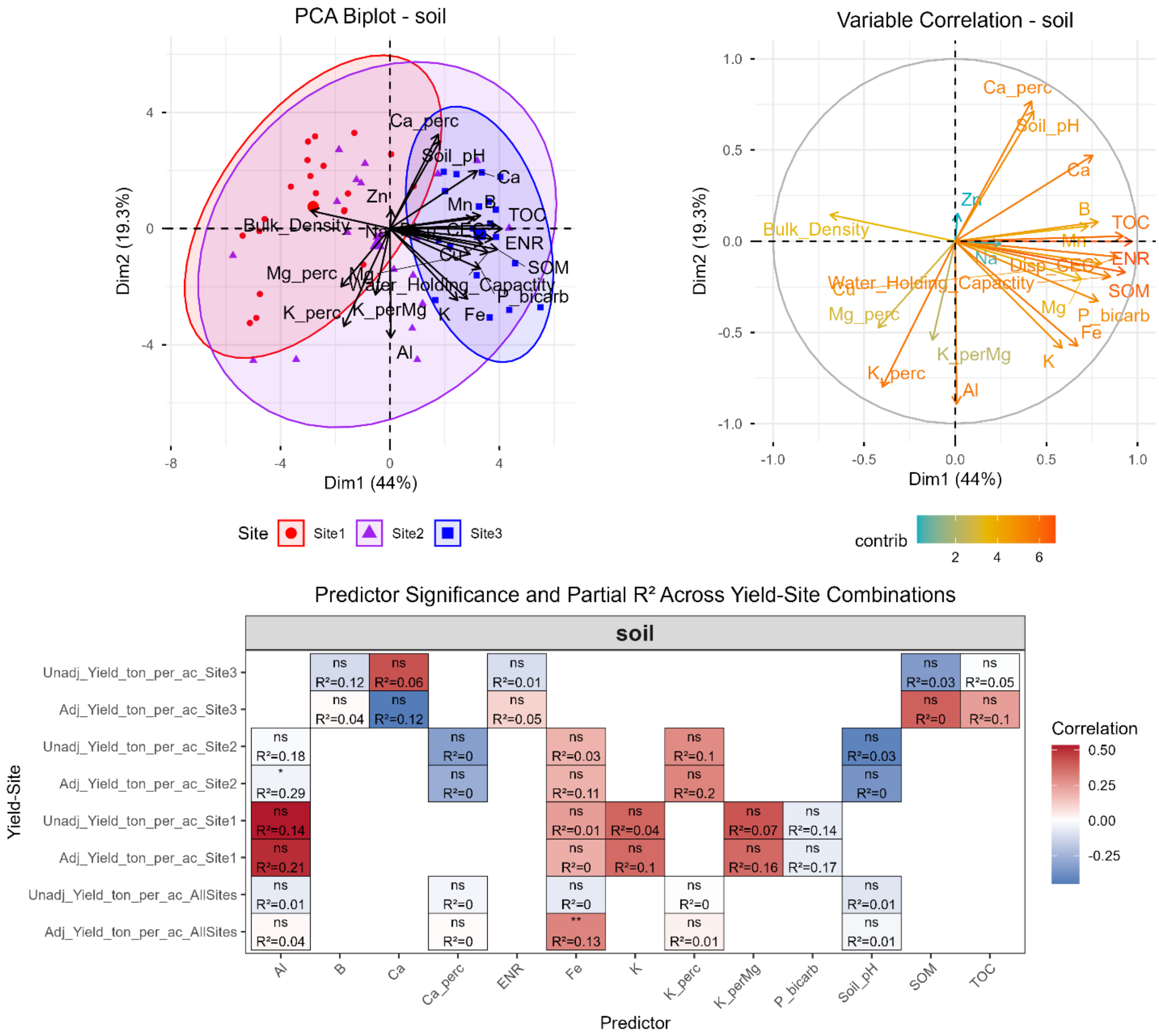


Figure S1: Soil Fertility and Yield

- Shows which soil fertility measures best predict yield within fields. The top chart groups soil properties by similarity, and the bottom chart shows how strongly each property relates to yield. Iron, aluminum, and the potassium-to-magnesium balance (K-perMg) stand out as important factors.

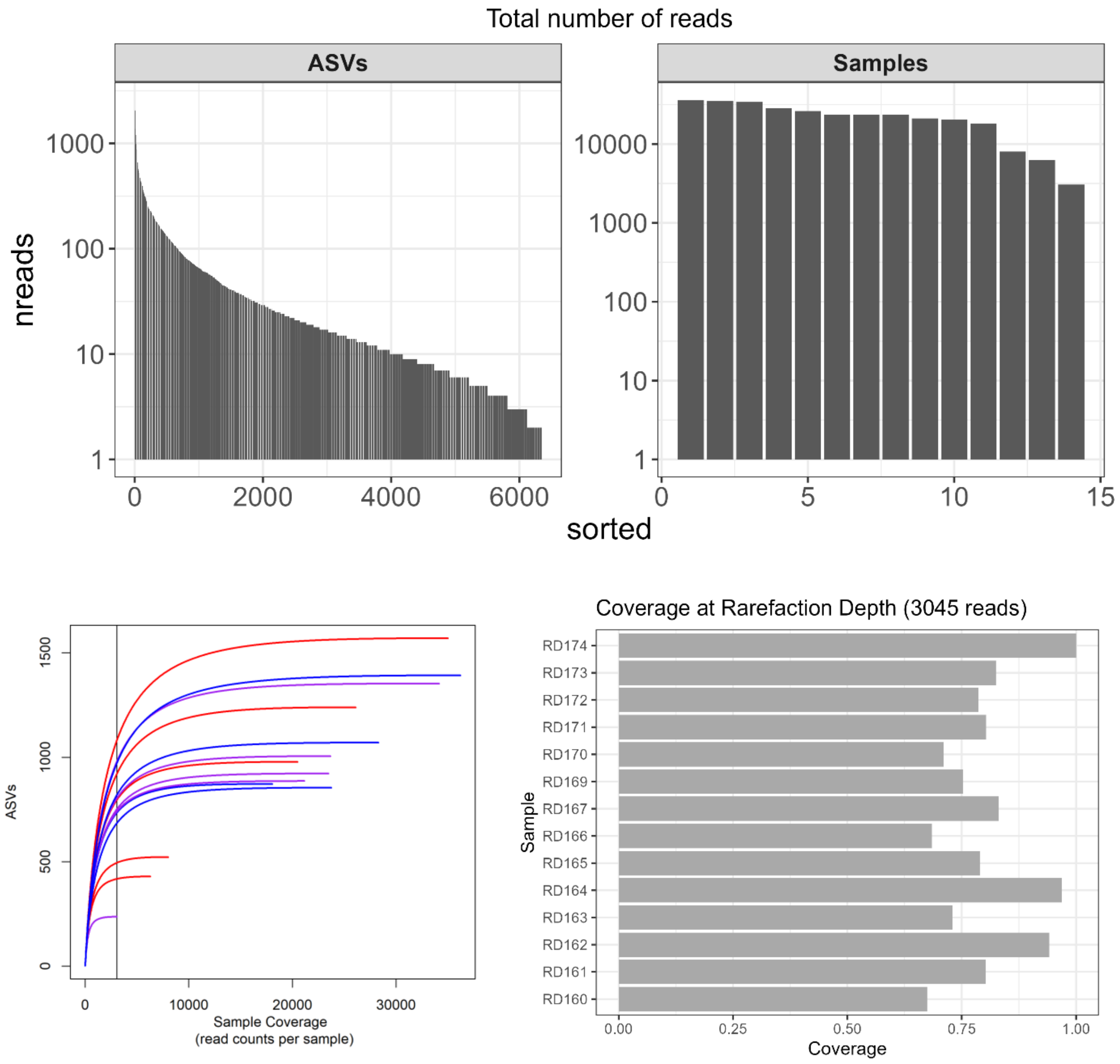


Figure S2: Sequencing Depth and Sampling Effort

- Top: Number of DNA reads per sample and per microbial variant (ASV)— few samples (3/14) with low (<10k reads) depth.
- Bottom: Rarefaction curve and coverage at rarefaction depth shows sequencing captured most microbial diversity present.

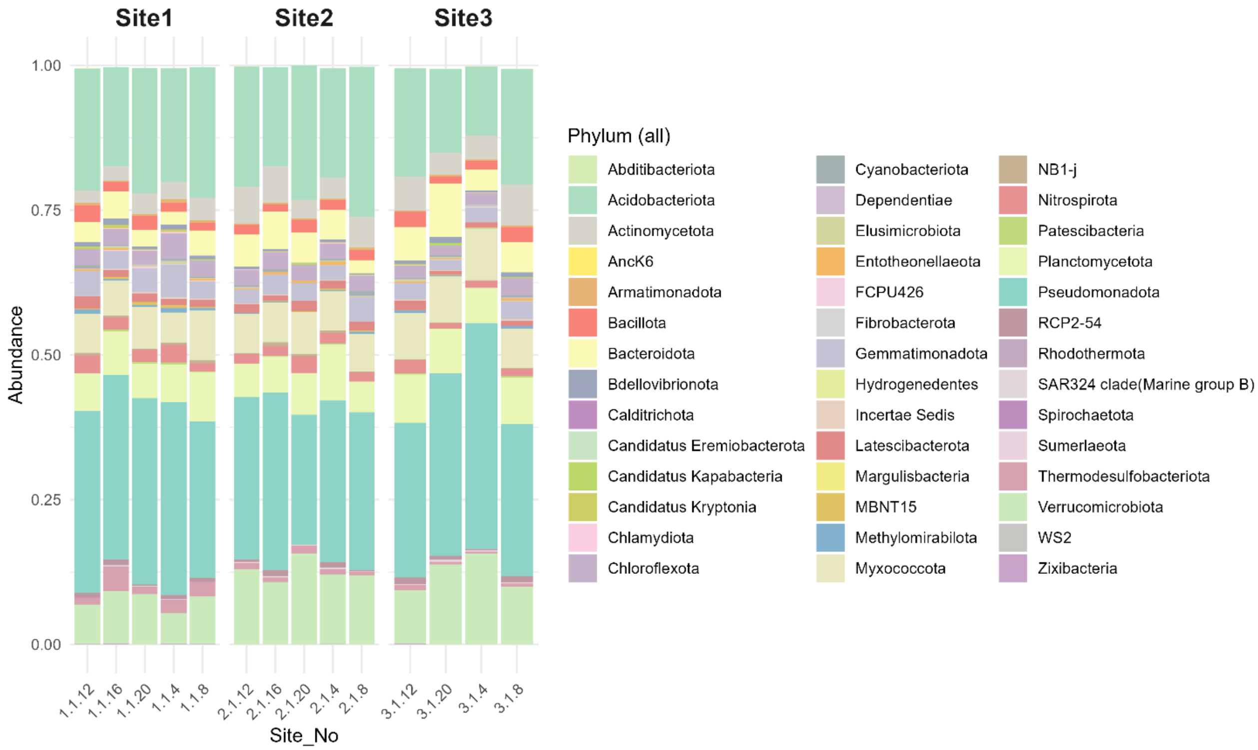


Figure S3: Microbial Composition by Phylum

- Compares the major microbial groups (at the phylum level) across the three fields sampled in 2024. While the overall mix is similar, some groups are more common in certain fields.