

# Current understanding of the food microbiome in the era of big data

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\*Eren, A.M., Maignien, L., Sul, W.J., Murphy, L.G., Grim, S.L., Morrison, H.G., Sogin, M.L. (2013). Methods Ecol. Evol. 4:1111-1119



How changes in process parameters can affect the distributions of the oligotyping and how this difference can affect the final characteristic of the products.





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# Correlation between *Pseudomonas fragi* oligotypes abundance and VOCs





#### Experimental approaches to study the ecology of foods





De Filippis, F.; Parente, E.; Ercolini, D. Recent Past, Present, and Future of the Food Microbiome. *Annu. Rev. Food Sci. Technol.* **2018**, *9*, 25.1-25.20.

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# Shotgun Metagenomics and Volatilome Profile of the Microbiota of Fermented Sausages

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FIG 4 Abundance of VOCs during ripening. Acetic acid, acetoin, and ethyl acetate concentrations over time (0, 3, 7, and 40 days) and under two fermentation conditions (red, inoculated; blue, spontaneous fermentation). Boxes represent the interquartile ranges (IQRs) between the first and third quartiles, and the lines inside represent the medians (2nd quartiles). Whiskers denote the lowest and the highest values within IQRs from the first and third quartiles, respectively. Circles represent outliers beyond the whiskers.





FIG 7 Liking test. (A) Radar graphs displaying the liking of appearance, odor, taste, flavor, and texture and overall liking expressed by consumers for the sausages made by spontaneous and inoculated fermentation. (B) Distributions of the liking scores of blavor and odor (P < 0.05) for fermentation conditions (red, inoculated, blue, spontaneous fermentation). Boxes represent the interquarilie ranges (DRB) between the first and third quartiles, and the lines inside represent the medians (2nd quartiles, thiskers denote the lowest and the highest values within IQRs from the first and third quartiles, respectively. Circles represent totiles beyond the whiskers.





#### **Metagenomics**



### **CulturOmics**



## Microbiota (reconstructed from metagenomic libraries) in fermented sausages





### Dominance of *L. sakei* never lower than 70% of the relative abundance in the three batches used



#### LAB culturable microbiota in fermented sausages



#### **Culturomics approach:**

- Y was characterized by the 77% of the colony isolated identified as *Lactobacillus sakei*, 23% of *Pediococcus pentosaceus*
- Z showed 62% of colony identified as L. sakei, 32% of colony identified as Lactobacillus curvatus
- X display 97% of *L. sakei* and 3% of colony of *P. pentosaceus*

It should be pointed out that *L. curvatus* was not isolated from X and Y and *P. pentosaceus* was never isolated from Z samples.





#### **×De novo extraction of microbial strains from metagenomes**







Strains	n° of reconstructed strains (completeness >20%, contamination <5%)
Lactobacillus curvatus	7
Lactobacillus sakei	22
Pediococcus pentosaceus	19
ТОТ	48



#### L. sakei REP PCR biotypes stratification







#### Single-Nucleotide Polymorphisms in *L. sakei* genomes





Phylogenetic tree built on concatenated L. sakei genes (1733 genes) extracted from assembled metagenomes.

### **Canopy-based algorithm of sausages genes**



To identify patterns of genetic variation among batches we determined co-abundance associations between genes and then clustered them, resulting in 14 co-abundance groups (CAGs)



CAG-02: enriched of KEGG genes releted to Butanoate metabolism

CAG-03: Fatty acid biosynthesis



#### **Carbohydrates metabolic routes**





- Y Butanoate:
  - alcohol dehydrogenase [EC:1.1.1.1],
  - (R,R)-butanediol dehydrogenase/diacetyl reductase [EC:1.1.1.4\_1.1.1.303]
- Z Propanoate:
  - alpha–glucosidase [EC:3.2.1.20], alpha–N–arabinofuranosidase
  - glyceraldehyde 3–phosphate dehydrogenase [EC:1.2.1.12]
  - acetate\_kinase\_[EC:2.7.2.1]



## CAGs significantly associated with the key metabolites and microbiota







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