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The oral examination of the doctoral thesis titled
**Influence of Crop Species and Weed Seedbank
Density on Extracellular DNA Degradation,
Bacterial Community Structure and Functional
Capabilities in Agricultural Soils in Manitoba,
Canada**

will be held on

Tuesday, December 19th, 2023, at 09:30 AM (CST)
134 Agriculture Building

Examining Committee

Advisor: Dr. Robert Gulden, Department of Plant Science

Examiners:

Dr. Martin Entz, Department of Plant Science

Dr. Mario Tenuta, Department of Soil Science

External Examiner:

Dr. Kari Dunfield

School of Environmental Studies

University of Guelph

Chair

Dr. Xiaopeng Gao, Department of Soil Science

Thesis Abstract

GENERAL ABSTRACT

Assessing the influence of crop species and weed seedbank density on the dynamics of extracellular DNA degradation potential, bacterial community structures and functional capabilities from agricultural soils in Manitoba, Canada.

Nucleic acids are abundant in terrestrial ecosystems and are degraded by DNases, mostly from microbial origin. However, the impact of agronomic practices on this soil function and the bacterial community involved has received little attention. An indoor and a long-term field study were used to determine the responsiveness of extracellular DNA (exDNA) degradation, extracellular DNase (exDNase) producing bacteria, bacterial diversity, community composition, and functional capabilities as influenced by crop species and weed seedbank density. A high-throughput DNA methyl green (DNA-MG) spectrophotometric assay was developed and successfully adopted for estimating instantaneous exDNA degradation in soils. The assay demonstrated that crop species, crop developmental stages and soil properties influenced instantaneous exDNA degradation, while weed seedbank density did not have a significant effect on this soil function. Moreover, crop species, crop developmental stages, and soil type influenced the populations of culturable exDNase-producing bacteria. Culturable exDNase-producing bacteria identified were dominated by Bacillota (Firmicutes) and Actinobacteria at the phyla level and the *Bacillus* genera group. The Proteobacteria and Actinobacteria phyla groups dominated the bacterial species in soils from the field study and those positively associated with instantaneous exDNA degradation. The chemical fallow and prairie treatments had distinct bacterial community structures and functional groups. In conclusion, this study provides new insights into the cycle of exDNA degradation by enzymatic restriction in agricultural soils, and how management practices contribute to shaping soil bacterial community and functions.