19.05.22

SO on the role played by the environment in the emergence and spread of antimicrobial resistance through the food chain

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PRO-FEM Agriclose Reference Workshop

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European Food Safety Authority

SCIENTIFIC OPINION

EFSA Journal

ADOPTED: 29 April 2021

doi: 10.2903/j.efsa.2021.6651

Role played by the environment in the emergence and spread of antimicrobial resistance (AMR) through the food chain

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In line with the EC AMR Action Plan

Self-task of the EFSA BIOHAZ Panel
In close collaboration with:

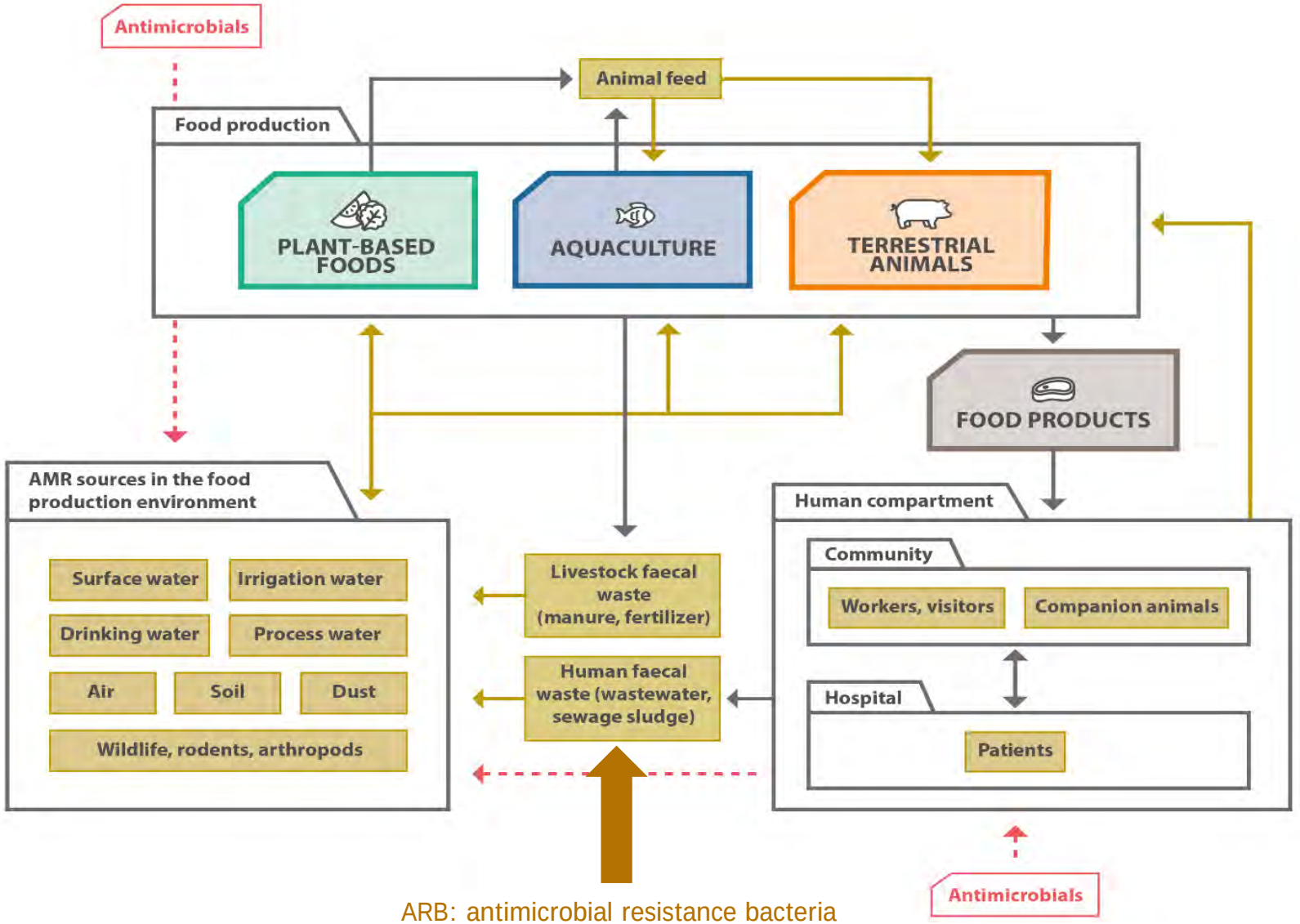
https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2021.6651

Interpretation of Terms of Reference

- **Food-producing environment: environments where food of animal or non-animal origin is produced or processed**, at both **pre-harvest** (primary production) and **post-harvest** level (processing: e.g. slaughterhouses, processing plants).

- **Three food sectors**:

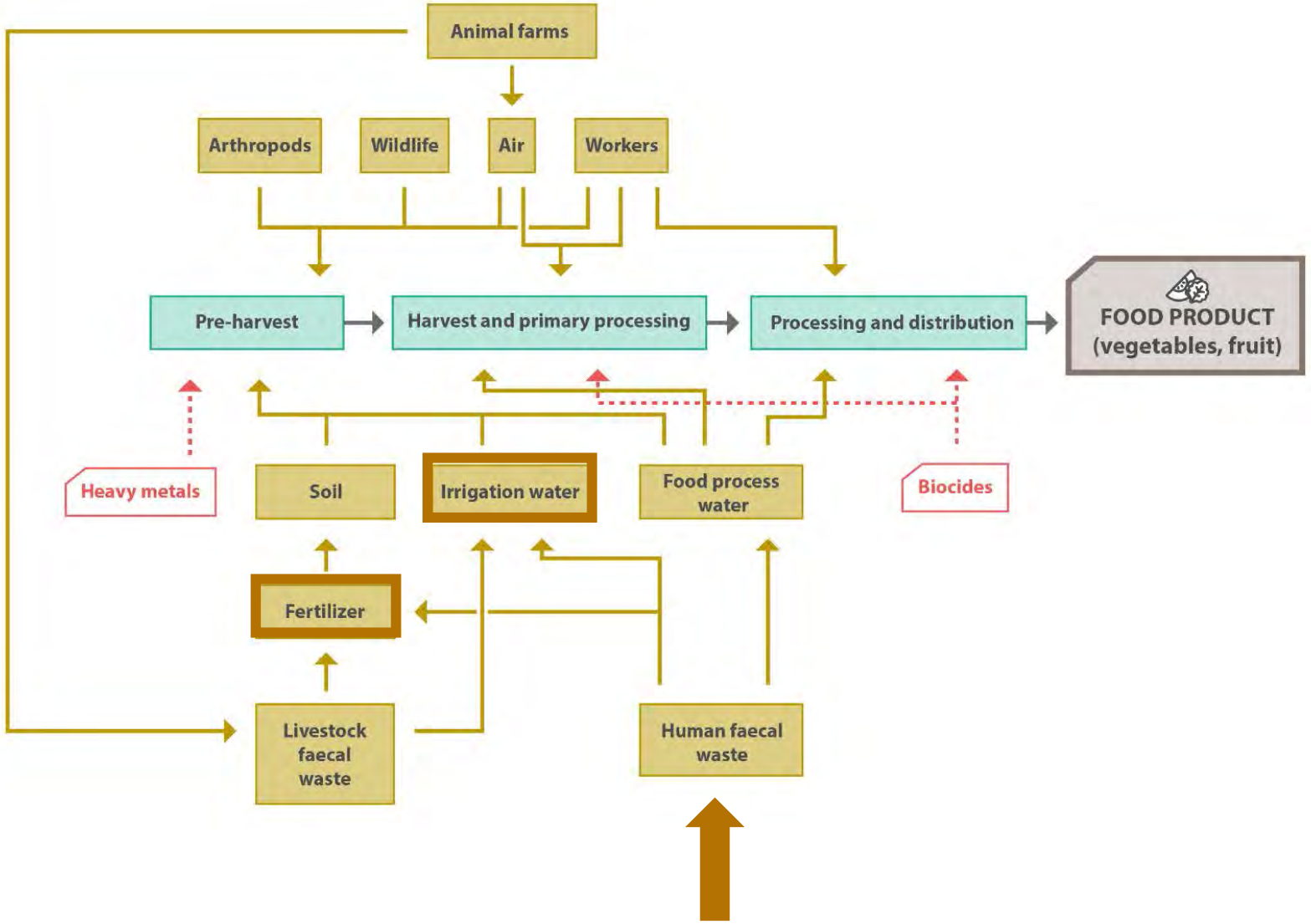
ToR1: Sources and Transmission routes



ARB: antimicrobial resistance bacteria
ARGs: antimicrobial resistance genes

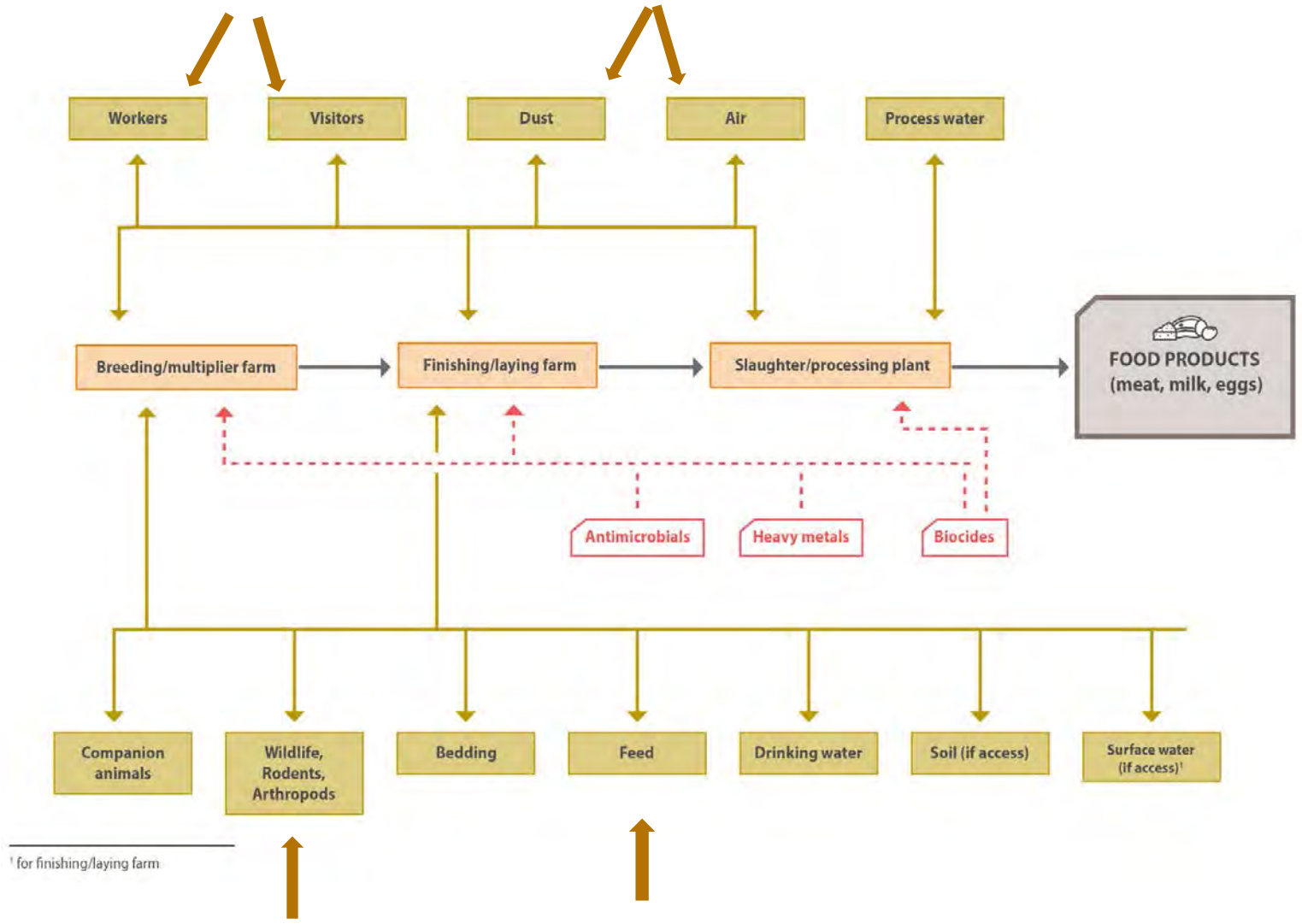
- Everything linked cyclical manner
- Most sources = transmission routes.
- Limited studies, but all known sources of pathogens.

ToR1: Plant-based food sources/routes



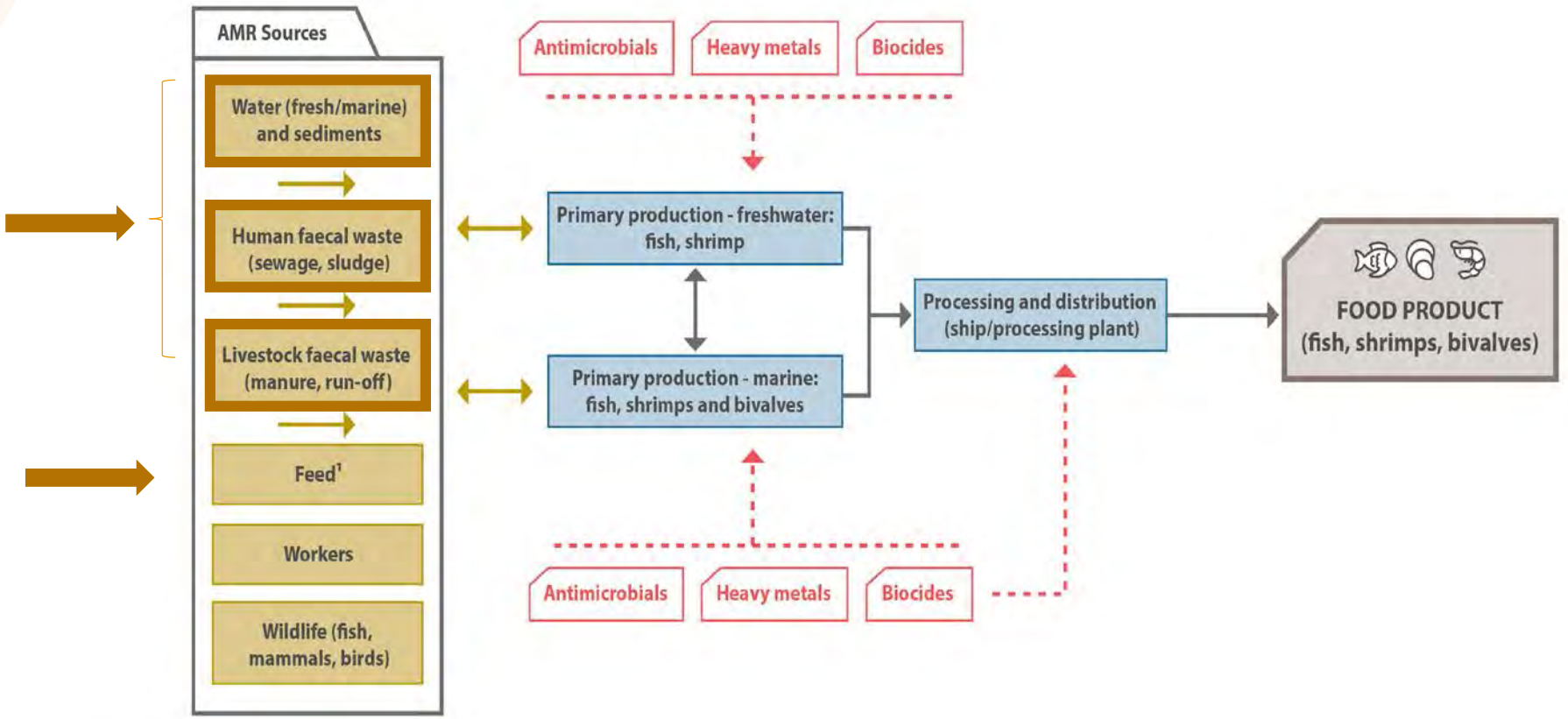
- Major transmission route: faecal matter through fertilisation and irrigation.

ToR1: Terrestrial animals sources/routes



- Not possible to stablish importance based on published evidence.
- Limited circumstantial evidence points to feed and, to a lesser extent, humans.

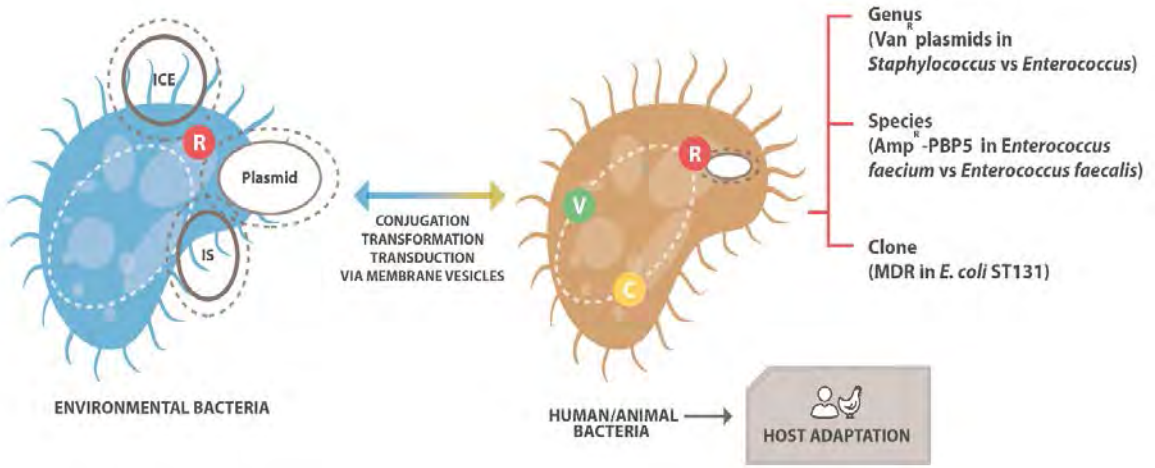
ToR1: Aquaculture



[1] only for fish and shrimps, not for bivalves

- Water was the main transmission route, with human and animal faecal material as important sources.

ToR2: Antimicrobial resistance- bacteria and genes (ARB and ARGs); Risk factors



In these food-producing environmental sources (including manure) we found:

- Group 1 ARB (pathogens resistant to last resort antimicrobials)
- Group 2 ARB (commensals/environmental with mobile ARGs)
- as well as highest priority genes

Risk factors for AMR linked to the food-producing environment:

- General factors (AMU, biosecurity, hygiene...)
- Bacterial traits (biofilm, HGT, metal/biocide tolerance, etc).
- Replacement of animals, persistent environmental contamination.
- Microbiota of natural environments (soil, water) source of genes.

Examples ARB and ARGs in manure

Main sources	Bacteria [antimicrobial resistance profiles and genes][a]	Detection of Group 1 ARB / highest relevant ARG [d,e] /comments	Factors influencing persistence and occurrence	Supporting references [f]
Poultry manure	**E. coli [3rd-GCs; ESBL-phenotype]**	?/ +	Antimicrobial residues in the manure, competing microflora, composting conditions (e.g. temperature, moisture)	Hering et al. 2016 Graham et al., 2009
Pig manure	**E. coli [MDR; 3rd-GCs; COL; aadA1, aadA2, $bla_{CTX-M-1}$, cmlA1-like, mcr-1, mph(A), sul3, tet(A)-like]; E. coli [3rd-GCs; $bla_{CTX-M-1}$; $bla_{CTX-M-15}$, $bla_{CTX-M-9}$] [b]** **E. faecalis [MDR; tet(M), tet(L), erm(B); aac(6')-Ie-aph(2')- Ia]** **E. faecium [VAN; vanA, tet(M), tet(L), erm(B)] [b]** **A. baumanii [CARBA; bla_{OXA-23}]**	?/ + Colistin resistance gene in IncX4 plasmid very similar to one of human clinical origin. ?/ + Numerous AMR phenotypes transferable by conjugation. +/ + Numerous AMR phenotypes transferable by conjugation including VAN-R ?/ +	Resistance to multiple antimicrobials including to antimicrobials commonly used in the animal production; AMR phenotypes usually horizontally transferable Tolerance to Cu with co-transference of resistance to several antimicrobials (e.g.vancomycin) under Cu selective pressure	García-Cobos et al. 2015;Guenther et al. 2017 Novais et al. 2013; Silveira et al., 2013 Hrenovic et al. 2019
Dairy or beef manure	**ESBL-E.coli [3rd-GCs; $bla_{CTX-M-14}$; $bla_{CTX-M-15}$; $bla_{CTX-M-27}$] [b]**	+/+ ST10 lineage in slurry and clinical isolates		Day et al. 2019

ToR3: Mitigation strategies/options

Apart from prudent antimicrobial use (AMU)...

- Correct implementation of effective general measures (good hygiene practices, biosecurity).
- Biological methodologies focusing on ARB/ ARGs (e.g. CRISPR-Cas, phages) are in the early phase of research and development.
- Priority for intervention:
  - activities at production stages which can widely disseminate large numbers ARB/ARGs.
  - reducing likelihood of faecal contamination.

ToR3. Mitigation strategies/options

- Reducing bacterial content of manure (e.g. by composting or anaerobic digestion), sewage sludge and irrigation water.

- Preventing transmission from other animals, dust, feed or surface run-off water.
- Proper implementation of cleaning/disinfection, and hygienic procedures for workers.

- High quality water by reducing/eliminating contamination with faecal waste.
- Reducing fish feed contamination.

- Water: wastewater treatment, reducing raw sewage discharges, multiple barrier approach to protect plant production and aquaculture.

ToR4: Knowledge/ Data gaps, …

Gaps:

- Large number of gaps (sources, routes, ARB/ARGs, effectiveness of mitigation measures).
- Most detailed studies in systems/areas not within the EU.
- ARB/ARGs, lack of systematic studies (similar sampling, detection methodologies, etc).
- Insufficient data to support assessment of quantitative impact of contamination of the EU production environment on foods or public health.
- Not sufficiently researched.

ToR4: …Some EU research needs

- One Health-based integrated studies, harmonised environmental AMR monitoring/surveillance strategies.
  - Priority plants-based and aquaculture sectors.
  - E.g focus among others faecal waste (manure, sewage), …

- To validate efficacy of practical mitigation methods.
  - Priority: e.g. disinfection/decontamination of highest priority ARB/ ARGs, treatment of faecal waste and wastewater used for fertilisation/irrigation or processing crops, feed heat treatment

- Studies linked to assessment of the effect of future policy developments (e.g. EU Green Deal, Circular Economy, and Veterinary Medicines products Regulation (EU) 2019/6) affecting food producing environments, AMU and climate change impacts.

SUBMISSION OF ABSTRACT
EXTENDED DEADLINE - 30.09.2021

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ANTIMICROBIAL RESISTANCE IN A FOOD PRODUCING ENVIRONMENTS

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