



BSI Standards Publication

Biotechnology — Inventory of methods for detection of microbiological contamination in mammalian cell culture

National foreword

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Biotechnology — Inventory of methods for detection of microbiological contamination in mammalian cell culture

*Biotechnologie — Inventaire des méthodes pour la détection de
la contamination microbiologique dans la culture cellulaire de
mammifères*

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Foreword

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The document was prepared by Technical Committee ISO/TC 276, *Biotechnology*, Subcommittee SC 1, *Analytical methods*.

Any feedback or questions on this document should be directed to the user's national standards body. A complete listing of these bodies can be found at www.iso.org/members.html.

Introduction

Cell culture plays an extremely important role in biotechnology and life science research. Therefore, the reliability of scientific data from cell culture is essential. One of the most common problems in cell culture is microbiological contamination. This usually results in catastrophic cell death or contamination sustained at low levels (sometimes due to the use of antibiotics), and thus impacts the reliability of experimental data derived from cell culture. Nonetheless, despite its prevalence and importance, the lack of open discussion discourages development and learning of best practices to avoid microbial contamination in cell culture. Microbial contamination is an economic issue as it affects the reproducibility of scientific data, the efficiency of in vitro cell culture work and most importantly, the safety of laboratory operators. It is therefore necessary to monitor microbial contamination through a full understanding of the source of contamination and employ good testing techniques before and during cell culture.

When cultured cells have been contaminated, first the various aspects of the contamination are identified, including the nature of contamination, the time of contamination and the operating environment. Contaminants can include bacteria, fungi, mycoplasma, viruses and other types of organisms. In order to demonstrate the absence of microbiological contamination in cell culture, it can be necessary to conduct a series of tests for likely organisms and such an approach will benefit from risk assessment of the cell type, cell origin and reagents used for their culture.

Environmental monitoring in areas where cells are cultured and stored can reduce the risk of microbial contamination from the processing environment.

This document provides an inventory of methods for the detection of microbiological contamination in mammalian cell culture in order to provide users with an overview that also includes information on pro- and contra indications for the listed methods in relation to the appropriate sample type.

Biotechnology — Inventory of methods for detection of microbiological contamination in mammalian cell culture

1 Scope

This document provides an inventory of methods for the detection of microbiological contamination in mammalian cell culture. This document includes considerations for the selection of methods to test the presence of common contaminants such as bacteria, fungi, viruses and mycoplasma. This document is not applicable to prions and protists.

This document is intended for use by biomedical researchers, biobank operators and others performing mammalian cell culture.

2 Normative references

There are no normative references in this document.

3 Terms and definitions

For the purposes of this document, the following terms and definitions apply.

ISO and IEC maintain terminology databases for use in standardization at the following addresses:

- ISO Online browsing platform: available at <https://www.iso.org/obp>
- IEC Electropedia: available at <https://www.electropedia.org/>

3.1

accuracy

closeness of agreement between a measured quantity value and the true quantity value of a measurand

[SOURCE: ISO/IEC Guide 99:2007, 2.13, modified — Notes to entry deleted.]

3.2

digital PCR

dPCR

procedure in which nucleic acid templates are distributed across multiple partitions of nominally equivalent volume, such that some partitions contain template and others do not, followed by PCR amplification of target sequences and detection of specific PCR products, providing a count of the number of partitions with a positive and negative signal for the target template

Note 1 to entry: Nucleic acid target sequences are assumed to be randomly and independently distributed across the partitions during the partitioning process.

Note 2 to entry: The count of positive and negative partitions is normally based on end point detection of PCR products following thermal cycling, however real-time qPCR monitoring of PCR product accumulation is additionally possible for some dPCR platforms.

[SOURCE: ISO 20395:2019, 3.10]