

# Rhizosphere functional microbiomes drive N availability to wheat

Vadakattu V.S.R. Gupta<sup>1</sup>, Marcus Hicks<sup>1</sup>, Stasia Kroker<sup>1</sup>, Mariano Cossani<sup>2</sup> and Victor Sadras<sup>2</sup>

<sup>1</sup> CSIRO Agriculture and Food, Waite Campus, Urrbrae, Australia SA 5064

<sup>2</sup> SARDI, Waite Campus, Urrbrae, Australia SA 5064

E-mail: [Gupta.Vadakattu@csiro.au](mailto:Gupta.Vadakattu@csiro.au)

## Abstract

Rhizosphere and root associated microorganisms regulate the cycling and availability of key macro (N, P and S) and micronutrients to plants. Capturing N benefits from improved plant-microbe interactions would be a more sustainable option for improved yield, and efficiency in the use of N and water. Successful exploitation of this approach requires selection of germplasm that more readily associate with beneficial microbiomes. We present findings on the abundances of N-cycling functional genes in roots and rhizosphere of agronomically adapted wheat varieties varying in root growth, and N uptake efficiency.

Keywords: Nitrogen, Rhizosphere, functional genes, nitrification, immobilization, microbiome

## 1. Background

In cereal crops, nitrogen (N) inputs account for a large part of production costs, and involve risk of unrealised profit in dry seasons. Selection for yield reduced the size of the root system but increased total N uptake (25% more N from soil) and N uptake per unit root system in Australian wheat varieties released over the last five decades (Aziz et al. 2017); reasons for improved efficiency are unknown. Plant-microbe interactions in the rhizosphere play a key role in the cycling and uptake of soil and fertilizer N (Gupta and Sharma 2021). We investigated differences in the abundance of key microbial functional genes and processes involved in N cycling and availability and relate them to variation in wheat yield and N uptake.

## 2. Materials and Methods

Rhizosphere and root samples for 14 wheat varieties released between 1958 to 2015 were collected 10 wks after sowing from field experiments at Roseworthy (Org C 2.05%, pH 8.2) and Riverton (Org C 2.15; pH 5.35) in South Australia during 2018 and 2019. All samples were analysed for microbial activity, microbial catabolic diversity and abundances of key N cycling functional genes (quantitative

PCR based). Crop yield and N uptake were measured at harvest.

## 3. Results and Discussion

Rhizosphere soils in both sites indicated differences ( $P < 0.05$ ) both in the total microbial activity and microbial catabolic diversity, suggesting that belowground C inputs (quantity and quality) varied with variety.

Variety	Ammonifying bacteria (npr)	NS-N <sub>2</sub> fixing bacteria (nifH)	Bacterial nitrifiers (AOB)	Archaeal nitrifiers (AOA)	Total Nitrifiers	Urease
Condor	■	■	■	■	■	■
Frame	■	■	■	■	■	■
Gamenya	■	■	■	■	■	■
Gladius	■	■	■	■	■	■
Halberd	■	■	■	■	■	■
Heron	■	■	■	■	■	■
Janz	■	■	■	■	■	■
Krichauff	■	■	■	■	■	■
Machete	■	■	■	■	■	■
Scepter	■	■	■	■	■	■
Spear	■	■	■	■	■	■
Warigal	■	■	■	■	■	■
Wyalkatchem	■	■	■	■	■	■
Yitpi	■	■	■	■	■	■
F-test	0.001	0.002	0.001	0.030	0.001	0.023
LSD (P<0.05)	■	■	■	■	■	■

Fig. 1: Abundance of microbial functional genes (copy number/gram soil) that regulate N cycling processes in the rhizosphere of wheat varieties, Roseworthy 2018.

In general, there was a significant varietal based variation in the rhizosphere abundance of various microbial groups involved in the different N cycling processes [mineralization of organic N (*npr*, *apr*), conversion of urea N into ammonia N (*ureC*), nitrification (B-*amoA*, A-*amoA*) and non-symbiotic N<sub>2</sub>-fixation (*nifH*)] (Figure 1). However, the magnitude of the variation between varieties was soil dependant.

Significant variation between varieties in microbial functional traits (genes) involved in N availability raises the potential for breeding this trait into modern, elite cultivars of wheat.

### **Acknowledgements**

SAGIT and CSIRO provided Financial support.

### **References**

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