

WELCOME TO THE

FEEDCO STAKEHOLDERS MEETING ON MICROORGANISMS



AGENDA 20TH JUNE 2023

Time	No.	Item	Presenter
09:00h	1	Welcome	EFSA FEEDCO Unit
09:05h	2	Brief introduction and in-house messages	EFSA FEEDCO Unit
09:15h	3	EFSA Guidance on the characterisation of microorganisms used as feed additives or as production organisms	EFSA FEEDCO Unit
09:30h	4	EFSA statement on the requirement for whole genome sequence analysis of microorganisms intentionally used in the food chain	EFSA FEEDCO Unit
		Microorganisms Pipelines Service - MoPS	
09.45h	5	Industry's views on the EFSA Guidance, Statement and MoPS	Industry representatives
10:30h	6	Questions and answers	All participants
11:20h	7	Concluding remarks	EFSA FEEDCO Unit
11:30h		End of the meeting	



SOME TIPS AND RULES - ONLINE



Keep your **microphone muted and camera off** at all times unless specifically asked by the Chair or an EFSA staff

Keep the **meeting chat box clean**. Use it only to signal technical problems or when indicated by the Panel Chair



Use "raise hand" function to ask the floor to submit questions or comments when indicated by the Chair

If you have problems with the connection, exit the meeting and rejoin



Use of headset recommended for better sound quality





EFSA Guidance on the characterisation of microorganisms used as feed additives or as production organisms



GUIDANCE UPDATE

Consolidating well-established and fitfor-purpose principles

2

New needs – bacteriophages

- Update to consider:
 - Recent advancements new technologies/tools
 - New data/information available
 - Experience gained



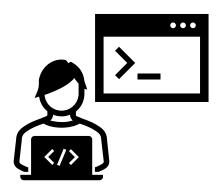


ADOPTED: 21 February 2018 doi: 10.2903/j.efsa.2018.5206

Guidance on the characterisation of microorganisms used as feed additives or as production organisms

EFSA Panel on Additives and Products or Substances used in Animal Feed (FEEDAP), Guido Rychen, Gabriele Aquilina, Giovanna Azimonti, Vasileios Bampidis, Maria de Lourdes Bastos, Georges Bories, Andrew Chesson, Pier Sandro Cocconcelli, Gerhard Flachowsky, Jürgen Gropp, Boris Kolar, Maryline Kouba, Marta López-Alonso, Secundino López Puente, Alberto Mantovani, Baltasar Mayo, Fernando Ramos, Maria Saarela, Roberto Edoardo Villa, Robert John Wallace, Pieter Wester, Boet Glandorf, Lieve Herman, Sirpa Kärenlampi, Jaime Aguilera, Montserrat Anguita, Rosella Brozzi and Jaume Galobart







UPDATE GUIDANCE - CONT....

MICROBIAL CHARACTERISATION – AMR SUSCEPTIBILITY

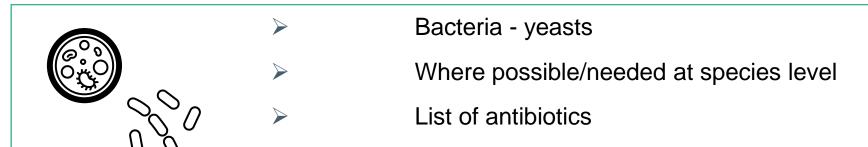
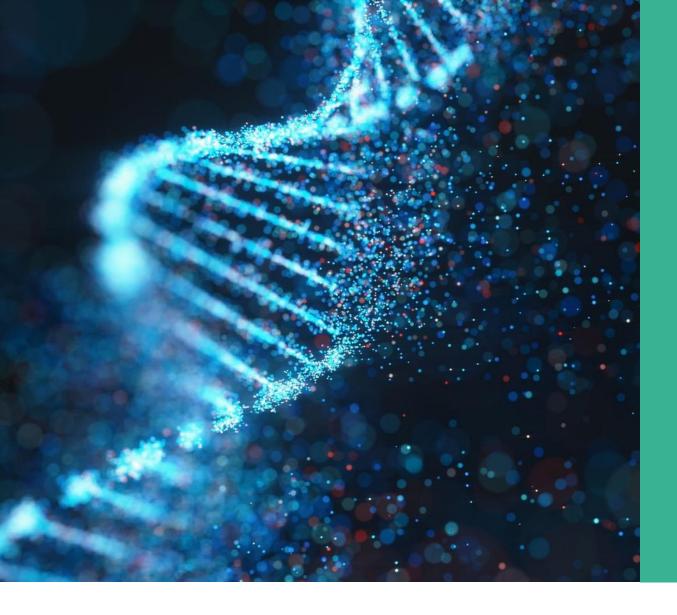


Table 2: Microbiological cut-off values (mg/L)

	Ampicillin	Vancomycin	Gentamicin	Kanamycin	Streptomycin	Erythromycin	Clindamycin	Tetracycline	Chloramphenico	Tylosin	Ciprofloxacin	Colistin	Fosfomycin
Lactobacillus obligate homofermentative(a)	2	2	16	16	16	1	4	4	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus acidophilus group	1	2	16	64	16	1	4	4	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus obligate heterofermentative(b)	2	n.r.	16	64	64	1	4	8 ^(c)	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus reuteri	2	n.r.	8	64	64	1	4	32	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus facultative heterofermentative(d)	4	n.r.	16	64	64	1	4	8	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus plantarum/pentosus	2	n.r.	16	64	n.r.	1	4	32	8	n.r.	n.r.	n.r.	n.r.
Lactobacillus rhamnosus	4	n.r.	16	64	32	1	4	8	4	n.r.	n.r.	n.r.	n.r.
Lactobacillus casei/paracasei	4	n.r.	32	64	64	1	4	4	4	n.r.	n.r.	n.r.	n.r.
Bifidobacterium	2	2	64	n.r.	128	1	1	8	4	n.r.	n.r.	n.r.	n.r.
Pediococcus	4	n.r.	16	64	64	1	1	8	4	n.r.	n.r.	n.r.	n.r.
Leuconostoc	2	n.r.	16	16	64	1	1	8	4	n.r.	n.r.	n.r.	n.r.
Lactococcus lactis	2	4	32	64	32	1	1	4	8	n.r.	n.r.	n.r.	n.r.
Streptococcus thermophilus	2	4	32	n.r.	64	2	2	4	4	n.r.	n.r.	n.r.	n.r.
Bacillus	n.r.	4	4	8	8	4	4	8	8	n.r.	n.r.	n.r.	n.r.
Propionibacterium	2	4	64	64	64	0.5	0.25	2	2	n.r.	n.r.	n.r.	n.r.
Enterococcus faecium	2	4	32	1,024	128	4	4	4	16	4	n.r.	n.r.	n.r.
Corynebacterium and other Gram-positive		4	4	16	8	1	4	2	4	n.r.	n.r.	n.r.	n.r.
Enterobacteriaceae		n.r.	2	8	16	n.r.	n.r.	8	n.r.	n.r.	0.06	2	8



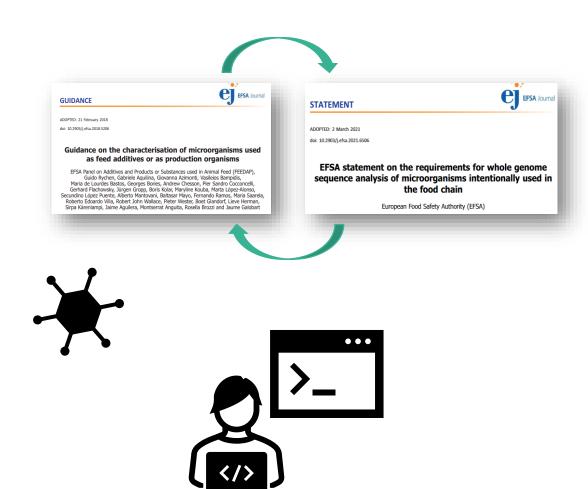


EFSA statement on the requirement for whole genome sequence analysis of microorganisms intentionally used in the food chain

WGS STATEMENT UPDATE

Complementing well-established guidance documents

- Expanding scope bacteriophages
- 3 Update to consider:
 - Most frequent questions
 - Recent advancements new technologies/tools
 - Development and implementation of the Microorganisms pipelines service





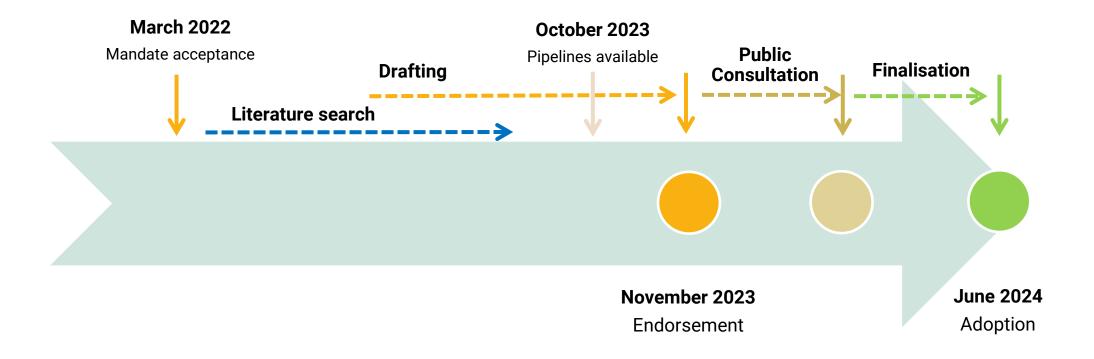
MAIN LIMITATIONS OF DATASET

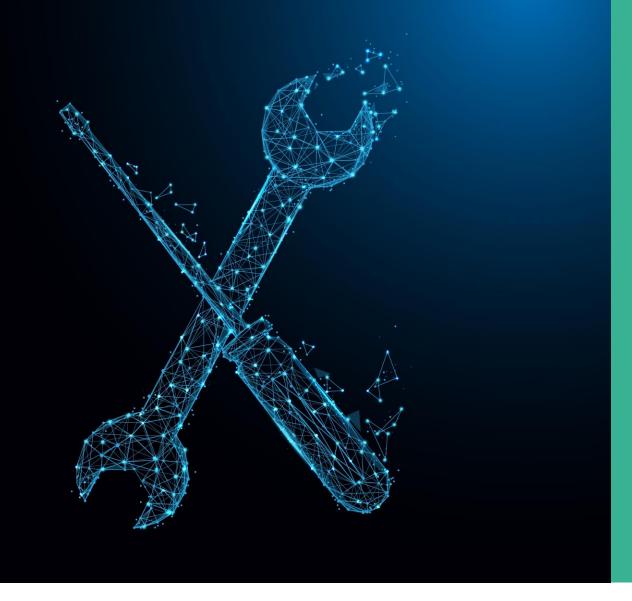
- Taxonomic identification reference strains
- Interrogation for the presence of genes of concern databases, reporting
- Antimicrobial activity test item
- Absence of viable cells and DNA of the production strain sampling, methodology, reporting, controls

Most frequent questions



TIMELINE - GUIDANCE AND STATEMENT





Microorganisms Pipelines Service -MoPS

MOPS IN A NUTSHELL

SCOPE



Develop and implement 3 pipelines (bacteria, yeasts/filamentous fungi, viruses) to support the risk assessment (RA) of WGS data

WHY



- Address the needs of different risk assessments domains
- Comprehensive microorganisms RA
- Standardised microorganisms WGS based data analysis

HOW



- Build a secure and confidential environment
- Perform the sequence quality check of the WGS data
- Use the WGS data to taxonomically identify and characterise the microorganism



TIMELINE - MOPS

April 2021 Start of the Project





Design of the project delivered

Design

October 2022

Pipelines





November 2022

Implementation of MoPS tool completed

Building

June 2023

Go Live for EFSA



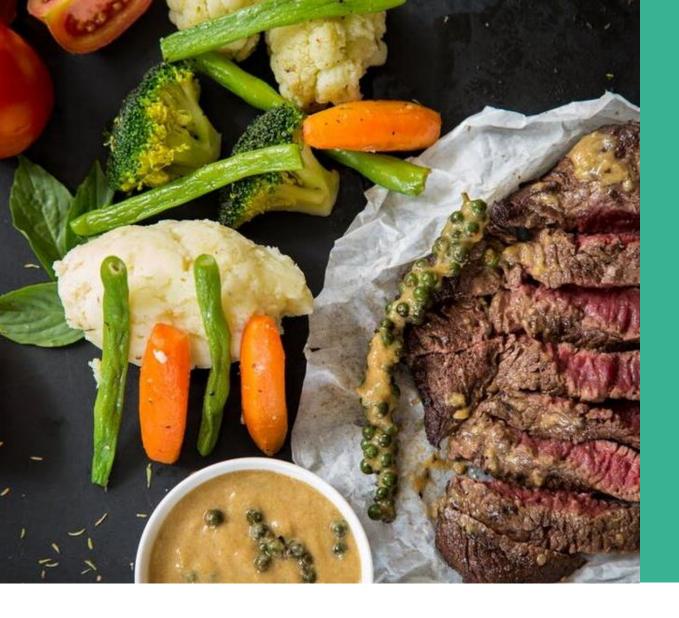


October 2023

Closure of the project

Testing





Industry's views on the EFSA Guidance, Statement and MoPS



Questions and answers

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