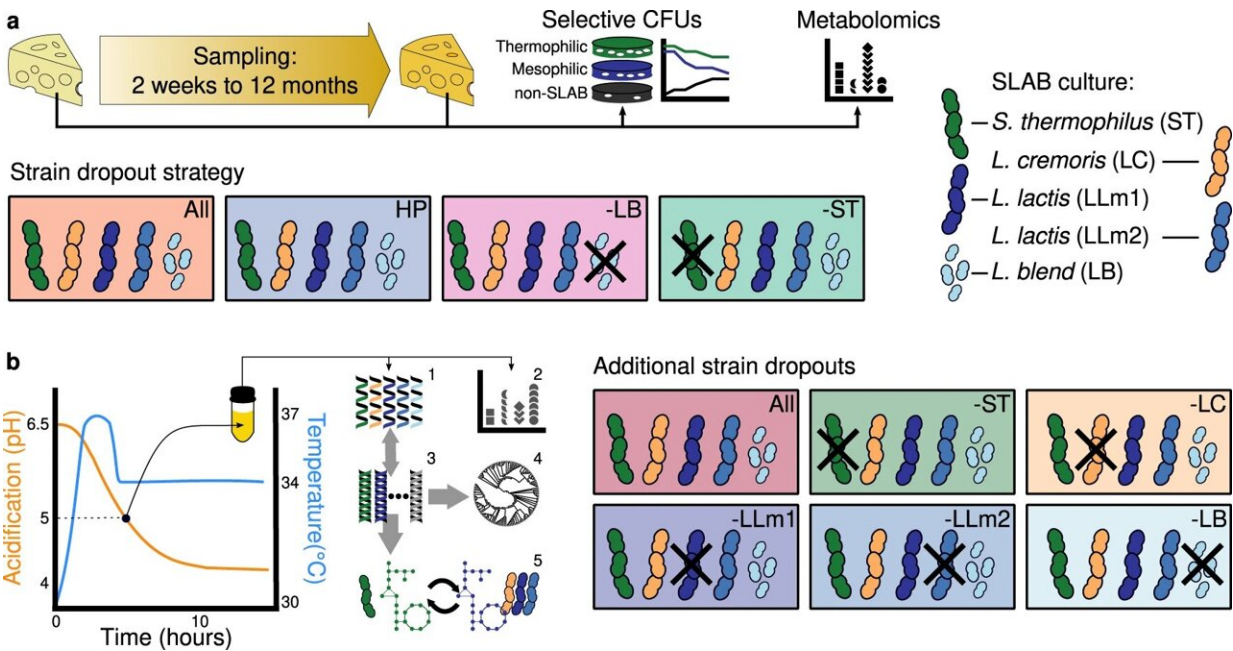


Investigating how microbial interactions shape Cheddar cheese's flavor profile

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Schematic representation of the experimental design and methods. **a** The 1 year long cheddar-making experiment. The SLAB culture is composed of one *S. thermophilus* (ST), two major *L. lactis* strains (LLm1 & LLm2), one major *L. cremoris* (LC), and a blend of *Lactococcus* strains (LB). Microbial population dynamics were quantified during cheese ripening using a selective method of viable cell counting, which discriminates between thermophilic cocci, mesophilic cocci and non-Starter Lactic Acid Bacteria (non-SLAB). Additionally, metabolic changes in the cheeses were measured using several targeted analytical chemistry approaches measuring acids, sugars, flavor-related organic compounds and peptides. **b** Schematic representation of the controlled milk experiment in the laboratory as well as of the methods (1–5) used in the controlled milk experiment. This second experiment involves the removal of additional strains,

namely the individual exclusion of three major *Lactococcus* strains. The numbers indicate the different types of data and analysis as follows: 1. metatranscriptomics, 2. metabolomics (i.e., acids, sugars, flavor-related organic compounds), 3. genomics, 4. phylogenomics and 5. genomes-scale metabolic models (GEMs) and community simulations. Our integrative systems biology approach combined: (i) the analysis of the SLAB community's genomes, (ii) the generation and simulation of their respective GEMs, (iii) the analysis of the metatranscriptomes across the different strain removal conditions and (iv) the quantification of key metabolites. Credit: *Nature Communications* (2023). DOI: 10.1038/s41467-023-41059-2

The combinations of microorganisms responsible for shaping the taste of Cheddar cheese—including fruity, creamy, buttery, and nutty flavors—are [investigated](#) in a *Nature Communications* paper.

Cheese fermentation and [flavor](#) formation are influenced by complex biochemical reactions driven by [microbial activity](#). Although the compositional dynamics of [cheese](#) microbiomes are relatively well-mapped, the mechanistic roles of microbial interactions in flavor formation are not fully understood.

To investigate how microbial interactions shape flavor profiles, Chrats Melkonian, Ahmad Zeidan, and colleagues prepared year-long batches of Cheddar cheese using variants of a starter culture containing different combinations of *Streptococcus thermophilus* and *Lactococcus* strains.

The authors identified the important role of *S. thermophilus* in boosting *Lactococcus* growth and in shaping the flavor profile. In turn, a strain of *Lactococcus cremoris* limited the formation of diacetyl and acetoin, which have a buttery flavor but lead to an off flavor when in excess.

Additionally, when *L. cremoris* was removed, four flavor compounds

were detected. These included 2,3-pentanedione (which gives the flavor of nuts, cream, and butter), and heptanal and hexanal (which taste fruity and fatty). When *L. cremoris* was present, another set of flavor compounds was detected in higher amounts, such as 2-methyl-3-thiolanone (which adds a meaty flavor) as well as the esters ethyl acetate and ethyl hexanoate (which adds a fruity flavor) the authors note.

Overall, the authors suggest their findings highlight the important role of competitive and cooperative microbial interactions in shaping the flavor of Cheddar cheese.

More information: Chrats Melkonian, Microbial interactions shape cheese flavour formation, *Nature Communications* (2023). [DOI: 10.1038/s41467-023-41059-2](https://doi.org/10.1038/s41467-023-41059-2).
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