





# 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:



Excellent	96-99	Μ	IALDI Biotyper®			0 5 10 15 20 met (10%)	analysis
Verygood	93-95			16S rDNA Sequencing kit	Contract, and the second secon		analysis
Good	89-92	Range	Interpretation		Andra, quand con, and any constru- Andra, guard construction of a particular Andra, guard construction of a particular Andra (construction)		after datak
Acceptable	85-88	2.00 - 3.00	High confidence species identification	Identification Level % Probability	Entry and the contraction of the second seco		
Unidentified or Inconclusive <9	<95	1.70 - 1.99	Low confidence species identification	Species ≥98.7	Sequence analysis and	Expansion of MALDI Biotyper® database	expansi
		0.00 - 1.69	No organism identification possible	Genus ≥97.0	phylogenetic evaluation	Expandion of MixEDI Diotypore database	

### **Results:**

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

