

10.5 Annual polycultures and soil health

Use of multispecies annual forage crops to promote healthy soil microbial communities and improve forage yield and sustainability

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MBFI Location(s): Brookdale Farm

Collaborating Partners: Mike Schellenberg, Research Scientist, AAFC

Start Date: 2016 **Status:** In progress

10.5.1 Introduction

This project aims to identify the benefits of diversity above and belowground and their potential contributions to sustainable and resilient forage production systems. Increasing plant diversity (both species and functional group richness) has the potential to increase crop productivity due to trait complementarity and increased functional redundancy, which reduces competition and increases stability. However, it is unclear how multi-species annual forage crop mixtures impact the function and diversity of soil microbial communities, which play an integral role in many important belowground ecosystem services. We plan to use two separate field studies to determine the effects of annual crop (1) diversity and (2) functional redundancy on soil microbial communities and forage productivity. The first field study at Brookdale and Swift Current is designed to broadly test the impact of increasing crop diversity, and the second field study at Swift Current will involve smaller plots to test the effects of plant functional groups (i.e., C₃, C₄, legumes, and brassicas) and functional redundancy on soil health and forage productivity. A combination of traditional and advanced molecular biology tools will be used to assess the taxonomic and functional microbial diversity. We will specifically determine (i) microbial biomass and activity, and (ii) composition and abundance of microbial taxa and functional groups/guilds (i.e., mutualists, saprophytes, pathogens, etc.). This approach will provide insights into the effects of crop mixtures and functional groups on the diversity and functional activity of soil microbial communities and their relative contribution to forage productivity.

10.5.2 Objectives

The first objective is to determine the effect of increasing crop diversity on forage productivity and the diversity and functional activity of soil microbial communities. The second is to determine the effect of plant functional groups and functional redundancy on forage productivity and diversity of microbial communities. And, the relative contribution of soil microbial communities to forage yield will be determined.

10.5.3 Project Design and Methods

The field study for the first objective was conducted at Brookdale and Swift Current and involved four treatments : (i) monoculture (oats); (ii) 3-species mixture (oats, forage peas, Graza); (iii) 6-species mixture (oats, forage peas, Italian ryegrass, hairy vetch, Winfred); and (iv) 9-species mixture (oats, forage peas, Italian ryegrass, hairy vetch, Winfred, sorghum, crimson clover, and Hunter). The treatments were replicated four times for a total of 16 plots at each location. The plots at Swift Current were 3.7 x 9.1 m with crop rows spaced 30.5 cm apart, and at Brookdale they were 12.2 x 152.4 m with a 15.2 cm crop row spacing. The Brookdale plots were fenced to allow for a grazing treatment on all plots (split-plots alternating among the blocks) that will be assessed in the second year of the study (2017). Field plots at Brookdale were managed by MBFI staff and by AAFC staff at Swift Current.

Soil samples were collected from each field site three times during the year: (i) April/May, (ii) July, and (iii) August/September. Soil samples were analyzed for soil nutrients at each time point and several microbiological measures (see below for more details). Aboveground biomass samples (up to six 1 m rows per plot) were collected in July and August to assess the forage productivity and nutrition of the mixtures compared to the monoculture. Plant tissue samples were oven dried and weighed for biomass and samples were subsequently ground to a fine powder for nutrition analyses.

The field study for the second objective was conducted at Swift Current and involved 11 treatments that included a fallow treatment, three monocultures (barley, peas, and radish), three two-species mixtures (barley and radish; peas and radish; barley and peas), three four-species mixtures (triticale, corn, peas, and radish; barley, corn, peas, and vetch; barley, oats, vetch, and turnip), and, one eight-species mixture (barley, triticale, oats, corn, peas, vetch, radish, and turnip). The treatments were replicated four times for a total of 48 plots that were 3.7 x 9.1 m. Soil samples were collected in May and July to assess soil nutrition and soil microbial communities (see below for more details). Aboveground biomass samples were collected in July to assess forage productivity (see paragraph above for details).

A similar soil sampling strategy was employed in both field experiments. We collected soil samples to a depth of 15 cm (2.5-cm diameter) from each plot prior to seeding the treatment mixtures in April/May 2016 to obtain a baseline. Soil sampling was also conducted in the growing season to monitor changes in soil properties and assess the diversity and functional activity of soil microbial communities. These included microbial biomass and activity, and composition and abundance of microbial taxa and functional groups. Microbial biomass and activity will be assessed using a combination of phospholipid fatty acid (PFLA) analysis and enzyme assays. Next generation sequencing (Illumina Miseq) will be used to assess the diversity and composition of the microbial communities, and bioinformatics tools will be used to predict functional profiles and relative abundance of key functional genes¹.

10.5.4 Results and Discussion

The first year of the field studies for objectives one and two were successfully completed. All plant tissue samples have been processed (dried, weighed, and ground) and we are waiting to receive the results from the nutrient and nutrition analyses. All soil samples have been initially processed and various

assays (dehydrogenase, acid phosphatase, and alkaline phosphatase) have been conducted. Molecular analyses (FAME and next generation sequencing) are well underway and should be completed in the near future. Soil samples have been submitted for chemical analysis.

Grazing was completed at the Brookdale site in September, and all aboveground biomass has been removed from the plots at both field sites in preparation for the second year of the project. Data is still being compiled and statistically analyzed. Results that were not available for this annual report will be published in the next year's report

During the first field season we observed good growth in the mixtures. Most plant species performed well, while other species underperformed likely due to poor emergence or competitive ability. Weather conditions may have also impacted the performance of the mixtures as we had above average precipitation at the field sites, which impacted site management (e.g. seeding dates and weed control). In late September, grazing took place at the Brookdale site, which will allow us to monitor the effects of grazing the mixtures on soil health and forage productivity during the second year of the project.

10.5.5 Summary

The first year of the field studies revealed the potential forage value of multispecies annual crop mixtures, but further analysis of the soil microbial communities will provide further insight into the effect on soil health. This information will be available at the conclusion of the project.

10.5.6 Acknowledgements

Technical staff and summer students at the Swift Current Research and Development Centre and MBFI staff at Brookdale.

10.5.7 References

Abhauer KP, Wemheuer B, Daniel R, and Meinicke P. Tax4Fun: predicting functional profiles from metagenomics 16S rRNA data. *Bioinformatics*. 2015; 31:2882-2884.



Fig. 10.5.1. Annual polyculture plots at Brookdale Farm, July 2016, photo by J. Van Parys.



Fig. 10.5.2. Nine-species mixture at Brookdale Farm, July 2016; photo by MBFI.



Fig. 10.5.3. Nine-species mixture at Swift Current Research Farm, August 2016; photo by J. Bainard.



Fig. 10.5.4. 6-species mixture at Swift Current Research Farm, August 2016; photo by J. Bainard.



Fig. 10.5.5. Three-species mixture at Swift Current Research Farm (August 2016, J. Bainard)