Rapid Detection and Identification of Bacteria and Yeasts in Food, Beverages and Water

Abstract

HybriScan[®] system is a new technology based on the detection of microbe-specific rRNA using sandwich hybridization. It allows comprehensive and reliable routine control of microbial contamination during food production, from raw materials to finished goods. The system is sensitive and specific since the method is based on molecular genetic identification, and it allows detection of a group of microorganisms as well as specific species. The signal read-out is triggered optically by an enzymatically generated color change. No PCR is required because the method is quantitative without cell counting (using standards) and uses standard laboratory equipment.

The HybriScan[®] method is an economical, high throughput, 96-well microplate format system. The test is performed in less than 3 hours (in addition to the prep time) and offers a time saving of up to 10 days compared to cultivation-based assays. It is ideal for safety and quality control of alcoholic and nonalcoholic beverages, water and food. Specific examples include the detection of food-borne pathogens like Salmonella, Campylobacter, Listeria and Cronobacter spp., and counting of Legionella in water, including the most relevant species, L. pneumophila. Organisms can be detected at any level of classification, from species or genus to higher ranks.

Introduction

Methods for a rapid, sensitive and reliable detection and quantification of micro- organisms and pathogens in food, beverages and water are receiving increasing attention. The sandwich hybridization method used in the HybriScan[®] Test system is a suitable alternative for such analysis. This test method is independent of the influence of sample matrices and is able to distinguish between live and dead cells. Furthermore, the detection of non-culturable microbes is possible.

The HybriScan[®] method is based on the detection of rRNA via hybridization events and specific capture and detection probes (Figure 1). Specificity is achieved by targeting conserved or unique rRNA sequences. A biotin-labeled capture probe is used to immobilize the target sequence on a solid support plate (streptavidin- coated microtiter plate). A digoxigenin-labeled detection probe provides an enzyme-linked optical signal read out. Detection results from application of anti- DIG-horseradish peroxidase Fab fragments. The bound complex is visualized by horseradish peroxidase substrate TMB (3,3',5,5'-tetramethylbenzidine). Photometric data are measured at 450 nm and compared with standard solutions. The HybriScan[®] software enables easy measurement and data analysis.





© 2021 Merck KGaA, Darmstadt, Germany and/or its affiliates. All Rights Reserved. Merck, the vibrant M and Millipore are trademarks of Merck KGaA, Darmstadt, Germany or its affiliates. All other trademarks are the property of their respective owners. Detailed information on trademarks is available via publicly accessible resources. MK_PS7745EN Ver. 1.0 05/2021

Discussion

Sandwich hybridization is very sensitive, detecting attomoles of the respective target rRNA molecules [1]. The ideal hybridization target for bacteria and yeast is rRNA. These cells contain a large number of rRNA-containing ribosomes; a single cell therefore contains several thousand copies of rRNA but only one DNA. Sandwich hybridization also provides sensitivity in crude biological samples because it is not susceptible to matrix interference. By using specific probes, the HybriScan[®] technology allows flexible group- and speciesspecific detection. It is applicable to many analytical fields, including monitoring the microbial content of beer, wine, non-alcoholic beverages, drinking water, a wide variety of foods and wastewater. The HybriScan[®] system rapidly and accurately identifies, detects and quantifies many important pathogenic species, including Salmonella, Campylobacter, Listeria and Legionella including the most relevant species L. pneumophila. [2,3,4]. The HybriScan[®] test system is ideal for the comprehensive and reliable routine control of raw materials and concentrates in all production steps up to the quality check of finished goods.



The HybriScan[®] method has significant time- and labor-saving benefits over traditional methods. It also has benefits over PCR and real time PCR, which, although highly sensitive, are susceptible to experimental interferences, like template inhibition from insufficient purification, and lack quantification accuracy due to biases associated with PCR and reverse transcription reactions [5]. In contrast, the HybriScan[®] method is nearly independent of the influences of sample matrix and detects only living cells. It also permits the detection of non-culturable microbes. **Table 1** compares the benefits and disadvantages of the various methods.

HybriScan[®] Listeria monocytogenes: An example for that rapid and innovative test system

One of the most important foodborne pathogens is *Listeria monocytogenes* (Figure 3), which poses a health threat in foods that have long, refrigerated shelf lives [6]. Listeriosis, caused by ingestion of foods contaminated with *Listeria monocytogenes*, has increased dramatically in recent years, causing a great deal of distress and even death. Milk, cheese, ice cream and meat contaminated with this pathogen have led to recent outbreaks of listeriosis [7]. *L. monocytogenes* proliferates at refrigeration temperatures and is able to grow over a wide pH range from 4.4 to 9.4.

Table 1: Advantages of HybriScan[®] system over other detection techniques Det tech HybriSo system

PCR

ELISA

Conven cultiva based

The life science business of Merck operates as MilliporeSigma in the U.S. and Canada.

Sensitivity, specificity, flexibility and applicability of HybriScan[®] technology

Figure 2: Workflow of HybriScan[®] test method

The HybriScan[®] system is a simple, time-saving assay that can be performed with standard laboratory equipment.



Benefits over conventional detection methods and PCR

		•
ection mology	Advantage	Disadvantage
can®	 Advantage detects only living cells minimal interference by sample matrix high specificity ow cross-reactivity easy handling cost-efficient read-out devices quantitative and qualitative high sample throughput (96-microwell plates) 	 - no differentiation of serotypes or subspecies - limited probe design (rRNA target)
	 detects non-culturable microbes high sample throughput sensitive quantitative 	 no live/dead cell differentiation sensitive to matrix interference (high extraction effort) susceptible to polymerase inhibition
	 differentiation of serotypes or subspecies high sample throughput (96-microwell plates) quantitative and qualitative 	 low sensitivity low specificity, higher cross- reactivity slow and expensive assay development
itional tion- methods	 relatively inexpensive simple specific widely accepted method 	 time-consuming (up to 10 days) no detection of non-culturable Microbes low sample throughput laborious

based methods often give false negatives.



need for further cultivation.

Figure 3. *Listeria monocytogenes* Colonies Grown on PALCAM Agar

Conventional culture-based methods to detect *L. monocytogenes* generally involve selective enrichment followed by culturing on selective medium, isolation and biochemical identification [8]. This laborious and time-consuming approach often takes several days to show results. Also, compared to molecular biological and immunological methods, culture-

HybriScan[®] Listeria monocytogenes is an excellent alternative to lengthy culture- based methods. It is as reliable and comprehensive as classical methods, but permits rapid detection and quantification with results available within 48 hours.

The species-specific probe permits direct detection of *L. monocytogenes*, thereby eliminating false positives caused by other *Listeria* species. Even more compelling, suspected single colonies can be identified within one hour using the HybriScan[®] identification kit without

Figure 4 shows the validation results of HybriScan[®] *Listeria monocytogenes*. Food samples were analyzed with the HybriScan[®] method and compared to the culture- based method according to 64-LFGB. Five different food categories were tested. 355 food samples were analyzed and compared to culture-based method according to 64-LFGB. The blue values are the number of analyzed food samples in each category. Validation was according to ISO 16140:2003 (ASU L00.00-22). Results of validation showed a relative accuracy of 99.2 %, relative specificity of 98.5% and relative sensitivity of 99.6%.

Two versions are available. HybriScan[®] *Listeria monoytogenes* is used for the extremely rapid, sensitive and economical identification of suspect colonies of

L. monocytogenes. HybriScan[®] Listeria monocytogenes is used for the detection, identification and quantification of *L. monocytogenes* in different food matrixes.

Figure 4: Validation of HybriScan[®] Listeria monocytogenes



References

- Tenhunen, J.; Eloranta, J.; Kallio, A.; Soderlund, H. A solution hybridization method for quantification of mRNAs: determining the amount and stability of oncogene mRNA. Genet. Anal. Tech. Appl. 1990, 7, 228-233.
- sandwich hybridisation method for detection of lactic acid bacteria in brewery samples. J. Microbiol. Methods 2007, 68(3), 543-53.
- quantitative detection of yeast RNAs in crude cell lysates. Microb. Cell Fact. 2003, 2(1), 4-12.
- Bustin, S.A. Absolute quantification of mRNA using real-time reverse transcription polymerase chain reaction assays. J. Mol. Endocrinol. 2000, 25, 169-193.
- Mellefont, L.A.; McMeekin, T.A.; Ross, T. Effect of relative inoculum concentration on Listeria monocytogenes
- growth in co-culture. Int. J. Food Microbiol. 2008, 121, 157-168. • McLauchlin, J. The relationship between Listeria and listeriosis. Food Control 1996, 7, 187-193.
- Donnelly, C.W. Detection and isolation of Listeria monocytogenes from food samples: implications of sublethal injury, J. AOAC Int. 2002, 85, 495-500.





• Huhtamella, S.; Leinonen, M.; Nieminen, T.; Fahnert, B.; Myllykoski, L.; Breitenstein, A.; Neubauer, P. RNA-based

• Leskela, T.; Tilsala-Timisjarvi, A.; Kusnetsov, J.; Neubauer, P.; Breitenstein, A. Sensitive genus-specific detection of Legionella by a 16S rRNA based sandwich hybridization assay. J. Microbiol. Methods 2005, 62(2), 167-79. • Rautio, J.; Barken, KB.; Lahdenpera, J.; Breitenstein, A.; Molin, S.; Neubauer, P. Sandwich hybridisation assay for



Rapid Test System for the Detection of Beer-Spoilage Bacteria

Frank Michel, Merck KGaA, Darmstadt, Germany; U.-M. Kohlstock, Katja Vetter and Mathias Zachlod, Scanbec GmbH, Bitterfeld-Wolfen/DE; Jvo Siegrist, Merck KGaA, Darmstadt, Germany

Abstract

Beer-spoiling microorganisms cause an increase of turbidity and unpleasant sensory changes in beer. Since the improved process technology in modern breweries has resulted in significant reduction of oxygen content in the final product, the role of strictly anaerobic bacteria like *Pectinatus* and *Megasphaera* has increased. Detection of these organisms, which is traditionally done by incubation on culture medium, takes a week or even longer. A rapid molecular test system is desirable for the detection of all known beer-spoiling microorganisms in one test only. Results of this study on a rapid test kit demonstrate that all beer-spoiling microorganisms can be detected and identified in a shorter time and in one test only.

Introduction

Beer continues to be a popular drink. It is important to maintain quality and enhance stability of beer during the production process through early detection of beer-spoiling microbes. The known beerspoiling species and genera listed in Table 1 can all be detected by HybriScan[®]**D** Beer, a rapid molecular test system for the detection of these microorganisms in one test.

Table 1: The Beer Spoiling Species and Genera that can be
 Detected by the HybriScan[®]D – Beer Test

Genus Lactobacillus

Lactobacillus acidophilus Lactobacillus brevis Lactobacillus brevisimilis Lactobacillus buchneri Lactobacillus casei Lactobacillus collinoides Lactobacillus coryniformis Lactobacillus curvatus Lactobacillus fermentum Lactobacillus fructivorans Lactobacillus lindneri Lactobacillus malefermentans Lactobacillus paracasei Lactobacillus parabuchneri Lactobacillus paraplantarum Lactobacillus plantarum Lactobacillus rhamnosus

Genus *Pediocoocus* Pediococcus acidilactici Pediococcus damnosus Pediococcus inopinatus Pediococcus parvulus Pediococcus pentosaceus

Genus Pectinatus

Pectinatus cerevisiiphilus Pectinatus frisingensis Pectinatus haikare Pectinatus portalensis Pectinatus spp.

Genus Megasphaera Megasphaera cerevisiae

HybriScan[®]**D** Beer test is based on the detection of target molecules from the microorganisms of interest by means of specific capture and detection probes in a so-called sandwich hybridization. The hybridization reaction of the target molecules with the Biotinlabeled capture and a DIG-labeled detection probe takes place in a streptavidin coated microtiter plate (Figure 1).

After coupling of the target molecule to the microtiter plate, an enzyme is attached in a subsequent incubation step. After several washing steps, reaction with a color substrate gives blue coloration that changes into yellow color after the addition of a stop solution. The yellow color enables highly sensitive photometric measurement at 450 nm (Figure 2). Comparison is made with the standard solutions contained in the test kit.



The life science business of Merck KGaA, Darmstadt. Germany operates as MilliporeSigma in the U.S. and Canada.

© 2021 Merck KGaA, Darmstadt, Germany and/or its affiliates. All Rights Reserved. MilliporeSigma, the vibrant M, and Millinore are trademarks of Merck KGaA Darmstadt Germany or its affiliates. All other trademarks are the property of their espective owners. Detailed information on trademarks is available via publicly accessible resources it Code MS_PS7663EN 35218 02/21

Experimental

In this study, beer samples with alcohol content between 2.5% and 6.7% were tested with HybriScan[®]D beer test kit. The beer samples were spiked with *L. brevis*, *L. coryniformis*, *L. lindneri*, *Ped.* damnosus, M. cerevisiae, and Pec. frisingensis in a range between 10³ and 10⁶ cfu/sample. The bacteria were cultivated in media according to DSMZ. The cultures were harvested and washed with sterile saline solution. The bacterial counts were then determined by measuring OD₆₀₀ and by counting colony forming units (cfu) on agar.

Afterwards cultures were inoculated into the beer.



Figure 1: Sandwich Hybridization between Target rRNA Capture and Detection Probe



total analysis time: ca. 2 hours



Additional 30 brewery samples were examined with the HybriScan[®]D beer test for beer-spoiling microorganisms. Up to 10 mL of the beer sample was processed according to the HybriScan[®]**D** protocol published by Sigma-Aldrich[®]. The results were controlled by cultivation on NBB agar.

For the development of further genera and species, specific test solution experiments were performed with 11 additional pure bacterial cultures of most common beer-spoiling micro-organisms for detection by HybriScan[®]**D** test experiments. These bacterial strains were also cultivated on media according to DSMZ and processed according to HybriScan[®]**D** protocol.

Results

In this study, a total of 178 samples, with alcohol content between 2.5% and 6.7%, were tested with HybriScan[®]*D* beer test. In order to confirm that it is possible to detect different beer-spoiling species with the test solution beer, the samples were spiked with *L. brevis*, L. coryniformis, L. lindneri, Ped. damnosus, Pec. frisingensis and *M. cerevisiae*. Results were compared with inoculated amount of bacteria. Results of 18 samples are presented in Figure 3. The bacterial counts in the beer samples which were determined by the HybriScan[®]**D** test were in the same range as the inoculated values.



Amounts.

Pec. frisingensis was detected only in beer sample with 2.5% alcohol. Results of the HybriScan[®]D test were below the counts of the inoculum. The number of microbes in beer is possibly diminished because the strain used in the study was not adapted to beer. Pec. *frisingensis* were not detected in beer with a higher alcohol content (data not shown). It was observed that beer with a low alcohol content is more prone to spoilage with *Pectinatus* and *Megasphaera* species (1). Pectinatus species are more resistant and can survive in acidic condition. The pH tolerance of these anaerobic bacteria is influenced by the presence of ethanol (2).

Real beer samples from the brewery were also tested with the HybriScan[®]**D** beer test for beer-contaminating bacteria. These samples were also simultaneously checked with NBB agar. The HybriScan[®]*D* test gave a positive signal for each sample. These results were confirmed on agar (Figure 4).

For a more sophisticated analysis, seven other test solutions "Pectinatus spp./Megasphaera spp.", "Pediococcus spp.", "Lactobacillus brevis", "L. lindneri", "L. collinoides", "L. rossiae" and "L. backii" were developed and optimized. Experiments were performed with 17 beer-spoiling bacteria strains. Eight different test solutions were tested with 10 beer-spoiling bacteria species. The experiment was performed with bacterial cultures which contained bacterial amounts $\geq 10^6$ cfu/sample.





Figure 3: Bacterial Counts of 18 Spiked Beer Samples Determined by the HybriScan[®]D Beer Compared to the Counts of Inoculated

Figure 4: Counts of Real Beer Samples Determinated by HybriScan[®]D Compared to the Counts of NBB Agar.

The test solution beer gave a positive signal with all used bacteria. The yellow signals at the microtiter plate confirm that the optimized test solutions react specifically and show no crossreactivity (Figure 5). The experiments for the optimization of the test solutions indicated that the detection limit of those test solutions differs for *Lactobacillus* spp. and the other mentioned beer spoiling genera between 10⁴ and 10⁵ cfu/sample.



Figure 5: Result of a HybriScan[®]D Test with 8 Different Test Solutions and 10 Different Beer Contaminating Bacteria after Addition of the Stop Solution following HybriScan[®]D Test Protocol

Conclusions

- It is a rapid and sensitive molecular biological test system that is comparable to the classical cultivation method.
- It offers qualitative and quantitative detection of the most wellknown beer-spoiling organisms in one test only.
- It is highly flexible as it allows combination with different read out technologies, and detection of rRNA and mRNA is possible.
- It is a robust test with easily predictable specificity of the probes, and easy synthesis of the oligonucleotide probes.
- It is a faster and cost-effective test with inexpensive read out device technology.

References

- 1. A. D. Paradh, W. J. Mitchell and A. E. Hill J. Inst. Brew. 117(4), 498 506 (2011).
- 2. Suzuki, K., 125th Anniversary review: Microbiological instability of beer caused by spoilage bacteria. J. Inst. Brew., 2011, 117, 131-155 (2011).
- HybriScan is a registered trademark of ScanBec GmbH.

Millipore.

Preparation, Separation, Filtration & Monitoring Products

Merck

Validation of shorter protocol for detection of *Salmonella enterica* subsp. Enterica in peanut butter samples followed by a rRNA detection system

Kathleen Merx¹ and Jvo Siegrist²

¹ BECIT GmbH, Edisonstr. 5, 06766 Wolfen, Germany ² Sigma-Aldrich Chemie GmbH, Industriestr. 25, 9470 Buchs Switzerland

Abstract

Food-borne pathogens Salmonella is commonly evaluated in manufacturing of peanut butter and other food products. For the HybriScan®D Salmonella Test (Cat. No. 55662) the ISO based enrichment method is recommended. That means sample pre-enrichment for 18 hours at 37 °C in buffered peptone water (BPW) followed by a selective enrichment step in Rappaport-Vassiliadis (RV) Broth for 24 hours at 41 °C. HybriScan®D Salmonella is a rRNA sandwich hybridisation detection system which needs at least 500 cfu/mL for the assay. This rapid molecular test system is desirable for the detection of Salmonella species like S. Enteritidis, S. Typhimurium, S. Typhi and S. Paratyphi. Results of this study on a rapid test kit demonstrate that Salmonella enterica subsp. enterica (ATTC[®] 13311[™]) can be detected and identified in a shorter time even in a difficult sample matrix like peanut butter.

Introduction

Peanut butter consist of about 20% carbohydrates, 25% proteins and 50% fat, Salmonella cells are just a very small component of the overall sample material and may be attached within the food matrix as single cells or clumps of cells. Normally before rapid detection methods can be used successfully, it is usually necessary to separate the target cells from the food matrix and from the background microflora. But even the HybriScan is as well a rapid molecular biological system it is practically insensitive to the sample matrix.

HybriScan®D Salmonella test is based on the detection of target molecules from the microorganisms of interest by means of specific capture and detection probes in a so-called sandwich hybridization. The hybridization reaction of the target molecules with the Biotin-labeled capture and a DIG-labeled detection probe takes place in a streptavidin coated microtiter plate (**Figure 1**).

Figure 1: Sandwich Hybridization between Target rRNA Capture and Detection Probe.



After coupling of the target molecule to the microtiter plate, an enzyme is attached in a subsequent incubation step. After several washing steps, reaction with a color substrate gives blue coloration that changes into yellow color after the addition of a stop solution. The vellow color enables highly sensitive photometric measurement at 450 nm (Figure 2). Comparison is made with the standard solutions contained in the test kit.

10 min

Figure 2: Work flow – HybriScan®D Salmonella.



Of the 107 inoculated with Salmonella enterica peanut butter samples, 106 were identified as clearly contaminated with Salmonella by the use of HybriScan[®]D Salmonella assay. The result of 1 sample was considered questionable. All negative controls gave negative results in the HybriScan®D Salmonella assay. See **Table 1– 4**.

Table 1					Table 3				
Code		Average	Sample	Cells/	Code	- · ·	Average	Sample	Cells
Date	Probe	O.D. 450 nm	0.D.%	10 µL	Date	Probe	0.D. 450 nm	0.D.%	10 µ
	51	0.046		0		51	0.058		0
	52	0.149		10.0		52	0.154		10.0
	53	0.377		30.0		53	0.356		30.0
1 6 2 4 2 5 4	54	1.017	0.0	90.0	02204252	54	0.982	2.0	90.0
1624251	1-1 N.C.	0.046	0.0		93294252	6-1 N.C.	0.046	-2.8	
	1-2	4.060	8/4.2			6-2	3.727	886.2	
	1-3	3.955	851.4			6-3	3.994	950.8	
	1-4	3.970	854.6			6-4	3.659	869.8	
	1-5	3.899	839.2			6-5	3.512	834.4	
	1-6	3.891	837.4			6-6	3.430	814.5	
	1-7	3.535	760.0			6-7	3.588	852.8	
	1-8	3.791	815.8			6-8	1./38	405.9	
	1-9	3.736	803.7			6-9	4.067	968.5	
	1-10	3.816	821.1			6-10	3.727	886.2	
1874251	2-1 N.C.	0.048	0.3		01304252	7-1 N.C.	0.046	-2.9	
	2-2	3.748	806.4			7-2	3.787	900.7	
	2-3	3.726	801.6			7-3	3.575	849.5	
	2-4	4.072	877.0			7-4	3.779	898.8	
	2-5	3.907	840.9			7-5	3.875	922.0	
	2-6	3.965	853.5			7-6	4.144	987.1	
	2-7	3.824	822.8			7-7	4.067	968.5	
	2-8	4.060	874.2			7-8	3.988	949.4	
	2-9	4.003	861.9			7-9	4.135	984.9	
	2-10	4.032	868.2			7-10	4.101	976.7	
					01304252	8-1 N.C.	0.053	-1.2	
						8-2	3.507	833.2	
Table 2						8-3	3.906	929.4	
Codo		Average	Comple			8-4	3.708	881.7	
Date	Droho	Average				8-5	3.672	873.1	
Date	S1	0.051	0.0.70			8-6	4.059	966.4	
	51	0.051		10.0		8-7	3.914	931.5	
	52	0.109		20.0		8-8	4.101	976.7	
	53	0.409		30.0		8-9	3.750	891.8	
	54	1.1/1		90.0		8-10	3.852	916.5	
01574251	3-1 N.C.	0.057	1.2						
	3-2	0.608	112.1		Table 4				
	3-3	1.665	324.6						
	3-4	0.289	47.9		Code	Durl	Average	Sample	Cells
	3-5	0.120	13.9		Date	Probe	0.D. 450 nm	0.D.%	10 µL
	3-6	1.146	220.2			51	0.047		0
	3-7	0.701	130.8			52	0.131		10.0
	3-8	0.251	40.2			53	0.339		30.0

3-9

0133425

0086425

S1= St

S2=Sta

S3=Sta

S4 = St

N.C.= inocula 0.981

187.0



20 min

Experimental

10 min

The matrix to be examined was Peanut Butter (9 different brand codes with 12 different code dates). The pre-enrichment time described in the protocol of the HybriScan[®]D Salmonella test takes 42 hours. In this experiment one target was to reduce the enrichment time to 24 hours in total. The cultivation time of the pre-enrichment peptone water culture took 18 hours; the incubation time of the selective enrichment culture in Rappaport-Vassiliades Enrichment Broth was shortened to 6 hours. Per peanut butter batch, one sample wasn't inoculated and carried as a negative control (N.C.), 9 to 10 samples were inoculated with Salmonella enterica subsp. Enterica (ATTC[®] 13311^M). Each Peanut Butter sample was treated as follows:

- 25 g of Peanut Butter (except the negative controls) were inoculated with 1 to 5 cells of Salmonella enterica ٠ subsp. Enterica.
- 225 mL buffered peptone water were added to each sample, the mixture was homogenised for 1 minute in a Stomacher and the sample were incubated for 18 hours at 37 °C.
- After 18 hours of incubation 0.1 mL of the pre-enrichment peptone water culture were transferred to 10 mL Rappaport-Vassiliades Enrichment Broth. The selective main enrichment was conducted for 6 hours at 41°C.

Cell lysis and the HybriScan®D Salmonella assay were completed as described in the HybriScan®D Salmonella test protocol. In addition, each negative control and inoculated sample were tested for Salmonella according to EN ISO 6579:2002.

Results

Evaluation of the samples was performed using the following formula as described in the HybriScan®D Salmonella assay:

Sample 0.D.% = $(0.D_{\text{sample}} - 0.D_{\text{N.C.}}) / (0.D_{\text{P.C.}} - 0.D_{\text{N.C.}}) \times 72.1\%$

P.C. positive control (S3)

N.C. negative control (S1)

Samples with O.D.% values under 10 are considered negative. Samples with O.D.% values from 10 to <20 are considered questionable. Samples with O.D.% values ≥ 20 are considered positive.



© 2021 Merck KGaA, Darmstadt, Germany and/or its affiliates All Rights Reserved. Merck, the vibrant M, and Millipore are trademarks of Merck KGaA, Darmstadt, Germany or its affiliates. All other trademarks are the property of their respective owners. Detailed information on trademarks is available via publicly accessible resources. MK_PS7653EN 35347 03/2021

The life science business of Merck operates

	3-10	0.359	62.0		9-2	2.749	668.2
2	4-1 N.C.	0.051	0.0		9-3	0.267	54.4
	4-2	3.737	741.4		9-4	1.231	292.9
	4-3	3.682	730.3		9-5	0.166	29.3
	4-4	3.927	779.6		9-6	1.516	363.3
	4-5	3.700	733.9		9-7	2.969	722.7
	4-6	3.780	750.1		9-8	1.921	463.5
	4-7	3.813	756.6		9-9	3.646	890.1
	4-8	3.915	777.1	008942	252 10-1 N.C.	0.050	0.7
	4-9	3.682	730.4		10-2	1.372	327.7
	4-10	4.091	812.6		10-3	3.943	963.6
2	5-1 N.C.	0.053	0.4		10-4	4.063	993.3
	5-2	0.232	36.4		10-5	3.913	956.2
	5-3	0.267	43.4		10-6	3.543	864.7
	5-4	0.740	138.7		10-7	3.803	929.0
	5-5	0.880	166.7		10-8	3.869	945.3
	5-6	0.736	137.8		10-9	4.112	1005.4
	5-7	0.561	102.7		10-10	3.615	882.4
	5-8	1.967	385.3	019042	252 11-1 N.C.	0.049	0.5
	5-9	2.093	410.7		11-2	3.537	863.1
	5-10	3.585	710.7		11-3	3.874	946.6
					11-4	3.988	974.8
					11-5	3.979	972.4
	ndard1 0 c	olle/10 ul			11-6	4.049	989.7
				11-7	3.881	948.2	
ır	ndard2 10.0	00 cells/µL			11-8	3.421	834.5
					11-9	3.984	973.7
I	ndard3 30.0	00 cells/10µ	L	0.070.00	11-10	3.635	887.3
а	ndard4 90.0	000 cells/101	ıL	007042	152 12-1 N.C.	0.051	0.9
-					12-2	2.225	538.6
Negative control: sample was not ted with <i>Salmonella spp.</i>			12-3	3.100	755.0		
			12-4	2.251	545.0		
					12-5	0.434	95.7
					12-6	1.037	244.7
					12-7	0.340	/2.5
					12-8	0.555	125.5
					12-9	0.293	60.7

00984252 9-1 N.C

0.060

3.1



Preparation, Separation, Filtration & Monitoring Products