



The Role of microorganism in the food industry

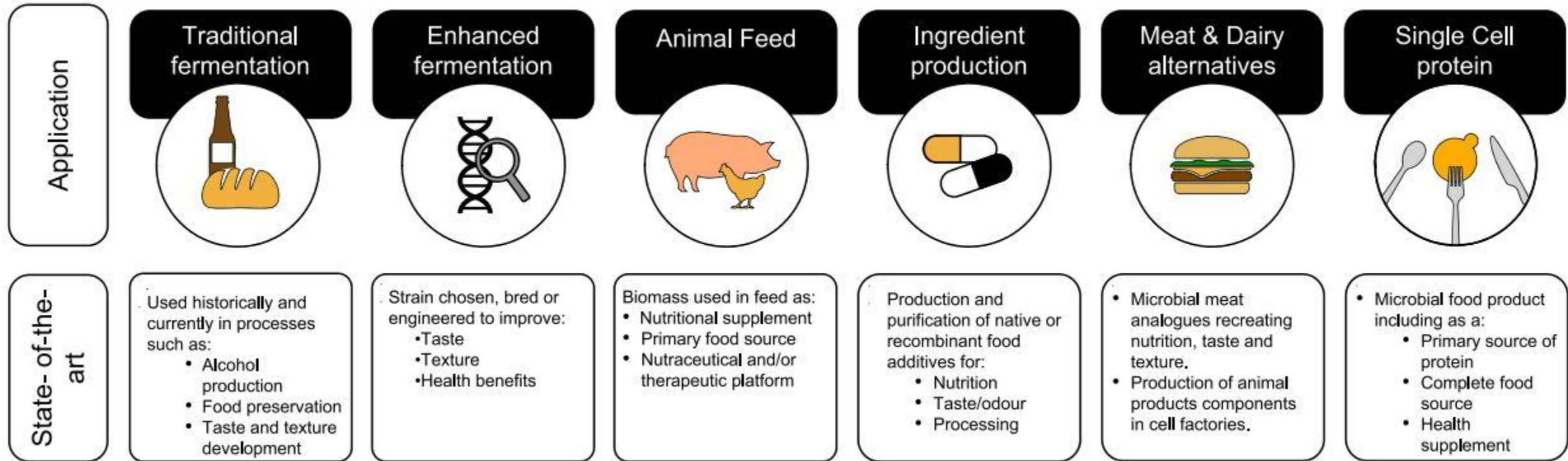
Presented by: Fardin Javanmardi

Department of Food Science and Technology

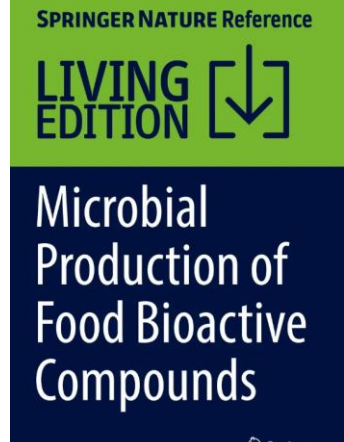
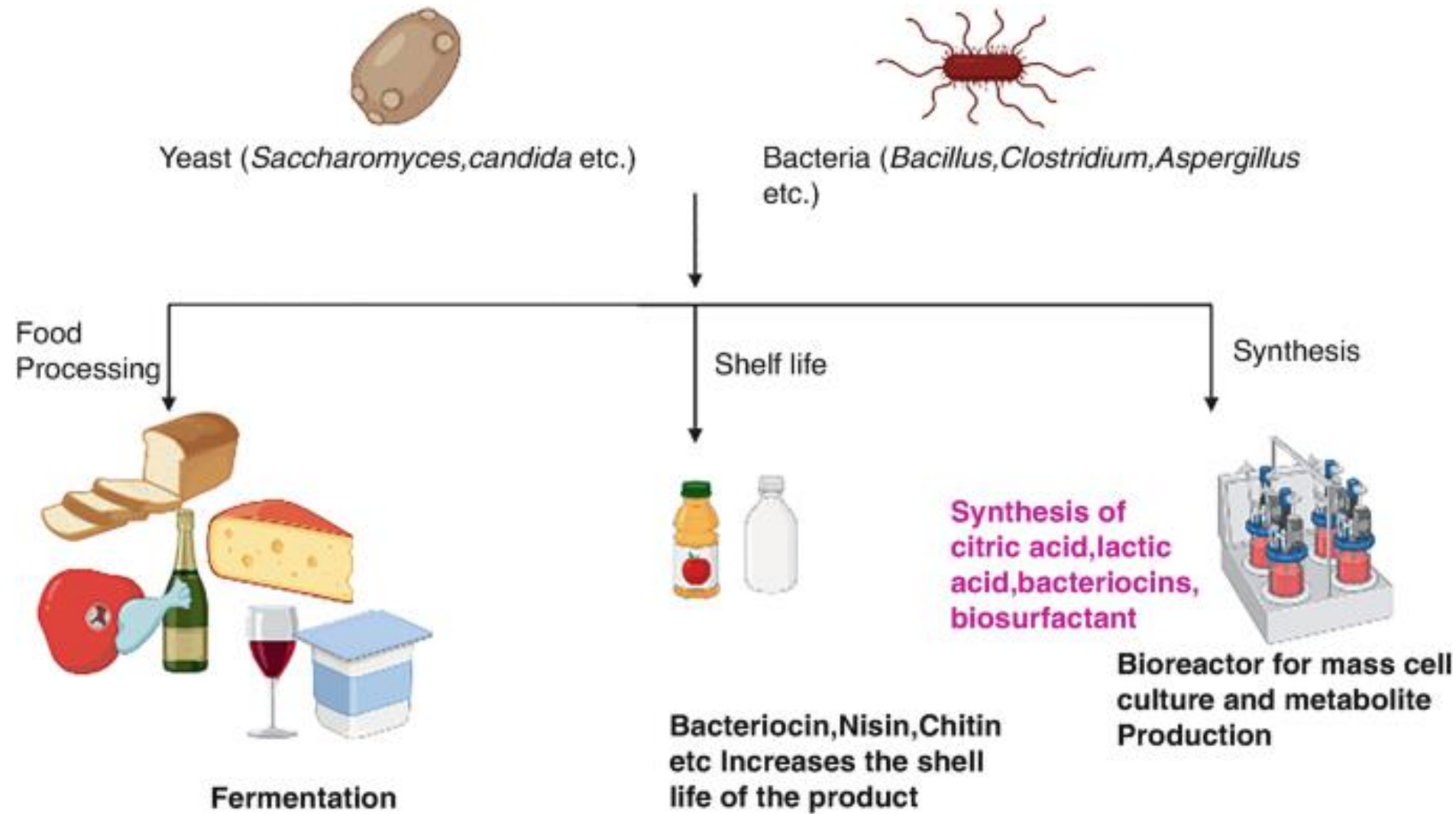
School of Nutrition and Dietetics

Tehran University of Medical Sciences

Timeline of the role of microbes in food



The role of microorganisms in the food industry



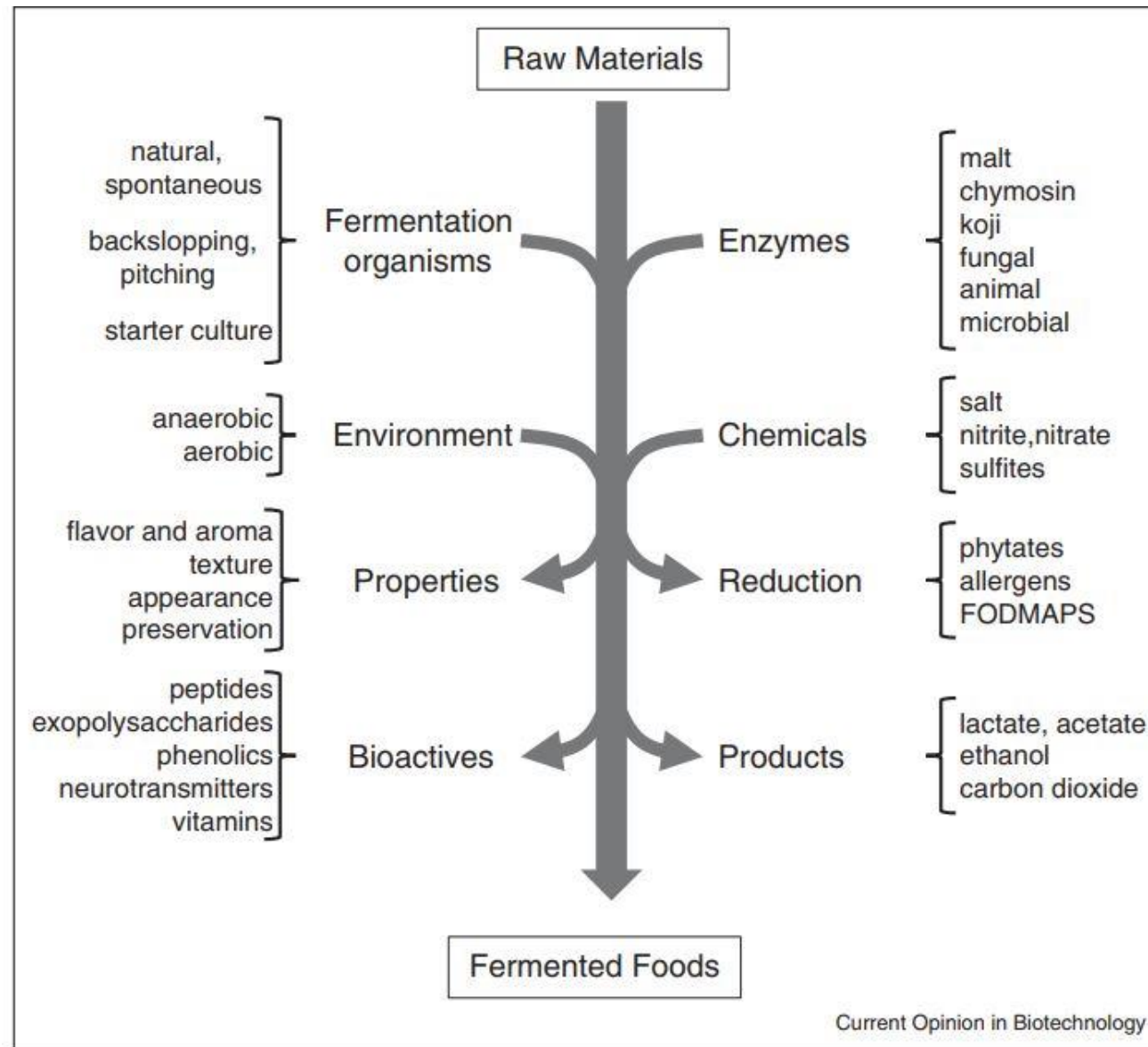
Editors: [Seid Mahdi Jafari](#),
[Farshad Darvishi Harzevili](#)

Fermented foods

- ✓ Limited Understanding of Microbial Composition
- ✓ Variability in Preparation
- ✓ Unexplored Health Benefits
- ✓ Food microbiome or food microbiota refers to the community of microorganisms, including bacteria, fungi, yeasts, molds, and sometimes viruses, that naturally exist in or on food.

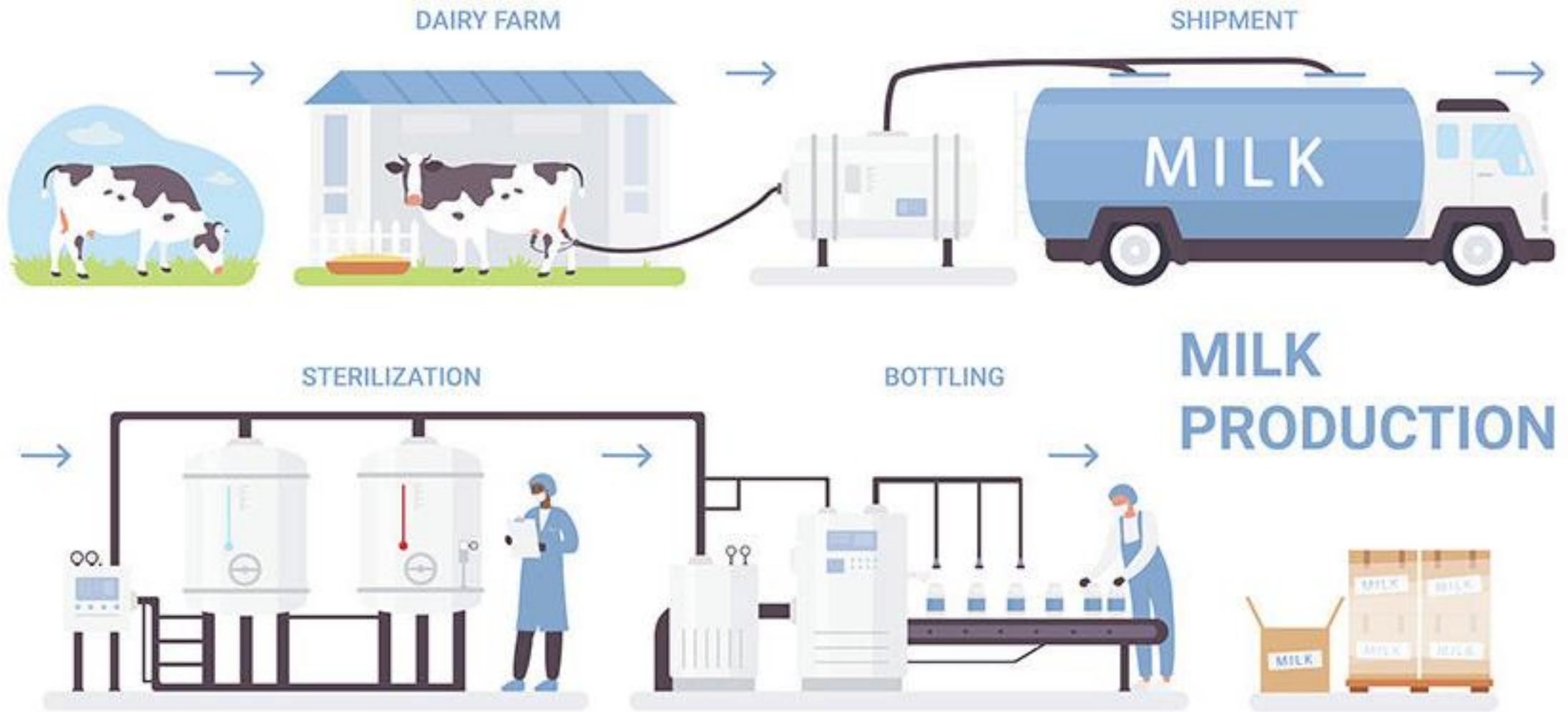


The transformative nature of fermented foods

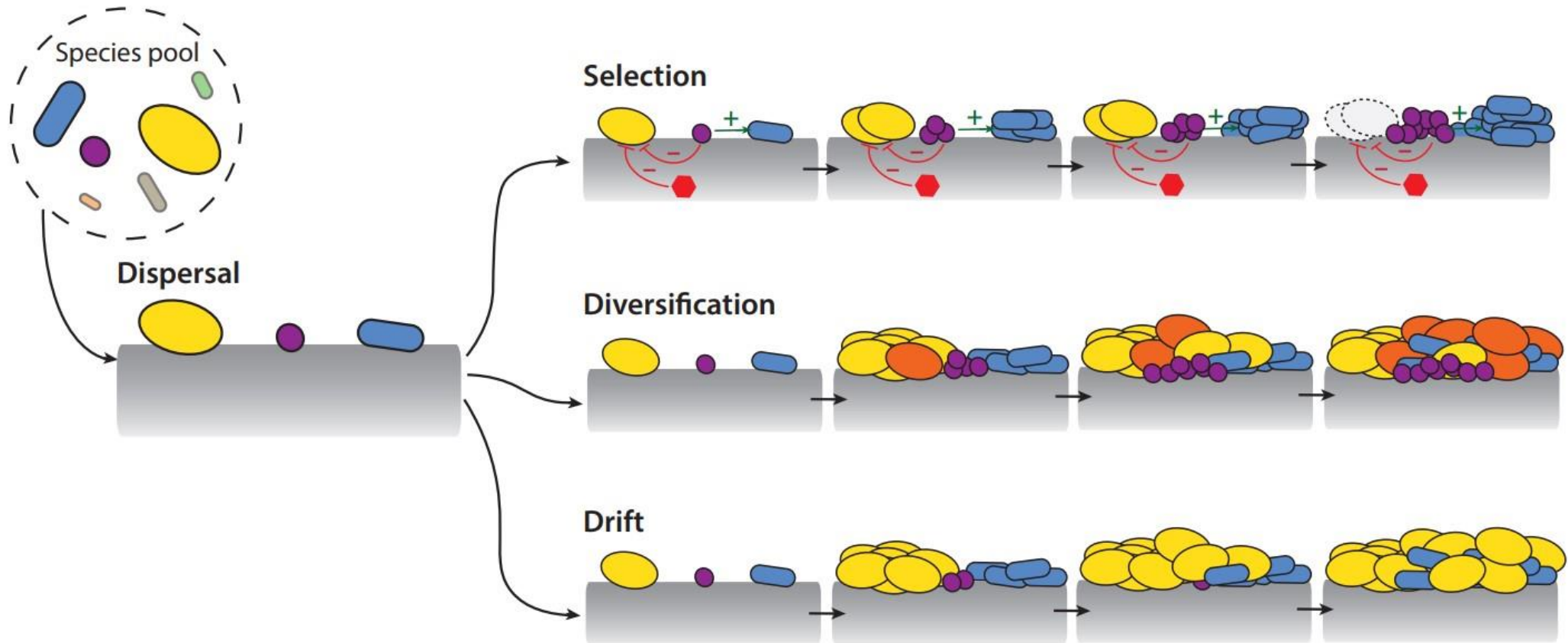


Marco, M et al. (2017). Health benefits of fermented foods: microbiota and beyond. *Current opinion in biotechnology*.

How is the microbiome of a food product formed?

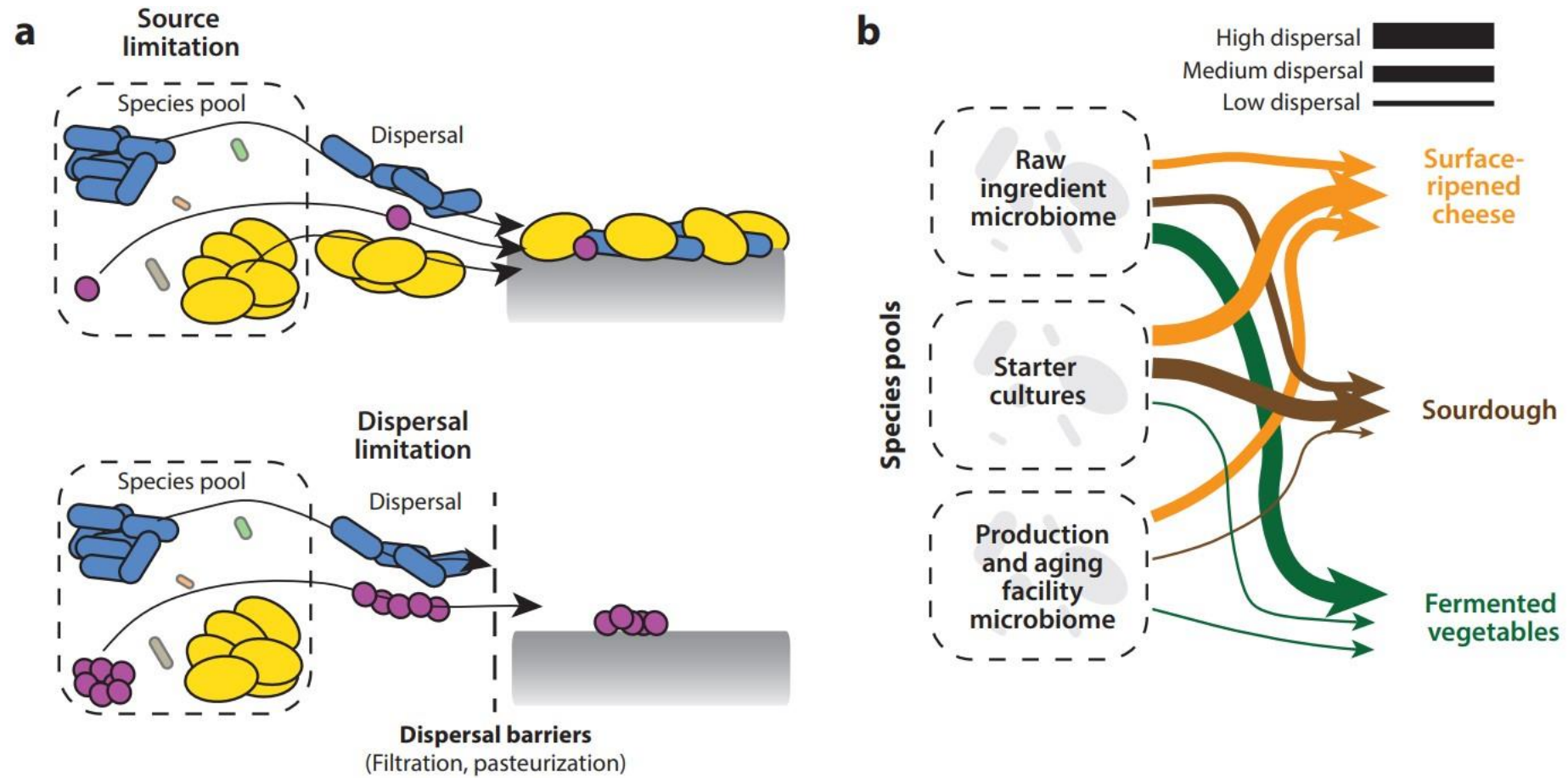


Microbial communities in food fermentations



Louw et al. (2023). Microbiome assembly in fermented foods. Annual review of microbiology.

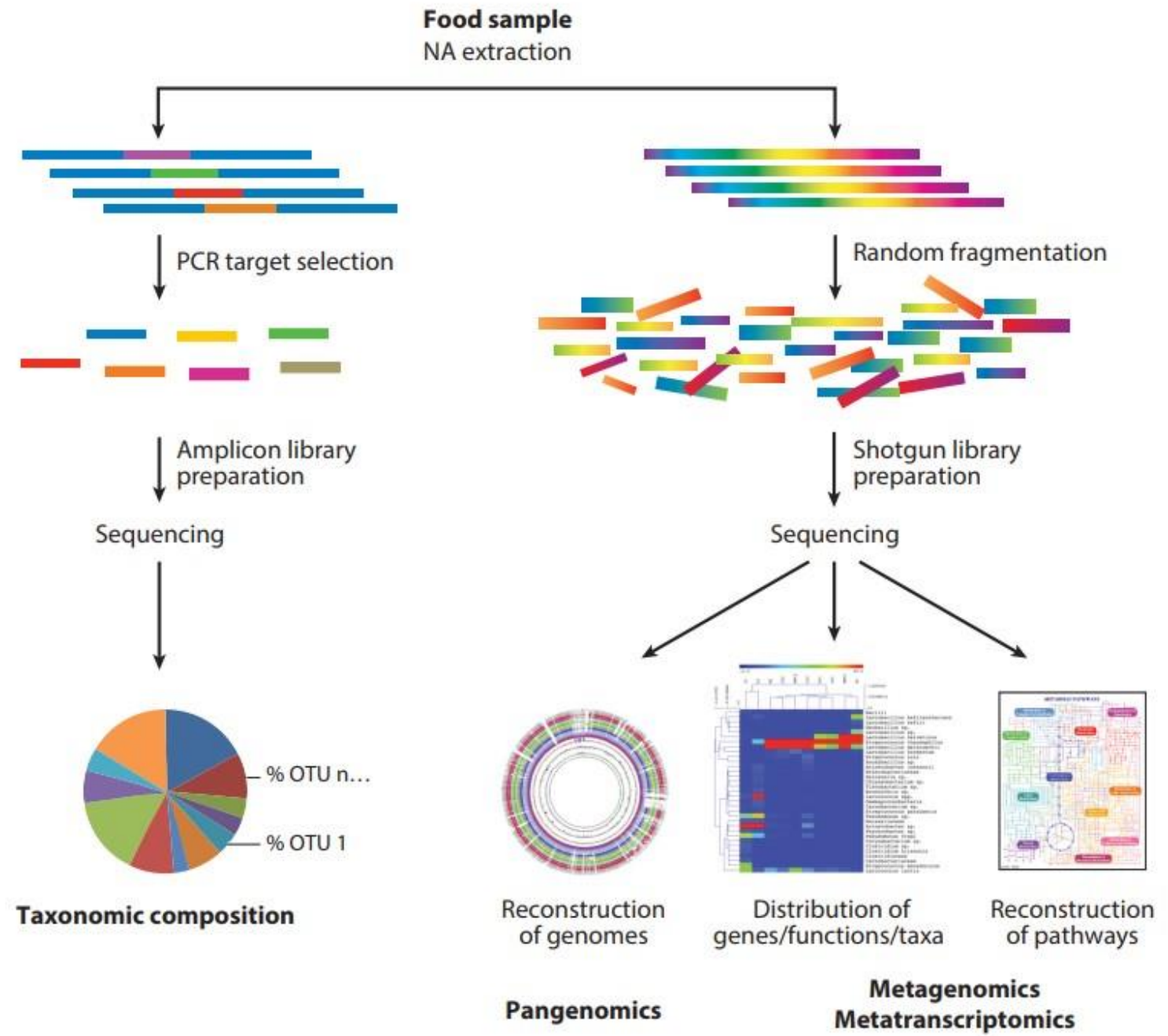
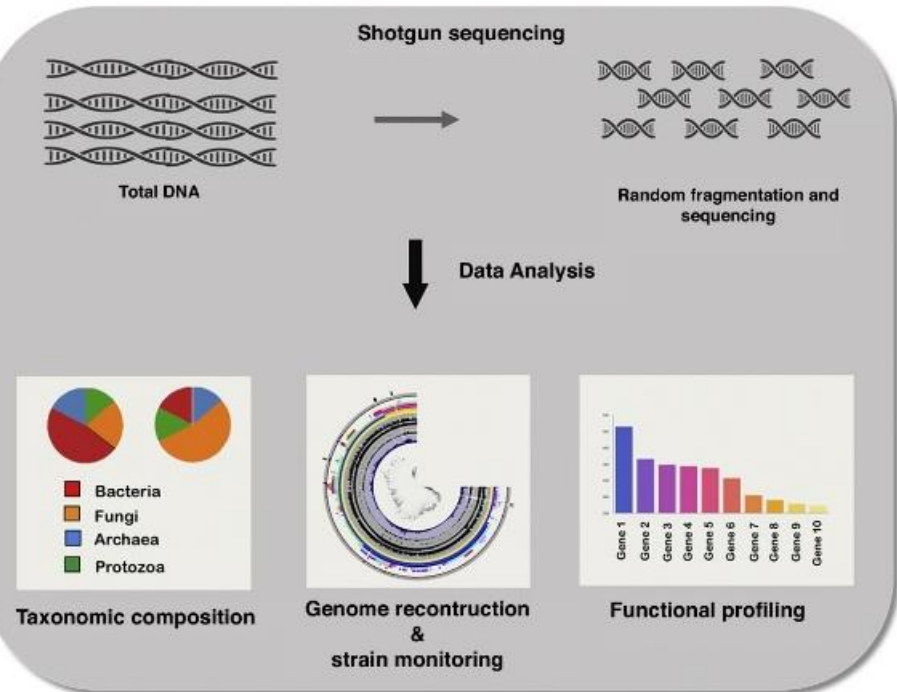
How is the microbiome of a food product formed?



Relationship between food microbiome and food quality and safety



Food microbiome characterization



Metatranscriptomics reveals temperature-driven functional changes in microbiome impacting cheese maturation rate

[Francesca De Filippis](#), [Alessandro Genovese](#), [Pasquale Ferranti](#), [Jack A. Gilbert](#) & [Danilo Ercolini](#)

[Scientific Reports](#) **6**, Article number: 21871 (2016) | [Cite this article](#)

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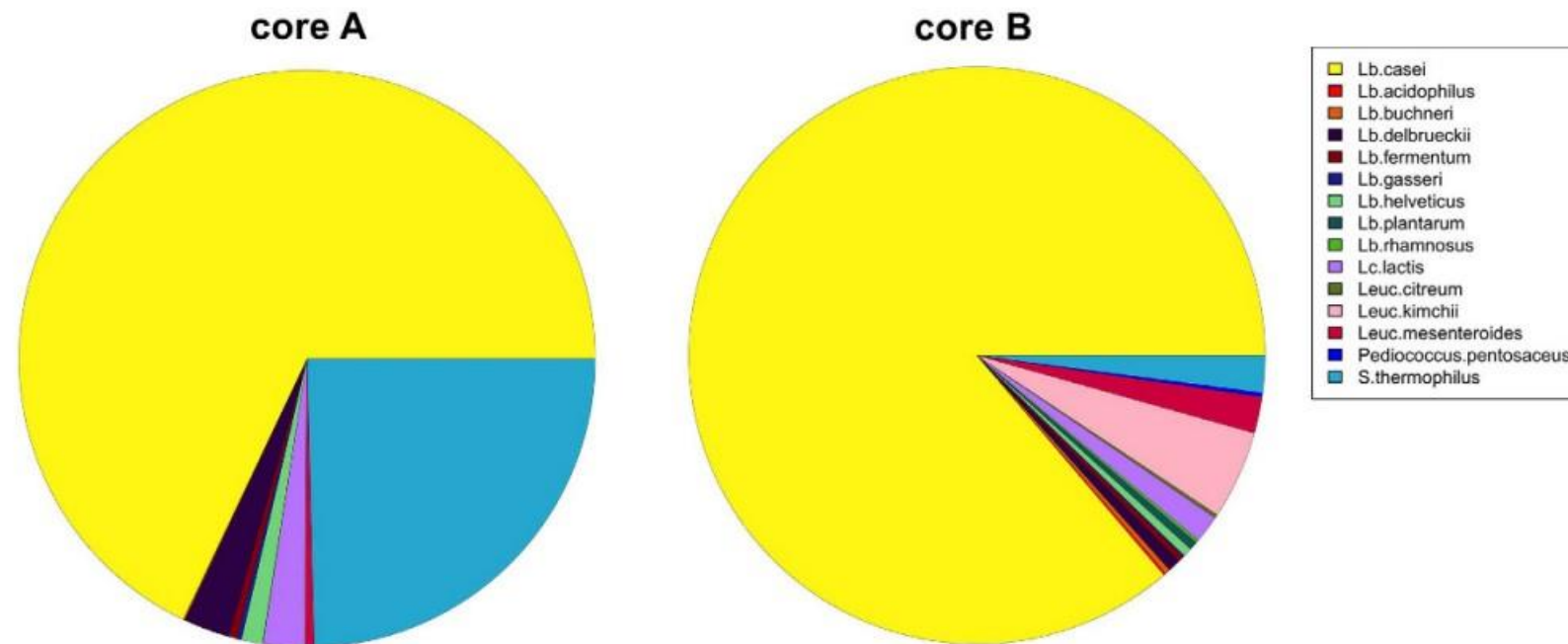


Figure 4. Higher temperature boosts NSLAB amino acid metabolism. Taxonomic assignment of the genes belonging to KEGG amino acid metabolism in the samples of cheese core from the second experiment, at 30 days of ripening. Only species belonging to Firmicutes are reported. A, ripening at standard conditions; B, higher temperature.

Which bacterial activities/pathways were highly expressed during the production and ripening of a cheese?

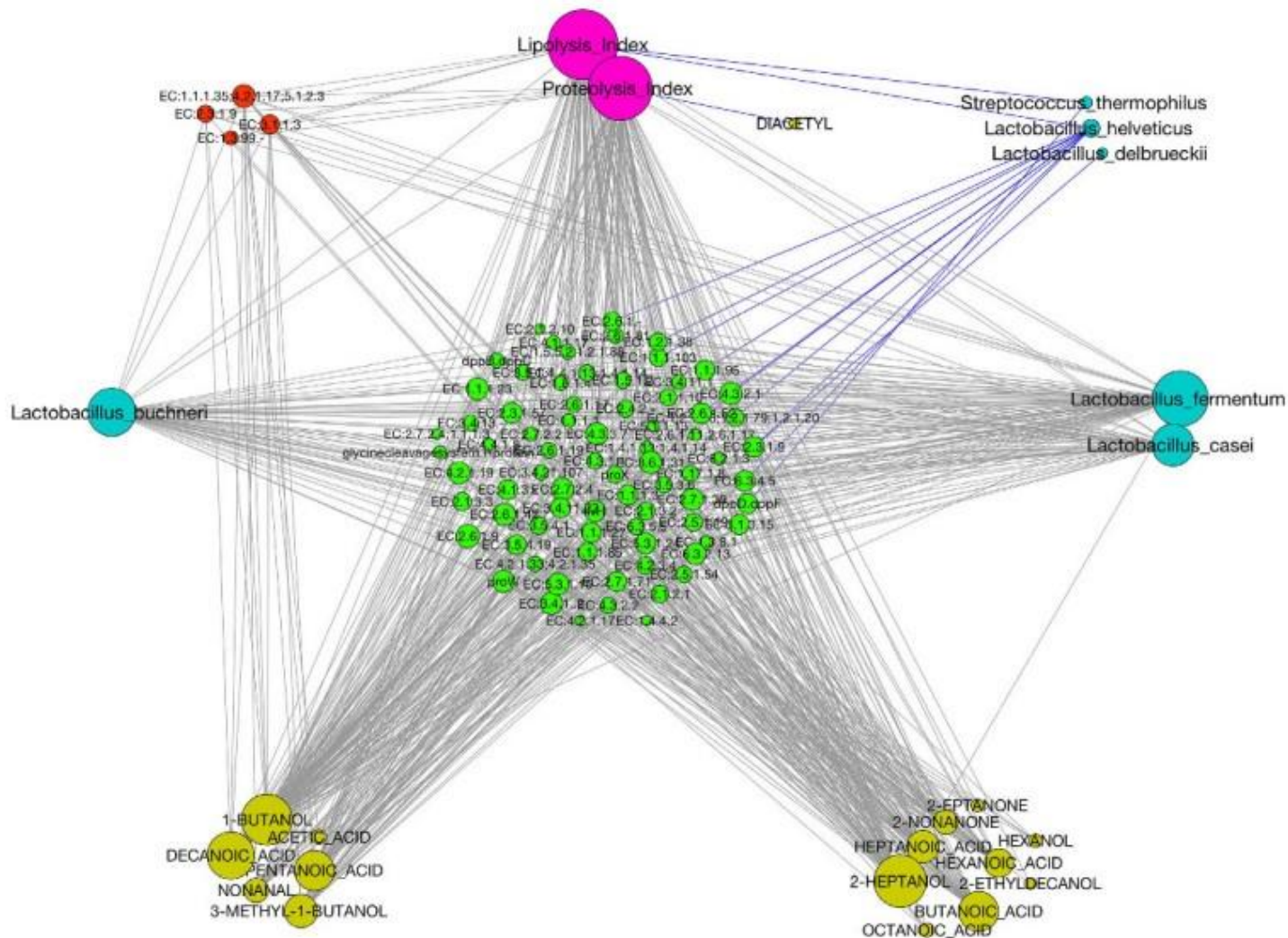
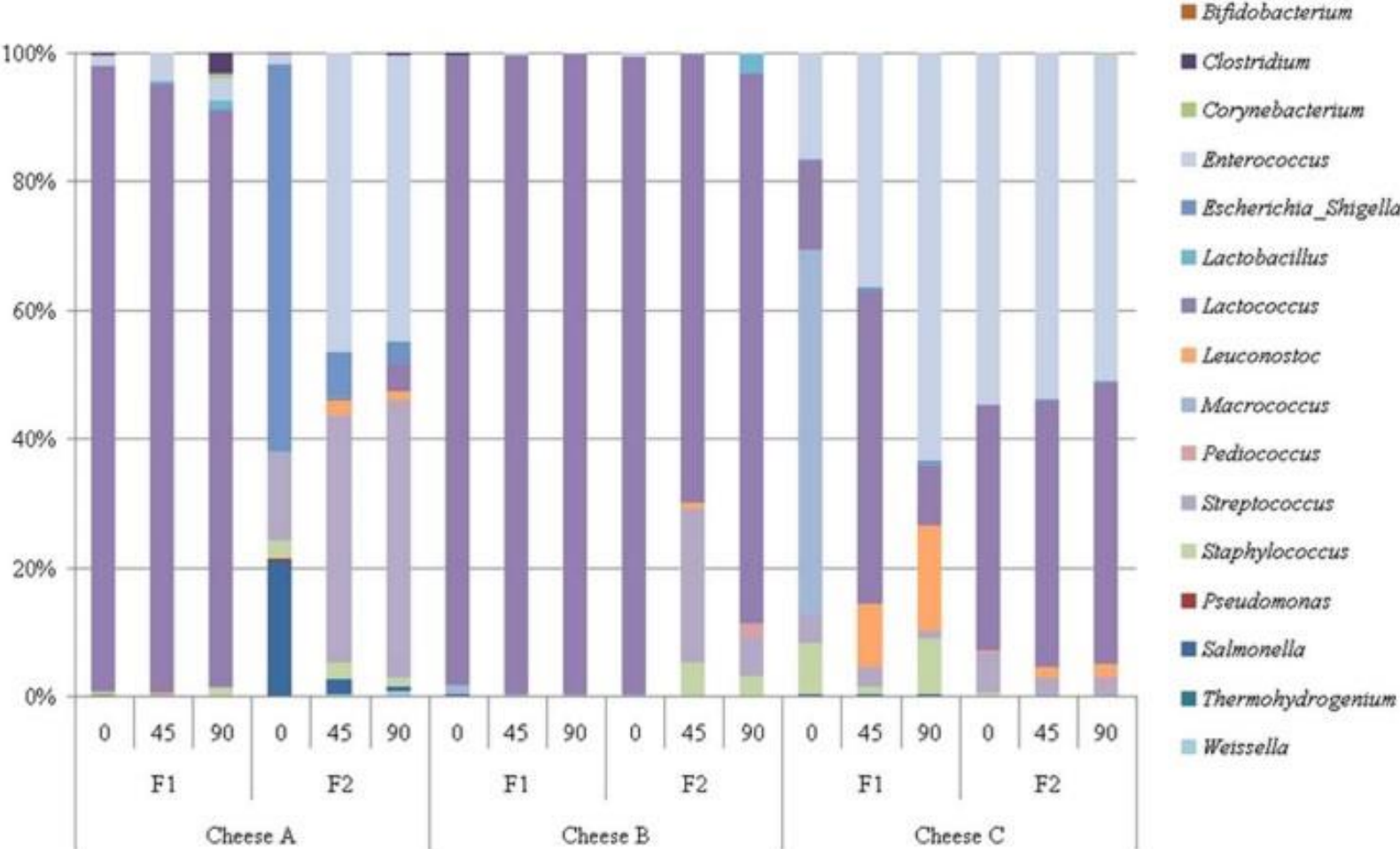


Figure 5. NSLAB abundance, ripening-related gene expression and metabolome are strongly linked. Network showing significant ($FDR < 0.1$) Spearman's correlations between KEGG genes belonging to amino acid and lipid metabolism, VOCs, lipolysis and proteolysis indices and OTUs belonging to Firmicutes identified through 16S rRNA sequencing. Node size was made proportional to the number of significant correlations. Edge color indicates negative (blue) or positive (grey) correlations. Node color was assigned as follows: green, KEGG genes related to amino acid metabolism; red, KEGG genes related to lipid metabolism; yellow, VOCs; magenta, chemical indices; cyan, Firmicutes OTUs.

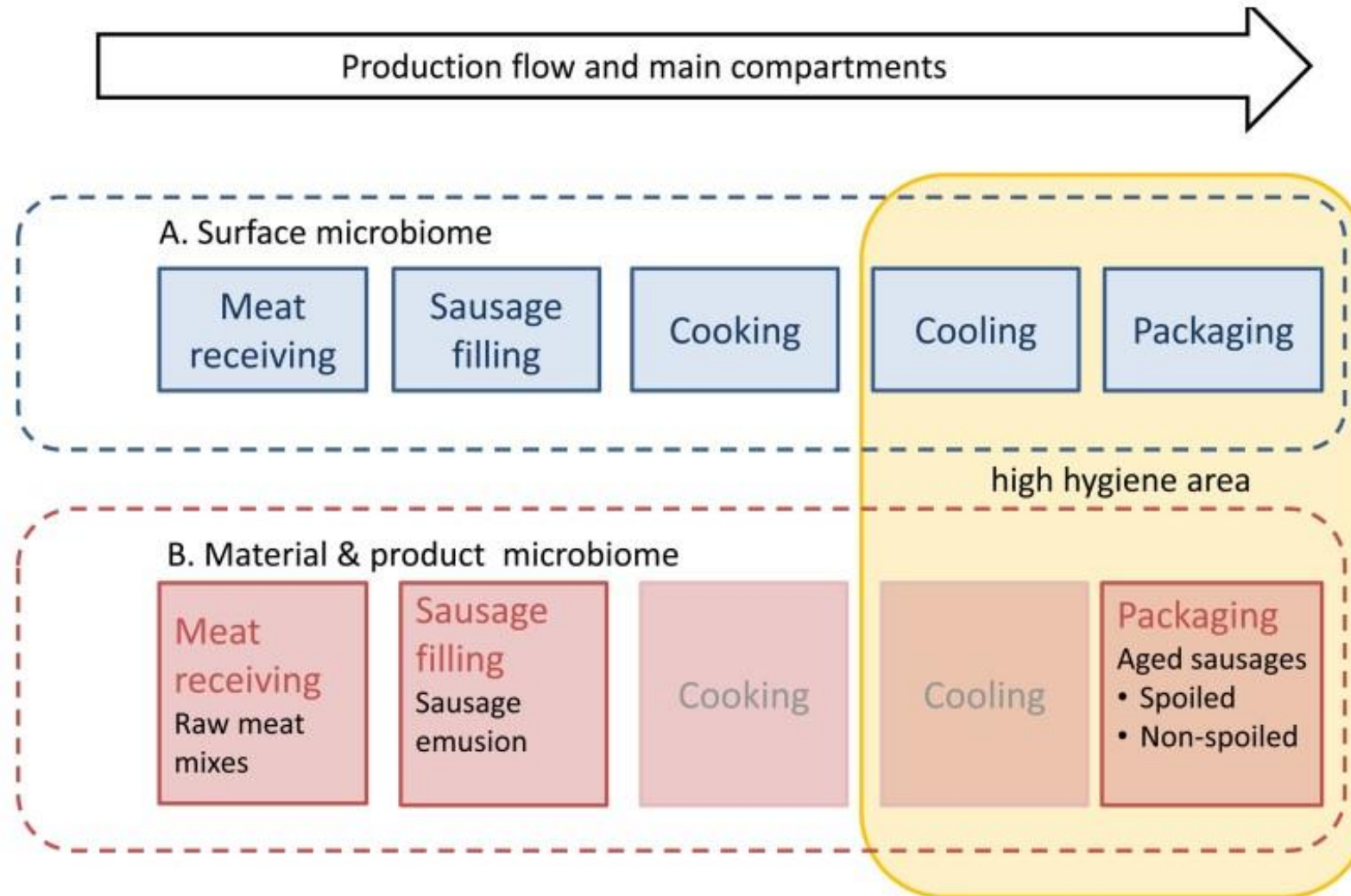
Dynamics of Bacterial Communities during the Ripening Process of Different Croatian Cheese Types Derived from Raw Ewe's Milk Cheeses

Mirna Mrkonjić Fuka^{1,2}, Stefanie Wallisch², Marion Engel², Gerhard Welzl², Jasmina Havranek³, Michael Schlöter^{2*}

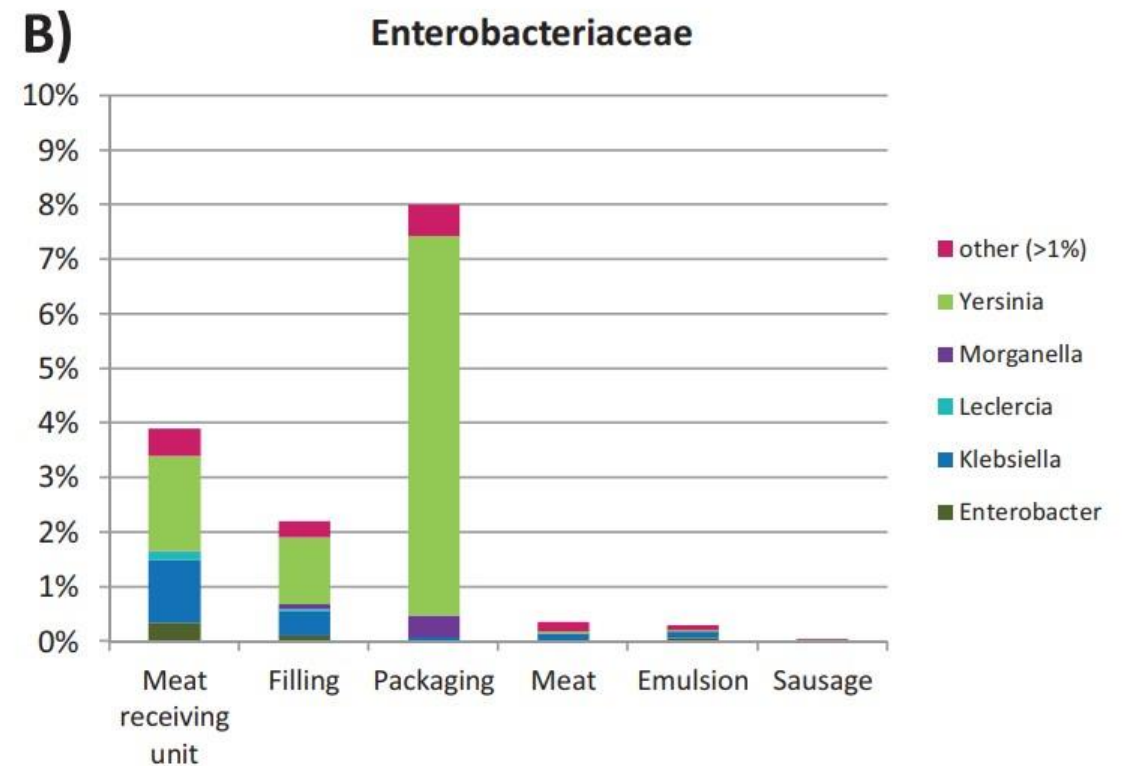
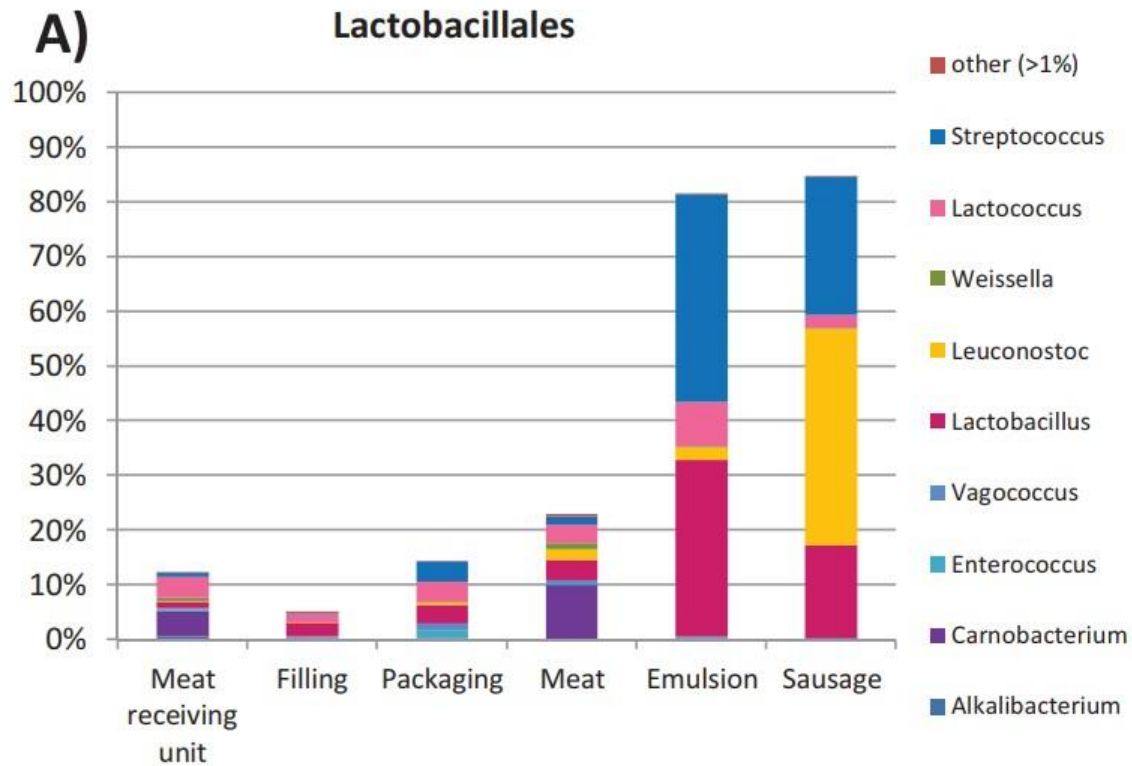
¹ Department Microbiology, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia, ² Research Unit for Environmental Genomics, Helmholtz Zentrum München, Neuherberg, Germany, ³ Department of Dairy Science, Faculty of Agriculture, University of Zagreb, Zagreb, Croatia



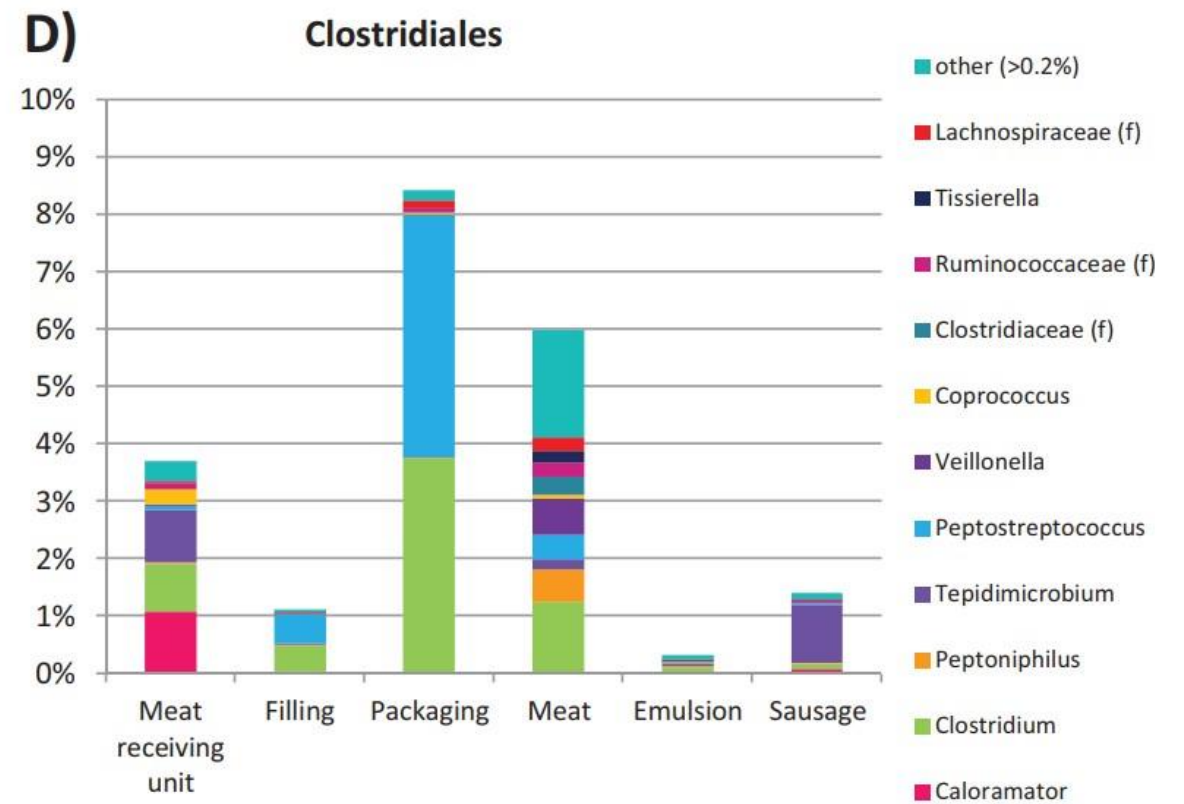
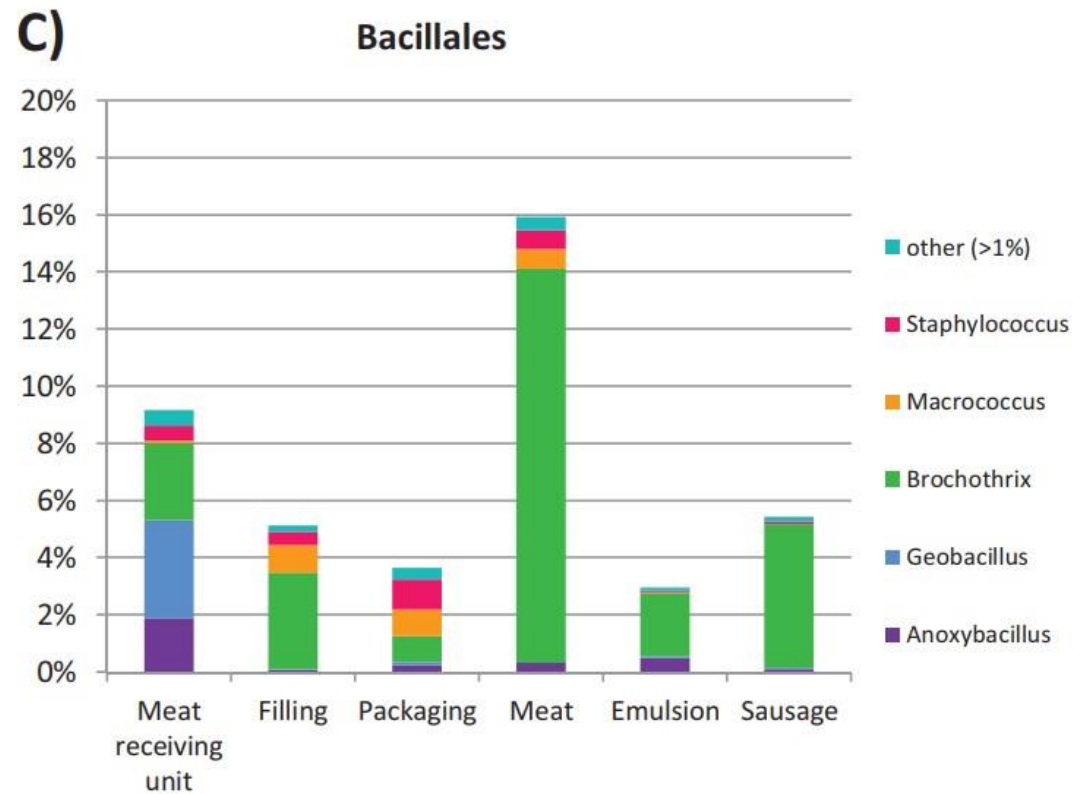
Tracking Microbial Contamination Routes and Monitoring Food Spoilage



Hultman et al. (2015). Meat processing plant microbiome and contamination patterns of cold-tolerant bacteria causing food safety and spoilage risks in the manufacture of vacuum-packaged cooked sausages. *Applied and environmental microbiology*.



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Conclusion

