

Influence of organic fertilization and cultural association practices on bacteria PGPR in a tomato field in Saguia (Niger): Density, morphological and biochemical traits

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Abstract

This study evaluates the impact of cultural practices and cultural associations on the density, morphological and biochemical characteristics of bacteria PGPR in a tomato experimental field in Saguia, Niamey region of Niger. After the experiments, morphological and biochemical analyses (Gram, API 20E) were carried out. The results show that the microbial density varies significantly with the type and dose of fertilizer, with maximum values observed below the recommended dose in ASD medium and under the poultry dropper in PDA medium. The bacterial genera PGPR identified are *Bacillus spp.*, *Serratia rubidaea*, *Burkholderia cepacia* and *Stenotrophomonas maltophilia*, as well as fungi such as *Candida non albicans* and *Aspergillus fumigatus*. Crop associations also influence microbial diversity, although less markedly than organic amendments. The study concludes that organic fertilizers, particularly at optimized doses, promote soil biological fertility by stimulating the density and diversity of beneficial microorganisms. These results support the adoption of sustainable agroecological practices to improve market productivity in Sahelian areas.

Keywords: PGPR; Organic Fertilization; Crop Association; Biological Fertility; Tomato

1. Introduction

In a context of climate change and the quest for sustainable agriculture in the Sahel, cultivation practices play a key role in soil health and crop productivity (Blanchard *et al.*, 2014). Soil fertility is based on three pillars: chemical, physical, and biological. Although important, soil fertility remains under-studied (Gobat *et al.* 2003). Agricultural productivity, particularly that of tomato, a strategic but demanding crop, is highly dependent on symbiotic microorganisms in the rhizosphere, such as plant growth promoters (PGPR) and arbuscular mycorrhizal fungi (Adjanohoun, 2017). These microorganisms improve mineral nutrition, stimulate plant growth, and enhance resilience to biotic and abiotic stress (Meddich *et al.*, 2017; Santoyo *et al.*, 2021), while contributing to organic matter degradation and nutrient availability (Yin *et al.*, 2012). If the use of organic amendments (cow dung, goat dung, poultry dung) and crop associations are recognized to improve soil quality and productivity (Boureima *et al.*, 2019; Dan Lamso & Guero, 2006), their specific effects on the density, diversity and morphological and biochemical characteristics of PGPR remain poorly documented, particularly in Niger's market gardening systems. This study, conducted in the Saguia area of Niamey, aims to assess how these practices influence the composition and abundance of bacteria PGPR in the tomato rhizosphere. By combining organic fertilization at different doses and rotational modalities, and then characterizing microorganisms via cultural methods (TSA/PDA), Gram staining and biochemical identification (API 20E), this research aims to identify the technical routes most favourable to biological fertility. Its results will provide a concrete scientific basis to guide

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producers towards sustainable agroecological practices, reducing dependence on mineral inputs while maintaining productivity in a constrained environment.

2. Presentation of the study area

The Niamey region is situated in the southwestern part of Niger, with geographical coordinates $13^{\circ} 24'$ "North" and $2^{\circ} 15'$ "East. Its altitude varies between 160 m and 250 m and its administrative area extends over 552.27 km², of which approximately 297.46 km² are urbanized (INS, 2016). The Saguia study area is located in the Niger River Valley, in District V of Niamey. The area has three distinct soil types: sandy-textured soils, including tropical ferruginous soils in the sandy valleys, used primarily during the rainy season. Hydromorphic soils located in the Niger River Valley, reserved for off-season crops. The soils of the carpeted trays, very degraded and not suitable for agriculture because of their depth, permeability and extreme aridity. The climate of the region is Sahelian, with a negative gradient of precipitation from south to north. Rainfall extends from late May to late September, marked by a southwestern flux associated with the monsoon. The ambient humidity is high, making the growing conditions often heavy. Average annual cumulative rainfall ranges from 200 to 500 mm from North to South (INS 2016; Ozer *et al.*, 2017). Temperatures remain high even during the dry season, ranging from an average of 18 °C (December-January) to 45 °C (March-April) throughout the year. The climate is divided into three distinct seasons: a dry and cold season from November to February, a dry and warm season from March to June, and a rainy season from July to October, characterized by alternating hot and cool periods (CRA, 2017; Ozer *et al.*, 2017).

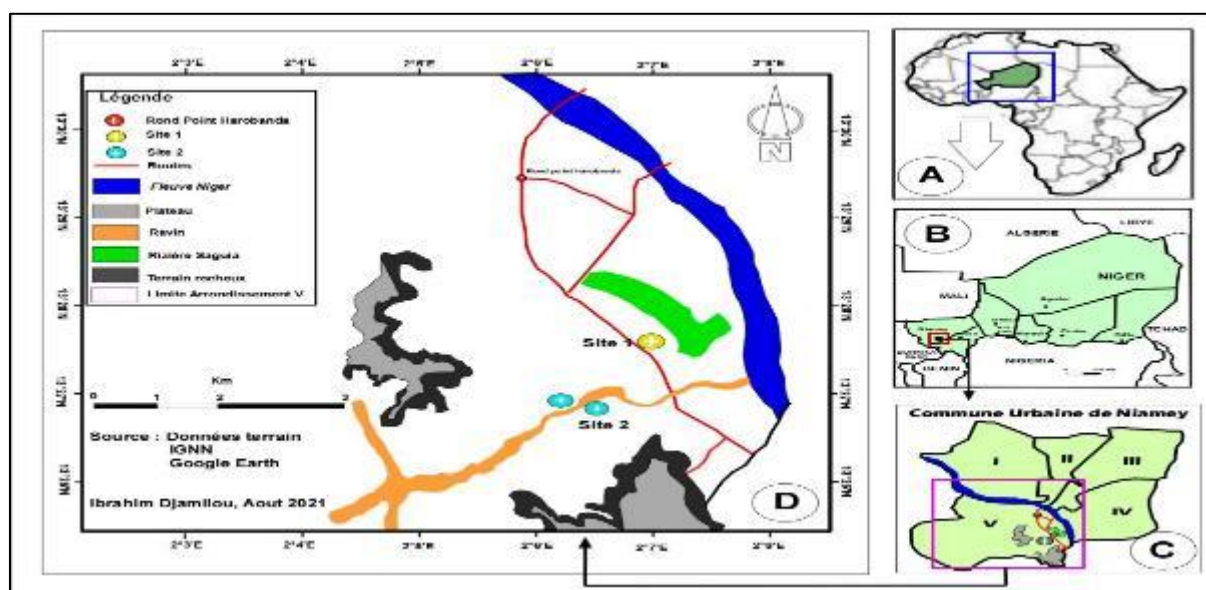


Figure 1 Map of the Saguia study area (Jamilou S.I., 2025)

3. Equipment and methods

The study was conducted in the Saguia area of the Niger River Valley in Niamey, Niger, characterized by Sahelian climate and off-season hydromorphic soils. An experimental device combining different methods of organic fertilization (cow's dung, goat's dung, poultry fiente) applied at three increasing doses, as well as cultivation systems (tomato monoculture and combinations with pepper, cabbage, maize, melon or carrot), has been put in place. The amendments were incorporated into the ground in background manure and micro-maintenance doses, in accordance with local agronomic recommendations. Rhizospheric soil samples were collected from each plot and analyzed in the laboratory to assess the density, diversity, and characteristics of microorganisms. The density of the rhizobacteria was determined by the decimal dilutions method (Speck, 1976) on TSA and PDA media, followed by the counting of the colony-forming units (CFU). Phenotypic identification focused on colony morphology (shape, size, color, surface), mobility, and Gram staining. The data obtained were subjected to statistical analyses (ANOVA, Kruskal-Wallis, ACP) using software R (version 4.0.2), in order to evaluate the significant effects of the treatments on the microbiological parameters studied.

4. Results

4.1. Morphological characteristics of rhizobacteria by culture medium

Table 1 presents morphological characteristics of germinated rhizobacteria in both culture media (ASD; PDA).

Table 1 Morphological characteristics of rhizobacteria

Growing environments	Size	Mobility	Color	Gram	Shape	Surface	Pigmentation
ASD	small	mobile/immobile	red, white, yellow, pink	G +/G-	round/oval/bacillary	smooth, rough,	pigmented/not pigmented
PDA	large	mobile/immobile	red, yellow, pink	G +/G-	round/oval/bacillary	smooth, rough,	pigmented/not pigmented

Morphological analysis of the rhizobacteria (Table 3) isolated from the tomato rhizosphere reveals significant diversity as a function of the culture medium used (ASD or PDA). In ASD, bacterial colonies are predominantly small in size, while those grown on PDA are generally larger in size. In both media, the bacteria observed show variable mobility (mobile or immobile) and adopt multiple forms: round, oval or bacillary. Their surface is either smooth, rough or curved, and their pigmentation is heterogeneous, ranging from white to red, through yellow and pink; some colonies are pigmented, others are not.

Gram staining confirmed the coexistence of Gram-positive (G⁺) and Gram-negative (G⁻) bacteria in both media, indicating high phenotypic diversity within the rhizospheric microflora. These results suggest that the differentiated nutrient and physico-chemical conditions offered by the ASD (less glucosed) and PDA (more sugars) media influence not only the abundance, but also the expression of the morphological traits of rhizobacteria. This phenotypic diversity is a preliminary indicator of a potential functional richness of the microbial community, justifying finer biochemical and molecular analyses to establish the taxonomic profiles and specific ecological functions of these microorganisms in the soil-tomato system.

4.2. Density of rhizobacteria according to the type of organic manure

Table 2 shows the density of the rhizobacteria (Nrhzio/1g of the soil) and their number of colonies in Gram + and Gram – as a function of the treatments applied.

Table 2 Density of rhizobacteria as a function of type of organic manure

	Densité_B ASD	Colo_G+	Colo_G-	Colo_TB	Densité_B PDA	Colo_G+	Colo_G-	Colo_TB
DR1	16000000	3	4	7	15000000	10	1	11
BV1	8000000	5	5	10	100000	6	2	8
BC1	19200000	6	2	8	1700000	6	2	8
FV1	4100000	6	4	10	950000	10	0	10
DR2	17000000	15	7	22	3100000	10	8	18
BV2	7500000	0	11	11	630000	5	0	9
BC2	5700000	6	5	11	720000	5	4	9
FV2	13300000	0	6	6	2500000	5	2	7
DR3	21300000	5	3	8	3400000	5	0	5

BV3	1210000	6	0	6	410000	5	2	7
BC3	11000000	5	0	5	800000	6	3	9
FV3	9000000	6	3	9	900000	5	0	5
P-value	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001	<0,001
DR	11000000	4	5	9	4600000	9	11	19
BV	5570000	5	5	10	380000	8	5	14
BC	10450000	2	2	4	1450000	10	7	17
FV	8800000	4	4	8	1073333	7	7	14
P-v	0,629	0,582	0,582	0,937	0,231	0,842	0,308	0,306
D1	8511111	3	3	6	3653333	9	11	19
D2	10875000	7	7	14	1737500	11	6	16
D3	10627500	2	2	4	1377500	5	5	10
P-v	0,778	0,000	0,000	0,015	0,515	0,160	0,034	0,08

Caption: Line: Processing; DR: Recommended dose; BV: Cow's bouse; BC: Goat dung; FV: Poultry fiente; D: Dose

Analysis of the density of cultivatable rhizobacteria (expressed as $\text{UFC}\cdot\text{g}^{-1}$ of soil) revealed significant variations according to the type and dose of organic manure applied, as well as according to the culture medium used (TSA or PDA). In ASD, the highest bacterial density ($2.13 \times 10^7 \text{ UFC}\cdot\text{g}^{-1}$) is observed at recommended dose 3 (DR3), while the lowest value ($7.5 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) is recorded with cow dung at dose 2 (BV2). A similar trend can be seen in the averages by type of fertilizer: the recommended dose (DR) induces the highest microbial abundance ($1.10 \times 10^7 \text{ UFC}\cdot\text{g}^{-1}$), followed by goat dung (CB) ($1.05 \times 10^7 \text{ UFC}\cdot\text{g}^{-1}$), poultry droppings (FV) ($8.80 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) and finally cow dung (BV) ($5.57 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$).

In the PDA medium, which is richer in carbohydrates, the recommended dose 1 (DR1) has the maximum density ($1.50 \times 10^7 \text{ UFC}\cdot\text{g}^{-1}$), while the cow dung at dose 1 (BV1) has the minimum value ($1.0 \times 10^5 \text{ UFC}\cdot\text{g}^{-1}$). At the fertilizer level, the recommended dose remains predominant ($4.60 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$), followed by goat dung ($1.45 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$), poultry droppings ($1.07 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) and cow dung ($3.80 \times 10^5 \text{ UFC}\cdot\text{g}^{-1}$).

Statistical analysis ($p < 0.001$ for all variables) confirms that these differences are highly significant, both between individual treatments and depending on the type of manure. Furthermore, the total number of colonies (Colo_TB) was the highest under DR2 (22 colonies in TSA and 18 in PDA), highlighting the stimulating effect of this combination on cultivable diversity. Finally, Gram-positive (G^+) bacteria dominate overall isolated populations, with the notable exception of treatment FV2, where no colony G^+ was detected.

4.3. Rhizobacterial density as a function of culture association

The density and number of colonies of rhizobacteria are given in the following table:

Analysis of the density of the rhizobacteria (expressed in $\text{UFC}\cdot\text{g}^{-1}$ of soil) revealed significant variations depending on the type of crop association used with the tomato. In ASD, the combination of tomato + pepper (APV) had the highest bacterial density ($1.10 \times 10^7 \text{ UFC}\cdot\text{g}^{-1}$), followed by tomato + cabbage (ACh) ($9.0 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) and tomato + maize (AMa) ($6.0 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$). In contrast, tomato + melon (AMe) ($1.3 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) and tomato + carrot (ACr) ($2.0 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$) had the lowest densities. These differences are highly significant ($p < 0.001$), indicating a marked effect of the plant partner on rhizospheric microflora stimulation.

In the PDA medium, the trend was partially reversed: the combination of tomato + melon showed maximum density ($6.0 \times 10^6 \text{ UFC}\cdot\text{g}^{-1}$), followed by tomato + pepper ($4.3 \times 10^5 \text{ UFC}\cdot\text{g}^{-1}$) and tomato + cabbage ($4.0 \times 10^5 \text{ UFC}\cdot\text{g}^{-1}$), while tomato + carrot remained the least favourable ($2.0 \times 10^5 \text{ UFC}\cdot\text{g}^{-1}$). This discrepancy between the two media suggests that the nutritional requirements and root exudates of each combination differentially influence the composition and abundance of culturable microbial communities.

In addition, the total number of colonies (Colo_TB) varied moderately between associations, ranging from 6 to 12 colonies depending on the medium. Gram-positive (G⁺) bacteria consistently dominate isolated populations, regardless of the combination tested - a trend consistent with that observed under the various organic amendments.

Table 3 Average density and colonies of rhizobacteria as a function of crop associations (Nrizzo/1g soil)

Treatment	D_B ASD	Colo_G+	Colo_G-		D_B PDA	Colo_G+	Colo_G-	
DR1	16000000	3	4	7	15000000	10	1	11
APv	11000000	5	4	9	4300000	6	2	8
ACh	9000000	6	3	9	4000000	6	0	6
AMa	6000000	7	3	10	630000	6	3	9
AMe	1300000	3	5	8	6000000	8	4	12
ACr	2000000	2	5	7	200000	6	0	6
P-value	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001
Mb	5860000	4	5	9	2517500	9	8	17
Asso	11200000	4	4	8	3026000	8	11	19
P-v	0.111	0.908	0.908	0.957	0.801	0.79	0.312	0.913
APM	5500000	8	4	12	11833333	4	10	14
APNM	6100000	9	4	13	8000000	11	11	22
P-v	0.292	0.926	0.994	0.833	0.559	0.181	0.573	0.10

Legend: D: Density; DR1: Recommended dose1; AMa: Tomato + But association; PVA: Tomato + Pepper Association; ACh: Tomato + cabbage association; ACr: Tomato + Carrot Association; Soul: Tomato + Melon Association; Mo: Monoculture; Asso: Association; MPA: Association with mycorrhizal plant; APNM: Association with non-mycorrhizal plant

4.4. Biochemical analyses of soil rhizobacteria by treatment

Table 4 Inventories of genera and species of rhizobacteroids and fungi by treatment

Name of Treatments	Culture medium 1 (Rhizobacteria)		Culture medium 2 (fungi)	
	Genus	Species	Genus	Species
DR1	<i>Serratia</i> , <i>Bacillus</i> , <i>Micrococcus</i>	<i>Serratia rubidaea</i> ; <i>Bacillus spp</i> , <i>Micrococcus spp</i>	<i>Candida</i>	<i>Candida albicans</i> non
BV1	<i>Micrococcus</i> , <i>Bacillus</i> , <i>klabsiette</i>	<i>Micrococcus spp</i> , <i>Bacillus spp</i> , <i>klabsiette oxytoca</i>	<i>Candida</i>	<i>Candida albicans</i> non
BC1	<i>Micrococcus</i> , <i>klabsiette</i>	<i>Micrococcus spp</i> , <i>klabsiette oxytoca</i>	<i>Candida</i>	<i>Candida albicans</i> non
FV1	<i>Serratia</i> , <i>Bacillus</i> , <i>Micrococcus</i>	<i>Serratia rubidaea</i> ; <i>Bacillus spp</i> , <i>Micrococcus spp</i>	-	-
DR2	<i>Bacillus</i> , <i>Micrococcus</i> , <i>Stenotrophomonas</i>	<i>Bacillus spp</i> , <i>Micrococcus spp</i> , <i>Stenotrophomonas maltophilia</i>	<i>Candida</i>	<i>Candida albicans</i> non
BV2	<i>Bacillus</i> , <i>Micrococcus</i> , <i>Burkholderia</i>	<i>Bacillus spp</i> , <i>Micrococcus spp</i> , <i>Burkholderia cepacia</i>	-	-
BC2	<i>Micrococcus</i> , <i>Bacillus</i> , <i>klabsiette</i>	<i>Micrococcus spp</i> , <i>Bacillus spp</i> , <i>klabsiette oxytoca</i>	-	-
FV2	<i>Micrococcus</i> , <i>klabsiette</i> , <i>Acintobacter</i>	<i>Micrococcus spp</i> , <i>klabsiette oxytoca</i> ,	<i>Candida</i>	<i>Candida albicans</i> non

		<i>Acimtotecter baumanu</i>		
DR3	<i>Micrococcus, klabsiette, Acimtotecter</i>	<i>Micrococcus spp, klabsiette oxytoca, Acimtotecter baumanu</i>	<i>Aspergillus, Mucor</i>	<i>Aspergillus fumigatus, Mucor spp</i>
BV3	<i>Bacillus, Micrococcus,</i>	<i>Bacillus spp, Micrococcus spp,</i>	<i>Candida</i>	<i>Candida non albicans</i>
BC3	<i>Micrococcus, Bacillus, klabsiette</i>	<i>Micrococcus spp, Bacillus spp, klabsiette oxytoca</i>	-	-
FV3	<i>Micrococcus, Bacillus, klabsiette</i>	<i>Micrococcus spp, Bacillus spp, klabsiette oxytoca</i>	<i>Candida</i>	<i>Candida non albicans</i>

Caption: Line: Processing; DR: Recommended dose; BV: Cow's bouse; BC: Goat dung; FV: Poultry fiente; D: Dose

These species are known for their ability to solubilize phosphates, fix nitrogen, produce phytohormones, or inhibit soil pathogens, positioning them as potential allies of plant growth in the Sahelian context.

At the same time, analysis of fungi culturable on PDA media revealed the presence of three fungal genera: *Candida non albicans*, *Aspergillus fumigatus*, and *Mucor spp*. Notably, *Candida non albicans* was detected in the majority of treatments, while *Aspergillus fumigatus* and *Mucor spp*. appear only under specific treatment conditions DR3 (recommended dose 3), suggesting sensitivity of these fungi to the intensity or nature of the organic amendments.

The microbial composition varies according to the type of manure: treatments based on goat dung and recommended dose tend to promote a greater diversity of bacterial strains PGPR, including *Bacillus* and *Serratia*, while poultry droppings (especially at the level of FV2 and FV3) is associated with the presence of *Acinetobacter baumannii*, a species less commonly reported in agricultural soils but possibly adapted to conditions of high organic mineralization.

4.5. Biochemical analysis of rhizobacteria and microscopic fungi based on culture association

This section therefore presents the results of the biochemical identification of rhizobacteria and microscopic fungi identified in the tomato rhizosphere in association with different vegetable species, with a view to identifying the most favourable configurations for the functional diversity of the soil microbiota.

Table 5 1Inventories of genera and species of rhizobacteroids and fungi by crop association

Types of association	Culture medium 1 (Rhizobacteria)		Culture medium 2 (fungi)	
Name of	Genus	Species	Genus	Species
APv	<i>Bacillus, Micrococcus, Burkholderia</i>	<i>Bacillus spp, Micrococcus spp, Burkholderia cepacia</i>	<i>Candida</i>	<i>Candida non albicans</i>
ACh	<i>Bacillus, Micrococcus, Stenotrophomonas</i>	<i>Bacillus spp, Micrococcus spp, Stenotrophomonas maltophilia</i>	<i>Candida</i>	<i>Candida non albicans</i>
AMa	<i>Micrococcus, Bacillus, klabsiette</i>	<i>Micrococcus spp, Bacillus spp, klabsiette oxytoca</i>	<i>Candida</i>	<i>Candida non albicans</i>
AMe	<i>Serratia, Bacillus, Micrococcus</i>	<i>Serratia rubidaea; Bacillus spp, Micrococcus spp</i>	<i>Candida</i>	<i>Candida non albicans</i>
ACr	<i>Bacillus, Micrococcus, Burkholderia</i>	<i>Bacillus spp, Micrococcus spp, Burkholderia cepacia</i>	<i>Aspergillus, Mucor</i>	<i>Aspergillus fumigatus, Mucor spp</i>

Caption: DR1: Recommended dose 1; AMa: Tomato + But association; PVA: Tomato + Pepper Association; ACh: Tomato + cabbage association; ACr: Tomato + Carrot Association; Soul: Tomato + Melon Association; Mo: Monoculture; As: Association; MPA: Association with mycorrhizal plant; APNM: Association with non-mycorrhizal plant; 1 ; Dose 1

In the system for growing tomatoes in combination, seven (7) genera are also observed, including five (5) species identified as rhizobacteria PGPR: *Micrococcus spp*, *Bacillus spp*, *Kluyvera ascorbata*, *Agrobacterium baumannii*,

Burkholderia cepacia, *Stenotrophomonas maltophilia* and *Serratia rubid.* Similarly, three genera, including two (2) species of microscopic fungi, were identified, namely *Candida non albicans*, *Aspergillus fumigatus* and *Mucor spp.* This diversity of microorganisms shows the effectiveness of tomato growing systems in combination in restoring soil biological fertility.

Biochemical analysis of the microorganisms isolated in the different tomato culture associations identified a diverse microbial community, composed of both bacteria PGPR and microscopic fungi. Seven bacterial genera were identified, corresponding to five species characterized as plant growth promoters: *Bacillus spp.*, *Micrococcus spp.*, *Serratia rubidaea*, *Kluyvera oxytoca* (formerly noted *Klabsiella*), *Burkholderia cepacia* and *Stenotrophomonas maltophilia*. These taxa are distributed in a variable manner according to the type of association:

- The combination of tomato + pepper (PVA) revealed the presence of *Bacillus spp.*, *Micrococcus spp.* and *Burkholderia cepacia*.
- The combination of tomato + cabbage (ACh) favoured *Stenotrophomonas maltophilia* in addition to the genera *Bacillus* and *Micrococcus*.
- The combination of tomato + maize (AMa) and tomato + melon (AMe) allowed the isolation of *Kluyvera oxytoca* and *Serratia rubidaea*, respectively.

Finally, the combination of tomato + carrot (ACr) was the only one to contain both *Burkholderia cepacia* and the two fungal genera *Aspergillus fumigatus* and *Mucor spp.*

For fungi, *Candida non albicans* was systematically detected in all combinations except monoculture (DR1) where it is also present, confirming its predominance in the rhizosphere studied. In contrast, *Aspergillus fumigatus* and *Mucor spp.* appear only in the tomato + carrot combination, suggesting a specific interaction between root exudates of these two species and fungal colonization.

5. Discussion

The results of this study are part of a global scientific consensus confirming that agroecological practices stimulate soil biological fertility by modulating the density and diversity of rhizospheric microorganisms. In Niger, our observations are similar to those of Maidoukia (2020) and Ibrahima (2022), which showed that organic amendments promote the proliferation of bacteria PGPR in millet and niébe cultures in Niamey. In West Africa, work in Burkina Faso and Senegal (Boureima et al., 2019; Zézé et al., 2007) also highlight the role of organic manure in soil microbiota enrichment. At the African level, studies in Kenya and Ethiopia (Giller et al., 2021) confirm the beneficial effects of cultural associations on the functional diversity of microorganisms. In Asia, including India and Bangladesh, the use of compost stimulates the presence of *Bacillus* and *Pseudomonas* (Santoyo et al., 2021), while in Europe, tests in France and Spain show that organic inputs enhance microbial resilience (Blanchard et al., 2014; Meddich et al., 2017). In the United States and Latin America, PGPR-fungi consortia are integrated into sustainable agricultural systems to improve yield and stress resistance (Glick, 2020). Globally, FAO (2021) now recognizes soil microorganisms as pillars of the agroecological transition. Thus, our results confirm that, in the Sahelian context, optimizing organic manure and crop associations is a local strategy aligned with sustainable solutions promoted around the world to reduce dependence on chemical inputs while supporting agricultural productivity.

6. Conclusion

This study demonstrates that cultivation practices, in particular organic fertilization (including goat dung and recommended doses) and certain crop associations (such as tomato + pepper or tomato + melon), significantly influence the density, diversity, morphological and biochemical characteristics of bacteria PGPR in the tomato rhizosphere in the Sahelian zone. Seven bacterial genera promoting growth (*Bacillus*, *Serratia*, *Burkholderia*, etc.) and several microscopic fungi (*Candida*, *Aspergillus*, *Mucor*) were identified, attesting to a functionally rich microflora. These results confirm that the optimization of organic inputs and plant associations is an effective agroecological strategy to strengthen the biological fertility of soils and sustainably support vegetable production in Niger.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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