New research shows that bacteria get 'hangry' too

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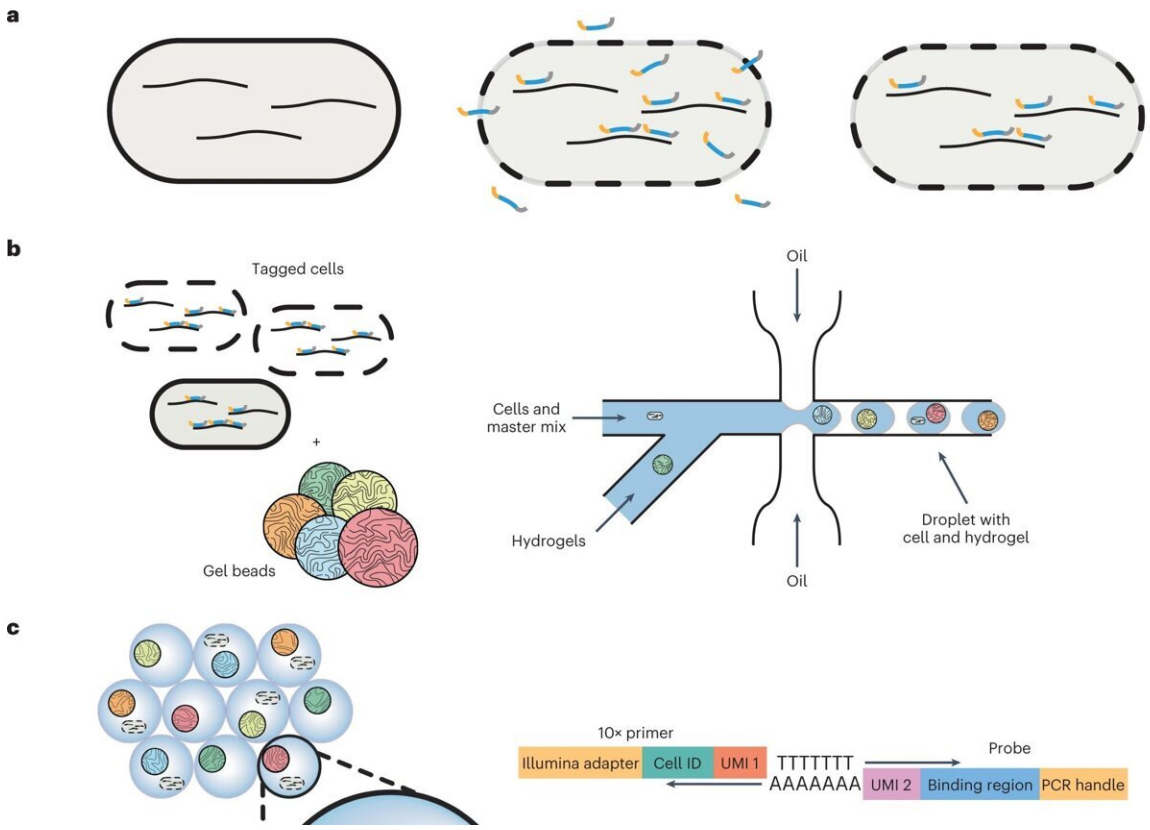

Microfluidic probe-based scRNA-seq method and validation. **a**, Cells were fixed and permeabilized to allow the penetration of thousands of unique, genome-specific oligonucleotide probes. Hybridized probes retrofitted transcripts with a poly-A tail and UMI, whereas unhybridized probes were washed away. **b**, Permeabilized cells with hybridized probes were flowed through a commercial microfluidic device that encapsulates single cells into droplets containing barcoded primers with poly-A capture sequence conjugated to a hydrogel microsphere and PCR reagents. **c**, Final droplets contain one or fewer cells and

one hydrogel with a unique cell barcode. Barcoded cDNA was generated from the mRNA:probe hybridized complex via in-droplet PCR. Droplets were then broken and the pooled cDNA amplified further before sequencing. Single-cell transcriptomes were resolved, clustered and visualized. **d**, Transcriptome quantification by hybridization of a probe library followed by PCR correlates (Pearson's correlation coefficient, $r = 0.73$) to traditional, bulk RNA-seq method (SMART-seq stranded kit, Takara) involving random priming of hexamers followed by reverse transcription (RT) and incorporation of template switching oligo. **e**, Species mixture ('barnyard') plot demonstrates that single cells of different bacterial species can be resolved by barcode after microfluidic encapsulation. **f**, Aggregated probe-based signal from thousands of single cells is well correlated (Pearson's correlation coefficient, $r = 0.94$) to the average probe-based signal obtained from the bulk population (pre-encapsulation). RPKM, reads per kilobase of exon per million reads mapped. Credit: *Nature Microbiology* (2023). DOI: 10.1038/s41564-023-01348-4

Have you ever been so hungry that you become angry, otherwise known as "hangry?" New research by Adam Rosenthal, Ph.D., assistant professor in the Department of Microbiology and Immunology, has found that some bacteria cells get hangry too, releasing harmful toxins into our bodies and making us sick.

Rosenthal and his colleagues from Harvard, Princeton and Danisco Animal Nutrition discovered, using a recently developed technology, that genetically identical cells within a bacterial community have different functions, with some members behaving more docile and others producing the very toxins that make us feel ill.

"Bacteria behave much more different than we traditionally thought," said Rosenthal. "Even when we study a community of bacteria that are all genetically identical, they don't all act the same way. We wanted to find out why."

The findings, published in *Nature Microbiology*, are particularly important in understanding how and why bacterial communities defer duties to certain cells—and could lead to new ways to tackle antibiotic tolerance further down the line.