

EVALUATION OF VITEK® MS PRIME FOR IDENTIFYING PHARMACEUTICAL STRAINS IN INDUSTRIAL QUALITY CONTROL



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SPECIES-LEVEL IDENTIFICATION: A REGULATORY IMPERATIVE IN PHARMA QC

Microbial identification is a cornerstone of pharmaceutical industrial quality control, ensuring product safety and compliance with regulatory standards. According to EU GMP Annex 1, Chapter 9.31, and USP <1113> guidance, manufacturers are required to identify microorganisms to the species level when investigating contamination or monitoring environmental trends. This level of precision is critical, as genus-level identification may overlook strain-specific risks such as pathogenicity, resistance profiles, or spoilage potential.

Modern technologies like MALDI-TOF mass spectrometry offer rapid, accurate, and cost-effective species-level identification, making them ideal for routine use in industrial QC. The VITEK® MS PRIME system exemplifies this advancement, providing robust microbial ID capabilities that align with regulatory expectations and support contamination control strategies.

Methods

The study was conducted by Labor LS SE & Co. KG, a leading independent contract laboratory in Europe renowned for its expertise in microbiological and physicochemical testing across the pharmaceutical, medical device, and cosmetics industries. The study was structured in two phases:

- **Phase I** involved a comprehensive performance assessment of the VITEK® MS PRIME system, a MALDI-TOF instrument, for species-level identification of pharmaceutical-relevant microorganisms.
- **Phase II** consisted of a comparative evaluation between VITEK® MS PRIME and the MicroSEQ™ ID system, one of the most commonly used sequencing-based identification platforms for pharmaceutical quality control in routine.

MicroSEQ™ ID system combines PCR amplification and DNA sequencing to identify microorganisms by targeting the 16S rDNA region for bacteria and the LSU D2 region for fungi.

In Phase I, 400 pharmaceutical strains randomly selected from routine pharmaceutical QC samples, including those recovered during environmental monitoring were analyzed using the VITEK® MS PRIME. The objective was to determine the system's accuracy and reliability in achieving species-level identification

For both phases, the strains were measured in triplicate (table 1) and then checked for plausibility based on the gram behavior and morphology.

The VITEK® MS PRIME was using the knowledge base V3.3.0.

Table 1: Listing example of the results with confidence-level for each strains

Sample no.	1. Result	Confidence	2. Result	Confidence	3. Result	Confidence
33	<i>Staphylococcus haemolyticus</i>	99.9	<i>Staphylococcus haemolyticus</i>	99.9	<i>Staphylococcus haemolyticus</i>	99.9
34	<i>Pseudomonas stutzeri</i>	99.9	<i>Pseudomonas stutzeri</i>	99.9	<i>Pseudomonas stutzeri</i>	99.9
35	<i>Staphylococcus capitis</i>	99.9	<i>Staphylococcus capitis</i>	99.9	<i>Staphylococcus capitis</i>	99.9
36	<i>Brevundimonas vesicularis</i>	99.9	No Identification		<i>Brevundimonas vesicularis</i>	99.9

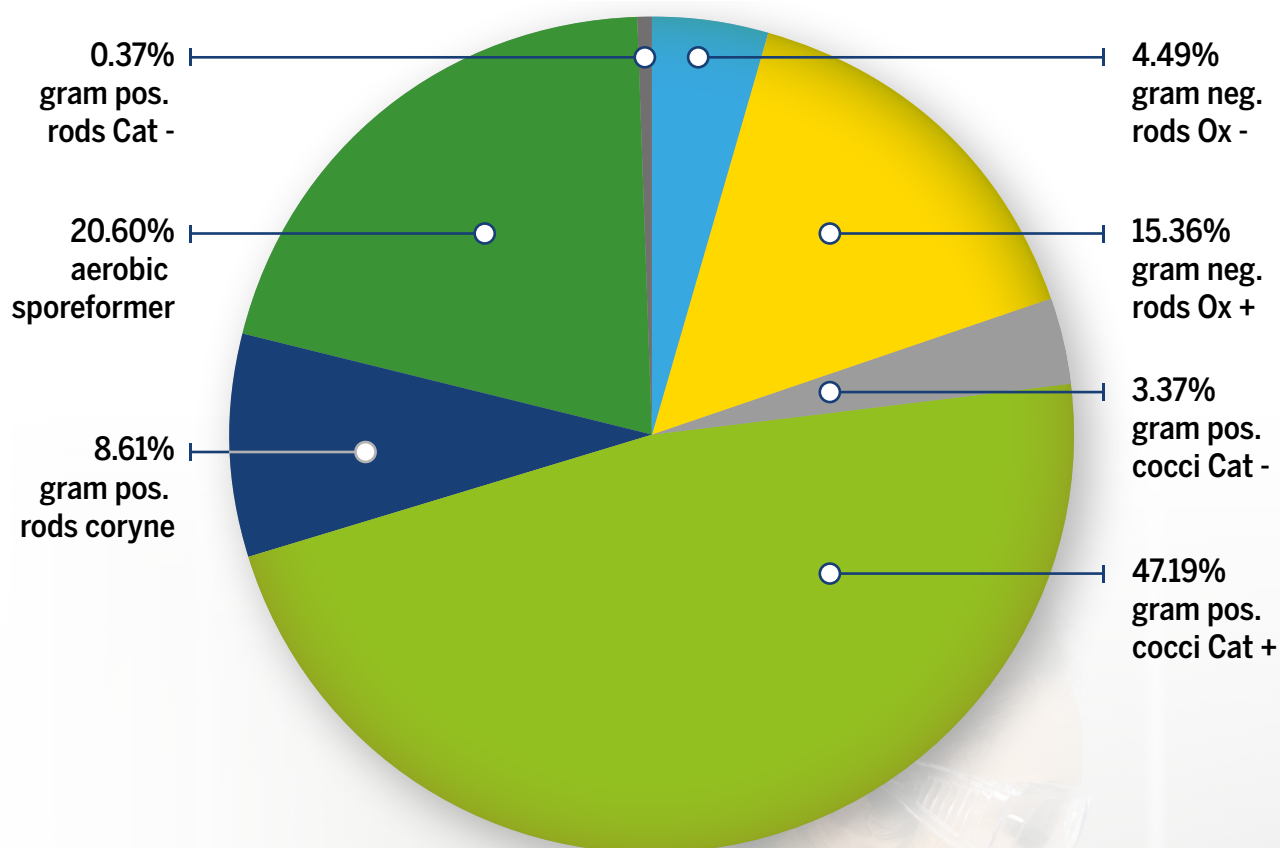
Phase I Results

From the 400 strains randomly selected from routine pharmaceutical quality control samples, 320 bacterial isolates, 40 yeasts, and 40 molds were identified.

These strains reflect the microbial diversity typically encountered in industrial pharmaceutical environments, particularly through environmental monitoring and other contamination control processes.

To guide microbial identification efforts, the distribution of bacterial species is presented in Figure 1, highlighting the taxa most frequently observed in routine pharmaceutical quality control.

Figure 1: Bacterial species distribution from routine pharmaceutical QC samples



For evaluation, two identification-rates were determined:

- **Overall-ID-Rate:** Corresponds to the successful identification rate on species level across all created spots.
- **Condensed-ID-Rate:** Corresponds to the successful identification rate on species level over the strains.

Table 2: Summary of the Identification rate

	All 400 strains	31 Yeasts	40 Molds
Successfull IDs	337	30	36
Overall-ID-Rate	73.33%	94.62%	85.00%
Condensed-IDRate	84.25%	96.77%	90.00%

Out of the 400 random strains, **84.25%** were successfully identified to the species level using VITEK® MS PRIME.

Please note that most samples come from routine QC processes, so are damaged or influenced by cleaning agents and disinfectants making identification more challenging.

These results demonstrate excellent species-level identification performance in a real-world context for a pharmaceutical industrial setting.

Phase II results

Phase II aimed to assess the performance of VITEK® MS PRIME versus sequencing for mold identification, a persistent challenge in pharmaceutical QC. Molds from Phase I were selected to simulate real-world conditions and evaluate the instrument's reliability in routine workflows.

31 molds were sequenced and tested in triplicate with VITEK® MS PRIME; results are shown in Table 3. Please find the summary below:

- 3 out of the 4 non-IDs were absent from Maldi-ToF database
- **Maldi-ToF yielded better** results over sequencing in **13 instances**
- **Maldi-ToF and sequencing yielded equivalent** result in **14 instances**
- **Sequencing yielded better** over Maldi-ToF results in **1 instance**.



Table 3: Comparison of mold identification results: MALDI-TOF vs. sequencing, with indication of superior method per case in the last column:

- Maldi-ToF** - better result with Maldi-ToF
- Seq. (MS-ID)** - better result with sequencing
- same** - equivalent result between Maldi-ToF and sequencing

Maldi-ToF	Value	Seq. MS-ID database 28S region	NCBI database 28S region	Comparison
<i>Aspergillus brasiliensis</i>	99,9	<i>Aspergillus awamori/brasiliensis/foetidus/niger</i> all 100%	<i>Aspergillus</i> spp.	Maldi-ToF
<i>Aspergillus sydowii</i>	99,9	<i>Aspergillus sydowii/versicolor</i> both 100%	<i>Aspergillus</i> spp. or <i>Cladosporium sphaerospermum</i> or <i>Pyricularia grisea</i> with 99,67 %	Maldi-ToF
<i>Aspergillus versicolor</i>	99,9	<i>Aspergillus versicolor</i> 100%	<i>Aspergillus</i> sp or <i>Agaricus sinodeliciosus</i> with 100%	same
<i>Cladosporium sphaerospermum</i>	99,9	<i>Cladosporium sphaerospermum</i> 99,63 %	<i>Cladosporium variabile</i> with 100%	same
<i>Cladosporium cladosporioides</i> complex	99,9	<i>Cladosporium</i> spp.	<i>Cladosporium</i> spp. or <i>Fonsecaea nubica</i> 99,66% or <i>Periconia cyperacearum</i> 99,66%	Maldi-ToF
<i>Aspergillus fumigatus</i>	99,9	<i>Aspergillus fumigatus</i> 100%	<i>Aspergillus fumigatus</i> or <i>Aspergillus tsunodae</i>	same
<i>Penicillium decumbens</i>	99,9	<i>Penicillium decumbens</i> 99,22 %	most closely related to <i>Penicillium</i> spp. or <i>Trichocomaceae</i> spp.	same
<i>Chaetomium globosum</i>	99,9	<i>Chaetomium</i> spp.	<i>Chaetomium</i> spp. or <i>Alternaria burnsii</i> or <i>cercophora thailandica</i>	Maldi-ToF
<i>Cladosporium fusiforme</i>	99,9	<i>Cladosporium fusiforme</i> 100%	<i>Cladosporium ruthsangerae/herbarum</i> both 100%	same
<i>Penicillium brevicompactum</i>	99,9	<i>Penicillium brevicompactum</i> 100%	<i>Penicillium</i> spp.	same
<i>Paecilomyces variotii</i> complex	99,9	<i>Paecilomyces</i> spp.	<i>Paecilomyces variotii/subglobosus</i> both 100%	Maldi-ToF
<i>Alternaria alternata</i>	99,9	<i>Alternaria alternata</i> 100%	<i>Alternaria</i> spp.	same
<i>Scopulariopsis brevicaulis</i>	99,9	<i>Scopulariopsis alboflavescens/brevicaulis</i> both 100%	<i>Scopulariopsis brevicaulis</i>	Maldi-ToF
no ID		<i>Penicillium oxalicum</i> (in Maldi DB) 99,62%	<i>Penicillium</i> spp. or <i>Eurotiales</i> sp or <i>Lophiostoma biappendiculatum</i>	Seq. (MS-ID)
<i>Rhizopus microsporus</i> complex	99,9	<i>Rhizopus</i> spp.	<i>Rhizopus microsporus</i> and var <i>rhizopodiformis</i>	Maldi-ToF
no ID		<i>Phialemoniopsis curvata</i> 100%	<i>Thyridium curvatum</i> 99,67%	
<i>Saprochaete capitata</i>	99,9	<i>Magnusiomyces capitatus</i> (=Synonym) 100%	<i>Magnusiomyces capitatus</i> 100%	same
<i>Penicillium chrysogenum</i>	99,9	<i>Penicillium chrysogenum/tardochrysogenum</i> both 100%	<i>Penicillium</i> spp.	Maldi-ToF
<i>Penicillium citrinum</i>	99,9	<i>Penicillium citrinum</i> 99,82%	<i>Penicillium citrinum/ochrosalmoneum/hetheringtonii</i> all 99,25%	same
<i>Penicillium glabrum</i>	99,9	<i>Penicillium glabrum</i> 100%	<i>Penicillium</i> spp.	same
<i>Penicillium corylophilum</i>	99,9	<i>Penicillium decumbens</i> (both in both DB) 99,63%	<i>Penicillium</i> spp.	Maldi-ToF
<i>Fusarium oxysporum</i> complex	99,9	<i>Fusarium</i> spp.	<i>Fusarium</i> spp. or <i>Alternaria hungarica</i> or <i>Coniella vitis</i>	Maldi-ToF
<i>Bjerkandera adusta</i>	99,9	<i>Bjerkandera</i> spp.	<i>Bjerkandera adusta/albocinera</i> or <i>Ceriporia inflata</i> or <i>Fomitopsis malicola</i> with 99,10%	Maldi-ToF
<i>Trichophyton mentagrophytes/interdigitale-tonsurans</i>	50/50	<i>Trichophyton tonsurans</i> (plausibility in Maldi was Tri. tonsurans) 100%	<i>Trichophyton</i> spp.	same
<i>Trichophyton benhamiae</i>		<i>Arthroderma benhamiae</i> (=Synonym) 100%	<i>Trichophyton</i> spp.	same
<i>Trichophyton mentagrophytes/interdigitale</i>	99,9	<i>Trichophyton tonsurans</i> (both in both DB) 100%	<i>Trichophyton</i> spp.	Maldi-ToF
<i>Purpureocillium lilacinum</i>	99,9	<i>Purpureocillium lilacinum</i> 100%	<i>Purpureocillium lilacinum/zongii/sodanum</i>	same
no ID		<i>Bipolaris</i> spp.(not in Maldi DB)	too many genus equally named no statement possible	
<i>Phoma glomerata</i>	99,9	<i>Didymella glomerata</i> or <i>Phoma herbarum</i> both 100%	too many genus equally named no statement possible	Maldi-ToF
<i>Acremonium sclerotigenum</i>	99,9	<i>Acremonium sclerotigenum</i> 99,63%	<i>Acremonium sclerotigenum/potronii/egyptiacum</i> all 100%	same
no ID		<i>Xenoseptoria</i> spp. (not in Maldi DB)	<i>Yunnanensis phragmitis</i> or <i>Tintelnotia deestructans</i> both 100%	

Conclusions

- VITEK® MS PRIME delivers high-performance for species-level microbial identification in pharmaceutical QC. With 84.25% accuracy at species level across 400 pharma-relevant strains, including bacteria, yeasts, and molds, it delivers robust results even under real industrial conditions.
- In mold identification, it outperformed sequencing not only in accuracy but also with a simpler workflow and faster turnaround time, making it ideal for routine industrial use.
- With recent regulatory updates, aligned with cGMP and USP <1113>, species-level microbial identification is now a critical requirement for pharmaceutical QC investigations. Genus-level identification is no longer sufficient when microorganisms are identified at atypically high rates, exceed alert limits, or are linked to sterility failures, making high-resolution solution like VITEK® MS PRIME essential for compliance and contamination control.
- By integrating VITEK® MS PRIME into their QC workflows, pharma manufacturers gain a rapid, reliable, and regulatory-compliant solution that helps accelerate investigations, strengthen contamination control, and safeguard product integrity.

