

MALDI BIOTYPER® DATABASE EXPANSION WITH A POSSIBLE NEW SPECIES OF GENUS *Aliidiomarina* ISOLATED IN AN IMMUNOBIOLOGICAL PHARMACEUTICAL INDUSTRY FACILITY: NEW APPROACHES TO CONTAMINATION CONTROL STRATEGY

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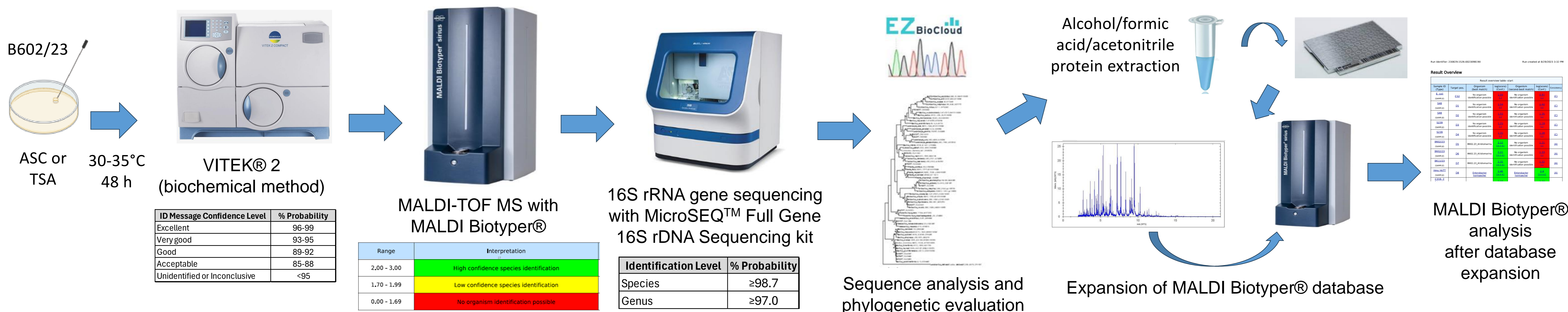
Introduction:

- Microbial identification is extremely relevant for parenteral drug pharmaceutical industry.
- Pre-requisite for a Contamination Control Strategy (CCS) implementation.
- Some microbial identification methodologies are not appropriate for environmental microorganism identification.
- Pharmaceutical production environments: potential for new species discovery; microbiota little explored and studied.
- Matrix-assisted laser desorption ionization-time of flight/mass spectrometry (MALDI-TOF/MS): fast and accurate methodology; limited database.
- *Aliidiomarina* spp.: Gram-negative, heterotrophic, aerobic and motile rods.

Objective:

The aim of this study was to expand the MALDI Biotyper® database with an *Aliidiomarina* strain isolated in an immunobiological pharmaceutical facility after 16S rRNA sequence analysis.

Methodology:

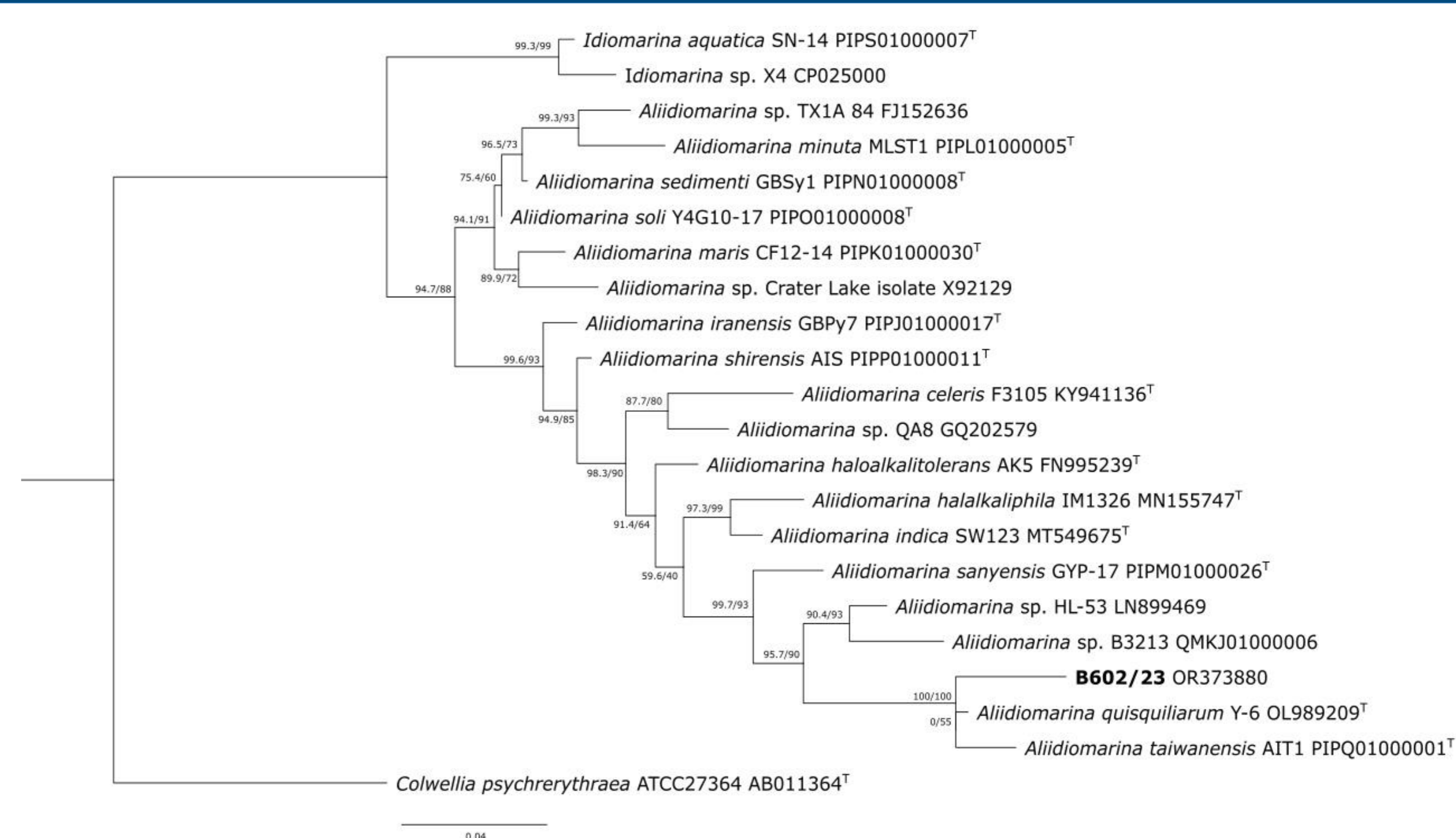


Results:

Strain	VITEK® 2	MALDI Biotyper®	16S rRNA sequencing (%)	MALDI Biotyper® after database expansion (score)
B602/23	Not identified	Not Identified	<i>Aliidiomarina quisquiliarum</i> (97.2%)	<i>Aliidiomarina</i> sp. (2.21)

Table 1: Results of B602/23 identification by VITEK@2, MALDI Biotyper® (before and after database expansion) and 16S rRNA sequencing.

Figure 1: Maximum-likelihood tree based on almost complete sequences of the 16S rRNA gene showing the phylogenetic position of B602/23 with the closest 20 strains. Values on the node indicate SH-aLRT/bootsrap values. *Colwellia psychrerythraea* ATCC 27364 was used as an outgroup. The scale bar represents changes per nucleotide position.



Conclusions:

- Molecular identification of *Aliidiomarina* spp. by full 16S rRNA gene sequencing and expansion of MALDI Biotyper® database is an effective tool to improve microorganism identification in pharmaceutical industry, contributing to CCS approaches.
- Whole genome sequencing, average nucleotide identity, genome-to-genome distance calculator and GC content will be necessary to better characterize B602/23 and maybe describe it as a new species of the genus *Aliidiomarina*.

Acknowledgments:

References: