

SARTORIUS

Simplifying Progress

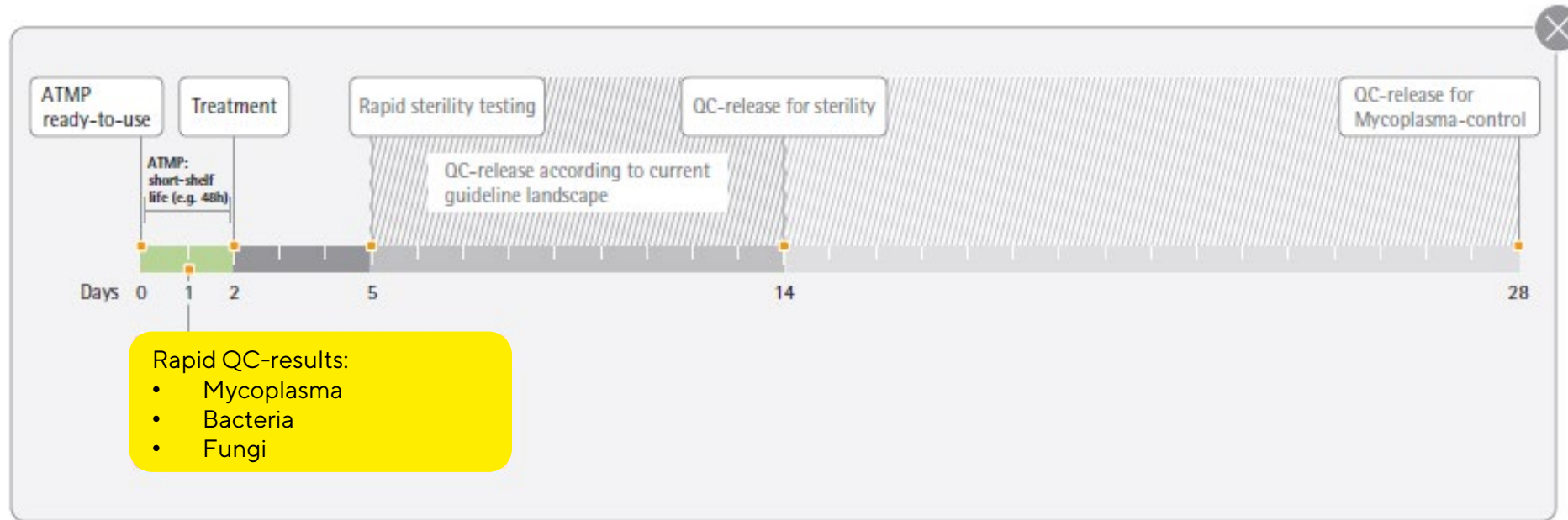


Rapid sterility of ATMPs prior treatment - Validation of a qPCR-based test

Alexandra Mueller-Scholz, Sartorius Lab Instruments

NIST RMTM Workshop - Apr 19, 2022

Safety of the Patient is a Risk



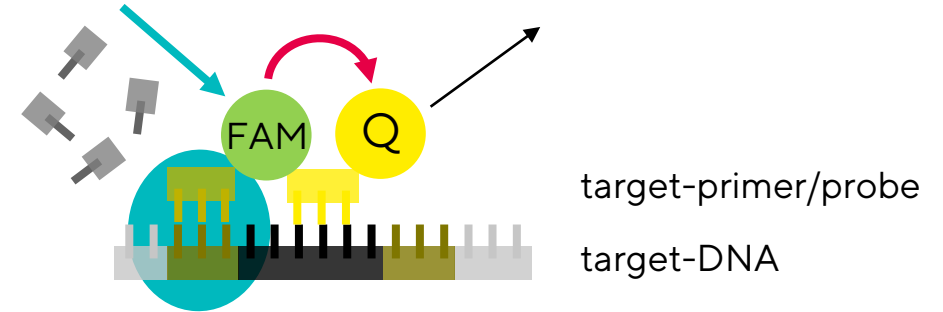
The Challenge:

- Growth-based QC-release takes too long.
- How do you ensure non-contaminated ATMPs?

Strategies to Reduce False Results

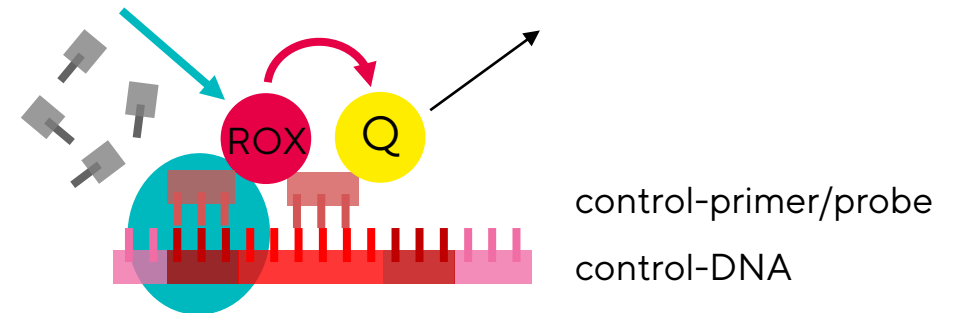
Reduce false-POSITIVES

- ✓ *specificity of TaqMan[®] system*



Reduce false-NEGATIVES

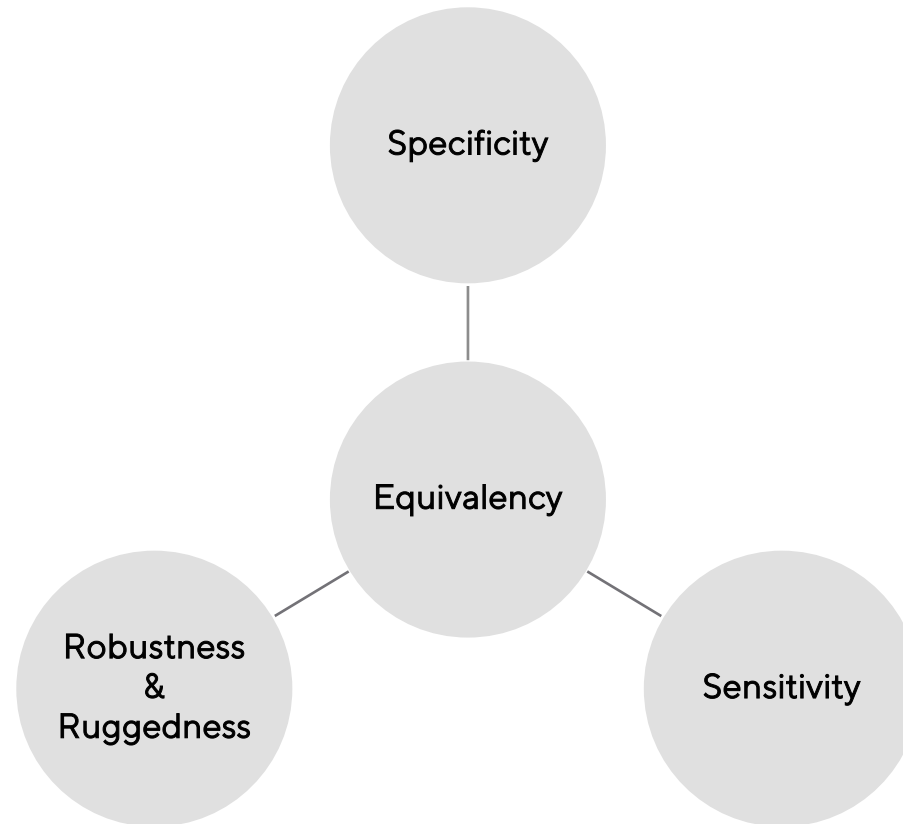
- ✓ *control of PCR-inhibition by integrated internal control*



Reliable Results for Bacterial and Fungal Detection in ATMPs PRIOR Treatment

Guidance for validation of rapid / alternativ methods:

- PDA, TR 33
- USP <1223>
- USP <1071>
- EP 5.1.6 part 4-1-1 primary validation by supplier
- EP 2.6.27



Including Guidance of the German Governmental Regulatory Agency (part of EMEA)

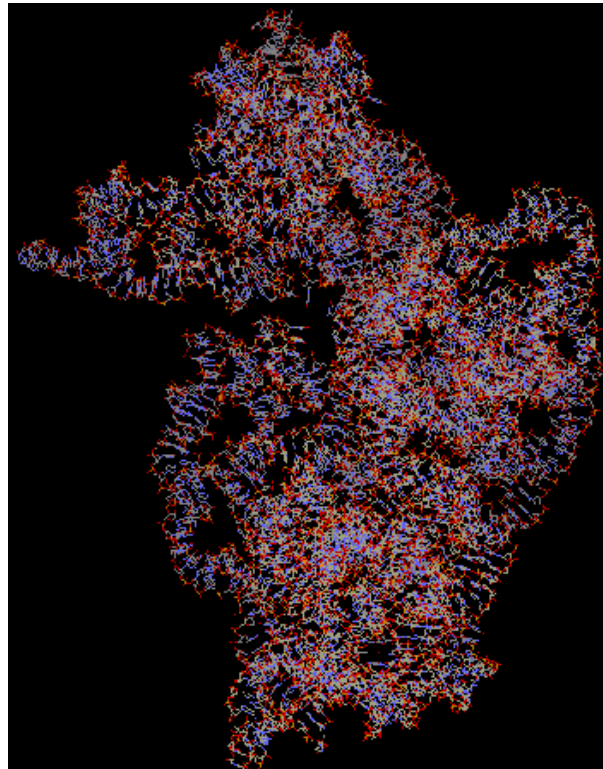


Challenge
To be accepted by regulatory bodies

In-silico prediction by sequence alignment and BLAST

Acceptance criterion: ≤ 3 nucleotides mismatch of primers and probe

16S / 18S rDNA



<http://www.biochem.umd.edu/biochem/kahn/bchm465-01/ribosome/16SrRNA.html>

example

NIH U.S. National Library of Medicine

BLAST® >> blastn suite

blastn blastp blastx tblastn tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

AGAGTTTGATCTGGCTCAG

Or, upload file

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Database

Human genomic + transcript Mouse

16S ribosomal RNA sequences (Bac

<https://www.ncbi.nlm.nih.gov/>

Detection Range - Bacteria

Acceptance criterion: ≤ 3 nucleotides mismatch of primers and probe

	Primer Mismatches			
	0	1	2	3
Bacteria	48.8 %	69.4 %	85.7 %	94.7 %
Archea	n.a	n.a	0.1%	40.4 %
Eukaryotes	0%	0%	0.1%	0.3 %



Detection Range - Fungi

Acceptance criterion: ≤ 3 nucleotides mismatch of primers and probe

Strains of all Fungi species which were part of this study	Primer Mismatches		
	Forward Primer	Probe	Reverse Primer
<i>Candida albicans</i> (HQ876034.1)	0	0	0
<i>Candida tropicalis</i> (EU348785.1)	0	0	0
<i>Candida glabrata</i> (AB094140.2)	0	0	0
<i>Candida guilliermondii</i> (AJ508274.1)	0	0	0
<i>Candida haemulonii</i> (AB013572.1)	0	0	0
<i>Candida parapsilosis</i> (AY497758.1)	0	0	0
<i>Aspergillus brasiliensis</i> (D63697.1)	0	0	0
<i>Aspergillus fumigatus</i> (AF548061)	0	0	0
<i>Penicillium crysogenum</i> (M55628.1)	0	0	0



37 % of the whole kingdom fungi are putatively detected based on sequence alignments.

Challenge
Do we detect enough species?

Cross Reactivity to Cell Lines / Sample Matrix Effects

Bacteria

		Results
Hela	No Cq	0/2
	No Cq	
Vero	No Cq	0/2
	No Cq	
CHO-K1	No Cq	0/2
	No Cq	
RK13	No Cq	0/2
	No Cq	
CHO-DG44	No Cq	0/2
	No Cq	
CHO XM111-10	No Cq	0/2
	No Cq	
L-9296 (NCTC)	No Cq	0/2
	No Cq	

Fungi

			Results
Hela	No Cq	No Cq	0/8
	No Cq	No Cq	
	No Cq	No Cq	
	No Cq	No Cq	
Vero	No Cq	No Cq	0/8
	No Cq	No Cq	
	No Cq	No Cq	
	No Cq	No Cq	
CHO-K1	No Cq	No Cq	0/8
	No Cq	No Cq	
	No Cq	No Cq	
	No Cq	No Cq	
HPBMC	No Cq	No Cq	0/8
	No Cq	No Cq	
	No Cq	No Cq	
	No Cq	No Cq	
Jurkat	No Cq	No Cq	0/8
	No Cq	No Cq	
	No Cq	No Cq	
	No Cq	No Cq	

26 species included in Validation

EP 2.6.1
USP<71>

Currently tested = 6



Bacillus subtilis
Clostridium sporogenes
Pseudomonas aeruginosa
Staphylococcus aureus

Candida albicans
Aspergillus brasiliensis

23/24 positive

regulatory advice;
EP 2.6.27; user feedback

Recommended Extension = 20

+ Colony Forming Units (CFU)

Streptococcus pyogenes
Bacteroides vulgatus
Escherichia coli
Pseudomonas protegens
Bacillus cereus
Enterococcus faecalis
Kocuria rhizophila
Staphylococcus epidermidis
Serratia marcescens
Propionibacterium acnes
Candida tropicalis
Candida glabrata
Candida krusei
Aspergillus fumigatus
Penicillium chrysogenum

Genome Copies (GC)

Bacteroides fragilis
Enterobacter cloacae
Klebsiella pneumoniae
Clostridium perfringens
Yersinia enterocolitica

8/8 positive

Limit of Detection (LOD₉₅): 99, 50, 25, 10, 5, 2.5, 1.25 CFU/ml

Limit of Detection (LOD₉₅) – Fungi

currently tested

recommended extension

Species (CFU-based)	Acceptance criterium	LOD ₉₅ (CFU/ml)	Acceptance passed?
<i>Candida albicans</i>	23/24	50	✓
<i>Aspergillus brasiliensis</i>	23/24	50	✓
<i>Candida tropicalis</i>	8/8	10	✓
<i>Candida glabrata</i>	8/8	25	✓
<i>Candida krusei</i>	8/8	50	✓
<i>Aspergillus fumigatus</i>	8/8	99	✓
<i>Penicillium chrysogenum</i>	8/8	99	✓

CFU-based

Challenge
Detect 1 CFU/ml

Example: *Candida albicans*

CFU/ml						Mean	
99	Run 1	31.32	31.90	32.78	32.80	32.20	24/24
	Run 2	32.96	32.88	33.07	32.25	32.79	
	Run 3	32.29	32.81	36.03	32.09	33.30	
	Run 4	32.46	32.14	32.29	32.33	32.30	
	Run 5	32.32	32.55	32.71	32.36	34.48	
	Run 6	32.58	31.48	31.89	32.43	32.09	
50	Run 1	33.15	33.79	34.11	34.44	33.87	23/24
	Run 2	34.25	33.86	33.04	35.03	34.04	
	Run 3	33.59	33.90	32.63	33.89	33.50	
	Run 4	34.04	32.94	34.27	33.81	33.76	
	Run 5	No Cq	34.77	32.82	34.48	34.02	
	Run 6	32.58	32.57	32.82	34.81	31.19	
25	Run 1	33.42	34.72	34.88	35.32	34.58	21/24
	Run 2	34.67	37.19	33.28	36.08	35.30	
	Run 3	34.96	37.20	38.18	No Cq	36.78	
	Run 4	37.96	34.90	35.11	34.59	35.64	
	Run 5	33.55	No Cq	35.77	No Cq	34.66	
	Run 6	34.51	35.33	36.17	34.90	35.23	
10	Run 1	35.85	36.48	37.27	37.38	36.74	14/24
	Run 2	No Cq	No Cq	37.00	34.65	35.82	
	Run 3	No Cq	No Cq	No Cq	No Cq	No Cq	
	Run 4	No Cq	35.93	No Cq	37.11	36.52	
	Run 5	35.04	No Cq	No Cq	38.91	36.97	
	Run 6	35.54	36.26	35.84	37.52	36.29	

Limit of Detection (LOD₉₅) – Bacteria

	Species (CFU-based)	Classification	Strain no.	LOD ₉₅ (CFU/ml)	Acceptance passed?
currently tested	<i>Bacillus subtilis</i>	Gram pos.	ATCC® 6633	25	✓
	<i>Clostridium sporogenes</i>	Gram pos.	ATCC® 19404	25	✓
	<i>Pseudomonas aeruginosa</i>	Gram neg.	ATCC® 9027	5	✓
	<i>Staphylococcus aureus</i>	Gram pos.	ATCC® 6538	10	✓
recommended extension	<i>Streptococcus pyogenes</i>	Gram neg.	ATCC® 19615	99	✓
	<i>Bacterioides vulgatus</i>	Gram neg.	ATCC® 8482	2,5	✓
	<i>Escherichia coli</i>	Gram neg.	ATCC® 8739	10	✓
	<i>Pseudomonas protegens</i>	Gram neg.	ATCC® 17386	10	✓
	<i>Bacillus cereus</i>	Gram pos.	ATCC® 10876	5	✓
	<i>Enterococcus faecalis</i>	Gram pos.	ATCC® 29212	99	✓
	<i>Kocuria rhizophila</i>	Gram pos.	ATCC® 9341	10	✓
	<i>Staphylococcus epidermidis</i>	Gram pos.	ATCC® 12228	99	✓
	<i>Serratia marcescens</i>	Gram neg.	ATCC® 14756	50	✓
	<i>Propionibacterium acnes</i>	Gram pos.	ATCC® 11827	25	✓

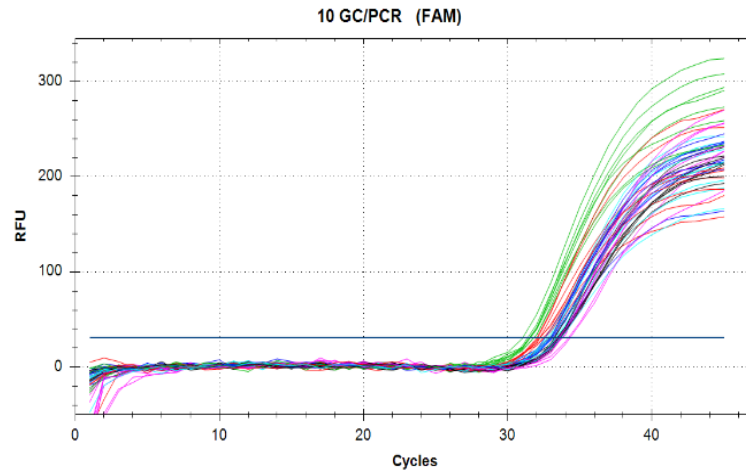
CFU-based

Limit of Detection (LOD₉₅) – Bacteria

recommended
extension

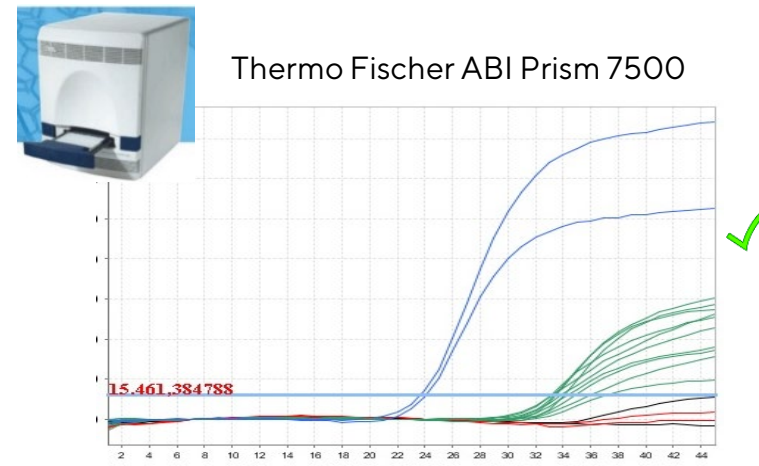
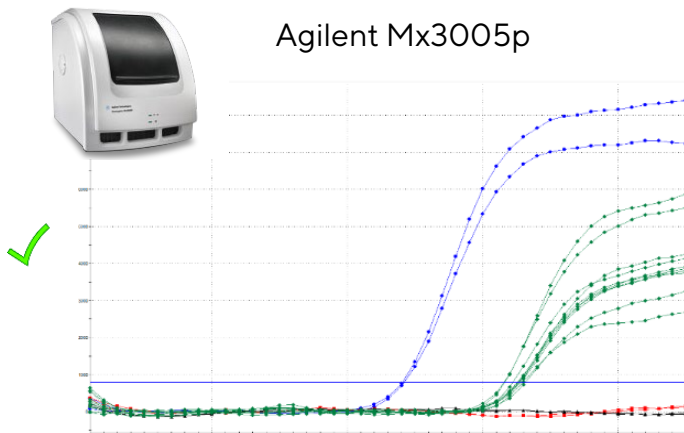
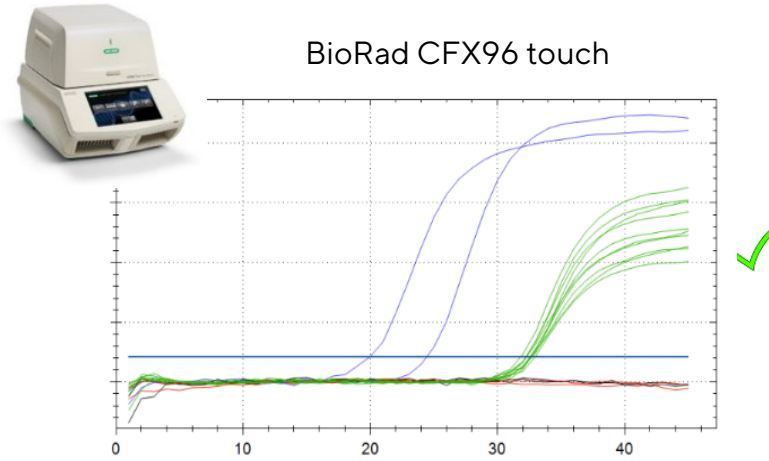
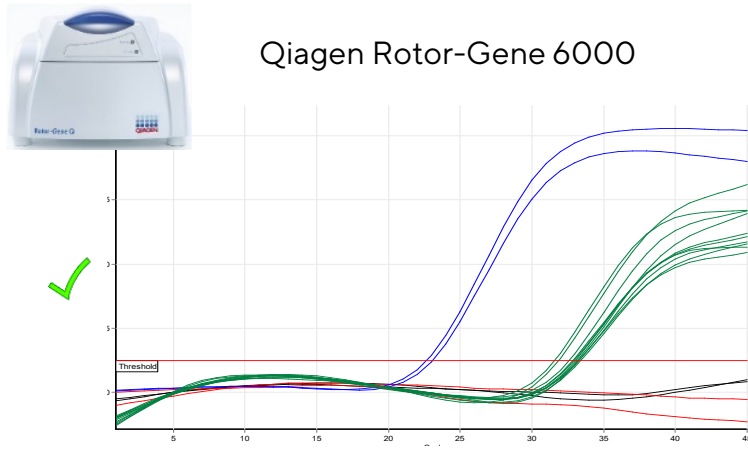
Species (GC-based)	Classification	Strain no.	LOD ₉₅ 10 GC/PCR	Acceptance passed?
<i>Bacteroides fragilis</i>	Gram neg.	ATCC® 25285	10	✓
<i>Enterobacter cloacae</i>	Gram neg.	ATCC® 13047	10	✓
<i>Klebsiella pneumoniae</i>	Gram neg.	ATCC® 13883	10	✓
<i>Serratia marcescens</i>	Gram neg.	ATCC® 13880	10	✓
<i>Clostridium perfringens</i>	Gram pos.	ATCC® 13124	10	✓
<i>Yersinia enterocolitica</i>	Gram neg.	ATCC® 27739	10	✓

GC-based



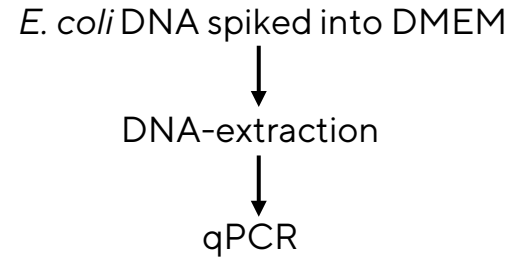
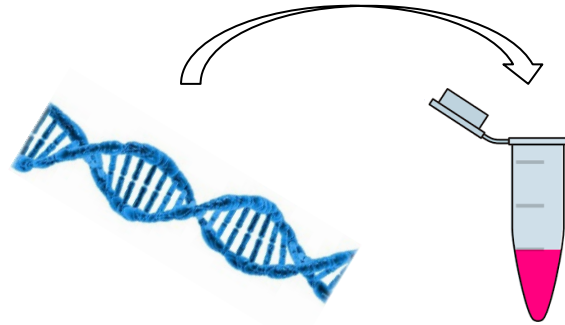
qPCR Device Comparability

Spiking 99 CFU/ml of the species with the highest LOD₉₅
Clostridium sporogenes (LOD₉₅ = 25)
Candida albicans (LOD₉₅ = 50)
Acceptance criterion 8/8 positive



False-Positives due to Free Microbial DNA?

Challenge
Discriminate live and dead microorganisms



failed		passed							
10 ⁴ GC/ml		10 ³ GC/ml		10 ² GC/ml		10 GC/ml		0 GC/ml	
Run 1	Run 2	Run 1	Run 2	Run 1	Run 2	Run 1	Run 2	Run 1	Run 2
39.00	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
39.93	39.89	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
39.38	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q
No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q	No C _q

Low risk of false-positive results

Is the Cell Culture Medium DNA-free?

Cell culture medium without spike
acceptance criterion
> 95 % negative

Fungi detection	Negative Results	ROX™	% Negative results
DMEM	8/8	8/8 Correct	100%
Fetal bovine serum (FBS)	8/8	8/8 Correct	100%
DMEM high Glucose, GlutaMAX	8/8	8/8 Correct	100%
DMEM w/o Na-Pyruvat mit stable Glutamin	8/8	8/8 Correct	100%
RPMI 1640	8/8	8/8 Correct	100%
MEM (1)	8/8	8/8 Correct	100%
MEM (2)	8/8	8/8 Correct	100%
KnockOut DMEM	8/8	8/8 Correct	100%
DMEM/F-12 GlutaMAX	8/8	8/8 Correct	100%
Opti-MEM Reduced Serum GlutaMAX	8/8	8/8 Correct	100%
McCoy's 5A Medium	8/8	8/8 Correct	100%
Leibovitz L-15 Medium	8/8	8/8 Correct	100%
Chondrocyte Differentiation Medium	8/8	8/8 Correct	100%
Human Osteoblast Differentiation Medium	8/8	8/8 Correct	100%
ChondroMAX Differentiation Medium	8/8	8/8 Correct	100%
Tahara Lympho One + HS	8/8	8/8 Correct	100%
RPMI, penicillin/Streptomycin, Glutamax, 5% FBS	8/8	8/8 Correct	100%

Low risk of false-positive results

Tolerance of Eukaryotic Cell Background

	<i>Aspergillus brasiliensis</i> 99 CFU (FAM™)			
	10⁶ cells/ml		10⁵ cells/ml	
Hela	37.54	31.26	33.72	32.10
	35.24	31.84	33.34	32.07
	4/4		4/4	
Vero	33.30	31.43	32.78	31.39
	34.45	32.76	33.48	31.60
	4/4		4/4	
CHO-K1	33.65	32.40	34.49	33.36
	34.70	32.83	33.89	32.40
	4/4		4/4	
HPBMC	32.21	31.59	33.80	32.12
	32.39	31.25	33.79	31.04
	4/4		4/4	
Jurkat	34.99	34.14	31.77	32.64
	34.80	33.50	34.30	33.81
	4/4		4/4	

February 20, 2020

Keywords or phrases:

Bacterial and fungal detection in high cell density ATMPs; Rapid microbial quality control, Real-Time PCR based ATMP release testing

Rapid, Real-Time PCR-Based Detection of Microbial Contaminations in High Cell Density Jurkat-, HPBMC- and CHO- Cultures using Microsart® ATMP Kits

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Abstract

In this study, we used Sartorius Real-time PCR kits for the rapid detection of bacteria, fungi, and mycoplasma to establish that these assays can detect microbial contaminants, even in the presence of high cell backgrounds, ranging from 10 to 40 million cells per milliliter (cells/mL). We observed that the cell density limit and assay robustness depend on cell types and media compositions. The detection limits for bacteria, fungi, and mycoplasma in Jurkat cells, HPBMC and CHO cells varies between 10 and 25 x 10⁵ cells/mL.

This study clearly demonstrates that Sartorius Microsart® ATMP kits tolerate higher cell density, still reaching the required sensitivity criteria (≤ 99 CFU, or colony forming units, for bacteria and fungi and ≤ 10 CFU for mycoplasma). The study also demonstrates the capability of Microsart® ATMP kits to sensitively detect microorganisms, even in the presence of high-density cell cultures, and thus contributes to risk-reduction and patient safety of cell therapy products.

Find out more: [sartorius.com/en/applications/quality-control-testing/microbiological-quality-control/rapid-testing](https://www.sartorius.com/en/applications/quality-control-testing/microbiological-quality-control/rapid-testing)

Comparability to Compendial Sterility Test

Sartorius



qPCR-based detection

L+S external contract lab



classical sterility test according to EP 2.6.1. and USP<71>

?
=

2x LOD₉₅

LOD₉₅

½ LOD₉₅

all 6 mandatory species

- Bacillus subtilis*
- Clostridium sporogenes*
- Pseudomonas aeruginosa*
- Staphylococcus aureus*
- Candida albicans*
- Aspergillus brasiliensis*

recommended extension

- Streptococcus pyogenes*
- Pseudomonas protegens*

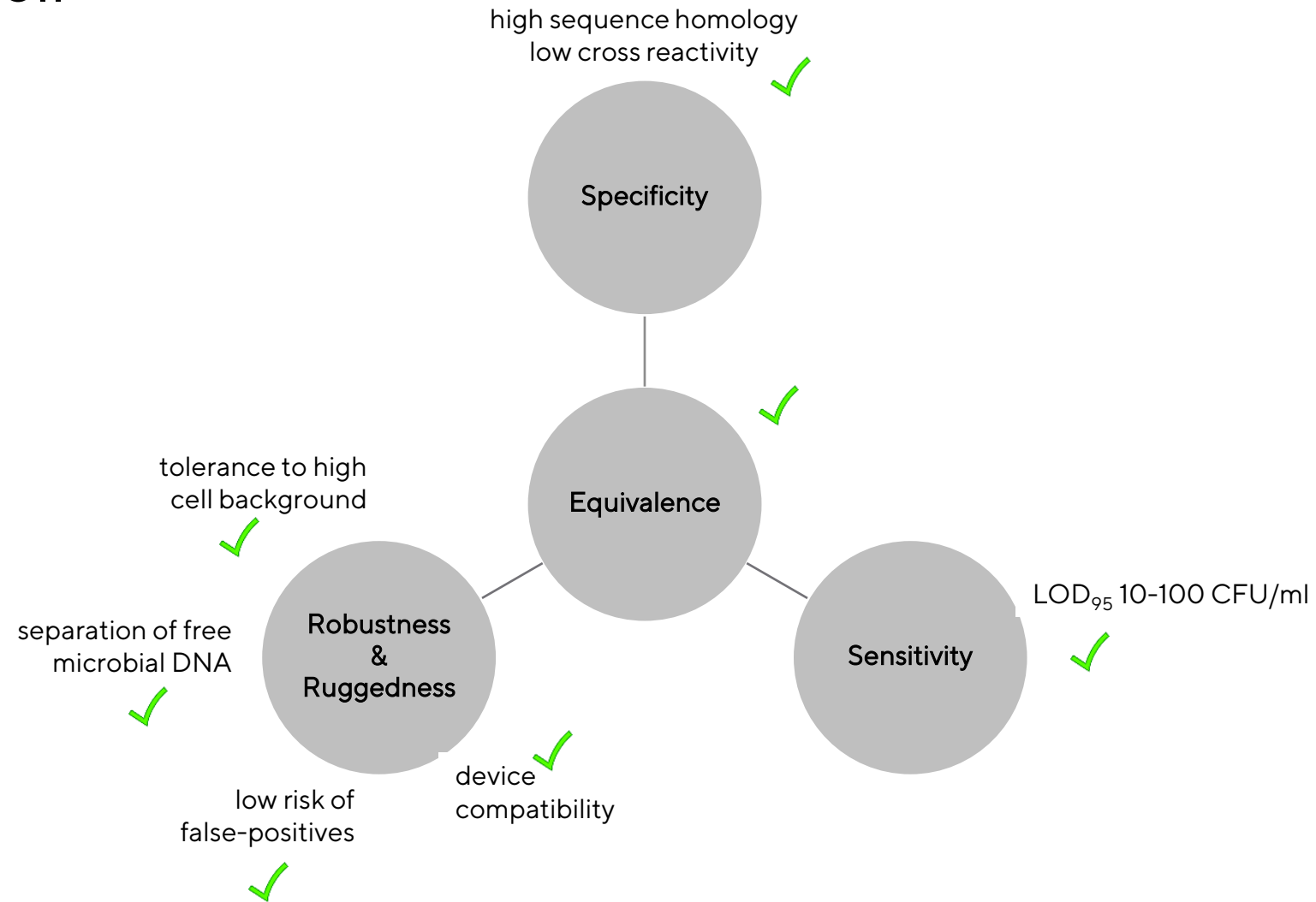
Comparability to Compendial Sterility Test

	Microsart® ATMP Bacteria			Compendial culture method (External)		
	2x LOD ₉₅	LOD ₉₅	LOD ₉₅ /2	2x LOD ₉₅	LOD ₉₅	LOD ₉₅ /2
<i>Bacillus subtilis</i>	33.16	34.23	35.47	<i>B. subtilis</i>	<i>B. subtilis</i>	<i>B. subtilis</i>
	33.23	34.32	34.38			
<i>Staphylococcus aureus</i>	35.42	35.77	36.56	<i>S. aureus</i>	<i>S. aureus</i>	<i>S. aureus</i>
	34.13	35.67	39.90			
<i>Clostridium sporogenes</i>	34.20	34.87	35.45	<i>C. sporogenes</i>	<i>C. sporogenes</i>	<i>C. sporogenes</i>
	34.10	33.43	35.61			
<i>Pseudomonas aeruginosa</i>	36.40	36.74	37.22	<i>P. aeruginosa</i>	<i>P. aeruginosa</i>	Negative
	36.22	37.96	No Cq			
<i>Streptococcus pyogenes</i>	34.89	35.53	36.55	<i>S. pyogenes</i>	<i>S. pyogenes</i>	<i>S. pyogenes</i>
	35.09	35.93	35.88			
<i>Pseudomonas protegens</i>	34.14	34.38	36.52	Gram - Oxidase +	Gram - Oxidase +	Gram - Oxidase +
	33.28	34.51	35.61			

Comparability to Compendial Sterility Test

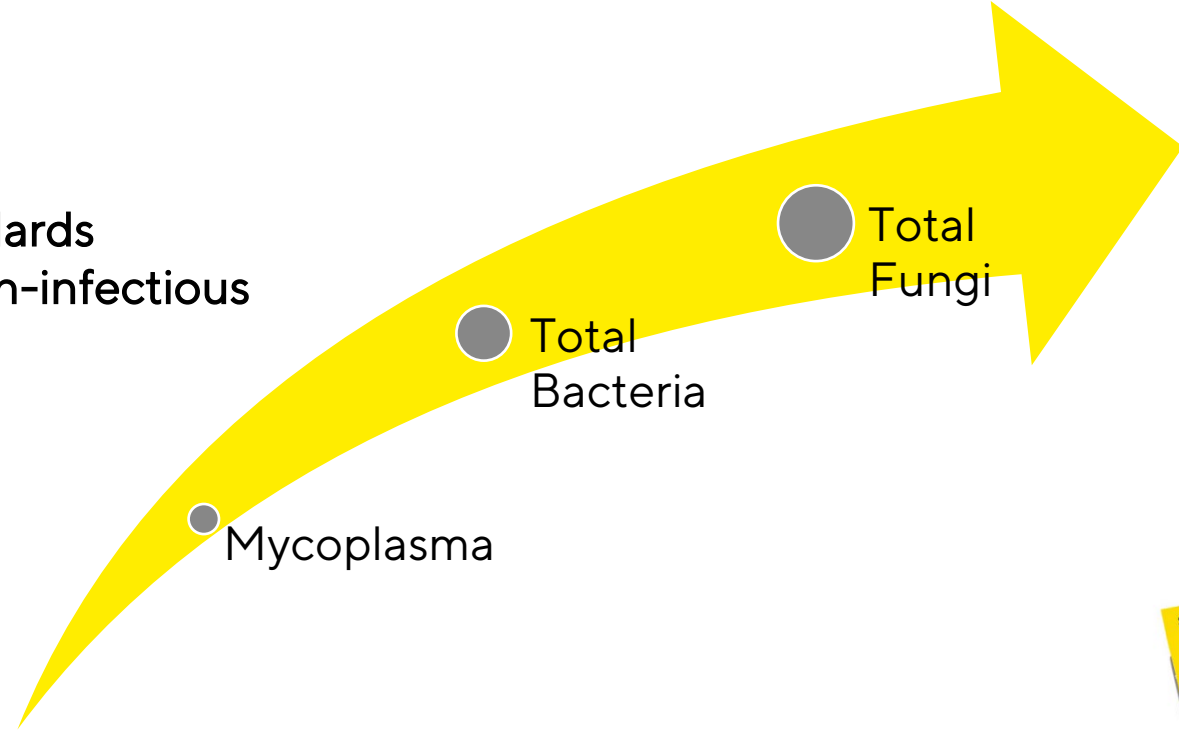
	Microsart® ATMP Fungi			Compendial culture method (External)		
	2x LOD ₉₅	LOD ₉₅	LOD ₉₅ /2	2x LOD ₉₅	LOD ₉₅	LOD ₉₅ /2
<i>Candida albicans</i>	32.25	32.27	32.96	<i>C. albicans</i>	<i>C. albicans</i>	Negative
	31.94	32.12	33.96			
<i>Aspergillus brasiliensis</i>	34.38	37.06	34.94	<i>A. brasiliensis</i>	<i>A. brasiliensis</i>	<i>A. brasiliensis</i>
	32.40	33.17	34.20			

Validation Results in a Nutshell



PCR@Sartorius.com

- DNA extraction
- qPCR reagents
- CFU Validation standards prequantified and non-infectious



Thank you.

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