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# Identification of a strain of the genus *Janibacter* isolated in a pharmaceutical industry using molecular and proteomic techniques

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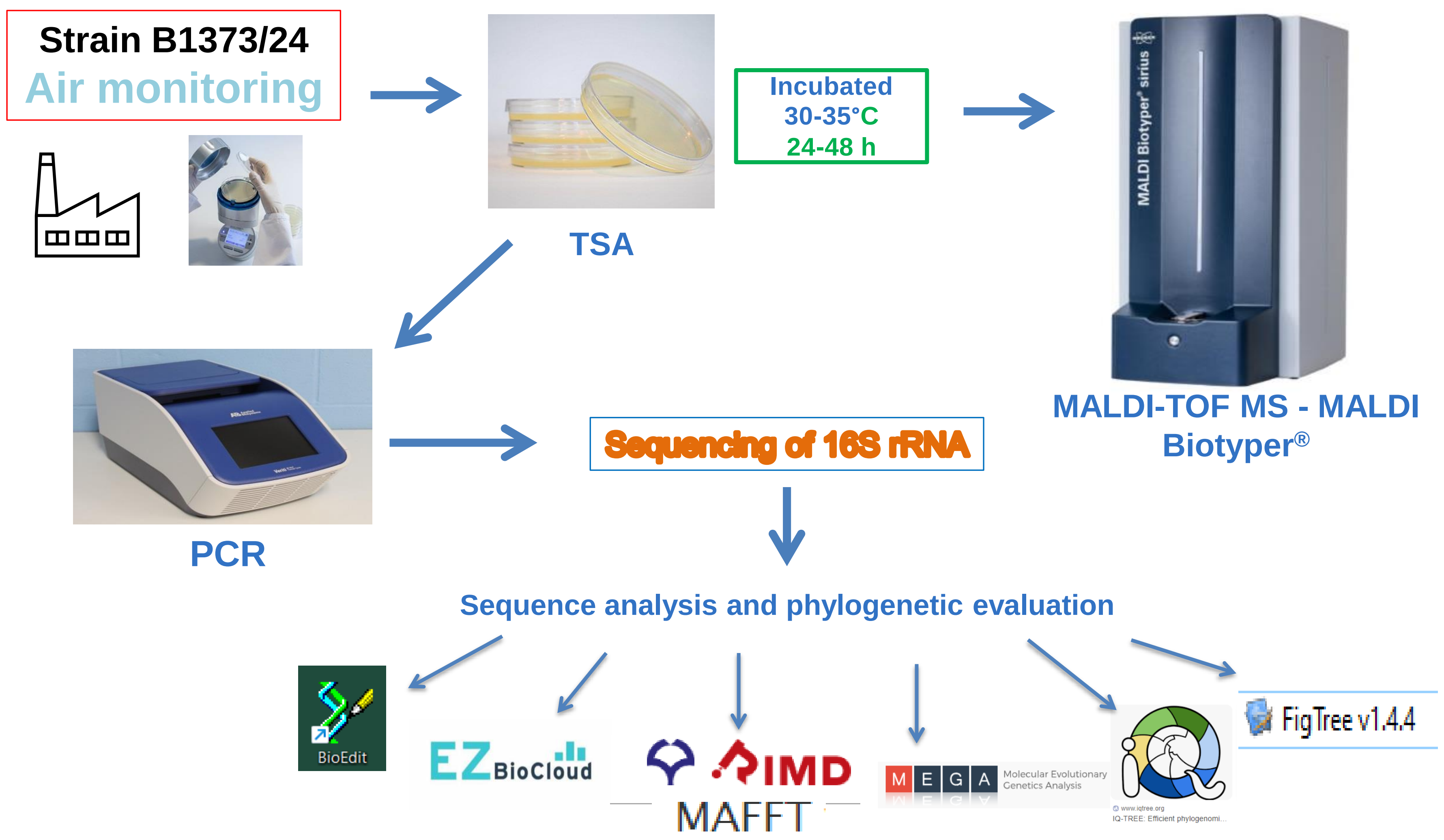
## INTRODUCTION & AIM

- The production of medicines and vaccines must comply with Good Manufacturing Practice (GMP) standards to ensure the safety of the manufactured products.
- Consequently, environmental monitoring of pharmaceutical production areas is essential to ensure compliance with recommended limits for microbiological contamination, and identifying microorganisms isolated from these areas supports preventive and corrective actions.
- This study aimed to identify, at the species level, the strain B1373/24, which was isolated during air monitoring in a viral vaccine production area of a pharmaceutical industry in Rio de Janeiro, Brazil.

## METHOD


**Strain B1373/24**
Air monitoring

TSA

Incubated
30-35°C
24-48 h

MALDI-TOF MS - MALDI Biotyper®

PCR

Sequencing of 16S rRNA

Sequence analysis and phylogenetic evaluation

## RESULTS & DISCUSSION

- ☐ The strain B1373/24 was initially analyzed using matrix-assisted laser desorption ionization time-of-flight mass spectrometry (MALDI-TOF MS) with the MALDI Biotyper® (Bruker); however, it was not be identified
- ☐ 16S rRNA gene of B1373/24 was sequenced→ EzBioCloud database→ ≥98.7% threshold for species-level identification.
- ☐ USP recommends relatedness less than or equal to 99% to be considered different species.
- ☐ The following species were proposed: *Janibacter anophelis* (100.0%), *Janibacter hoylei* (98.82%), and *Janibacter cremeus* (98.75%).
- ☐ The species was confirmed as *Janibacter anophelis* through phylogenetic analysis. This confirmation allowed the spectrum of strain B1373/24 to be incorporated into the MALDI Biotyper® system, contributing to the expansion of its database (DB).

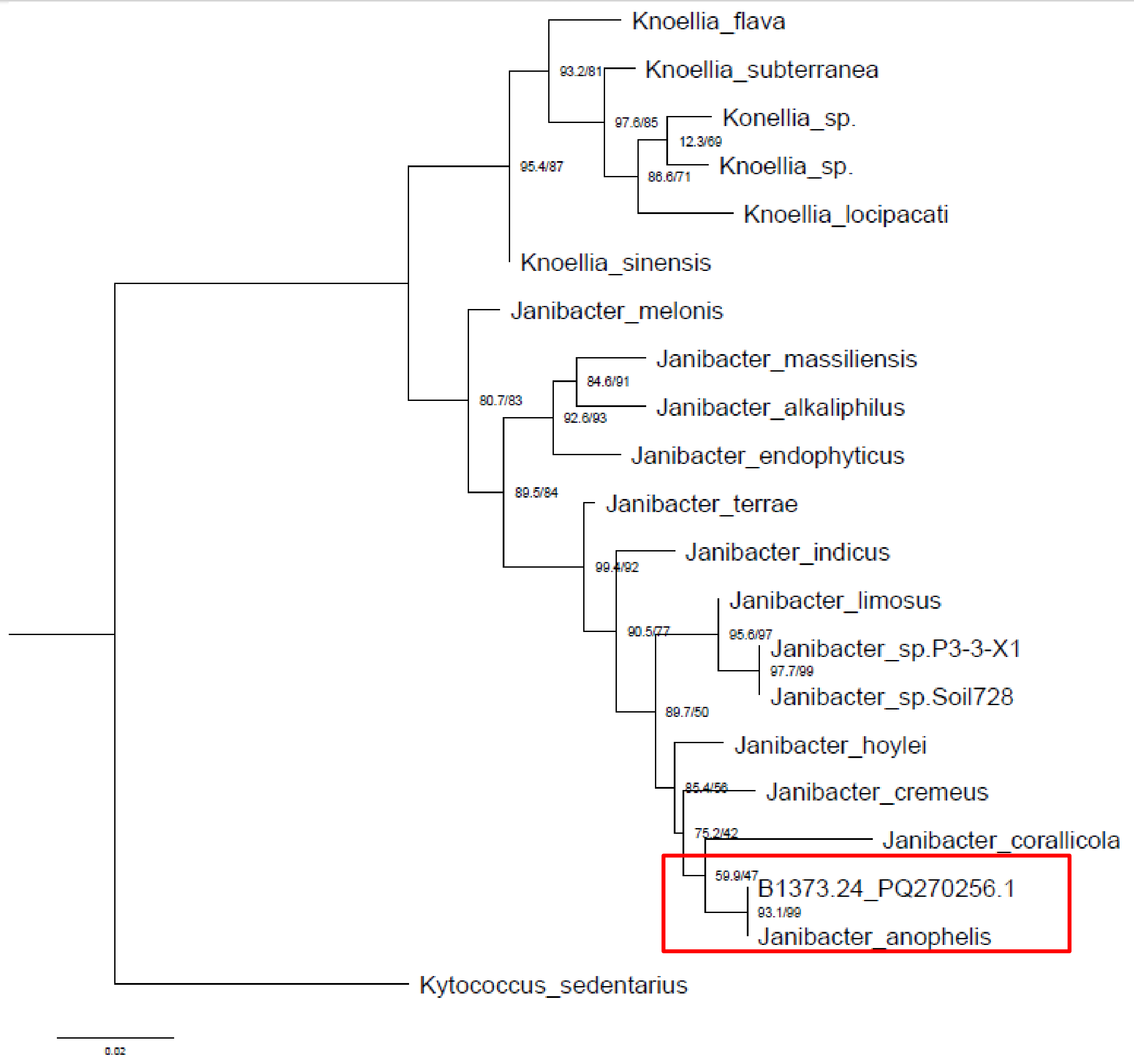


**Figure 1**: *Maximum Likelihood Phylogenetic Analysis* based on the sequence ).) of the 16S gene (using the substitution model (e.g., GTR+G+I), the alignment included 1,448 base pairs (bp).) of t of B1373/24 with the closest lineages. Nodes indicate the bootstrap values. *Kytococcus sedentarius* was used as an outgroup.

## CONCLUSION

- A subsequent reanalysis of B1373/24 using MALDI-TOF MS successfully identified it as *Janibacter anophelis*, confirming the validity of the newly added spectrum within the system's DB.
- The identification of B1373/24 as *Janibacter anophelis* highlights the importance of combining molecular tools to expand the MALDI-TOF MS database, thereby improving its capacity to identify environmental microorganisms.
- This study underscores its significant technological and scientific value for the pharmaceutical industry.

## REFERENCES

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