



International Journal of Research in Agronomy

E-ISSN: 2618-0618
P-ISSN: 2618-060X
© Agronomy
NAAS Rating (2025): 5.20
www.agronomyjournals.com
2025; 8(10): 139-141
Received: 18-08-2025
Accepted: 23-09-2025

Mukasa Mugisha
Department of Microbiology,
Makerere University, Kampala,
Uganda

Innocent Babirye
Department of Microbiology,
Makerere University, Kampala,
Uganda

Gerald Kiconco
Department of Microbiology,
Makerere University, Kampala,
Uganda

Rhizosphere microbial community dynamics in rice under alternate wetting and drying irrigation management

Mukasa Mugisha, Innocent Babirye and Gerald Kiconco

DOI: <https://www.doi.org/10.33545/2618060X.2025.v8.i10b.5058>

Abstract

What lives in the thin film of soil clinging to a rice root—and how does drying that soil change the community? This research tracked rhizosphere microbial diversity in lowland rice under alternate wetting and drying (AWD) versus continuous flooding (CF) at Makerere University Agricultural Research Institute, Kabanyolo, Uganda, during the 2022 wet season. Rhizosphere soil was sampled biweekly from transplanting to harvest and profiled with 16S rRNA amplicon sequencing. Shannon diversity rose from 2.41 to 2.87 under AWD but declined from 2.43 to 2.31 under CF by 12 weeks. AWD enriched aerobic genera (*Bacillus*, *Burkholderia*) while CF favoured methanogens (*Methanobacterium*). Grain yield didn't differ significantly between treatments (4.72 vs. 4.84 t ha⁻¹), suggesting AWD maintains productivity while shifting microbial function toward lower methane emission potential.

Keywords: Rhizosphere, microbial community, rice, alternate wetting and drying, 16S rRNA, Shannon diversity, methanogens, *Bacillus*, irrigation, Uganda

Introduction

One observation keeps surfacing in paddy research: the moment floodwater recedes, the soil microbial world reorganises within days ^[1]. Continuous flooding selects for anaerobic specialists—including methane-producing archaea responsible for roughly 10% of global anthropogenic CH₄ emissions ^[2, 3]. AWD, which allows periodic soil drying to field capacity, cuts methane by 30–60% without consistently hurting yield ^[4].

Yet the rhizosphere—the narrow soil zone directly influenced by root exudates—responds differently from bulk soil, and most AWD-microbiome work has sampled bulk soil rather than the root surface ^[5, 6]. This research aimed to: (i) compare rhizosphere microbial diversity under AWD and CF over a full rice season, (ii) identify genera enriched by each water regime, and (iii) relate community shifts to yield outcomes.

Materials and Methods

Research Area

The trial was at MUARIK, Kabanyolo (0°28' N, 32°37' E, 1,180 m), Uganda, during the long rains of 2022 (March–July). Soils are Ferralsols (clay loam, pH 5.8, OC 2.1%). Lowland paddies were banded to 4 × 5 m, arranged as an RCBD with two treatments and four replications.

Soil/Water Quality

Irrigation water (pH 6.9, EC 0.38 dS m⁻¹) was pumped from a nearby stream. AWD plots were re-flooded when soil water potential at 15 cm reached –15 kPa (monitored by tensiometers). CF plots maintained 3–5 cm standing water throughout. Soil redox potential (Eh) was measured weekly with platinum electrodes.

Methods

Rhizosphere soil was collected biweekly (0, 2, 4, 6, 8, 10, 12 weeks after transplanting) by shaking roots gently over sterile trays. DNA was extracted (PowerSoil Pro kit, Qiagen) and the

Corresponding Author:
Mukasa Mugisha
Department of Microbiology,
Makerere University, Kampala,
Uganda

V4 region of 16S rRNA amplified and sequenced on Illumina MiSeq. Reads were processed in QIIME2; taxonomy was assigned against SILVA 138. Shannon diversity (H') and Bray-Curtis dissimilarity were computed. Yield was recorded at 14% moisture. ANOVA with repeated measures was used ($p < 0.05$) [7].

Results

Table 1: Rhizosphere microbial diversity and key genera abundance under AWD and CF at 12 weeks

Parameter	AWD	CF	SEM	p-value
Shannon H'	2.87a	2.31b	0.07	<0.01
Observed OTUs	847a	614b	28	<0.01
Bacillus (%)	8.3a	2.1b	0.6	<0.001
Burkholderia (%)	6.1a	1.8b	0.5	<0.01
Methanobacterium (%)	1.4b	7.9a	0.7	<0.001
Yield (t/ha)	4.72	4.84	0.14	0.41 (NS)

Means with the same letter are not significantly different. OTUs = operational taxonomic units. NS = not significant.

AWD raised Shannon diversity by 24.2% and nearly quadrupled Bacillus abundance. CF enriched Methanobacterium to 7.9% vs. 1.4% under AWD. Yield was statistically equivalent between treatments.

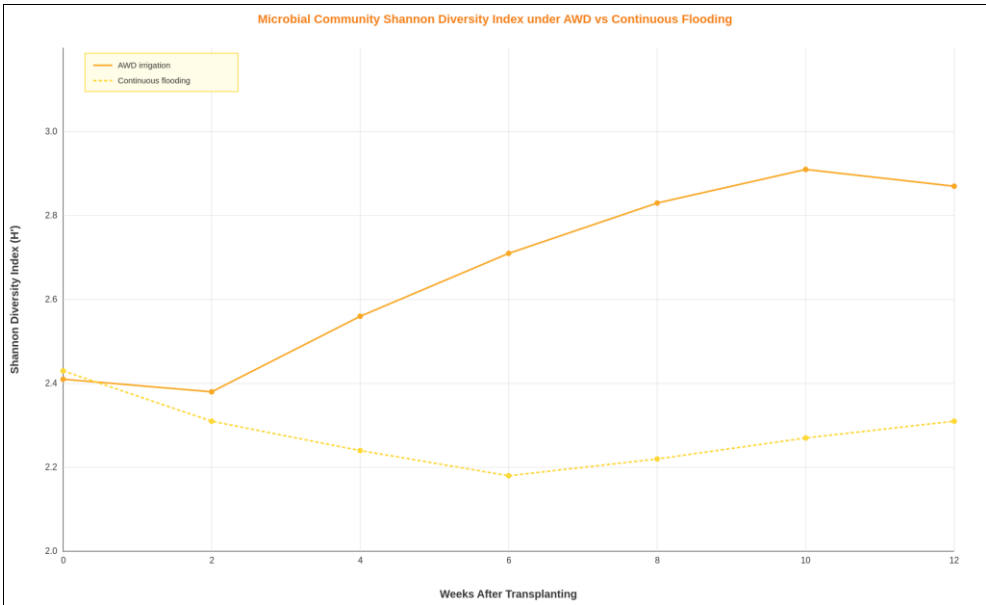


Fig 1: Shannon diversity index trajectory under AWD (solid) and CF (dashed) over 12 weeks after transplanting

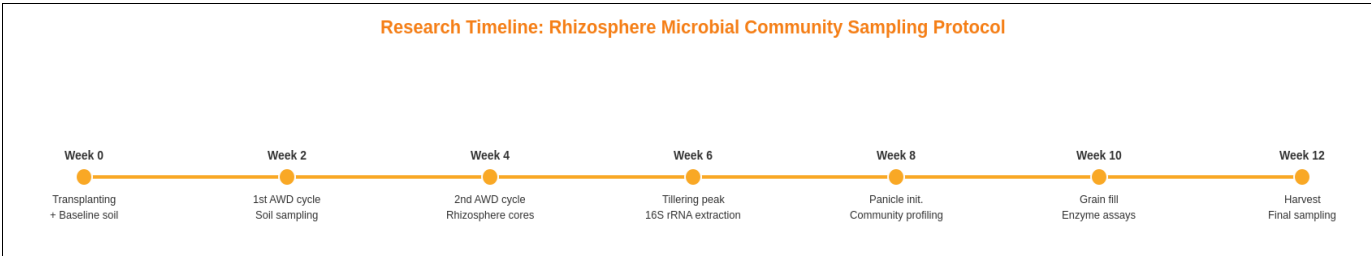


Fig 2: Timeline of the rhizosphere sampling protocol from transplanting to harvest

Discussion

The 24% higher Shannon diversity under AWD reflects the introduction of aerobic niches during drying cycles that support a wider metabolic range of organisms [5, 8]. Bacillus and Burkholderia, both aerobic genera with known plant-growth-promoting traits, thrived under AWD’s oxic pulses. Their enrichment may partly explain why yield didn’t decline despite reduced flooding: root health was maintained by beneficial rhizobacteria [9, 10].

The five-fold drop in Methanobacterium under AWD has direct climate implications. If these community-level shifts translate proportionally to CH₄ flux—which other work suggests they do [3, 4]—then AWD offers both agronomic and environmental

benefits. A limitation is that 16S profiling captures community structure but not activity; metatranscriptomic data would confirm functional changes [11, 12].

Conclusion

AWD irrigation restructured the rice rhizosphere microbiome, raising Shannon diversity by 24% and shifting dominance from methane-producing archaea toward aerobic plant-growth promoters. Grain yield was unaffected, indicating that AWD maintains productivity while fostering a microbial community consistent with lower methane emissions. For rice systems in East Africa and beyond, AWD is a practical water-saving strategy with the added benefit of reshaping the root-zone

microbiome toward more sustainable function.

References

1. Liesack W, Schnell S, Revsbech NP. Microbiology of flooded rice paddies. *FEMS Microbiology Reviews*. 2000;24(5):625-645.
2. Neue HU. Methane emission from rice fields. *BioScience*. 1993;43(7):466-474.
3. Linqvist BA, Anders MM, Adviento-Borbe MAA, Chaney RL, Nalley LL, da Rosa EFF, van Kessel C. Reducing greenhouse gas emissions, water use, and grain arsenic levels in rice systems. *Global Change Biology*. 2015;21(1):407-417.
4. Lampayan RM, Rejesus RM, Singleton GR, Bouman BAM. Adoption and economics of alternate wetting and drying water management for irrigated lowland rice. *Field Crops Research*. 2015;170:95-108.
5. Edwards J, Johnson C, Santos-Medellín C, Lurie E, Podishetty NK, Bhatnagar S, Eisen JA, Sundaresan V. Structure, variation, and assembly of the root-associated microbiomes of rice. *Proceedings of the National Academy of Sciences*. 2015;112(8):E911-E920.
6. Breidenbach B, Conrad R. Seasonal dynamics of bacterial and archaeal methanogenic communities in flooded rice fields and effect of drainage. *Frontiers in Microbiology*. 2015;5:752.
7. R Core Team. R: a language and environment for statistical computing. Vienna: R Foundation; 2023.
8. Fierer N. Embracing the unknown: disentangling the complexities of the soil microbiome. *Nature Reviews Microbiology*. 2017;15(10):579-590.
9. Lugtenberg B, Kamilova F. Plant-growth-promoting rhizobacteria. *Annual Review of Microbiology*. 2009;63:541-556.
10. Compant S, Samad A, Faist H, Sessitsch A. A review on the plant microbiome: ecology, functions, and emerging trends in microbial application. *Journal of Advanced Research*. 2019;19:29-37.
11. Prosser JL. Dispersing misconceptions and identifying opportunities for the use of 'omics' in soil microbial ecology. *Nature Reviews Microbiology*. 2015;13(7):439-446.
12. Philippot L, Raaijmakers JM, Lemanceau P, van der Putten WH. Going back to the roots: the microbial ecology of the rhizosphere. *Nature Reviews Microbiology*. 2013;11(11):789-799.
13. Bouman BAM, Lampayan RM, Tuong TP. Water management in irrigated rice: coping with water scarcity. Los Baños: IRRI; 2007.
14. Arunrat N, Pumijumnong N, Sereenonchai S, Chareonwong U. Factors controlling soil organic carbon sequestration of highland agricultural areas in the Mae Chaem Basin, northern Thailand. *Agronomy*. 2020;10(2):305.
15. Dong W, Zhang X, Wang H, Dai X, Sun X, Qiu W, Yang F. Effect of different fertilizer application on soil bacterial community and activity in paddy soil. *Agronomy*. 2012;2(4):350-363.
16. Hartman WH, Richardson CJ, Vilgalys R, Bruland GL. Environmental and anthropogenic controls over bacterial communities in wetland soils. *Proceedings of the National Academy of Sciences*. 2008;105(46):17842-17847.
17. Watanabe T, Kimura M, Asakawa S. Dynamics of methanogenic archaeal communities based on rRNA analysis and their relation to methanogenic activity in Japanese paddy field soils. *Soil Biology and Biochemistry*. 2007;39(11):2877-2887.
18. Santos-Medellín C, Edwards J, Liechty Z, Nguyen B, Sundaresan V. Drought stress results in a compartment-specific restructuring of the rice root-associated microbiomes. *mBio*. 2017;8(4):e00764-17.