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## REVIEWER'S REPORT

Manuscript No.: IJAR-54891

**Title: Diagnosis and characterization of the bacterial flora of mango (Mangifera indica L.) in western Senegal.**

**Recommendation:**
Accept as it is .....
Accept after minor revision.....
Accept after major revision .....
Do not accept (*Reasons below*) .....

| Rating | Excel. | Good | Fair | Poor |
|---|---|---|---|---|
| Originality | | x | | |
| Techn. Quality | | | x | |
| Clarity | x | | | |
| Significance | | x | | |

Reviewer Name: Dr. Hari Prashad Joshi

## *Detailed Reviewer's Report*

**Recommendation: Accept after Major Revision**

This manuscript presents a valuable and timely study on the diagnosis and characterization of bacterial flora associated with mango in Senegal's Niayes region. It provides the first baseline dataset on this topic for western Senegal, which is a significant contribution to the field of plant pathology and has important implications for regional biosecurity and mango production.

The experimental design is generally sound, employing a combination of morphological, biochemical, and molecular methods to identify bacterial isolates. The absence of the high-concern pathogen Xanthomonas citri pv. mangiferaeindicae is a noteworthy and reassuring finding for the region, while the prevalence of genera like Pseudomonas and Stenotrophomonas offers crucial data for future disease management.

However, several major revisions are required before the manuscript can be accepted for publication:

Pathogenicity Assessment: The most significant weakness is the lack of pathogenicity tests. Isolating bacteria from symptomatic tissue does not fulfill Koch's postulates. The discussion on potential pathogenicity remains speculative without experimental validation. The authors must conduct pathogenicity assays on mango plants to confirm which of the identified species are true pathogens versus endophytes or saprophytes.

Clarification of Methods and Results: The sampling strategy and isolate selection process need clarification. The rationale for sampling only three locations and the absence of isolates from one site should be explained. Furthermore, the results section is disjointed, with data split between tables and text. The presentation of biochemical (Table 5) and molecular (Table 4) data should be streamlined and cross-referenced more clearly with the main findings.

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Resolution of Taxonomic Ambiguity: The limitations of 16S rDNA sequencing for distinguishing between closely related species (e.g., within Bacillus and Pseudomonas) are correctly noted. The authors should employ additional techniques, such as multi-locus sequence analysis (MLSA) or the use of species-specific primers, to provide more definitive species-level identification for key isolates, particularly those with high similarity to known pathogens.

Refinement of Discussion: The discussion should be refocused to more critically interpret the results in light of the study's limitations (e.g., no pathogenicity data). The relevance of identifying primarily opportunistic human pathogens (e.g., P. aeruginosa, B. cepacia) in a phytopathological context needs a more nuanced discussion, clearly differentiating between their established and potential roles.

This study has a strong foundation and represents an important step forward. Addressing these points will substantially strengthen the manuscript and its contribution to the literature.