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LET'S CONNECT!

IDEA

Contamination of foods by **existing and emerging pathogenic bacteria** raises public health concerns. We need in-depth genomic knowledge on foodborne pathogens to discover their virulence- and antibiotic resistance-related genes as well as niche-adaptation genetic traits. This research will help us better understand the potential risk associated with each pathogen and each food supply chain

HOW

Bacteria such as **Arcobacter, Staphylococcus, Bacillus, and Enterobacteriaceae** will be isolated from representative food supply chains, like meat and vegetables, and subjected to whole genome sequencing followed by in-depth genomic characterization and comparative genomic analyses. Bacterial isolates and genomic sequences can be deposited in **publicly available repositories** for open utilization and ongoing scrutiny by the scientific community

RESULTS

This approach will enhance genomic understanding of existing and emerging foodborne pathogens unveiling the presence of **distinctive virulence and antibiotic-resistance genes, and specific niche-adaptation genetic traits**. It will also allow the development of **targeted molecular methods** useful for their early detection in the relevant food matrices in order to improve monitoring and control measures

IMPACT

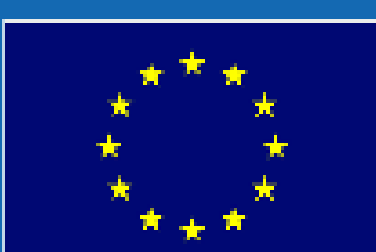
Overall, this approach will help to facilitate the risk assessment within the Food Safety Risk Analysis Framework in Europe and contribute to the advancement in the food safety diagnostics field

ACKNOWLEDGEMENTS

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EU FOOD SAFETY
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“Youngs acting for the future of Food Safety in EU”

