The canola effect: quantifying root-derived carbon and microbial uptake in Saskatchewan soils

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1 INTRODUCTION

- Canola (*Brassica napus* L.), a major oilseed crop with distinctive root characteristics, influences soil carbon (C) dynamics differently from mycorrhizal cereal and legume crops in agricultural systems[1]. Hence, it is important to understand its influence on belowground C dynamics and storage[2].
- Quantifying root C contributions of canola relative to other widely cultivated crops to soil functional pools and microbial communities across different soil types is crucial for understanding and maintaining soil health and productivity in agricultural systems.

We aim to quantify and compare canola root biomass and rhizodeposition contributions compared to wheat and field pea, (2) trace the distribution of root-derived carbon into soil organic carbon (SOC) pools, and (3) examine how soil microbial communities process and store this carbon across two contrasting soil types.

2 METHODS

➢ $^{13}CO_2$ stable isotope pulse-labelling of canola (InVigor L233P), wheat (AAC Brandon), and field pea (CDC Meadow) to track belowground photosynthate C allocation and rhizodeposition in two soils.

➢ Soil organic matter (SOM) fractionated into mineral-associated OM (MAOM; <53μm) and particulate OM (POM; >53μm); quantification of root-derived ^{13}C to obtain mineral-associated C (MAOC) and particulate C (POC) [3].

➢ Soil microbial communities were analyzed using cell structural phospholipid (PLFA) and storage neutral lipid fatty acid (NLFA) analyses. The $\delta^{13}C$ of individual fatty acid methyl esters, was used to quantify the plant root-derived ^{13}C incorporation into different microbial functional groups[4].
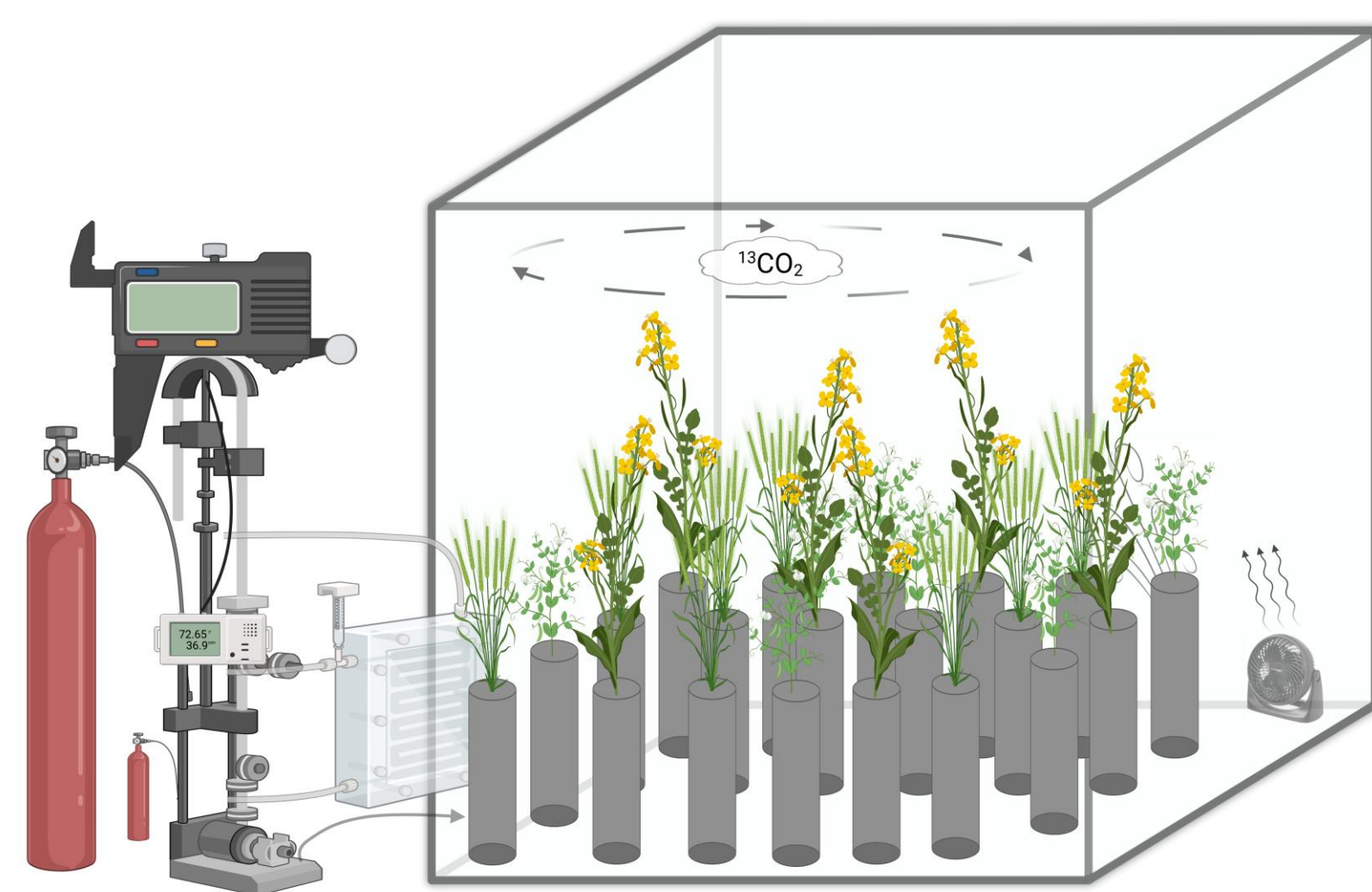
Table 1. Soil physical and chemical properties.

Soil types	Clay (%)	Sand (%)	Silt (%)	WHC (%)	CEC (meq/100 g)	OC (%)	Total N (%)
Goodale	19	47	34	18.89	27.27	1.8	0.196
Central Butte	23	41	36	20.46	30.13	2.0	0.185

Lipid extraction and separation

Methyl esterification and GC &GC-IRMS analyses

Fig. 1. A schematic showing plants in experimental pots being pulse-labeled with $^{13}CO_2$ in a transparent chamber.
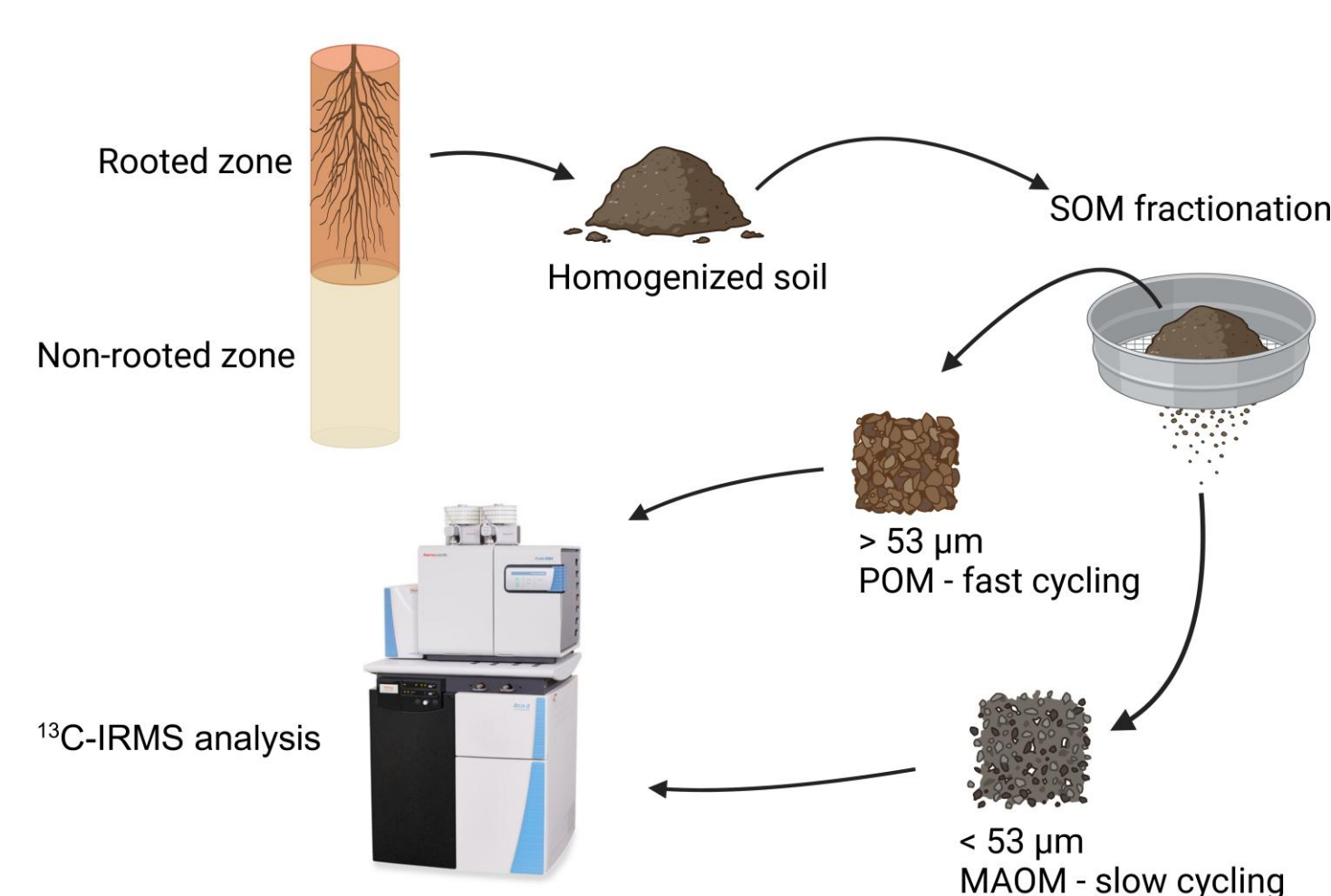
Fig. 2. Soil particle size fractionation and ^{13}C stable isotope analysis performed on each size fraction.
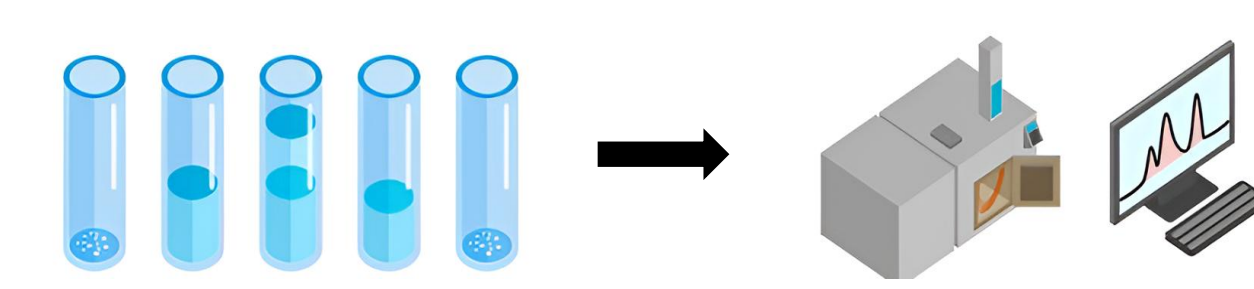
Fig. 3. Main steps of lipid extraction, separation, derivatization and analysis by gas-chromatography (GC) and GC-isotope ratio mass spectrometry (GC-IRMS). ^{13}C-PLFA and ^{13}C-NLFA represent microorganisms that have utilized plant root-derived C.
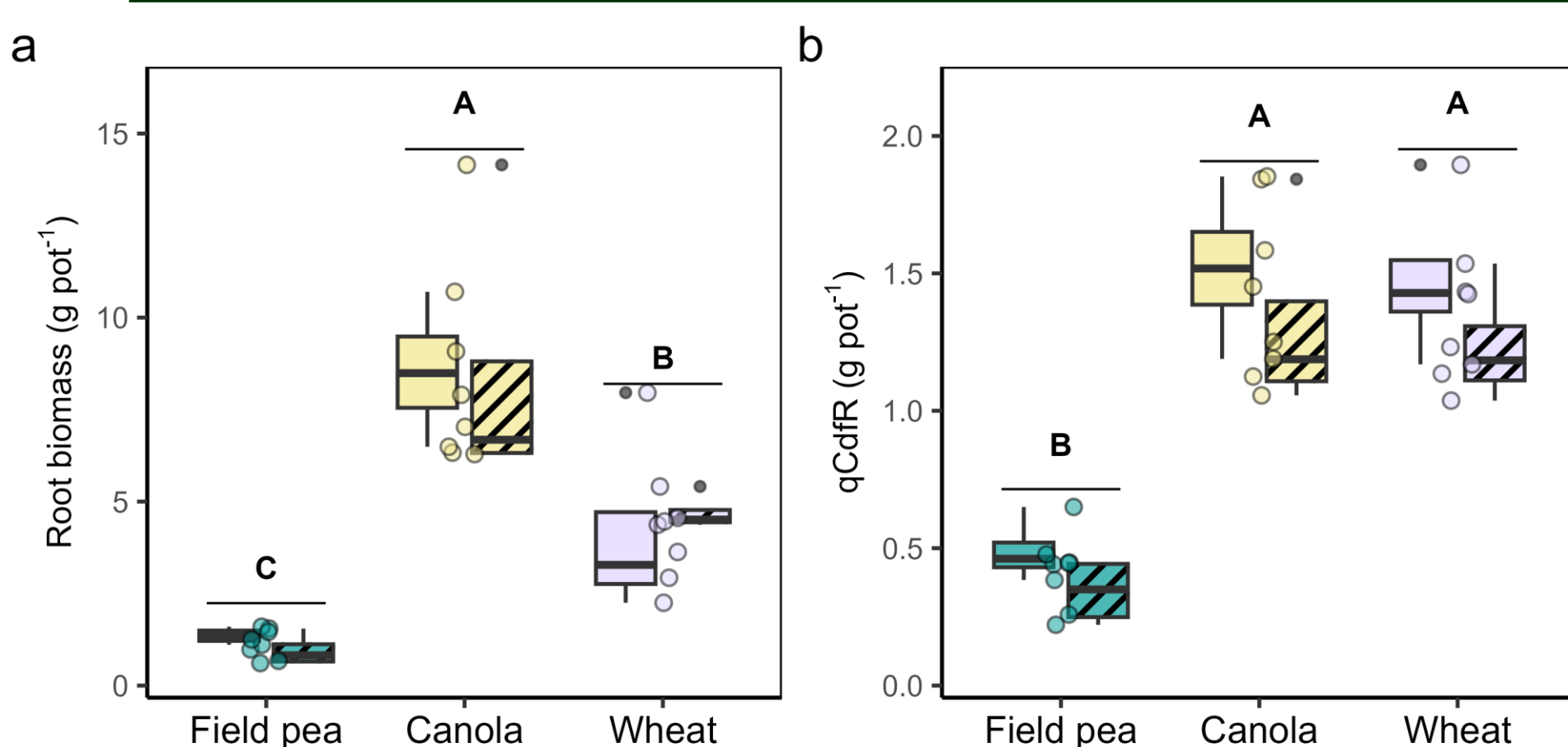
3 RESULTS

Fig. 4. Root biomass (a), and quantity of C derived from rhizodeposition (qCdfR) (b) of crop roots in Goodale (solid boxes) and Central Butte (hatched boxes) soils.
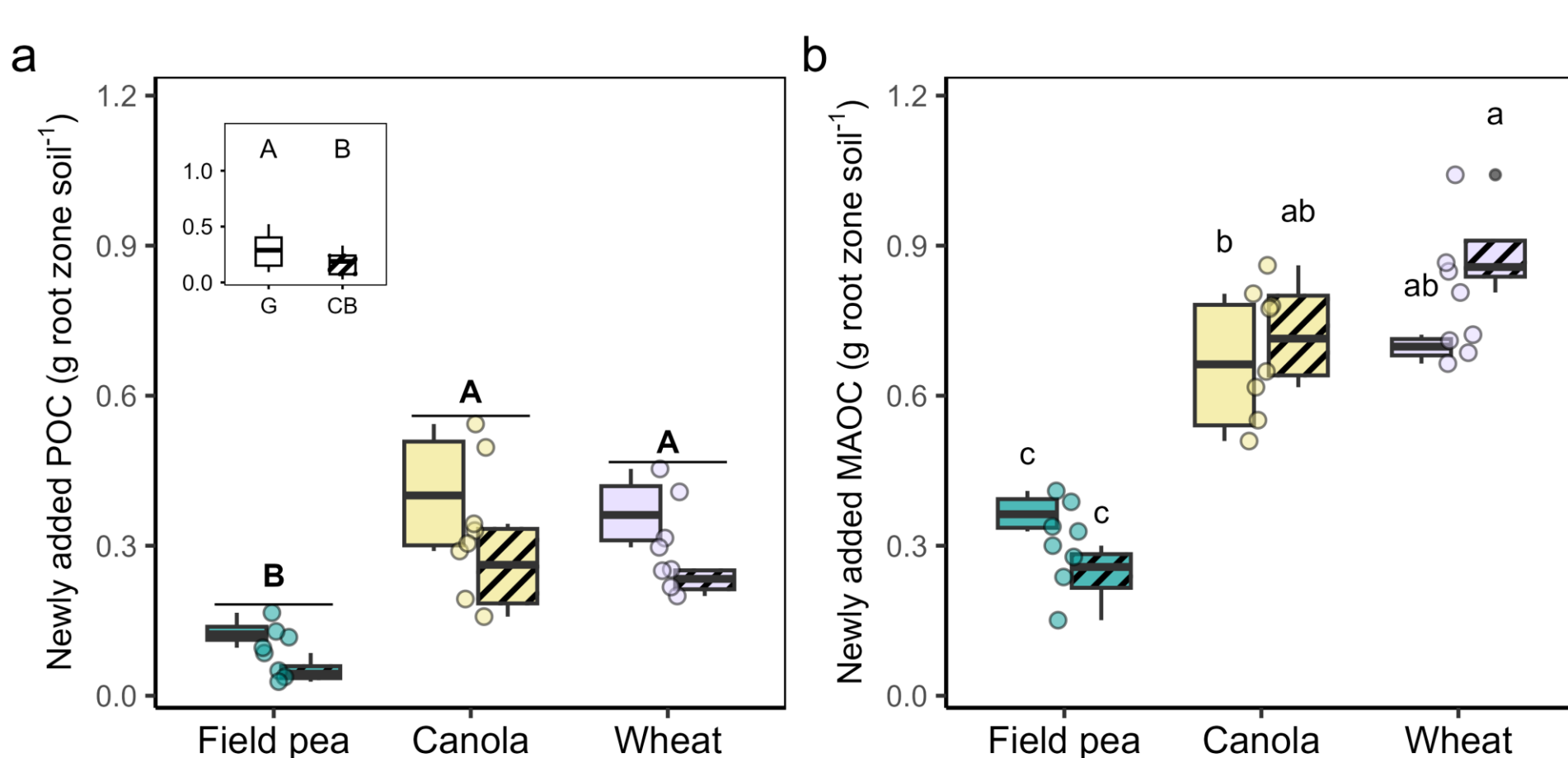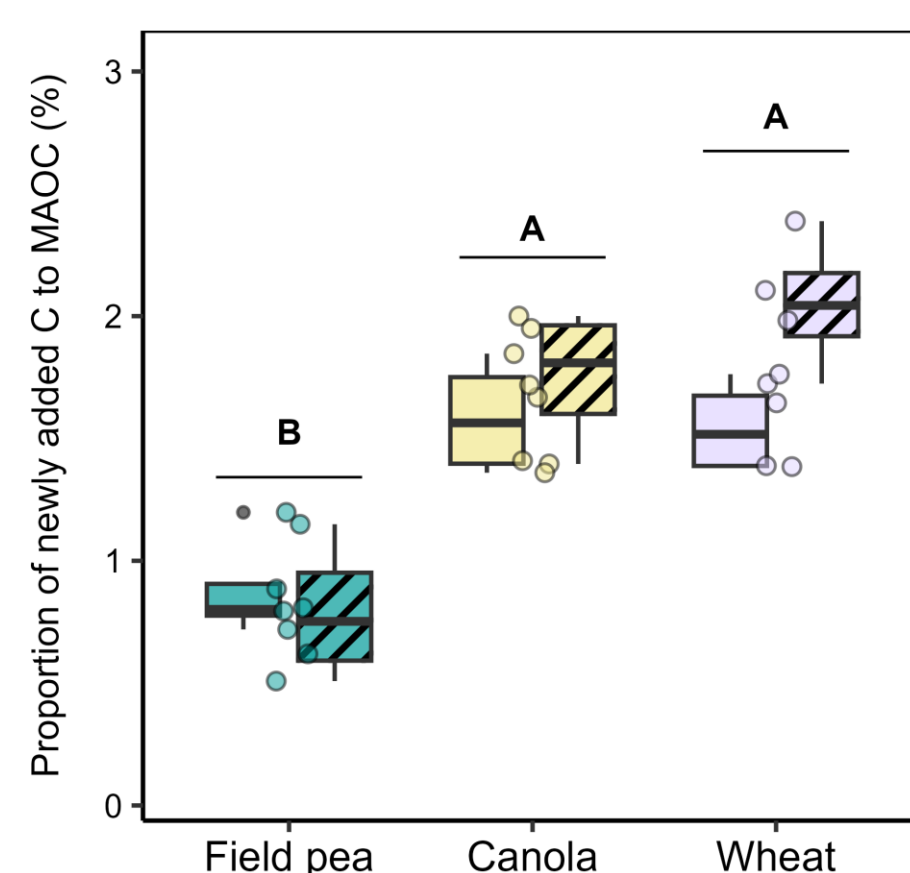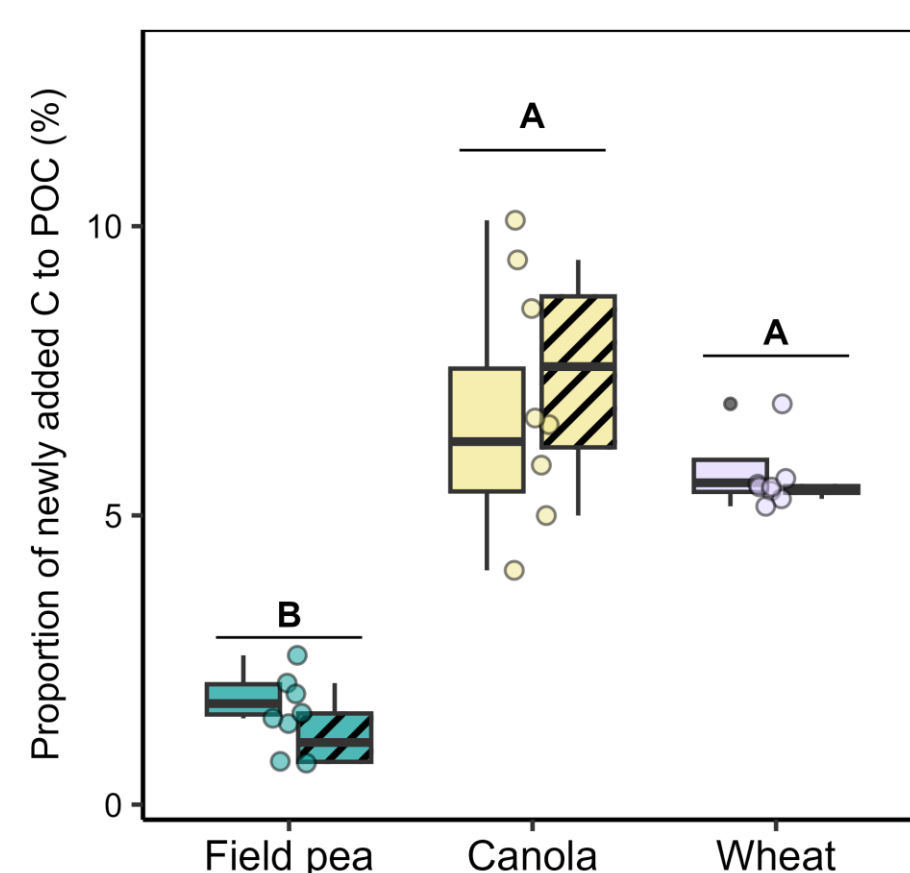

Fig. 5. Newly added C into POC and MAOC to root zone soil from crop roots in Goodale (G-solid boxes) and Central Butte (CB-hatched boxes) soil types.

Root C contributions from canola and wheat to mineral-associated (MAOC) and particulate (POC) carbon pools were greater than field pea

Longer-term microbial turnover of root-derived MAOC and POC is currently unknown, but will affect soil C cycling and sequestration
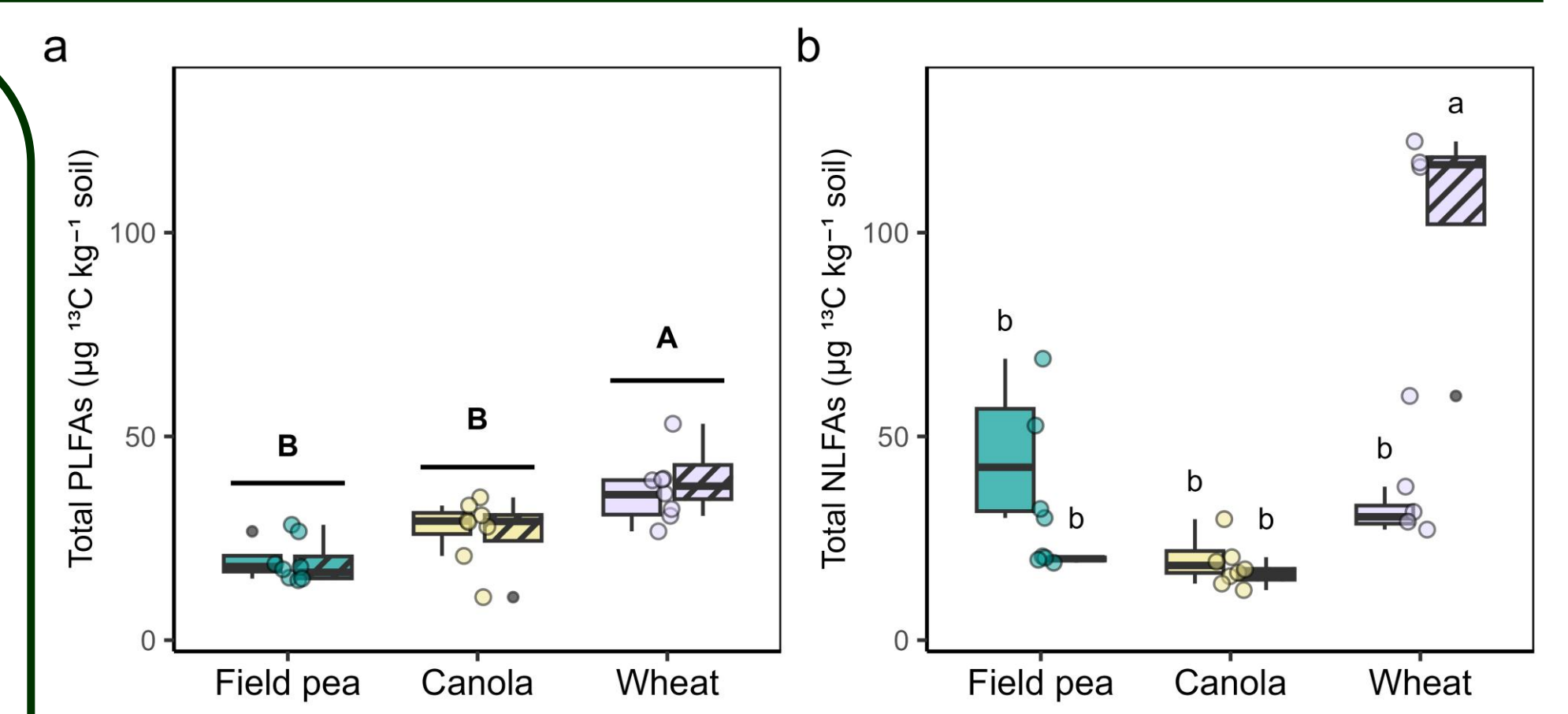

Fig. 6. Incorporation of crop root-derived ^{13}C into total PLFA (a) and NLFA (b) microbial functional groups in Goodale (solid boxes) and Central Butte (hatched boxes) soil types.
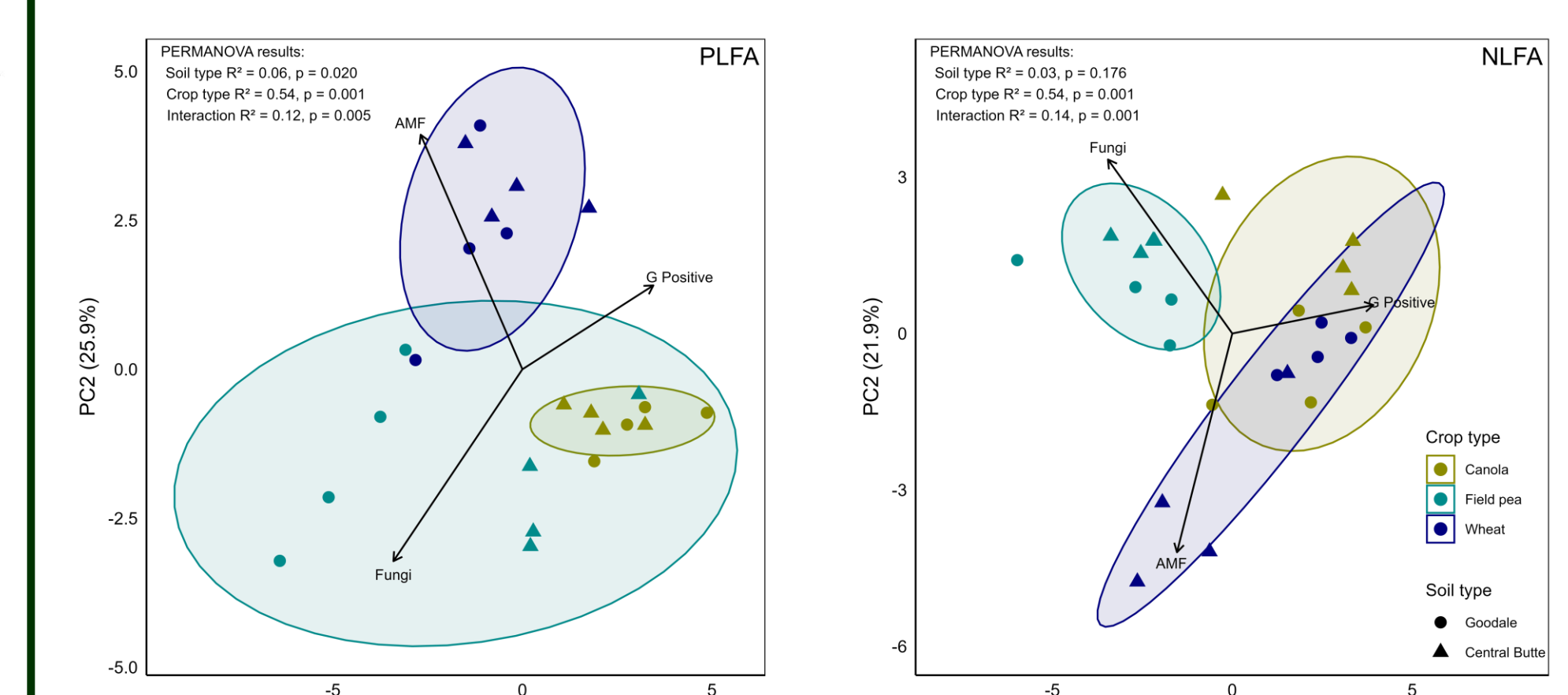

Fig. 7. Microbial community structure (by PCA) showing the distribution of crop root-derived ^{13}C into active (PLFA) and storage (NLFA) microbial functional groups in Goodale and Central Butte soils.

Root-microbe interactions are beginning to reveal canola's distinct carbon legacy in Saskatchewan soils.

4 DISCUSSION & CONCLUSION

- Canola exhibited the highest root biomass and, along with wheat, contributed significantly more root-derived C compared to field pea. Both canola and wheat contributed more C to the POC fraction than field pea, with significant soil type effects. MAOC showed significant crop × soil type interactions, with canola resulting in up to 10% higher MAOC in Central Butte compared to Goodale soil. Canola showed consistent ^{13}C incorporation patterns between soils, contrasting with wheat's more soil-dependent responses in both PLFA and NLFA profiles.
- Microbial community structure (by PCA) of the active microbial community ^{13}C-PLFA and ^{13}C-NLFA profiles showed the dominance of ^{13}C incorporation into Gram-positive bacteria under canola, with a prevalence into fungi in Central Butte soil.

We measured ca. 2.4 times more root-derived C from canola compared to field pea, but only 5% more than wheat, with distinct patterns of microbial C processing. The short-term fate of root-derived C varied between two soil types, highlighting the importance of soil-type specific predictions and accounting of root C contributions to soil organic C pools.

REFERENCES

1. Town et al. (2023). Environ. Microbiome, 18(1):40. 2. Gan et al. (2012). Int. J. Life Cycle Assess., 17:58-68. 3. Haddix et al. (2020). Geoderma, 363:114160. 4. Gorka et al. (2023). Soil Biol. Biochem., 187:109205.

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