THE SOURDOUGH JOURNEY

Inside the Invisible World of Sourdough Starters

A 14-Month DNA Study of Sourdough Starter Stability, Maturity, and Microbial Change

Appendices

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Appendix A: Experiment Design and Maintenance History

Experiment Design Details

The experiment began in February 2025, when I purchased a live sample of a commercially available starter. I sequestered my other sourdough starters to reduce risk of cross-contamination. I used all new jars, lids, disposable utensils, etc. I do not use commercial baker's yeast in my kitchen, reducing one potential source of *S. cerevisiae* cross-contamination.

I was seeking a "Type 1" starter when I conceived the experiment, but I did not send the sample for DNA testing when it was received. The cost was prohibitive to send an initial sample for DNA testing at that time. I froze a portion of the original starter I received in 2025, and I still have that frozen sample and plan to test it in the future.

For clarity, this experiment tests two starters, which **diverged from the same source**, then both samples were tested 14 months later, not against a static starting point in February 2025. This is a test of "**divergence**," of two samples from the same source, not longitudinal change of one sample.

Table 11: Experiment Timeline Highlights

February 2025	• Acquired 30g of live starter from the source. • Sequestered my existing starter to avoid cross contamination. • Purchased fresh bag of flour and new flour containers. • Began maintaining and using the starter • Baked many loaves with well-documented details (baking notes, videos, photos) • Observed excellent baking results, generally fuller fermentation, more open crumb, faster rise time and milder flavor than my previous starters. • Generally fed twice per day during this period using Kirkland All Purpose Flour, with good results
March 2025	• One month travel with starter in New York City • Fed NYC tap water and King Arthur Bread Flour (non-organic) Generally, once-per-day feedings
April-August 2025	• The starter was well-maintained with once or twice-a-day feedings. Fed Kirkland All Purpose Flour or Bob's Red Mill Artisan Bread Flour
June and August 2025	• Benchmark "starter strength tests" • See *Appendix J: Changes in Starter Rising Power*
Sept 2025-March 2026	• Extensive travel with many "vacation holds" • Starter was unfed and stored at 50°F (10°C) with "dry top off" • See below for Vacation Hold Protocol
List of Vacation Holds	• 8/8/25 – One-week hold • 9/15/25 – One-week hold • 10/4/25- Three days unfed at room temperature • 10/11/25- Three-week hold • 11/4/25 – Three-day hold (no dry top off) at 50°F (10°C) • 12/26/25 – One-week hold

	• 1/21/26 – Two-week hold • 2/15/26 – Two-week hold • 6 vacation holds with dry top off and 50°F (10°C), 2 other methods
March 2026	• Noted improved dough rising performance while recording a video series • 75% rise at 5.5 hours and 78°F (26°C) dough temperature • Previous benchmark was 50% rise in same conditions
April 2026	• Acquired a fresh sample of the original starter from the source • Sent that sample and a sample of my 14-month-old version of that starter to LabID in Bolzano, Italy for DNA sequencing
Summer 2026	• Assessed results, conducted additional starter strength testing, conducted research, and summarized observations • See *Appendix J: Changes in Starter Rising Power*

"Vacation Hold" Protocol

The largest deviation in my maintenance schedule was a "vacation hold" protocol. I was doing a lot of international travel during the testing period, so I devised a method to put the starter on hold while I was away for one, two, and three-week trips.

My typical feeding method was to discard down to 10 grams of starter and feed it 30 grams flour and 30 grams water (a 1:3:3 feeding ratio). For the vacation hold, I used this method, then topped off the mixed starter with about 1 inch (2.5 centimeters) of dry flour.

I chose to store the starter in a temperature control device (Brod and Taylor Sourdough Home) at 50°F (10°C). I chose 50°F (10°C) based on some research showing that some microbes commonly found in "bakery" starters can be negatively impacted when stored at temperatures at or below 40°F (4°C) (Gänzle/Reinhart Video 2021).

At the end of the hold period, the starter generally would "volcano" up through the top of the dry flour and remain in a semi-hydrated state, like clay or putty. The dry top off provided ample food for the starter, and it slightly dried the starter so it did not turn acidic or "hoochy" (covered with alcohol). The starter ended in a type of suspended animation – not dehydrated, and not liquid – somewhere in between – and clearly still alive.

To refresh the starter after the hold period, I would shake out approximately half of the excess dry flour on top, then add approximately 30g water and vigorously mix the starter, essentially using some of the remaining dry flour as the "feeding" with a slightly higher than 100% hydration to create a wet mix. I would then let the starter sit at room temperature until it was completely covered with bubbles. Then I would perform a normal discard and feeding routine until it regained full strength.

After a one-week duration hold, the starter would generally return to full strength in one or two feedings. After a three-week hold, the starter would require three to five feedings to return to full strength. In all cases, the starter would "reactivate" (actively bubbling) after just one feeding, but additional feedings were required to bring it back to expected rising times after feeding. The starter occasionally seemed "stressed" after the hold period, but I have no evidence that the vacation holds materially altered the starter based on its recovered aroma, rising power, or other observable criteria.

Prof. Michael Gänzle noted that this method is possibly a unique and previously untested method of using a cooling device at 50°F (10°C) which retained the presence of *F. sanfranciscensis,* unlike typical refrigeration at 40°F (4°C) which can negatively impact the persistence of that bacteria. My experiment did not include storage at 40°F (4°C).

When considering total "unfed days," it should also be noted that during my normal maintenance routine, I missed or skipped a daily feeding approximately 10% of the time, or roughly 30–40 times per year.

Starter Performance Observed

Table 12: Observations of Different Flour Feedings

February 2025	• Kirkland All Purpose Organic Flour • Starter performed well and smelled sweet and yeasty
March 2025	• Moved starter to New York City • Fed King Arthur Bread Flour (non-organic) • Developed slightly acidic aroma and did not perform as well as with the Kirkland flour
April 2025	• Fed Kirkland All Purpose Organic Flour
April 2025	• Tested a 50/50 mix of King Arthur Bread Flour (Organic) and King Arthur Whole Wheat (Organic). The starter did not perform well with this mix.
Summer 2025	• Fed Bob's Red Mill Artisan Bread Flour and King Arthur Organic Bread Flour with good results and slightly acidic aroma.
Fall 2025 – April 2026	• Fed Kirkland All Purpose Organic Flour with good results

Starter Performance During the Test Period: Rising Power / Fermentation

My first bake with the new starter in February 2025 was notable. The starter was clearly a very fast-rising, gassy starter. It exhibited strong rising power and was a more robust riser than starters I had used in my prior six years of sourdough baking. For example, my previous starters would raise my dough approximately 30% in volume in 5.5 hours 78°F (26°C) dough temperature. This starter raised the dough taller and faster, to a 50% rise in the same time at the same temperature. This test became my baseline for "dough rising power" of the starter.

In March 2026, I noted the starter was raising the dough more quickly than I had seen in the past, with a 75% rise at 5.5 hours and 78°F (26°C) dough temperature.

See *Appendix J: Changes in Starter Rising Power* for more details.

Starter Performance During the Test Period: Aroma

The aroma of the starter was a notable change during the test period. In February 2025, the original starter had a more "dairy-forward" aroma with very little to no acidity. Over time, my starter exhibited a brighter, slightly acidic aroma. The aroma also changed as I cycled through

different types of flour for feeding. Following a series of twice-a-day feedings, the acidic aroma would dissipate and return to a more yeast-forward, yeasty and creamy aroma.

At the end of the test period, when I acquired a fresh sample of the source starter, the source had a more dairy-forward aroma, and mine had a slight acidic aroma, but both clearly smelled like "siblings." It was very clear to me the two starters shared many similarities.

Starter Performance During the Test Period: Flavor

When I baked my first loaves with the new starter in February 2025, I was surprised at the mild flavor of the starter. My previous starters had more complex, sour notes. This new starter had a "one note" flavor – mildly sour with little depth or complexity to the flavor.

The flavor did not materially change over the course of the experiment. As noted above, the aroma periodically would take on brighter acidic notes, but this generally did not translate into a different flavor in the baked loaves.

Source Starter Owner's Maintenance Protocol

I did not collaborate directly with the owner of the source starter during the study period. He feeds the starter twice a day and never refrigerates it. When I purchased the starter in February 2025, he sent me a small bag of flour with the starter sample. The flour was Central Milling Organic Type 70 Malted Bread Flour. He generally uses Central Milling Flours and feeds his starter with an organic "bread flour" (not whole wheat or rye). During the study period, the owner of the source starter relocated to an adjacent state, so the source starter also experienced a change in geographic location and household environment, but retained its maintenance routine.

Is the 2026 source starter sample representative of the original 2025 source?

I don't know for certain. I have a frozen sample of the original February 2025 source starter, which I plan to test in the future to help answer this question.

For purposes of this study, I've assumed that the source starter's microbial community remained relatively stable between the two sample dates. This assumption is based on the owner's consistent twice-daily feeding schedule throughout the intervening period, with no known significant changes in maintenance practices.

While consistent maintenance does not guarantee an unchanged microbial community, it reduces one potential source of variability. Without testing the original 2025 sample, however, we cannot confirm that the source starter's microbial composition remained unchanged.

This experiment examines the divergence between two starters after 14 months of separate maintenance, while acknowledging that the precise microbial changes in each starter cannot be independently determined or attributed at this time.

Appendix B: DNA Testing Protocol

DNA Testing Protocol

The two starter samples were analyzed by LabID S.r.l. in Bolzano, Italy using **Next Generation Sequencing (NGS) with 16S/ITS amplicon metabarcoding**. LabID uses targeted DNA sequencing to separately characterize the bacterial and yeast populations in complex sourdough samples.

The analysis targets 16S ribosomal RNA (rRNA) gene regions for bacteria and Internal Transcribed Spacer (ITS) regions for fungi/yeasts. The laboratory workflow includes DNA extraction, library preparation, DNA sequencing, and data analysis, with quality-control procedures performed throughout the process.

The resulting analysis identifies microorganisms taxonomically and reports their **relative abundance within the bacterial and yeast populations separately**. Species representing more than 1% of a population are reported individually in the primary tables; organisms below 1% are grouped as "Others," with identified organisms above 0.01% reported separately elsewhere in the report.

Important Limitations of the DNA Analysis

- The results report relative abundance of DNA associated with each identified species; they are not direct microbial cell counts.
- Yeast and bacterial populations are analyzed separately. The testing does not determine the overall yeast-to-bacteria ratio.
- The primary analysis used in this report identifies organisms at the species level. The species profile does not by itself establish whether changes occurred at the strain or subspecies level.
- Relative abundance should therefore be interpreted as a comparison of the microbial composition of each population, not as an absolute measurement of the number of organisms present.

Taxonomy Name Changes

Two important sourdough organisms discussed in this report have undergone recent name changes. *Lactobacillus sanfranciscensis* was reclassified as *Fructilactobacillus sanfranciscensis* in 2020.

More recently, *Kazachstania humilis* was reclassified as *Maudiozyma humilis* in 2024. Older scientific literature therefore uses several different names for the same organisms.

For consistency with previous studies referenced here, I am using:

- *Fructilactobacillus sanfranciscensis, and*
- *Kazachstania humilis*.

Appendix C: Additional DNA Results: Below-Species-Level Diversity

Intra-Species Sequence Diversity

Although the dominant species profiles of the two starters remained remarkably similar, the DNA analysis does not demonstrate that the starters remained genetically unchanged **below the species level**. Individual microbial species can contain substantial genetic variation among strains and lineages.

This distinction was specifically raised during my review of the testing results by Michael Gänzle and another researcher who **independently cautioned** that meaningful changes could have occurred below the species level even while the species-level fingerprint remained stable.

The LabID report provides an additional measure of this variation by examining DNA sequence diversity within individual taxonomic species. These results should not be interpreted as identification of specific strains or subspecies. Amplicon metabarcoding can detect different sequence variants within the amplified 16S and ITS regions.

These differences may reflect:

- Different strains,
- Multiple copies of ribosomal genes,
- Minor mutations,
- Sequencing artifacts, or
- Closely related lineages.

NGS metabarcoding cannot reliably distinguish individual strains.

Accordingly, the results below are best interpreted as **intra-species sequence diversity**, rather than a direct count of strains or subspecies.

Description of Sub-Species Diversity (*Source: LabID Report*)

Your Sourdough's Biodiversity

In the previous section, we showed the taxonomy, while the biodiversity score looks at the presence, abundance, and distribution of different genomes from the same taxonomic species, as well as all the species found below the 1% cut-off level. In this section, we will look at the dominance and diversity scores on two different levels: the species level and 'intra-species' level (= alpha diversity).

a. Dominance vs Diversity scores

The difference between these two scores is that the dominance score measures the probability that two species or two DNA sequences are different. The diversity score, on the other hand, indicates the probability that your sourdough contains a variety of species or DNA sequences and their abundance.

b. Species vs Intra-species level

We analysed your sourdough at the DNA sequence level. It is important to understand that different DNA sequences can be associated with the same species. Therefore, we make a distinction between the species level and the DNA sequence level (intra species level).

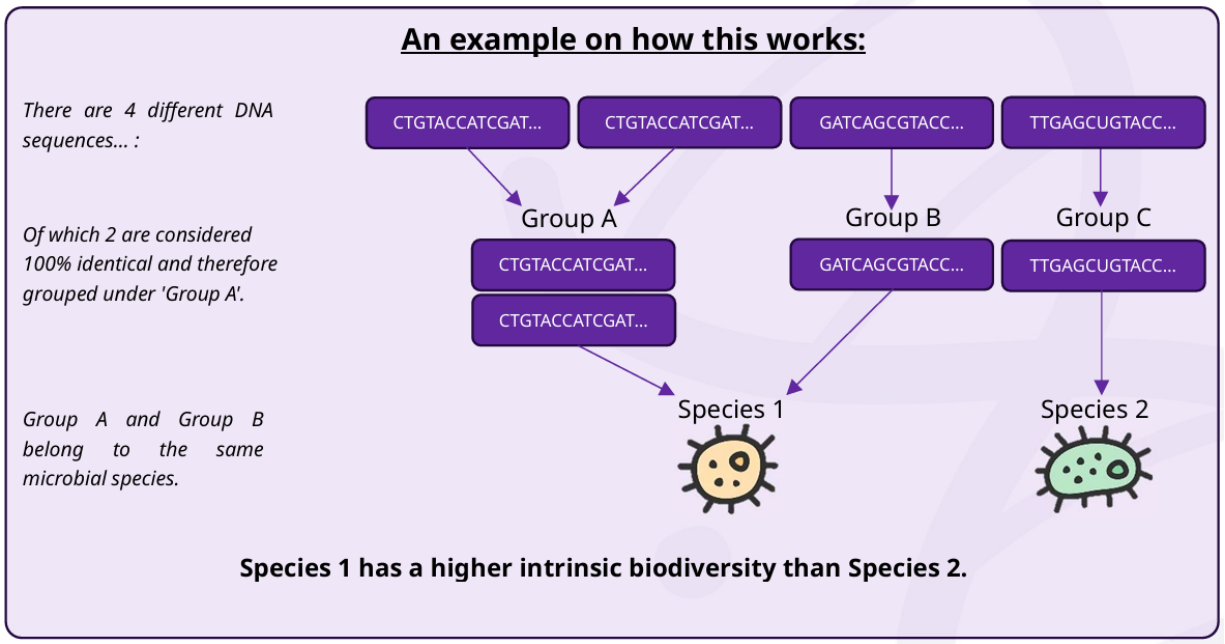

Image Source: Lab ID Report

Intra-Species Findings

Table 13: Intra-Species Findings: Distinct Sequence Variants

Measure	Source Starter	My Starter
Total Bacterial DNA Sequences	**63**	**76**
Fructilactobacillus Sequences	41	64
Total Yeast DNA Sequences	**21**	**20**
S. cerevisiae Sequences	2	6
M. humilis (K. humilis) Sequences	7	3
Bacterial Intra-species Diversity Score	**0.498**	**0.461**
Bacterial Intra-species Dominance	**0.830**	**0.812**
Yeast Intra-species Diversity Score	**0.266**	**0.276**
Yeast Intra-species Dominance	**0.509**	**0.509**

Observations

The two starters remained remarkably similar at the species level, but **differences were detectable within species** at the DNA sequence level.

Both starters contained approximately the same total number of yeast DNA sequence variants, with 21 detected in the source starter and 20 in my starter. However, their distribution among the two dominant yeast species differed.

My starter contained **more detected sequence variants assigned to *S. cerevisiae*,** with six compared with two in the source starter. *S. cerevisiae* was also the dominant yeast species in my starter.

Conversely, the source starter **contained more sequence variants assigned to *K. humilis*,** with seven compared with three in my starter. *K. humilis* was the dominant yeast species in the source starter.

This raises an interesting question: **Does the dominant yeast species within a mature starter tend to exhibit greater detectable intra-species sequence diversity?** The two samples in this experiment cannot answer that question. More abundant species generally provide more sequencing reads and therefore more opportunities to detect rare variants. The pattern may be worth examining in a larger dataset.

The bacterial results were also mixed. My starter contained more total bacterial sequence variants and more *Fructilactobacillus* sequence variants, yet its bacterial intra-species diversity score was slightly lower than that of the source starter.

Yeast diversity scores were nearly identical, with my starter slightly higher.

I initially considered whether the differences might reflect the more variable maintenance schedule, flour sources, and environmental exposures experienced by my starter. Unfortunately, these data do not establish such a relationship. With only two samples, the impact of maintenance history cannot be separated from normal biological variation or sequence-level variations.

The Bottom Line

Species-level stability does not necessarily imply genetic uniformity below the species level.

The two starters had remarkably similar dominant species profiles after 14 months of separate maintenance, while also showing **measurable differences in DNA sequence diversity** within those species. The most notable yeast pattern was that each starter contained more sequence variants from its own dominant yeast species.

Whether these differences resulted from maintenance practices, flour exposure, environmental conditions, normal microbial variation, or other factors cannot be determined from this experiment.

Appendix D: Newly Created Starters – The Research

2025 Taheri et al. Study of Newly Created Starters

As part of my research, I consulted a recent 2025 study by Taheri et al. that tracked the microbial development of 18 new sourdough starters created from scratch. The researchers performed DNA sequencing of the flour used to create the starters, and at multiple points during the first 28 days. This study provides a fascinating look at how the microbial ecology of a new starter changes as it becomes established.

While this study does not relate directly to my analysis of mature starters, it provides an important backstory. The microbial fingerprints of these newly created starters look very different from the mature starter in my experiment. This raises an obvious question: **How does the microbial fingerprint of a starter change as it matures?**

Conventional wisdom says that new starters are seeded from flour, water, and their environment. However, this study showed that most of the organisms that established in the new starters were **traceable to the flour.** Some species, including *S. cerevisiae*, may have entered from the surrounding environment or been present in flour below the detection threshold. Taheri et al. specifically identify bakers, vessels, and utensils as plausible sources of *Saccharomyces*.

The First 28 Days of a New Sourdough Starter

Table 14: Week-by-Week Summary of Microbial Succession in New Starters

Time	Yeast / Fungi	Bacteria	What Is Happening
Flour, before first feeding	Diverse flour-associated fungi, including *Alternaria*, *Cladosporium* and *Filobasidium*. *Kazachstania* and *Saccharomyces* are absent or present at low abundance in many flour samples.	Dominated largely by flour-, plant- and environment-associated organisms, particularly *Pantoea* and *Cutibacterium*. Sourdough-associated bacteria occur at low abundance.	Starting population. Many organisms present in flour will not ultimately thrive in the sourdough environment.
Week 1	*Alternaria* and other flour-associated fungi decline sharply. *Kazachstania* rises dramatically.	*Pantoea*, *Weissella*, *Kosakonia* and *Cutibacterium* decline sharply. Sourdough-associated bacteria begin increasing.	Major ecological turnover. The developing starter environment strongly favors some organisms over others.
Week 2	*Kazachstania* becomes overwhelmingly dominant across most starters.	*Companilactobacillus*, *Lactiplantibacillus*, *Levilactobacillus*, *Furfurilactobacillus* and *Acetobacter* increasingly dominate.	A recognizable sourdough ecosystem is emerging. Diversity declines as a smaller number of organisms become dominant.
Week 3	*Kazachstania* remains dominant. Flour-associated fungi are now minor.	Sourdough-associated bacteria dominate, with the population mix varying somewhat by flour type.	The microbial community continues to consolidate.
Week 4 / Day 28	*Kazachstania* remains dominant, but *Saccharomyces* begins increasing late, including in starters where it was not initially detected.	A small number of sourdough-associated bacterial genera dominate, with proportions differing by flour type.	Continued consolidation around typical sourdough-associated species, with continued movement among yeast species.

Source: Taheri, et al. 2025

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Important Observations from this Study

Many flour-associated organisms disappear rapidly. Focusing on the species we typically see in mature starters:

- *Kazachstania* becomes dominant very early.
- *Saccharomyces* is scarce or undetected in the starting flour and emerges in a few starter samples in the Day 28 testing.
- *F. sanfranciscensis*, despite its importance in mature Type 1 starters, is not a typical flour organism and was not detected in any of the starters in the first 28 days.

How do microorganisms enter a new sourdough starter?

The microorganisms in a new sourdough starter originate primarily from flour, with potential additional contributions from the surrounding kitchen environment, including human contact, utensils, equipment, work surfaces, and airborne particles. Water may also introduce microorganisms, although research suggests its mineral composition may be more important in influencing which microbes develop.

The evidence differs for bacteria and yeasts. Reese et al. (2020) found that sourdough-associated bacteria are commonly detected in air and dust, while yeasts are relatively uncommon in dust samples. Although yeasts can travel through the air, flour and contact with the surrounding kitchen environment, including hands, utensils, and work surfaces, are plausible sources of the yeasts that establish themselves in new starters. The relative contributions of these sources remain uncertain.

Minervini et al. (2015) identified sourdough-associated bacteria and yeasts on bakery equipment, suggesting that **contact** with the kitchen environment provides additional opportunities for microbial introduction.

New and mature starters behave differently. In a new starter, microorganisms encounter a developing ecosystem in which the dominant community has not yet become established. In a mature starter, repeated fermentation and feeding cycles have already selected a microbial community adapted to its maintenance conditions. Minervini et al. (2019) demonstrated this distinction: different tap waters influenced the bacterial communities developing in new starters, but produced little change in an established Type 1 starter over nine days of propagation.

Arrival does not guarantee establishment, and establishment does not guarantee persistence. Microorganisms may enter a starter through several pathways, but the fermentation conditions and subsequent maintenance history determine which organisms become dominant and remain part of the microbial community.

Relevance to Type 1 Starters

The absence of *F. sanfranciscensis* from the developing starters is particularly relevant to my experiment because of its prominence in mature Type 1 communities.

In a separate study, McKenney et al. analyzed 10 different starting flours and found that the early microbial communities largely reflected flour- and plant-associated bacteria. As fermentation progressed, these organisms were replaced by bacteria better adapted to the sourdough environment. ***Fructilactobacillus,*** *a genus commonly found in mature starters,* **was not reported among the bacterial genera detected in their starting flours.** This raises interesting questions regarding the source of *F. sanfranciscensis* in Type 1 starters.

This is particularly striking when compared with my starter's DNA results. *F. sanfranciscensis* represented **99.8% of the bacterial** population, yet it was not commonly detected in flour in these two studies.

Together, these studies demonstrate an important principle: **some microorganisms that ultimately become prominent in mature and Type 1 sourdough starters do not necessarily begin as prominent, or even detectable, members of the flour microbiome.**

The studies also lay the foundation for an important follow-up question:

If some signature microbes of mature Type 1 starters are scarce or undetected in the starting flour, where do they come from, and how do they become established and eventually dominant?

Related Experiments: New Starter Creation

In 2023, I conducted an extensive experiment on the creation of new sourdough starters from scratch. I tested several popular methods and ultimately **created 40 new starters** under highly controlled conditions. I did not have access to DNA testing during my experiments, but many of my observations tracked remarkably closely with the microbial succession documented by Taheri et al.

Taheri's DNA sequencing provides a fascinating microbial view of changes I could only observe indirectly through aroma, acidity, bubbling and rising activity.

Functional Maturity is Not Microbial Maturity

The 28-day timeline observed by Taheri et al. should not necessarily be interpreted as a typical timeline for creating a functional starter.

In a separate 2023 study by McKenney, Nichols, Dunn et al., researchers created 40 starters (coincidentally, the same number of starters I created in my independent study), using 10 different flours under a protocol specifically designed to mimic home baking practices. Those starters reached what the researchers called **"functional maturity," or readiness for baking, at approximately Day 10**. This closely matches the timeline I observed independently in my own 2023 experiments creating 40 new starters.

McKenney et al. analyzed 30 samples from 10 different flours and followed the bacterial development of 40 new starters.

- *Fructilactobacillus*, the genus containing *F. sanfranciscensis*, was not reported among the bacterial communities of any of their Day-14 starters.

In the Taheri study, which provided greater species-level resolution, *F. sanfranciscensis* was not detected in any of the 18 newly created starters.

A starter can become **functionally mature** without developing anything resembling the bacterial ecology of a mature Type 1 starter.

F. sanfranciscensis appears to be something of a **"late joiner"** to the sourdough ecosystem, characteristic of many long-maintained Type 1 starters but notably absent from the newly created starters examined here.

Interpreting the Taheri Timeline

Based on my 2023 experiments creating 40 new starters, it is important to note several differences between the Taheri study and the methods that I, and many other bakers, use when creating sourdough starters from scratch.

I believe new starters generally follow the broad sequence of microbial succession documented in the Taheri study, but the timeline in this study appears somewhat slower than what I and others have typically observed. Several differences in methodology may help explain this:

1. **Flour choices:** The Taheri study used three commercial supermarket flours. In my experiments, higher-quality, stone-ground, organic whole-grain flours generally produced faster starter development.
2. **Feeding regimen:** In my typical starter creation method, flour and water are mixed on Day 1 and the mixture is not discarded and refed daily during the first three days. In the Taheri study, starters were discarded and refed daily from the beginning. In my experiments, early daily discard and feeding sometimes delayed the appearance of strong yeast activity.
3. **Feeding ratio:** The Taheri study used approximately a 1:0.5:0.5 ratio of carryover starter, flour, and water by weight. Many starter creation methods use higher feeding ratios, such as 1:1:1 or 1:2:2. A larger feeding dilutes the accumulated acids in the carryover starter more substantially, raising the pH and potentially giving yeast a longer period to reproduce before the starter acidifies again. This difference could affect the development timeline.
4. **Refrigeration:** Newly created starters are not typically refrigerated during their first few weeks. In the Taheri study, the starters were refrigerated without feeding each weekend. This represents another significant difference from the methods used in my experiments, and could have slowed their development.

For these reasons, I would not interpret the specific Day 7, Day 14 or Day 28 observations in the Taheri study as a universal timetable for new starter development.

Appendix E: Type 1 Starters

What Is a Type 1 Sourdough Starter?

The term **“Type I sourdough”** dates at least to a 1995 classification proposed by Böcker, Stolz and Hammes, who divided sourdoughs into three types based primarily on their production and maintenance methods. Type I described traditional sourdough starters maintained through **continuous propagation and frequent refreshments**, while Types II and III described increasingly industrialized sourdough processes. For readability in this paper, I use the Arabic numeral 1 (‘Type 1’) rather than the Roman numeral I (‘Type I’).

Subsequent work by De Vuyst and colleagues, Minervini and colleagues, Gänzle and others has continued to refine this classification and, importantly, has characterized the **distinctive microbial communities** associated with traditional Type 1 sourdoughs.

For purposes of this paper, I bring these two ideas together and consider a **“Type 1 starter”** as having two important elements**:** the starter's **maintenance history** and its **microbial profile**.

This distinction is important.

Some Household starters (albeit a small percentage at 3.8% per the Landis study cohort) have the signature species profile of a Type 1 starter, however, they do not follow the requisite maintenance routine.

Similarly, some home bakers feed their starters every day and do not refrigerate them, but if they do not possess the characteristic Type 1 species profile, they are not Type 1.

For purposes of this analysis, I use the following two characteristics:

1. Type 1 Maintenance Protocol

A mature starter that has undergone long-term, continuous propagation, frequent refreshments, generally once or more per day, relatively short fermentation cycles, ambient or warm fermentation temperatures, and little or no routine refrigeration.

A long lineage often associated with traditional bakery starters is also common, but **age alone is not a separate criterion.** An old starter is not necessarily Type 1, but many Type 1 starters are old because they develop and persist through repeated generations under a sustained maintenance regime.

2. Type 1 Starter Signature Species Profile

Type 1 starters are characterized by a specific species profile.

Among the most characteristic are ***Fructilactobacillus sanfranciscensis*** among the bacteria and ***Kazachstania humilis***, or **other *Kazachstania* species**, among the yeasts. ***Saccharomyces cerevisiae*** is also found in Type 1 starters and can sometimes be the dominant yeast.

In his 2023 review (Gänzle 2023), Michael Gänzle describes Type 1 sourdough communities as globally similar at the species level, with *F. sanfranciscensis* as the predominant bacterium and *K. humilis* as the predominant yeast in the vast majority of cases. He also acknowledges other

Kazachstania species. A 2024 study of artisan bakeries in Valencia identified *F. sanfranciscensis, K. humilis,* and *S. cerevisiae* as predominant species (Sanmartín et al., 2024).

These organisms should not be treated as a rigid microbial checklist. Not every Type 1 starter contains exactly the same species, and their relative abundances can vary considerably.

In this paper, therefore, "Type 1 starter" refers to a mature starter that combines a specific long-term maintenance protocol with a generally consistent microbial profile.

Note: While there is no generally accepted scientific definition of a "Type 1 species profile," in this paper, I use the above species profile as a **highly indicative marker** of a Type 1 starter rather than a definitive criterion.

Representative species patterns commonly found in Household and Type 1 starters are included in *Appendix I: Commonly Recurring Species Patterns and Co-Occurrence.*

The Path to a Type 1 Microbial Profile

What is the path to a Type 1 starter? Do new starters, or household starters "evolve" into Type 1 starters?

Let's begin with the characteristic species of Type 1 starters:

- *K. humilis* and/or other *Kazachstania* species
- *S. cerevisiae*
- *F. sanfranciscensis*

These species have been found to follow patterns of occurrence on the path to Type 1.

See the Microbial Signpost table in *Part 5: The Starter Maturity Model*, to follow the typical occurrences of these species in New, Household and Type 1 starters.

How does one create a Type 1 starter?

Once Type 1 starters are understood, they inevitably raise some fascinating questions. Can a Type 1 starter be created from scratch? How long would it take? Could an established Household starter become Type 1? Could we create one in a laboratory by introducing the desired microorganisms? And would that engineered community be stable from Day 1?

The short answer is that **we don't know**.

However, the Arrival, Selection, and Maintenance framework introduced in the Maturity Map provides a useful way to explore these questions.

For purposes of this discussion, I use the Type 1 target species profile proposed in this paper: *Fructilactobacillus sanfranciscensis* together with *Kazachstania* spp. and/or *Saccharomyces cerevisiae*. This is a proposed microbial fingerprint, not a universally accepted definition of Type 1 sourdough.

The Arrival, Selection and Maintenance model is discussed in Part 2 and Part 5 of this document. The following section covers more nuanced details not included in those sections. Consult Part 2 and Part 5 for more complete coverage.

1. Arrival: The Microorganisms Must Be Present

Before microorganisms can become dominant in a starter, they must first have an opportunity to enter it. There are several possible pathways:

Initial colonization (chance). A newly created starter could, by chance, contain all the desired microorganisms from the beginning. It could essentially win the "microbial lottery." This is plausible, although the target organisms may be uncommon in the initial ingredients. As discussed, *F. sanfranciscensis* is often not detected in flour samples.

Intentional inoculation. Microorganisms can be deliberately introduced through selected ingredients, environmental materials, an existing starter, or laboratory cultures. Three options to consider:

- Debra Wink has experimented with inoculating starters using materials such as wildflowers and other natural sources (Wink / Janjigian, 2024).
- An existing starter could be inoculated with another known, Type 1 starter.
- The desired microbial community could theoretically be assembled in a laboratory.

None of these approaches guarantees that the introduced organisms will establish dominance.

Ongoing environmental introduction. “Arrival” is not necessarily a one-time event. Sourdough starters are an “open system.” Microorganisms may enter during routine feedings through flour, water, equipment, insects, human contact, or other environmental sources.

In every case, arrival is only the first condition. **The presence of the desired microorganisms does not guarantee that they will become dominant.**

2. Selection: The Conditions Must Favor Their Dominance

Once the target microorganisms have arrived, they must encounter conditions that favor their growth and establishment.

We don't know precisely which combination of conditions would reliably produce the proposed Type 1 species profile. The answer may involve many familiar sourdough variables, including flour type, hydration, temperature, feeding ratios, and feeding frequency.

One potentially important factor is the **number of feeding cycles**. Each refreshment repeatedly exposes the microbial community to changing environmental conditions and competitive pressures, creating opportunities for some microorganisms to gain an advantage over others.

But the absolute number of cycles alone may not tell the whole story.

For example, 500 feeding cycles at 12-hour intervals may not produce the same microbial community as 500 feeding cycles at 24-hour intervals. The number of cycles is identical, but the microorganisms experience different periods of growth, acidity, nutrient availability, and competition.

The timing and conditions of feeding cycles likely influence which species become dominant. More frequent feeding might accelerate selection under favorable conditions, but it could also favor different organisms. The outcome may depend partly on how each organism's **growth pattern aligns with the feeding schedule**.

And one fundamental limitation continues:

- More frequent feeding cannot select for microorganisms that have never arrived.

Simply feeding a starter more often, or maintaining it for many years, does not guarantee that it will develop a Type 1 microbial profile.

3. Maintenance: Achieving Dominance Is Not the Same as Sustaining It

Even if the desired microorganisms arrive and become dominant, a third condition remains: Maintenance.

The starter must continue to experience conditions that allow the resulting microbial community to persist.

Consider an extreme hypothetical example. Imagine we could identify the exact day a starter first achieved the desired Type 1 species profile and confirmed it with a DNA test. What happens if, the next day, the baker materially changes the feeding routine?

Would the starter maintain the Type 1 species profile?

We don't know. But the conditions that originally favored the community have changed dramatically, and we cannot assume its dominance would be preserved.

How do Type 1 starters maintain their stability? Consider two possible explanations.

1. **Intrinsic ecological stability.** At one extreme, a mature microbial community might become highly resistant to change when its microorganisms achieve dominance and develop mutually beneficial relationships which collectively create conditions favoring their own persistence and excluding competitors. These starters may remain stable even when maintenance conditions change.
2. **Maintenance-dependent stability.** At the other extreme, the microbial community might be relatively fragile, remaining stable primarily because the baker consistently repeats the same feeding protocol. Change those maintenance conditions, and the microbial community might change as well.

These explanations **are not mutually exclusive**. Both mechanisms could operate simultaneously, and their relative importance may differ for bacteria and yeasts.

Without longitudinal testing under changing maintenance conditions, we cannot reliably distinguish between a community that is inherently resistant to change and one that remains stable because its environment is consistently maintained.

How does *F. sanfranciscensis* get into a sourdough starter?

The Taheri study of newly created starters in Appendix D illustrates an interesting paradox. *F. sanfranciscensis*, one of the organisms most strongly associated with mature Type 1 sourdough starters, was not detected in any of the 18 newly created starters. McKenney et al. also did not detect it in the 10 flours they tested.

If it is not commonly found in flour, how does it get into a starter in the first place?

Research suggests that the answer may be **dispersal from the surrounding environment**. A fascinating experiment by Debra Wink explored the possibility of deliberately "seeding" newly created sourdough starters with plant and other natural materials as potential sources of sourdough microorganisms (Wink/Janjigian, “Flowers and Flours” 2024).

Other research has similarly identified bakery environments as potential reservoirs for sourdough microorganisms. Minervini et al., for example, specifically studied **"house microbiotas as sources of lactic acid bacteria and yeasts in traditional Italian sourdoughs."**

Michael Gänzle provides a much more colorful historical example. In a 2021 presentation, he described two bakeries that reported originally starting their sourdough starters with **livestock manure (horse and cow)** to seed it with desired microbes. The practice was straightforward: a small amount was added to the initial sourdough mixture, followed by dilution with repeated refreshments before the starter was eventually used for baking.

The manure example sounds shocking to modern bakers, but the ecological principle is important. **The flour does not have to contain every microorganism that eventually becomes established in the starter.** Microorganisms can arrive from other environmental sources, and perhaps intentional inoculation.

The original natural habitat of *F. sanfranciscensis* remains uncertain. Evidence increasingly points toward an association with insects, particularly insects that infest stored grain. DNA surveys have detected *F. sanfranciscensis* in the intestinal material and frass of grain beetles, suggesting that insects may introduce the organism into grain and flour before it ultimately enters a sourdough starter.

This does not mean that *F. sanfranciscensis* can never arrive through flour. Microorganisms can be introduced through incidental environmental contamination of the grain or flour itself.

Michael Gänzle once illustrated this point to me with a characteristically colorful example: a single rodent hair or insect in flour could potentially introduce enough microorganisms to inoculate a starter with specific microbes**.** In other words, identifying flour as the immediate source does not necessarily mean the microorganism originated from the wheat itself. Flour can be the vector without flour being the natural ecological reservoir.

What about the well-known “Baker's Hands” study?

A widely cited study by Reese et al. (2020) found substantial microbial similarities between sourdough starters and the hands of the bakers who maintained them. This is often interpreted as evidence that bakers introduce their own microbes into established starters.

However, an important detail is frequently overlooked: the researchers studied **newly created starters**, not long-established sourdough cultures. They also could not definitively establish the direction of microbial transfer between hands and starters.

During early starter development, microbes introduced from flour, hands, and the environment may influence the developing community. Once a stable microbial community becomes established, however, newcomers must compete with organisms already adapted to that environment.

The study provides valuable evidence about microbial exchange during **new starter creation**. It does not establish that handling a mature starter will significantly alter its established microbial community.

Is *F. sanfranciscensis* the Type 1 "Gatekeeper?"

F. sanfranciscensis plays an important role on the path to Type 1.

As discussed, we know it is one of the three characteristic Type 1 organisms.

Consider the potential arrival paths:

- *Kazachstania* spp. are frequently detected in flour.
- *S. cerevisiae* is found in flour, the environment, and the vast majority of Household starters.

F. sanfranciscensis is the outlier.

- It is the dominant bacterium in the **overwhelming majority** (over 90%) of the Type 1 starters examined in this paper. De Angelis et al. described it as **the "key lactic acid bacterium"** of Type 1 sourdough.
- It is not commonly detected in flour, suggesting that other sources may be important for its arrival.
- It is uncommon in new starters, and relatively uncommon in Household starters occurring as the dominant bacterium in 17.4% of the Landis Household cohort and only 11.5% of household starters not originating in a bakery or other commercial source.

For these reasons, I think of *F. sanfranciscensis* as a potential **"gatekeeper"** organism in the development of Type 1 microbial ecosystems. (A small percentage of Type 1 starters have other dominant bacterial species so it is not a universal requirement).

A plausible pathway to Type 1 is:

1. *F. sanfranciscensis* arrives through an environmental source, and less likely through flour.
2. Frequent refreshments and infrequent refrigeration favor its establishment and eventual dominance.
3. Once *F. sanfranciscensis* becomes dominant, the community may develop the characteristic Type 1 combination: this bacterium alongside *K. humilis* or other

Kazachstania species. The co-occurrence analysis in *Appendix I: Commonly Recurring Species Patterns and Co-Occurrence* reports this species pair as occurring more frequently than would be expected at random.

4. Sustained maintenance supports the microbial community exhibiting the characteristic Type 1 fingerprint.

Another interesting possibility: Household starters already dominated by *F. sanfranciscensis* may represent a relatively small pool of promising candidates for conversion to Type 1 through intensive maintenance, essentially bypassing steps 1 and 2 above.

These are proposed pathways. The research does not yet establish how individual Household starters transition into Type 1 starters, or whether *F. sanfranciscensis* dominance makes that transition more likely.

Nevertheless, its striking prevalence in Type 1 starters, contrasted with its relative rarity as the dominant bacterium in Household starters, makes it a **strong distinguishing indicator** and a promising subject for future research.

In *Appendix F: What Happens When Type 1 Maintenance Stops* we examine five case studies showing exceptional resistance to change by *F. sanfranciscensis* under varying maintenance conditions. Once it is established, it appears difficult to displace.

In addition to the "gatekeeper" role, is *F. sanfranciscensis* also ***"the last to leave?"*** See *Appendix F.* for more discussion on this topic.

Why is *S. cerevisiae* so dominant in Household starters, but less characteristic of Type 1 starters?

S. cerevisiae is extremely successful in Household starters. In the Landis dataset, it was by far the most common yeast and frequently dominated the yeast population in 80.2% of samples.

Type 1 starters present a different ecological environment. Years of frequent feeding strongly favor a narrower group of microbes adapted to continuous growth under increasingly specialized conditions. In that environment, *F. sanfranciscensis* frequently becomes the dominant bacterium, and *Kazachstania* yeasts become much more common. The positive relationship between these species of yeast and bacteria is known as "co-occurrence." See *Appendix I: Commonly Recurring Species Patterns and Co-Occurrence.*

The Landis co-occurrence data provide an important clue. *F. sanfranciscensis* showed positive associations with *Kazachstania* species such as *K. humilis*, and a **negative association with *S. cerevisiae***. That does not prove a direct cause-and-effect relationship, but it suggests that the microbial environment favored by *F. sanfranciscensis* may also favor *Kazachstania* over *S. cerevisiae*.

The "dance partner" analogy is useful:

- *S. cerevisiae* is an excellent performer, but it may not be the preferred dance partner of *F. sanfranciscensis*. *Kazachstania* often appears to be.

That helps explain the apparent paradox. *S. cerevisiae* is not a weak, underperforming species or excluded from Type 1 starters. In fact, it dominates some Type 1 starters. But the highly selected Type 1 ecosystem appears to create conditions which favor a different yeast-bacteria partnership.

Type 1 Starters and "Elimination of Dispersal Limitation"

Michael Gänzle and others describe one condition associated with the development of Type 1 starters as the **"elimination of dispersal limitation."** I struggled with this wording at first, so let's unpack it.

The introduction of new microorganisms into a starter is referred to as **dispersal**. Starters are open systems. Every feeding creates another opportunity for microorganisms from flour, water, and the surrounding environment to enter a starter.

Dispersal has a cumulative effect. More feedings create more dispersal opportunities for new microbes to enter a starter. A newly created starter **is limited** in its opportunities to encounter new species simply because it is new and feeding cycles take time to accumulate. A newer starter may therefore be described as **dispersal limited**.

A starter that has been fed frequently for many years has had far more opportunities to encounter new microbes. Repeated feeding cycles can then progressively and cumulatively "**eliminate" the dispersal limitation**.

Mature starters have been exposed, again and again, to potential new entrants resulting in ***"elimination of dispersal limitation."*** In colloquial, though not literal, terms, they have had a chance to "see everything."

This leads to an interesting paradox:

A mature Type 1 starter may have had more opportunities for microorganisms to arrive, yet ultimately contain fewer dominant species.

As discussed in Part 2 and Part 5 of this document, the "Arrival" and "Selection" conditions help explain this process. Over many years and thousands of feeding cycles, many organisms may arrive, but only a small number may repeatedly win. And the winners have been "selected" from an extremely broad pool of candidate microbes.

Can a Household starter perform as well as a Type 1 starter?

I have not performed controlled side-by-side tests of Household and Type 1 starters, so I cannot answer that definitively. Based on years of baking notes and starter-strength testing, however, I would not assume that Type 1 automatically means "better."

The source starter in this study rises faster than my previous starters, which were presumably Household starters. But faster rising is not necessarily better. My previous starters produced nearly identical loaves; they simply fermented and rose somewhat more slowly.

I have also tested how much a Household starter can improve through intensive maintenance. In one six-day feeding experiment, I increased the starter's rising power by about **250%**. That test is

documented in my YouTube video, *When Is Bulk Fermentation Done?: Episode 6 (2021)*. I have seen similar improvements using the **Peak-to-Peak Feeding Method**, which I introduced in my 2020 video *How to Strengthen a Weak Starter*.

Different yeast species and strains can vary substantially in carbon-dioxide production. Performance also depends on the entire starter community, including carbon dioxide produced by some bacteria and interactions among microorganisms. A starter's potential therefore depends on its microbial makeup, while its **health and maintenance** influence how much of that potential it achieves.

Chasing a particular yeast species may not produce the desired improvement. Strain-level differences and the surrounding microbial community also matter.

My practical conclusion is simpler: **a Household starter can often be made dramatically stronger through intensive feeding, even if that maintenance is only temporary.** Whether it can match or exceed a particular Type 1 starter depends on the organisms and strains present.

Appendix F: What Happens When Type 1 Maintenance Stops

Type 1 Stability Is Conditional

Once a starter has developed the maintenance history and characteristic microbial ecology of a Type 1 starter, that does not mean it will remain unchanged forever. **The same maintenance conditions that helped create its highly specialized microbial ecosystem also help maintain it.**

Frequent feedings and uninterrupted maintenance are the hallmarks of Type 1 starters. These starters thrive in a continuous state of turnover. They are a product of their **momentum.** Like spinning plates, their stability depends on continued activity.

Type 1 starters can be remarkably stable, but that stability is not absolute. Their microbial communities have been selected through hundreds or thousands of feeding cycles under a relatively consistent maintenance regime. Feeding frequency, feeding ratio, temperature, hydration, flour, storage conditions and the surrounding microbial environment all contribute to the selective conditions under which that community developed.

When those conditions change, **the selective pressures also change**. Organisms that were highly competitive under the original maintenance routine may become less competitive, while other organisms already present in the starter, or newly introduced from the environment, may gain an advantage.

This does not mean that changing a Type 1 maintenance routine will immediately change the identity of the starter. As the studies below demonstrate, established microbial communities can be remarkably resilient. But significant or prolonged changes in maintenance can increase the opportunity for microbial community shifts, including changes in the relative abundance of existing species and, potentially, the loss or replacement of organisms characteristic of the original Type 1 ecology.

The direction and magnitude of that shift are not predetermined. They depend on what changes, how long the new conditions persist, and how well the existing microbial community competes under the new conditions.

Put simply: **Change the maintenance conditions, and you change the competitive landscape. Change the competitive landscape and you can change the microbial makeup of the starter.**

What does "Reversion" mean?

In this paper, I use "**reversion"** to describe **movement away from the characteristic Type 1 species profile** after that maintenance routine is substantially relaxed or changed. *See Part 5: Starter Maturity Model: The Complete Guide* for additional discussion of "reversion."

Reversion should not be thought of as an instantaneous switch from "Type 1" to "Household." A starter may first experience changes in the population mix of organisms that are already present.

With continued changes in maintenance, characteristic Type 1 organisms may decline, disappear, or be replaced by organisms better adapted to the new environment.

Reversion is therefore better understood as a **continuum**.

A starter can drift substantially without losing its defining microbial identity. Conversely, a sufficiently large or prolonged change in maintenance conditions may eventually produce a microbial profile more characteristic of a Household starter.

The following case studies illustrate the concept of reversion in Type 1 starters.

Case Study 1: Urien et al. (2019) and Michel et al. (2023): Different Bakery Practices, Different Yeast Communities

The Setup

Urien et al. (2019) studied the fungal communities of traditional French sourdoughs (a.k.a. sourdough starters) made with organic wheat flour. The study included sourdoughs from two types of producers: conventional artisan bakers and "farmer-bakers," who grow grain, mill flour and bake bread on a generally smaller and less frequent production schedule.

The researchers characterized sourdough yeasts using culture-based methods and DNA metabarcoding.

What Was Different

The two groups followed substantially different bread-making practices. Most relevant here, the artisan bakers generally operated more intensive production schedules with shorter fermentation cycles, while farmer-bakers tended to bake less frequently, often only once or twice per week, and stored their sourdoughs for longer periods between baking cycles.

Michel et al. (2023) also associated *K. humilis* with artisan-like practices and *K. bulderi* with farmer-like practices.

What Happened

The yeast communities differed substantially between the two groups.

K. humilis was the characteristic dominant yeast among the artisan bakers, while the starters maintained with farmer-like practices contained a broader collection of *Kazachstania* species, including *K. bulderi*, *K. unispora*, *K. saulgeensis*, *K. barnettii* and another unidentified *Kazachstania* species.

Related bacterial studies found *F. sanfranciscensis* broadly across both groups.

Why It Matters

This study suggests that different maintenance practices can favor different yeast communities.

That suggests an important possibility**:** different members of a mature sourdough ecosystem, namely **yeast versus bacteria,** may respond differently to changes in maintenance conditions.

That pattern is particularly relevant to my experiment. The two starters differed substantially in yeast proportions, while *F. sanfranciscensis* accounted for almost all bacterial reads in both. Together, these findings suggest that yeast and bacteria **need not respond alike** to differences in maintenance.

Important limitation: This study was an observational comparison of established starters maintained under different practices, not a controlled experiment in which the same starter was subjected to different maintenance regimes. The study therefore demonstrates an association between bakery practices and microbial composition, but does not by itself establish that reduced feeding frequency caused the observed differences.

Case Study 2: Pham et al.: The "Retired Baker"

The Setup

Pham et al. examined the long-term persistence of bacteria in established bakery sourdoughs. One starter, identified as **Sourdough C**, provides an unusually useful natural experiment.

It was sampled in 2005 while being maintained as a bakery starter. In 2009, the bakery operation and a copy of the starter were transferred to another baker, who continued maintaining it for commercial bread production. The original baker also retained a copy but began using it only for personal baking, approximately once per week. Both descendants were later sampled again.

What Changed

Before 2009, Sourdough C was refreshed **twice daily**, fermenting at relatively cool temperatures of approximately 12–18°C.

After the bakery transfer, the commercial copy continued under intensive maintenance, although its protocol changed to once-daily feeding.

The original baker's personal copy underwent a much larger change. Instead of twice-daily bakery propagation, it was maintained approximately **once per week** at the household level. Importantly, however, the starter was still kept under cool conditions in a "cold room," approximately 12–18°C. **It was not refrigerated** at typical refrigerator temperatures of 40°F (4°C).

Descendants of the same established bakery starter therefore followed dramatically different maintenance paths for roughly 15 years.

What Happened

The bacterial community proved remarkably resilient.

The original Sourdough C was dominated by ***F. sanfranciscensis***. Both descendants remained overwhelmingly dominated by the same species. The researchers reported that *F. sanfranciscensis* represented **more than 99% of viable bacterial cell counts** in the original and both descendant starters.

The study also **went beyond species-level identification**. Whole-genome analysis showed that the *F. sanfranciscensis* isolates remained genetically very closely related, supporting **long-term strain-level persistence.**

In a later conversation I had with the retired baker who maintained the household descendant, she provided another useful piece of context. Despite the dramatic reduction in feeding frequency, she described the starter approximately 15 years later as **"exactly the same as it was in the bakery."** That is a baker's observation rather than a microbial measurement, but it is notable. The starter had apparently retained the functional, and observable characteristics she associated with the original bakery culture even after many years of much less intensive maintenance.

Why It Matters

A dramatic reduction in feeding frequency, from twice-daily bakery maintenance to approximately once-weekly household maintenance, did **not** eliminate the dominant *F. sanfranciscensis* population.

Approximately 15 years after the maintenance routines diverged, *F. sanfranciscensis* still accounted for more than 99% of viable bacteria in both descendants, with very close alignment at the strain level. And, from the baker's perspective, the household starter still behaved much as it had during its bakery years.

Changing Type 1 maintenance can create an opportunity for microbial drift, but substantial drift is not inevitable. Some components of an established Type 1 ecosystem can be extraordinarily persistent even after the maintenance regime changes dramatically.

There is, however, an important limitation: the Pham study focused on bacterial persistence and **did not provide a comparable longitudinal analysis of the yeast community.** It therefore cannot tell us whether *K. humilis*, *S. cerevisiae*, or other yeasts changed after the transition from bakery to household maintenance.

That missing information matters. The bacterial population may remain extraordinarily stable even while the yeast community changes substantially, as seen in Case 1. The retired baker's observation that the starter seemed unchanged is compelling supporting context, but without historical and contemporary yeast data, we cannot know whether the underlying yeast population was equally stable.

Case Study 3: Minervini et al.: Bakery vs. Laboratory Maintenance

The Setup

Minervini et al. studied seven mature Type 1 starters from artisan bakeries in southern Italy.

Each starter continued to be maintained at its original bakery while a second sample was propagated for 80 days in a laboratory. The researchers attempted to reproduce the principal process parameters, including flour and ingredients, inoculation level, fermentation temperature and fermentation time.

What Changed

Unlike the previous examples, the researchers deliberately attempted to keep the feeding and fermentation variables similar.

The major change was the broader maintenance environment: **a working artisan bakery versus a controlled laboratory environment.**

What Happened

Despite efforts to preserve the principal process parameters, significant microbial changes occurred in several starters.

The most dramatic changes involved the yeast populations. In one starter, the viable yeast population declined by approximately 99.99% during laboratory propagation, with substantial declines also observed in several other starters. Changes in lactic acid bacteria species and strains were also observed.

Importantly, the seven starters did not respond identically. Some microbial populations were considerably more stable than others.

Why It Matters

The mechanism behind these changes is not entirely clear, and the study should **not** be interpreted to mean that simply changing the geographic location of a starter causes microbial drift.

The meaningful change was broader: the starters were removed from their established bakery maintenance environment and propagated in a laboratory.

Minervini therefore provides an important counterpoint to the extraordinary persistence observed in the Pham study. Even when researchers attempted to preserve many of the obvious maintenance variables, changing the broader propagation environment was associated with substantial microbial change.

The study reinforces an important limitation in our understanding: **we may not yet know all of the variables that contribute to the stability of an established Type 1 starter.**

Case Study 4: A Tale of Two Starters (Cucuzza): 14 Months of Different Maintenance

The Setup

The experiment described in this paper provides another example of Type 1 starter stability under changing maintenance conditions.

Two samples originating from the same mature Type 1 starter were separated and maintained independently for 14 months. The source starter continued under its established, highly consistent maintenance routine, while my sample was subjected to a substantially different and more variable maintenance regimen.

Unlike several of the published examples above, DNA sequencing measured the relative abundance of both yeast and bacterial populations, allowing all three dominant organisms to be compared.

What Changed

The source starter was maintained using a highly consistent feeding schedule, flour, feeding ratio, temperature and other maintenance practices.

My starter experienced considerably more variability. During the 14-month period, I changed flours, feeding frequency, feeding ratios, temperatures and storage conditions. The starter was also subjected to several extended "vacation holds" at 50°F (10°C) lasting from one to three weeks.

In short, the starter was removed from a highly consistent Type 1 maintenance routine and subjected to multiple changes over an extended period.

What Happened

Despite those maintenance differences, the same three dominant species were found in both the source starter and my starter 14 months later.

The bacterial population was remarkably stable:

F. sanfranciscensis
Source: **99.7%**
My starter: **99.8%**

The yeast population differed more substantially:

K. humilis
Source: **57.3%**
My starter: **17.8%**

S. cerevisiae
Source: **40.7%**
My starter: **78.0%**

The ranking of the two dominant yeasts reversed.

Why It Matters

This experiment illustrates both the **stability** and the **capacity for drift** within an established Type 1 starter.

The core microbial fingerprint proved remarkably resilient despite 14 months of substantially different maintenance. At the same time, that stability did not mean the microbial community remained static.

The result is also consistent with the two partial pictures provided by Urien et al. and Pham. Urien et al. found *K. humilis* associated with more intensive bakery maintenance, while Pham

demonstrated extraordinary persistence of *F. sanfranciscensis* after bakery maintenance was greatly reduced.

In my experiment, both patterns appeared together: *K. humilis* abundance differed substantially between the two starters, while *F. sanfranciscensis* abundance was virtually identical.

Type 1 stability therefore does not necessarily mean that the proportions of organisms remain fixed. **A starter can retain its defining microbial species while the balance among those species changes substantially.**

What can we learn from these studies?

Taken together, these studies paint a more nuanced picture of Type 1 starter stability.

Type 1 starters can be remarkably persistent. Established microbial communities do not necessarily disappear when maintenance changes. Pham et al. demonstrated extraordinary long-term persistence of *F. sanfranciscensis* even after a bakery starter transitioned from twice-daily feeding to approximately weekly household maintenance.

But Type 1 starters are not impervious to change. Urien et al. found important differences in yeast communities associated with different bakery practices, while Minervini demonstrated that substantial microbial changes can occur when established bakery starters are propagated under a different maintenance environment.

My experiment demonstrated both characteristics simultaneously. After 14 months of substantially different maintenance, the three dominant species remained the same. *F. sanfranciscensis* was virtually the same in both starters, while the relative abundance of the two dominant yeasts diverged.

Several general observations emerge:

1. **Type 1 starters are highly stable, but not permanently fixed.** Their established microbial communities can persist through substantial changes in maintenance, sometimes for many years.
2. **Different organisms may respond differently to the same maintenance change.** The available evidence suggests particularly strong persistence by *F. sanfranciscensis*, while yeast populations may be more responsive to change.
3. **Relaxing or changing Type 1 maintenance creates an opportunity for microbial drift, but does not predetermine the outcome.** The direction, magnitude and timing of that drift depend on the starting community, the changes imposed and their duration.
4. **Microbial drift does not necessarily mean loss of microbial identity.** A starter may retain its characteristic species while their relative proportions change substantially.
5. **There is probably no single "reversion switch."** Feeding frequency is clearly important, but temperature, storage, flour, hydration, fermentation conditions and the broader maintenance environment may all influence which organisms remain competitive.

The larger implication is that **Type 1 should not be viewed as a permanently fixed microbial state that, once achieved, is retained indefinitely.** Its ecology reflects an ongoing relationship between the organisms already present and the conditions under which they continue to be propagated.

Case Study 5: Testing the Limits of Type 1 Starter Stability (Wardhana et al. 2026)

In a 2026 study, Wardhana and colleagues examined the stability of two established industrial Type 1 sourdough starters under prolonged, infrequent feeding conditions.

Both starters initially contained the characteristic species *F. sanfranciscensis* and *M. humilis* (formerly *K. humilis*). The researchers conducted separate experiments using weekly feeding for four weeks and feeding every three weeks for 39 weeks, with refrigeration at 4°C between feedings.

The table below focuses on the 39-week experiment, which produced strikingly different microbial outcomes. Importantly, the two starters came **from different sources** and differed in hydration, feeding ratios, and fermentation temperatures and durations. Consequently, the study provides valuable evidence about microbial stability under these maintenance conditions, but does not establish which individual factor caused the differences.

Table 15: Wardhana Study of Extreme Maintenance Conditions on Type 1 Starters

Comparison detail	IB-A: Firm Starter (60% hydration)	IB-B: Semi-Liquid Starter (100% hydration)
Original starter	Established industrial wholemeal wheat sourdough	Established industrial wholemeal wheat sourdough (different source from IB-A)
Initial signature species	*F. sanfranciscensis* and *M. humilis (K. humilis)*	*F. sanfranciscensis* and *M. humilis (K. humilis)*
Feeding ratio (starter: flour: water)	1 to 3.12 to 1.87	1 to 0.5 to 0.5
Retained starter as % of final mix	16.7%	50%
Warm fermentation after feeding	24 hours at 24–27°C	16 hours at 30°C
Storage between feedings	4°C (39°F) refrigeration	4°C (39°F) refrigeration
39-week feeding schedule	Feed every 3 weeks for 39 weeks (13 cycles)	Feed every 3 weeks for 39 weeks (13 cycles)
pH range during 39-week study	3.7–4.0	3.7–4.0
Highest recorded TTA during 39-week study	25.9 mL (week 24)	32.9 mL (week 21)

LAB outcome after 39 weeks	*F. sanfranciscensis* **persisted** through week 39; *L. parabrevis* also appeared	*F. sanfranciscensis* **displaced** in cultured isolates by *L. parabrevis* (~week 12); *P. parvulus* later prominent
Yeast outcome after 39 weeks	*M. humilis* **persisted** through week 39; transient other yeasts	*M. humilis* last cultured week 15; cultured yeasts **below detection** after ~weeks 15–18
Source: Wardhana et al. 2026		**© The Sourdough Journey, 2026**

Key Findings

This extraordinary study, published in September 2026, is essentially an "extreme version" of the "vacation hold" regimen in my study. The starters were maintained with only 13 feedings over 39 weeks (once every three weeks) and extended refrigeration storage at 4°C (39°F).

The feeding ratio of the liquid starter (IB-B) was very low, and what I would characterize as a "starvation feeding" with only half as much flour and water as carryover starter added in each feeding.

This study gives us two remarkable, complementary findings about Type 1 starters:

1. **Persistence:** An established Type 1 ecosystem can be extraordinarily resistant to change, even under infrequent maintenance. Both samples retained their dominant species profiles for many weeks of infrequent feedings and refrigeration. The firm starter sample (IB-A) retained both characteristic Type 1 species through all 39 weeks, despite some changes in the broader microbial community.
2. **Vulnerability:** That persistence is not guaranteed. Maintenance conditions appear to matter, although this experiment cannot isolate which variables were responsible. The characteristic Type 1 species in the liquid starter sample (IB-B) were displaced after 12-15 weeks of unconventional maintenance.

Perhaps the most striking finding is that an established Type 1 microbial community remained remarkably stable through 39 weeks of infrequent feeding and prolonged refrigeration, while another underwent substantial microbial replacement under a different maintenance regimen.

Why did the two samples react differently?

The two samples were from two independent sources. They are not two branches of the same original starter. In addition, while the study characterizes the two starters as "firm" and "semi-liquid" the more notable difference, based on my experiments and experience, is the very different feeding ratio.

The firm starter was fed **nearly six times as much flour** as the semi-liquid starter, relative to both of their carryover starter amounts with each feeding. A higher feeding ratio provides a greater supply of fresh nutrients for the starter to persist during a long period without feeding (three weeks between feedings in this example). Higher feeding ratios also dilute initial acidity which can impact starter performance.

This study challenges some commonly repeated claims about the fragility of established Type 1 sourdough starters, including suggestions that brief refrigeration or missed feedings can rapidly eliminate their characteristic microorganisms.

Additional Frequently Asked Questions

Can Reversion be reversed?

Possibly. And the persistence of *F. sanfranciscensis* may be the key.

A starter that moves away from Type 1 maintenance does not necessarily lose all of its Type 1 organisms. The Pham "retired baker" case is particularly important here: after roughly 15 years of approximately weekly Household-style maintenance, *F. sanfranciscensis* still represented more than 99% of the viable bacterial population.

That suggests an intriguing possibility. If *F. sanfranciscensis* persists after a starter moves toward Household maintenance, the starter may retain one of the most difficult pieces of the Type 1 ecological puzzle.

Recall the three requirements described in this paper:

Arrival → Selection → Maintenance

For a completely new starter, ***F. sanfranciscensis* must first arrive** before Type 1-style selection can favor it. But in a reverted or partially reverted starter in which *F. sanfranciscensis* remains present, that arrival step has already been satisfied.

The yeast side may present a lower barrier. *Kazachstania* yeasts, including *K. humilis*, appear to have more direct routes of introduction through flour and the grain-associated environment. If *K. humilis* remains at low abundance, as it did in my starter, it does not need to be reacquired at all. If it has disappeared, reacquisition may still be more readily achievable than reacquisition of *F. sanfranciscensis*.

Restoring frequent Type 1-style refreshments could then re-establish the **selection pressure** favoring those organisms. This leads to a useful hypothesis:

A former Type 1 starter that still contains *F. sanfranciscensis* may retain the biological ingredients needed to cross the Type 1 boundary again.

In that sense, persistent *F. sanfranciscensis* may **"hold the key" to reentry**. The starter may no longer display a Type 1 signature species fingerprint, but it **has not necessarily lost the organism that may be hardest to reacquire.**

There is currently no demonstrated scientific "reset protocol" for a reverted Type 1 starter. But if *F. sanfranciscensis* survives the transition to Household maintenance, the path back may be considerably shorter than the path by which a new starter reaches Type 1 in the first place.

If I were to begin feeding my starter used in this experiment twice a day, would the population mix revert back to *K. humilis* dominance?

Short Answer: I think it might.

Because we have two endpoint samples of my starter and the source starter, we cannot attribute changes to either starter. For this thought exercise, **assume the difference arose through a change in my starter**.

A working hypothesis under that assumption is that the shift from *K. humilis* dominance toward *S. cerevisiae* dominance was caused, at least in part, by my less consistent and less frequent maintenance routine. If that is correct, returning the starter to the source starter's twice-daily feeding schedule could gradually shift the competitive balance back toward *K. humilis*.

Importantly, *K. humilis* is still there. It represents nearly 18% of my yeast population, so it would not need to be reintroduced. It would only need to regain relative abundance.

Would it return all the way to the source starter's original 57.3% mix of *K. humilis*? **I have no idea.**

There is also an important assumption buried in this question: **that the source starter's original yeast ratio represented an ideal Type 1 state that my maintenance somehow disrupted.** The available Type 1 data do not support that assumption. As shown in *Part 5: Table 10,* the source starter's relatively even *K. humilis* / *S. cerevisiae* mix is uncommon among mature Type 1 bakery starters.

So, a presumed change in my starter should not automatically be interpreted as "damage" to a previously ideal microbial balance. Both samples remained strongly consistent with Type 1 ecology; the principal change was the relative abundance of two yeast species that were already present. And my starter continues to produce excellent sourdough bread.

That leads to the more practical question: **Does it matter?**

I did not observe any deterioration in starter performance over the 14-month period. So, at least from a baking standpoint, I see no compelling reason to try to force the starter back toward *K. humilis* dominance. There is evidence that my starter's rising power increased in the latter months of the study. See *Appendix J: Changes in Starter Rising Power* for more information.

If a baker stops feeding a Type 1 starter every day, will it lose its Type 1 identity?

Short Answer: Not necessarily, but it can.

The case studies above demonstrate that Type 1 starters can tolerate substantial departures from traditional daily maintenance without necessarily losing their characteristic microbial signature.

In my experiment, I missed or skipped approximately 10% of daily feedings and used extended vacation holds at 50°F (10°C) without losing the characteristic Type 1 species.

Wardhana et al. (2026) demonstrated even more remarkable persistence. One established Type 1 starter retained its characteristic bacteria and yeast through 39 weeks of feeding only once every three weeks, with refrigeration at 40°F (4°C) between feedings. However, a second starter maintained under a different set of conditions experienced substantial microbial replacement and loss.

These findings suggest that less frequent feeding, refrigeration, and other changes in maintenance do not necessarily cause a Type 1 starter to lose its microbial identity. But that identity is not guaranteed to persist indefinitely, as the Wardhana study also demonstrates.

How quickly a starter changes, and whether it changes at all, depends on its existing microbial community and the conditions under which it is maintained.

Appendix G: A 20-Year Household Starter Comparison

The Auerbach Natural Experiment

The Auerbach comparison provides one of the most unusual natural experiments in the Global Sourdough Project.

Rather than comparing unrelated starters, it compares **two descendants of the same starter after approximately 20 years of separate maintenance**.

In 2017, David Auerbach submitted Starter #867 to the Global Sourdough Project. Approximately 20 years earlier, he had given a portion of the same starter to another baker. That independently maintained descendant was also submitted to the project as Starter #742. The two samples therefore represented a roughly 20-year fork of the same starter lineage.

Despite two decades of separation, their microbial fingerprints were remarkably similar.

The Starter's Earlier History

The lineage can be traced farther back.

According to Auerbach, his starter descended from the **"Russian" culture distributed by Ed Wood and Sourdoughs International**. Wood's Russian culture was described as originating in Palekh, Russia**,** approximately 200 miles northeast of Moscow, and as a particularly fast-leavening culture suited to heavy whole-wheat doughs.

The broader history of Wood's collection is also relevant. Wood collected sourdough cultures from around the world, particularly while traveling through Europe and the Middle East. Accounts of his collecting describe seeking out traditional or old-fashioned bakeries and obtaining pieces of their sourdough cultures.

This raises the possibility that the Russian culture originated in a traditional bakery environment. However, **that cannot presently be established**.

I attempted to trace the Palekh culture far enough back to determine whether Wood's original Russian sample came specifically from an artisan bakery, which might suggest that it had been maintained under a Type 1 protocol. That trail ended without a definitive source.

The safest conclusion is therefore:

The Auerbach starter descended from Ed Wood's Russian culture, a lineage collected during Wood's worldwide search for traditional sourdough cultures, but its specific bakery origin cannot be confirmed.

Microbial Fingerprints After Approximately 20 Years of Separation

The following is the complete comparison reported from the original Global Sourdough Project results.

Table 16: Auerbach 20-Year Starter Comparison: Complete Microbial Fingerprint: Yeast

Microorganism	Starter #867	20-Year Fork #742
YEAST		
***Saccharomyces cerevisiae* strain 2**	49.62%	53.90%
***Saccharomyces cerevisiae* strain 1**	44.64%	45.48%
Combined *S. cerevisiae*	**94.26%**	**99.38%**
***Candida* sp. strain 2**	3.11%	—
***Candida* sp. strain 1**	2.03%	0.05%
***Wickerhamomyces anomalus* strain 1**	0.33%	0.10%
***Wickerhamomyces anomalus* strain 2**	0.03%	0.18%
***Wickerhamomyces anomalus* strain 3**	0.02%	—
***Kazachstania humilis* strain 4**	0.07%	—
***Kazachstania humilis* strain 3**	0.02%	—
Candida glaebosa	0.07%	—
Candida quercitrusa	—	0.16%
Meyerozyma guilliermondii	—	0.05%
Kazachstania wufongensis	0.02%	0.04%
***Kazachstania bulderi* strain 1**	—	0.01%
***Kazachstania servazzii* strain 2**	—	0.01%
***Hanseniaspora uvarum* strain 4**	0.03%	0.02%
***Debaryomyces hansenii* strain 1**	—	0.01%
Kluyveromyces marxianus	0.02%	—

The remarkable feature is not merely that *S. cerevisiae* dominates both samples. Even the **two separately reported *S. cerevisiae* sequence variants (variant 1 and variant 2) remained in remarkably similar proportions** after approximately 20 years.

Starter #867 contained 49.62% and 44.64% of the two types.

Starter #742 contained 53.90% and 45.48%.

That is an unusually close microbial fingerprint for two starter populations maintained independently for approximately two decades.

Table 17: Auerbach 20-Year Starter Comparison: Complete Microbial Fingerprint: Bacteria

Microorganism	Starter #867	20-Year Fork #742
BACTERIA		
***"Lactobacillus* sp. 7"**	**99.62%**	**99.65%**
***Lactobacillus brevis* strain 1**	0.14%	0.08%
Lactobacillaceae sp. 7	0.08%	0.05%
Lactobacillaceae sp. 1	0.05%	0.04%
Lactobacillaceae sp. 3	0.03%	0.04%
***Pediococcus* sp. 1**	0.02%	0.02%
Lactobacillus paralimentarius	0.01%	0.03%
Lactobacillus plantarum	0.01%	0.05%
***Lactobacillus zeae* strain 1**	0.01%	—
***Pediococcus ethanolidurans* strain 1**	0.01%	—
Lactobacillaceae sp. 2	0.01%	—
***Lactobacillus brevis* strain 3**	—	0.02%
***Lactobacillus* sp. 2**	—	0.01%
***Pediococcus* sp. 2**	—	0.01%
Lactobacillaceae sp. 5	—	0.01%
***Leuconostoc* sp. 1**	—	0.01%

Source: Auerbach comparison as reproduced in Mike Avery, "Another Delicate Matter," SourdoughHome, 2019.
Note: Strain designations are reproduced from the original report and should not be interpreted as independently confirmed strain-level identifications.

Identifying *"Lactobacillus* sp. *7"*

When these results were originally reported, the dominant bacterium was identified only as ***"Lactobacillus* sp. *7."*** That left the most important bacterial organism in the comparison apparently unidentified.

The published Landis et al. dataset makes it possible to resolve that label.

The Global Sourdough Project sample numbers can be cross-referenced to the samples used in the final Landis dataset:

- Auerbach **#742 = Landis sample S_250**
- Auerbach **#867 = Landis sample S_392**

In the final sequence-level taxonomy, the overwhelmingly dominant bacterium in these samples maps to ***Lactobacillus sanfranciscensis***, subsequently renamed ***Fructilactobacillus sanfranciscensis***.

The Landis sequence data show approximately:

Sample	Final Identification	Relative Abundance
#742 / S_250	*F. sanfranciscensis*	~99.92%
#867 / S_392	*F. sanfranciscensis*	~99.76%

The small numerical differences from the earlier public report reflect the later sequence-processing and taxonomy pipeline. The important point is not the difference between 99.6% and 99.9%. It is the identity of the organism.

Both descendants were essentially monocultures of *F. sanfranciscensis* on the bacterial side after approximately 20 years of independent maintenance.

That makes the Auerbach comparison considerably more relevant to the Type 1 discussion than the original public report suggested.

What Changed?

Surprisingly little at the dominant-organism level.

After approximately 20 years:

- Both starters remained approximately **94–99% *S. cerevisiae*** on the yeast side.
- The two major *S. cerevisiae* sequence types remained in remarkably similar proportions.
- Both remained approximately **99.8–99.9% *F. sanfranciscensis*** on the bacterial side.
- *K. humilis* was essentially absent, appearing only at trace levels in #867 and not as a meaningful component of #742.

The minor organisms differed more substantially, particularly among the yeasts, but the dominant microbial architecture remained strikingly similar.

This is not simply a case of both starters independently ending up with common sourdough organisms. They retained an unusually specific shared fingerprint.

Maintenance History

In August 2026, I contacted David Auerbach directly to clarify the maintenance history of the starter lineage.

Auerbach reported that his maintenance protocol has changed somewhat over the years. He currently keeps the starter at **66% hydration**, stored either in the refrigerator or, more recently, in a temperature controlled "Sourdough Home" at **50°F (10°C)**. Before baking, he refreshes the starter in **three stages, roughly tripling the quantity at each stage**, with the final refresh becoming the levain. The retained starter itself is maintained on **white flour**, even when different levain builds are used for specialty breads such as high-rye formulas.

Auerbach also indicated that his baking and refresh frequency has varied over time. Approximately a decade earlier, he estimated that he was refreshing and baking with the starter **more than 80 times per year**. More recently, that frequency had declined to approximately **66 times per year**, although he noted that it was beginning to increase again.

Regarding the separately maintained branch, Auerbach could speak less definitively, but said that the other holder of the starter was, to the best of his knowledge, using a **similar maintenance protocol**.

This additional history makes the 20-year comparison even more interesting. The two branches were maintained independently, but apparently not under radically different regimes. The available evidence therefore does not support interpreting the case as a controlled comparison of contrasting maintenance environments. Instead, it demonstrates the remarkable persistence of a dominant microbial fingerprint across two independently maintained branches of the same lineage over approximately two decades.

What Does the Auerbach Case Suggest?

The Auerbach comparison demonstrates something important about the long-term persistence of an established sourdough ecosystem.

A mature starter lineage can retain its dominant microbial fingerprint for decades.

That finding complements the long-term persistence seen in established Type 1 bakery starters. It also provides a useful counterpoint to the 14-month experiment presented in this paper, where two branches of the same starter developed a substantial divergence in their dominant yeast proportions.

The Auerbach lineage shows the other possibility. **Sometimes, remarkably little changes.**

But the case also presents an intriguing combination of microbial characteristics.

Its bacterial population is nearly pure ***F. sanfranciscensis***, one of the strongest microbial signposts associated with mature traditional Type 1 sourdough ecosystems.

Its yeast population, however, is almost entirely ***S. cerevisiae*** rather than the *Kazachstania*-dominated profile frequently associated with traditional Type 1 starters.

This is one reason the Type 1 fingerprint should not be reduced to a single organism or a rigid formula. *F. sanfranciscensis* dominance alone is not sufficient to identify a Type 1 starter. The broader microbial fingerprint and maintenance history must also be considered.

Was the Auerbach starter originally Type 1?

Possibly. Perhaps even plausibly. But the evidence does not allow that conclusion to be confirmed.

From what we know about Ed Wood and his search for traditional sourdough cultures around the world, including cultures obtained from old-fashioned bakeries, that provenance makes a bakery origin entirely credible, but not confirmed.

There is no historical DNA sample from the original Russian culture, so its earlier microbial composition cannot be known. However, the present-day fingerprint raises an intriguing possibility.

One possible scenario is that the shared Russian source had **already reverted from a more typical Type 1 microbial configuration before the two branches separated**. Under this hypothesis, both branches inherited an overwhelmingly *S. cerevisiae*-dominated yeast population. The near-total dominance of *F. sanfranciscensis*, the lineage's possible traditional bakery origin, and the low-abundance *Kazachstania* species detected in both starters are consistent with this possibility, but do not establish it.

This cannot be demonstrated from the available data. It is a hypothesis, not a reconstruction of what actually occurred.

But the resulting ecosystem illustrates an important feature of reversion. Once *S. cerevisiae* becomes overwhelmingly established, the competitive environment has fundamentally changed. A small incoming population of *K. humilis* would no longer be entering an open ecological niche; it would be competing against an already dominant and apparently highly persistent yeast population.

S. cerevisiae could be similar to a "shark in the guppy tank." Once the shark has taken over the tank, simply adding a few guppies does not restore the previous ecosystem.

Under this hypothesis, the Auerbach comparison suggests that a reverted state could itself be highly persistent: both branches had essentially the same dominant yeast configuration when tested after approximately 20 years of independent maintenance. Without baseline testing, however, we cannot establish when that configuration arose or whether it persisted throughout the separation.

The Auerbach starters are one of the most remarkable long-term comparisons in the Global Sourdough Project.

A Useful Contrast With the 14-Month Experiment

The two natural experiments point in different directions.

In the experiment presented in this paper, two branches of the same starter experienced a significant divergence in the relative abundance of their dominant yeasts in only 14 months.

In the Auerbach comparison, two branches retained strikingly similar yeast populations after approximately 20 years.

Neither result contradicts the other.

Together, they illustrate one of the central themes of this paper:

Sourdough ecosystems can be remarkably stable, but they are never guaranteed to remain static.

Maintenance creates selective pressure. Sometimes that pressure produces measurable population change. Certain species or sub-species may be more sensitive to changes in maintenance procedures. Sometimes an established ecosystem appears resilient enough to preserve its dominant structure for decades.

Understanding why one starter changes while another remains stable is one of the most interesting questions that remains.

Appendix H: Landis Sample Size Adjustment

The comparison below, used earlier in the paper, progressively narrows the microbial populations from **all species identified** to **commonly found species** and finally to the much smaller set of organisms likely to dominate an individual starter.

For simplicity in this Appendix, I refer to this progression as the **Walkdown**.

Table 3: Yeast and Bacteria Species in Sourdough Starters

	"Household" (*Landis*)	"Type 1" (*von Gastrow*)
Yeast Species Identified	61	14
Bacteria Species Identified	93	11
Possible Total Combinations	**2.28×10^{46}**	**33.5 million**
Commonly Found Yeast Species	12	5
Commonly Found Bacteria Species	9	2
Possible Commonly Found Combinations	**2 million**	**93**
Typical Dominant Yeast Species in a Starter	1-2	1-2
Typical Dominant Bacteria Species in a Starter	1-3	1-2
Likely Dominant Yeast + Bacteria Combinations	10,062	45

Note: "Commonly Found" species occur in at least 10% of all starter samples in the population.

Does sample size affect the Walkdown?

When comparing the Landis and von Gastrow datasets, there is an obvious difference in sample size. The Landis "Household" study included approximately **500 starters**, while the von Gastrow study "Type 1 / Bakery" included **46**.

That raises an important question:

Is the difference in sample size materially affecting the summary data shown in the Walkdown?

A larger study has more opportunities to detect rare species, so some difference in the total number of species identified would be expected even if the underlying populations were otherwise similar.

To test the effect, I repeated the Landis analysis using **10,000 random draws of 46 starters** from the full Landis dataset. For each draw, the species-occurrence calculations were rebuilt from the underlying sample-by-species abundance data.

This created an equal-sized comparison: **46 randomly selected Landis household starters versus 46 von Gastrow mature bakery starters.**

Sample-Size Adjustment

Table 18: Landis Data Adjusted for Sample Size (10,000 random draws of n=46)

Metric	Landis full n=500	Landis random n=46 median (95% range)	von Gastrow n=46
YEAST			
Identified species	61	31 (25–37)	14
Species in ≥10% of samples	12	12 (9–15)	5
Species in ≥20% of samples	5	6 (3–8)	2
Tail abundance (<10% occurrence)	10.9%	9.3% (2.9–17.2%)	13.9%
BACTERIA			
Identified species	93	37 (29–47)	11
Species in ≥10% of samples	9	9 (7–12)	2
Species in ≥20% of samples	6	5 (4–7)	2
Tail abundance (<10% occurrence)	22.5%	18.6% (10.2–28.0%)	0.6%

Source: Landis et al. (2021)

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The adjustment produces one clear material change: **the raw species counts fall substantially when the Landis sample is reduced to 46 starters.**

The median number of identified yeast species falls from **61 to 31**, and identified bacterial species fall from **93 to 37**.

The species counts shown at the top of the Walkdown are therefore **correct for the actual published datasets**, but they are less useful as a direct relative comparison because the two studies contain very different numbers of samples. A larger study has more opportunities to detect rare organisms.

As the Walkdown progresses, however, the comparison becomes less sensitive to that difference. The analysis shifts from all species detected to species that recur across a meaningful portion of the population.

The methodology used in the original Walkdown table filtered the “commonly found” results based on occurrence in at least 10% of samples.

At the **10% occurrence threshold**, the full Landis dataset contains **12 yeast species and 9 bacterial species**. After reducing the equivalent sample size to 46, the **median results remain 12 yeast and 9 bacteria**.

A **20% threshold** is also shown for sensitivity analysis, and the results also remain similar.

In other words, the sample-size difference matters most at the top of the Walkdown, where every detected species is counted. It matters very little in the later stages, because the **10% occurrence threshold used to define “Commonly Found” species filters out many of the rare species most affected by sample size.** That is also why the comparison at the bottom of the Walkdown is the more meaningful relative comparison between the two populations.

The original Walkdown therefore remains useful as presented. The raw species totals accurately describe the organisms detected in each published dataset, while the later stages provide a more meaningful comparison of the recurring microbial populations.

This sample-size adjustment is included here for completeness and to demonstrate that the primary Household versus Type 1 pattern in the Walkdown is **not** simply an artifact of comparing approximately 500 Landis starters with 46 von Gastrow starters.

Additional Observations

The calculated species combinations in the original Walkdown (Table 3) overlap only slightly. Just 9 of the 45 Type 1 combinations also appear among the 10,062 Household combinations; the remaining 36 (80%) fall outside the Household set.

Appendix I: Commonly Recurring Species Patterns and Co-Occurrence

The tables in this appendix reproduce the commonly occurring species-pattern tables presented in Part 5 of this paper. They are repeated here as a convenient reference, with additional co-occurrence analysis.

Note: In this section, "dominant" means **the single species with the highest relative abundance** in each sample, with yeast and bacteria assessed separately. This classification does not use the collective ≥95% abundance rule used in other parts of this report.

How to Use the Tables

If you have a DNA report for your starter, compare the dominant yeast and bacteria species from your starter to the matching line items on these tables. This can help you determine whether your starter's microbial profile more closely resembles the Household or Type 1 patterns identified in this study. Once you've identified the closest matching group, you can compare your specific species combination with the more than 500 starter profiles analyzed for this study, and determine if your species profile is common or uncommon relative to this population.

How the Patterns Were Constructed

The purpose of these tables is not to reproduce every unique microbial composition found in the underlying studies. Instead, individual samples were grouped into **sensible, biologically meaningful categories** that make recurring community patterns easier to see.

For each sample, the dominant yeast and bacterial species were identified and combined into a simplified yeast/bacteria pattern. Related patterns were then grouped into broader reporting categories where appropriate.

This approach necessarily compresses some of the underlying microbial detail. A single pattern may therefore contain samples with different secondary or low-abundance organisms. The tables should be interpreted as a way of identifying **recurring community structures**, rather than as a catalog of identical microbial communities.

Other is a residual reporting category. It includes samples that share the listed dominant yeast but whose dominant bacterial species was not one of the bacterial pairings separately enumerated in the table. For example, if *S. cerevisiae* + *L. brevis* is listed as its own category, then *S. cerevisiae* + *Other* excludes *L. brevis* (and other individually enumerated bacteria).

The same grouping rules were applied consistently within each dataset. Because the underlying studies differ in sample population, sequencing methods, and sample size, the resulting percentages are most useful for understanding patterns **within each study** and for broad comparison between starter populations, rather than as precise population estimates.

Signature Species Patterns: Household Starters

Table 9: Observed Species Patterns in Mostly Household Starters (Landis n=499)

Rank	Dominant Yeast	Dominant Bacterium	n	%	Cumulative %
1	*S. cerevisiae*	*L. brevis*	78	15.6%	15.6%
2	*S. cerevisiae*	*F. sanfranciscensis*	59	11.8%	27.5%
3	*S. cerevisiae*	*L. paralimentarius*	59	11.8%	39.3%
4	*S. cerevisiae*	*Other*	56	11.2%	50.5%
5	*Other yeasts*	*Other*	49	9.8%	60.3%
6	*S. cerevisiae*	*P. parvulus*	49	9.8%	70.1%
7	*S. cerevisiae*	*L. plantarum*	39	7.8%	78.0%
8	*Kazachstania* spp.	*Other, excluding F. sanfranciscensis*	31	6.2%	84.2%
9	*Kazachstania* spp.	*F. sanfranciscensis*	19	3.8%	88.0%
10	*S. cerevisiae*	*L. sakei*	19	3.8%	91.8%
11	*S. cerevisiae*	*L. paracasei*	12	2.4%	94.2%
12	*S. cerevisiae*	*L. rossiae*	11	2.2%	96.4%
13	*S. cerevisiae*	*A. malorum*	10	2.0%	98.4%
14	*S. cerevisiae*	*L. parabrevis*	8	1.6%	100.0%

"Dominant" is the species with the highest relative abundance in each sample. Yeast and bacteria are classified separately.
"Other" categories represent species or species combinations not separately enumerated in the table. "Other yeasts" includes samples whose most abundant yeast species is not individually listed. "Other bacteria" includes samples whose most abundant bacterium is not separately listed for the corresponding yeast category.
Individual yeast–bacterium combinations are shown separately when they occur frequently enough to represent meaningful recurring patterns in the dataset.
"n=499" The Landis dataset examined 500 starters. One sample lacked reported abundance data and is excluded here.
Source: Landis et al. (2021)
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Observations: Household Starter Signature Species Patterns

S. cerevisiae is clearly the dominant yeast in this mostly-household dataset, occurring as the single dominant yeast species in 80.2% of the 499 starters.

Kazachstania spp., which are much more characteristic of Type 1 starters, were dominant in only 10.0% of the Household starters. Their presence alone, however, does not identify a starter as

Type 1. *Kazachstania* species can also occur in developing New starters and in stable Household starters.

F. sanfranciscensis, the bacterial species most strongly associated with Type 1 starters, was the dominant bacterium in only 17.4% of the Household starters.

Among the 59 Landis starters on Row 2 with dominant *S. cerevisiae and F. sanfranciscensis*, 56 (94.9%) had less than 1% detectable *Kazachstania* spp., including 35 with none detected. Although this combination also occurs in mature Type 1 starters, the near-absence of *Kazachstania* in most of these Household samples is noteworthy. These profiles may represent different positions along the proposed maturity continuum, including possible reversion, but their maintenance histories are not known.

Row 9, the combination of *Kazachstania* spp. and *F. sanfranciscensis*, 3.8% of the samples, most closely resembles the signature species pattern commonly found in Type 1 starters. However, these Landis samples were not documented as being maintained under the defining Type 1 protocol of frequent refreshments without refrigeration. This illustrates an important limitation of species-level classification: a microbial fingerprint can strongly resemble Type 1 ecology without, by itself, establishing that the starter is being maintained as a Type 1 starter.

Additional observations

First, **Household starters are much more diverse on the bacterial side than on the yeast side.** The yeast population is heavily concentrated around *S. cerevisiae*, while that same yeast appears with many different dominant bacteria. That suggests the bacterial community is doing much more of the work in distinguishing one Household starter fingerprint from another.

Second, there is **no single canonical Household species pair**. The most common specific pairing, *S. cerevisiae* + *L. brevis*, represents only 15.6% of the dataset. Even the top six patterns together account for only 70.1%. Household starters are not one microbiological "type;" they occupy a wide ecological middle ground between New and Type 1 starters.

Third, *S. cerevisiae* appears to be **remarkably ecologically flexible**. It is paired here with *L. brevis, F. sanfranciscensis, L. paralimentarius, P. parvulus, L. plantarum, L. sakei, L. rossiae, L. paracasei, A. malorum,* and *L. parabrevis*. That is a striking contrast to the much tighter species associations we see in Type 1 starters.

Fourth, the table illustrates the **overlap between New, Household and Type 1 starters rather than hard microbial borders**. The Type 1-associated organisms do occur in Household starters, just at much lower frequencies. So, neither *Kazachstania* nor *F. sanfranciscensis* alone functions as a Type 1 "proof."

Signature Species Patterns: Mature Type 1 / Bakery Starters

Table 10: Observed Species Patterns in Type 1 / Bakery Starters (von Gastrow n=46)

Rank	Yeast pattern	Dominant bacterium	n	%	Cumulative %
1	*Kazachstania* spp. dominant; *S. cerevisiae* <1%	*F. sanfranciscensis*	17	37.0%	37.0%
2	Other yeast pattern	*F. sanfranciscensis*	10	21.7%	58.7%
3	*S. cerevisiae* dominant; *Kazachstania* spp. <1%	*F. sanfranciscensis*	8	17.4%	76.1%
4	*S. cerevisiae* dominant; *Kazachstania* spp. ≥1%	*F. sanfranciscensis*	4	8.7%	84.8%
5	*Kazachstania* spp. dominant; *S. cerevisiae* ≥1%	*F. sanfranciscensis*	3	6.5%	91.3%
6	Various yeast pattern	*Other bacteria*	4	8.7%	100.0%

Note: *Kazachstania spp. = each Kazachstania-dominant sample was dominated by one of the following species: K. humilis (8), K. bulderi (6), K. servazzii (3), K. barnettii (2), Kazachstania sp.(2) or K. unispora (1). Other Kazachstania species could also be present at lower abundance.*

Kazachstania spp. includes multiple species within the genus. "Other yeast pattern" includes alternative dominant yeasts and two samples without a usable yeast classification. "Other bacteria" includes three samples dominated by C. paralimentarius and one by Lactobacillus sp.

Source: von Gastrow et al. (2023)

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Observed Species: Mature Starters Type 1 / Bakery

Yeasts from the *Kazachstania* genus frequently dominate mature Type 1 starters. Across this dataset, *Kazachstania* spp. were the dominant yeast in 47.8% of starters, while *S. cerevisiae* was dominant in 30.4%.

Notably, 10 of the 46 starters (21.7%) exhibited other yeast patterns. Eight starters (17.4%) were dominated by alternative yeast species, including *Metschnikowia*, *Naumovozyma*, *Candida saitoana*, *Meyerozyma caribbica*, and *Saccharomyces uvarum*. Two additional starters (4.3%) had no usable yeast classification.

Some of these alternative yeast communities also contained *Kazachstania* spp. and/or *S. cerevisiae* at lower abundances. For example, one starter dominated by *Metschnikowia* (39.8%) also contained substantial populations of *S. cerevisiae* (34.5%) and *Kazachstania* spp. (25.6%).

Despite this yeast diversity, *F. sanfranciscensis* was overwhelmingly the dominant bacterium, occurring in 42 of 46 starters (91.3%), including all ten starters in the "Other yeast pattern" category.

These findings suggest that the **bacterial signature was considerably more consistent** than the yeast signature within this cohort. While *Kazachstania* spp. and *S. cerevisiae* represented the principal yeast patterns, several alternative yeast communities were also observed.

Co-occurrence Analysis

Co-occurrence describes whether two microbial species are found together across samples more often, less often, or about as often as would be expected by chance.

A **positive co-occurrence** means that two species tend to appear together more frequently than expected. A **negative co-occurrence** means that two species appear together less frequently than expected from their individual occurrence rates.

Co-occurrence does **not** by itself demonstrate that the organisms directly help, inhibit, or compete with one another. It identifies a statistical association across samples, which may also reflect shared environmental preferences or different maintenance conditions.

The Landis Household starter study provides a useful co-occurrence map for many of the organisms discussed throughout this report.

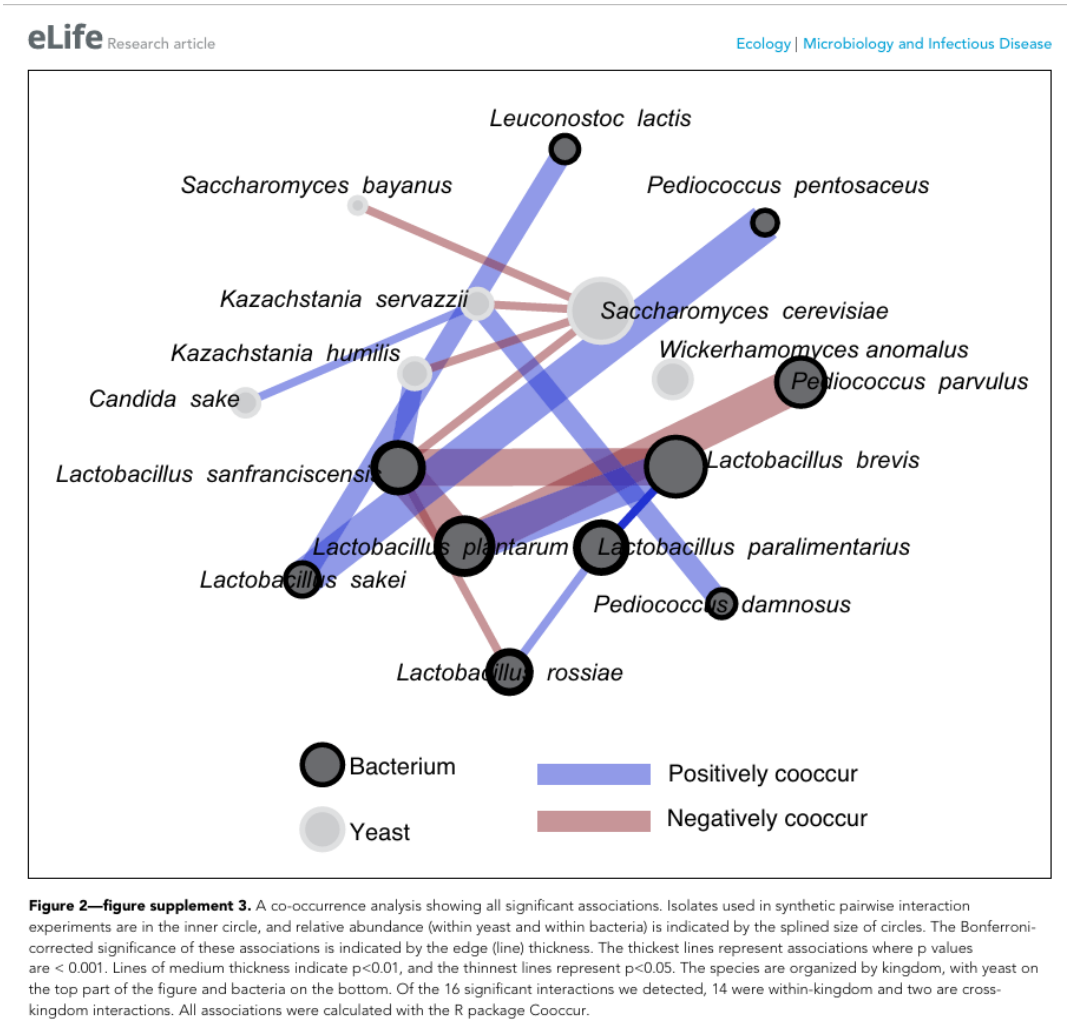

Figure 2—figure supplement 3. A co-occurrence analysis showing all significant associations. Isolates used in synthetic pairwise interaction experiments are in the inner circle, and relative abundance (within yeast and within bacteria) is indicated by the splined size of circles. The Bonferroni-corrected significance of these associations is indicated by the edge (line) thickness. The thickest lines represent associations where p values are < 0.001. Lines of medium thickness indicate p<0.01, and the thinnest lines represent p<0.05. The species are organized by kingdom, with yeast on the top part of the figure and bacteria on the bottom. Of the 16 significant interactions we detected, 14 were within-kingdom and two are cross-kingdom interactions. All associations were calculated with the R package Cooccur.

Source: Landis et al. (2021). The diversity and function of sourdough starter microbiomes. eLife, 10:e61644. Figure 2, Figure Supplement 3: Co-occurrence analysis of sourdough bacteria and yeasts. DOI: *10.7554/eLife.61644*, Direct link to figure: *Landis et al. figures and supplementary data*.

Co-occurrences Most Relevant to This Study

Three relationships in the Landis household-starter population are especially relevant to the Household versus Type 1 patterns discussed throughout this report.

In this section, a species "occurred" when its relative abundance exceeded 1% within the respective yeast or bacterial community, following the method used by Landis. Household occurrence percentages use all 500 samples.

The following occurrence percentages differ from the preceding signature pattern tables, which identify the "dominant species" rather than all species present above 1% abundance. Most notably, *F. sanfranciscensis* is reported there as 17.4% based on **dominance** not **occurrence.**

The "Type 1 dataset" referenced below is the Type 1 / "bakery" dataset from the von Gastrow study, used elsewhere throughout this document.

1. *S. cerevisiae* and *K. humilis*: Negative co-occurrence

Landis found a negative co-occurrence between the yeast species *S. cerevisiae* and *K. humilis*. Both species occur together in only 3.4% of samples.

S. cerevisiae was overwhelmingly the dominant Household yeast, accounting for more than 50% of fungal reads in 77% of samples, and it occurs in 90.2% of total samples. By comparison, *K. humilis* was much less prominent, occurring in only 5.6% of samples.

The negative co-occurrence between *S. cerevisiae* and *K. humilis* is particularly interesting. **It closely parallels the broader pattern seen in this report**: Household starters are strongly associated with *S. cerevisiae*, while *K. humilis* becomes much more prominent in traditional Type 1 starter populations.

The relationship is not exclusionary. Both species can coexist, as they did in the two starters analyzed in this experiment. The Landis result describes a population-level tendency rather than a rule governing individual starters.

These individual occurrence rates provide context for the broader pattern discussed in this report: *S. cerevisiae* is widespread in Household starters, while *K. humilis* is considerably more frequent in the Type 1 dataset.

These species also occur together in the Type 1 dataset. The pairing was about 2.6 times as common in the Type 1 dataset (8.7% versus 3.4% in the Household dataset, counting both species above 1% relative abundance).

2. *S. cerevisiae* and *F. sanfranciscensis*: Negative co-occurrence

Landis found a negative co-occurrence between *S. cerevisiae* and *F. sanfranciscensis*. Both species occur together in 18.0% of samples.

S. cerevisiae occurs in 90.2% of samples, and *F. sanfranciscensis* occurs in 22.8%.

This is notable in a Household population where *S. cerevisiae* is overwhelmingly common, while *F. sanfranciscensis* appears above 1% abundance in a narrower subset of starters. However, **they**

do not randomly overlap across the population. They occur together less often than statistically expected.

Again, this does not mean they cannot coexist. They clearly can, including in both starters examined in this study. But at the population level, the Landis data reinforce the broader distinction between the typical Household microbial pattern and the Type 1 pattern.

This pairing occurred in both populations, but was about 2.3 times as common in the Type 1 dataset (41.3% versus 18.0%, counting both species above 1% relative abundance).

3. *K. humilis* and *F. sanfranciscensis*: positive co-occurrence

Landis found a positive co-occurrence between *K. humilis* and *F. sanfranciscensis*. Both species occur together in 3.4% of samples. However, both appear in a relatively small percentage of samples: *K. humilis* occurs in 5.6% of Household samples, and *F. sanfranciscensis* occurs in 22.8% and is the dominant bacterium in 17.4% of samples.

This is the classic Type 1 pairing discussed throughout this report: a sourdough-adapted yeast, *K. humilis*, occurring with the bacterium *F. sanfranciscensis*.

This pairing also occurs in Household starters, but was about **seven times as common** in the Type 1 dataset (23.9% versus 3.4%, counting both species above 1% relative abundance).

Additional Analysis: Comparing the Study Samples to Datasets

Table 19: Cucuzza Study Samples Dominant Species Profile Match to Datasets

Dataset	Matching Samples (n)	Denominator: Classifiable Samples	Frequency	Sample Numbers
Landis	4	499	0.8%	S_428, S_481, S_482, S_515
von Gastrow	2	44	4.5%	B11, B31
Combined	6	543	1.1%	

Method: Relative abundances were normalized separately within each dataset's selected yeast and bacterial pools. Yeast species were ranked by abundance and accumulated until reaching ≥95%; matching profiles contained exactly *K. humilis* and *S. cerevisiae*, in either order, with *F. sanfranciscensis* comprising ≥95% of the bacterial pool. Thresholds were applied before rounding. Three samples without usable yeast profiles were excluded: Landis S_351 and von Gastrow B14 and B59. Frequencies describe the analyzed datasets and should not be interpreted as population-wide estimates.

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Appendix J: Changes in Starter Rising Power

Introduction, Timeline, and General Observations

I observed the following changes in my starter's rising power during the study period:

- **February 2025 to February 2026:** No observed change in rising power
- **March 2026:** First observed faster dough rising times
- **March-August 2026:** Faster rising performance continued
- **August 2026:** Repeated controlled starter-strength tests and confirmed increased rising power compared with 2025 benchmarks

These observations came from two different sources: routine baking records and controlled pressure-vessel testing of starter CO_2 production.

The DNA comparison covered 14 months, from February 2025 to April 2026. The follow-up rising-power tests described here were conducted in August 2026, four months after the DNA testing and approximately 18 months after I acquired the starter.

Observed Changes in Dough Rising Times

When I acquired the source starter in February 2025, I immediately observed that it rose faster and taller than my previous starter.

I keep detailed baking records, and a new bulk fermentation benchmark quickly emerged. Under my standard conditions and using the new starter, bulk fermenting dough would typically reach approximately a **50% rise in about 5.5 hours** at 78°F (25.6°C). My previous starter generally produced only about a **30-40% rise over the same timeframe**.

That new **50% benchmark** for the new starter remained remarkably consistent throughout 2025.

In March 2026, approximately 13 months into the study period, I was recording a new video series when I noticed that the dough was rising faster and higher than the established benchmark. In subsequent bakes, the pattern continued. Under otherwise similar conditions, the dough was now reaching approximately a **70-75% rise in 5.5 hours.**

Because I routinely track dough temperature, flour type, formula, fermentation time, and other process variables, the change was noticeable against a well-established baseline.

The increased rising performance continued in subsequent bakes through the summer of 2026.

Observed Changes in Starter Rising Power

In 2023, I developed a testing system for measuring the actual gas-producing capacity, or "rising power," of a sourdough starter.

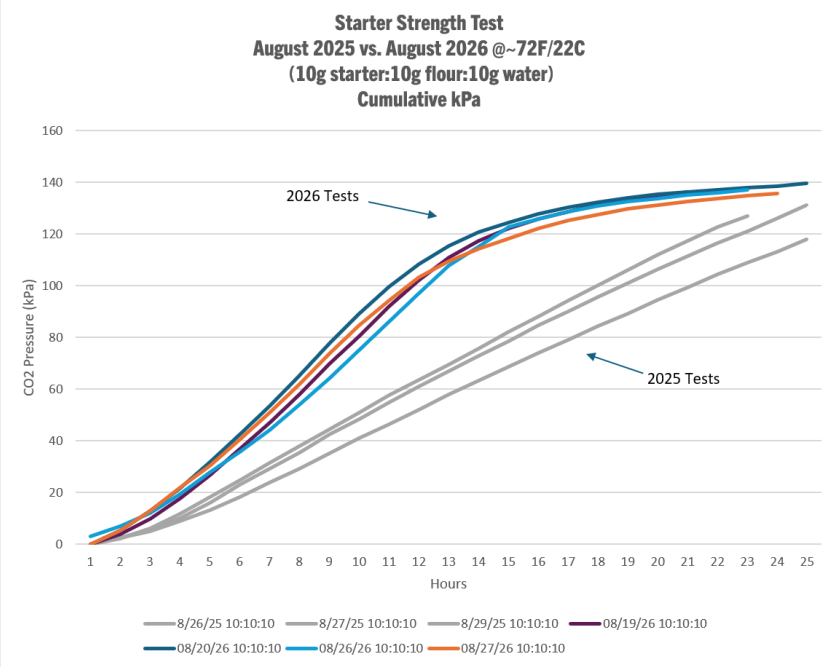
The method uses sealed pressure vessels to measure CO_2 generation directly rather than relying only on indirect visual indicators such as starter height, time-to-peak, or volume increase.

See **Starter Strength Testing Methodology** below for additional details.

The first controlled strength tests of the new starter were conducted during the summer of 2025. I repeated comparable tests in August 2026, using the same starter, approximately one year later.

The 2026 tests showed **materially greater CO_2 production** than the earlier benchmark tests.

Based on my experience running hundreds of the comparative tests, these test results are a clear indication of distinct variability in microbial activity.



Observations and Conclusions

Two independent observations point in the same direction:

1. Dough fermented substantially faster/taller than the established 2025 benchmark.
2. Controlled pressure-vessel testing showed increased CO_2 production compared with the 2025 tests.

Together, these results support a straightforward conclusion:

My starter's rising power materially increased between the 2025 benchmark period and August 2026.

What the tests do not establish is why that increase occurred.

Does *S. cerevisiae* produce more CO_2 than *K. humilis*?

There is evidence that *S. cerevisiae* can produce more CO_2 than *K. humilis* under some conditions, but this is not a universal species-level rule.

Some sourdough studies have reported greater CO_2 production by *S. cerevisiae* than by *K. humilis* under the conditions tested. In one comparison, *S. cerevisiae* produced approximately 35% more CO_2 than *K. humilis* after 20 hours.

More recently, Aiki et al. (2026) directly compared sourdough isolates of the two species and found that *S. cerevisiae* produced more gas and demonstrated greater leavening ability than *K. humilis*, resulting in bread with greater specific volume.

However, the opposite has also been demonstrated. Sánchez-Adriá et al. (2023), for example, tested sourdough yeast isolates and found that some *K. humilis* strains produced more total CO_2 and showed 54% higher gassing rates than a commercial *S. cerevisiae* baker's yeast control.

The most important point is that CO_2 production is **highly dependent on the specific strain** and the environmental conditions in which it is tested.

The DNA analysis in this study identifies organisms primarily at the species level. It does not show whether the particular *S. cerevisiae* strain in my starter is inherently more gas-producing than the particular *K. humilis* strain. Nor do the two endpoint samples establish whether my starter shifted from *K. humilis* dominance toward *S. cerevisiae* dominance during the study period.

Such a shift, if it occurred, could plausibly have contributed to the observed increase in rising power, but the DNA results alone do not demonstrate that it did.

The observed changes are directionally consistent with published differences in yeast behavior and CO_2 production, but this experiment does not establish causation.

Summary

Over approximately 18 months, the starter showed a measurable increase in rising power.

The change first appeared in routine baking records in March 2026 and was later confirmed through controlled CO_2-generation testing in August 2026.

The endpoint DNA tests showed different relative abundances of the two main yeast species: the source starter was dominated by *K. humilis*, while my starter was dominated by *S. cerevisiae*.

That difference in yeast composition offers a plausible explanation for at least part of the performance change, but existing research shows substantial strain-to-strain and condition-dependent variation in CO_2 production.

The strongest conclusion is therefore limited but clear:

The starter became measurably stronger. Differences in species abundance between the source starter and my starter offer a plausible explanation, but these tests cannot establish the cause. Strain-level differences, which these tests do not resolve, may also have contributed.

Starter Strength Testing Methodology

Starter strength was evaluated using a custom sealed pressure-vessel system designed to measure CO_2 production over time under controlled feeding and temperature conditions. The method provides a quantitative measure of fermentation performance independent of visual indicators such as starter height, bubble formation, or time-to-peak.

Each vessel contained a measured quantity of starter, flour, and water and was fitted with a digital pressure gauge. As fermentation proceeded, CO_2 accumulated in the fixed headspace and increased vessel pressure, recorded in kilopascals (kPa). A parallel open-air sample, fitted with a pH meter, was used to monitor rise rate, volume, time-to-peak, pH, and other observable characteristics.

Tests generally ran for approximately 24 hours and approximately 72°F (22.2°C). Pressure, pH, and temperature were recorded at regular intervals from time-lapse video. The resulting pressure curves were used to evaluate both the **rate of CO_2 production** and **cumulative CO_2 production** over the test period.

The method does not directly measure the mass of CO_2 produced, and absolute pressure values depend on temperature, vessel volume, headspace, and other physical conditions. It was therefore used primarily as a **comparative method under matched conditions**, with the strongest comparisons made among tests using the same feeding ratio, hydration, sample mass, temperature, vessel configuration, and test duration.

Within these limitations, the system provided a repeatable means of comparing starter gas-producing capacity over time and distinguishing changes in fermentation rate from changes in total gas production.

Four-vessel sourdough starter CO_2 testing apparatus. Digital pressure gauges measure CO_2 accumulation in sealed vessels under controlled experimental conditions, with parallel open-air samples used to measure visible attributes and pH.

Appendix K: The Starter Maturity Map: Supporting Research

The following table is included in Part 5 of this report and repeated here for convenience. This appendix includes supporting research for each cell in the table.

The chart illustrates how the "Big 3" microbial classifications are shown to change over the lifecycle of the Starter Maturity Map described in this report.

Table 7: Microbial Signposts Across the Maturity Map – The "Big 3"

	New Starters	Household Starters	Type 1 Starters	Reversion
YEAST: ***K. humilis*** ***Other K.* spp.**	**Appears early** in new starters. May be displaced by *S. cerevisiae* with time	**Not typically dominant**. Can persist in some household starters	**Characteristic Type 1 yeast;** well-adapted to the mature sourdough ecosystem	**May decline** in dominance with less rigorous maintenance, or other stressors
YEAST: ***S. cerevisiae***	Fast-growing competitor; **may establish early** if conditions favor it	**The most common dominant yeast.** Persists with infrequent feedings and refrigeration	**Can dominate,** but is less characteristic than *Kazachstania* spp.	**May gain dominance** when Type 1 maintenance is relaxed
BACTERIA: ***F. sanfranciscensis***	**Uncommon.** Not typically found in measurable quantities in flour	**Uncommon.** Can be dominant and persistent, but dominance is infrequent	**Hallmark bacterium** of mature Type 1 starters; strongly selected by frequent propagation	**Persistent**; may decline or be displaced under substantially altered maintenance conditions

Sources: See Table 6.
Classification note: A Type 1-like microbial fingerprint is characteristic of mature bakery starters but uncommon in household starters.
In the Landis dataset, only 3.8% of starters had both *Kazachstania* spp. and *F. sanfranciscensis* as the most abundant yeast and bacteria species, giving this combination useful discriminatory power. © The Sourdough Journey, 2026

Microbial Evidence Supporting the Maturity Model

The descriptions in the Maturity Map are intentionally qualitative. The available scientific evidence is not equally strong for every organism at every stage, and the four stages do not represent rigid microbial categories. Rather, the organism patterns and occurrences function as **microbial signposts**: recurring patterns that help determine an individual starter's potential position on the map.

The following notes identify the principal evidence supporting each cell of the Microbial Signposts table, along with important limitations and qualifications.

New Starters

New Starter: *Kazachstania humilis* and other *Kazachstania* spp.

Taheri et al. provide the strongest evidence for the early appearance of *Kazachstania* during spontaneous starter development. *Kazachstania* rapidly emerged and became a prominent, and in many cases predominant, yeast across their experimentally created starters.

The evidence is stronger at the **genus level** than specifically for *K. humilis*. Other starter-succession studies have also produced different yeast communities, demonstrating that flour, temperature, feeding schedule, and other environmental conditions can strongly influence which yeasts establish.

The New Starter stage is inherently transitional rather than a stable microbial state. The table therefore uses the broader and more defensible description: ***Kazachstania* appears early in new starters and may later be displaced by *S. cerevisiae*.**

New Starter: *Saccharomyces cerevisiae*

Taheri found *Saccharomyces* at relatively low abundance through much of the 28-day starter-development experiment, followed by a substantial increase later in the succession process. Other studies demonstrate that the timing and direction of yeast succession can vary considerably among starters.

A 2009 study by Siragusa et al. found *S. cerevisiae* to be the dominant yeast in 10 newly prepared starters by day 10.

Therefore, *S. cerevisiae* should not be characterized simply as a late-arriving organism. It is a fast-growing and highly competitive yeast that may establish relatively early when conditions favor it.

The table therefore describes *S. cerevisiae* as a **fast-growing competitor that may establish early if conditions favor it.**

New Starter: *Fructilactobacillus sanfranciscensis*

This cell has relatively strong independent support. Taheri found little or no meaningful establishment of *F. sanfranciscensis* across the newly created starters during the 28-day experiment. McKenney et al., following newly created starters made from multiple flour types, likewise did not identify *F. sanfranciscensis* in early starter development.

This is consistent with an important ecological observation: *F. sanfranciscensis* is strongly associated with established sourdough ecosystems but is not typically detected in measurable abundance in flour itself.

These studies do not demonstrate that *F. sanfranciscensis* can never occur in flour or in a newly created starter. The table therefore uses the conservative description: ***uncommon in new starters and not typically found in measurable quantities in flour.***

Household Starters

Household Starter: *Kazachstania humilis* and other *Kazachstania* spp.

Landis et al.'s survey of nearly 500 household sourdough starters provides the primary evidence for this stage. *Kazachstania*, including *K. humilis*, occurs in household starters and can sometimes reach high abundance, but it is not the typical dominant yeast across the household population.

The table is not suggesting that *Kazachstania* is absent or exceptionally rare in household starters. Rather, compared with mature Type 1 starters, it is **less consistently selected for dominance**.

Accordingly, the table describes *Kazachstania* as **not typically dominant, but capable of persisting in some household starters.**

Household Starter: *Saccharomyces cerevisiae*

This is one of the strongest cells in the model. Landis et al. found *S. cerevisiae* to be by far the most common dominant yeast among household starters. In my analysis of the Landis dataset, *S. cerevisiae*-dominated communities account for a substantial majority of the recurring household yeast patterns.

This broad prevalence is consistent with the organism's ability to perform well under the varied maintenance conditions characteristic of household starters, including relatively infrequent feeding and, in many cases, refrigeration.

The table therefore describes *S. cerevisiae* as **the most common dominant yeast in household starters.**

Household Starter: *Fructilactobacillus sanfranciscensis*

Landis again provides the principal evidence. *F. sanfranciscensis*, despite its strong association with Type 1 bakery starters, is infrequently dominant in the household starters in the Landis dataset.

In that dataset, *F. sanfranciscensis* is found to be the dominant bacterium in 17.4% of samples. However, the study also records reported “origin” for 490 of the 500 samples.

F. sanfranciscensis dominance occurs in 87 samples. (17.4% of total). Of the 87 *F. sanfranciscensis* samples:

48 samples report “Individual” origin (9.6% of total)
36 samples report “bakery or other commercial source” origin (7.2% of total)
3 samples report no origin (0.6% of total)

Across the entire dataset, *F. sanfranciscensis* is the dominant bacterium in:

48 of 417 “individual” origin samples (11.5% of “individual…”)
36 of 73 “bakery or other commercial source” origin samples (49.3% of “bakery…”)
3 of 10 “no reported origin” (30.0% of “no reported…”)

The frequent occurrence of *F. sanfranciscensis* in the "bakery or other commercial source" samples may reflect an inherited bakery-associated community, although neither prior Type 1 status nor subsequent reversion can be established from these data, but the implication is notable.

When *F. sanfranciscensis* is present in a household starter, it can become a major or dominant component of the bacterial population, and the Auerbach study provides one example of extraordinary persistence.

The table therefore states: **Uncommon. Can be dominant and persistent, but dominance is infrequent.**

Type 1 Starters

Type 1 Starter: *Kazachstania humilis* and other *Kazachstania* spp.

The broader Type 1 literature identifies *K. humilis* as one of the organisms most strongly associated with traditional, continuously propagated starters. More recent datasets reinforce this pattern while also showing that the relevant signal is broader than a single species.

In the von Gastrow mature bakery cohort, *Kazachstania* species form one of the major yeast signatures of mature Type 1 starters. *K. humilis* is the most typical and most familiar example, but other *Kazachstania* species can occupy a similar ecological position.

The Maturity Map does not treat *K. humilis* itself as a requirement for Type 1 classification. Instead, ***Kazachstania* spp. are characteristic Type 1 yeasts, well adapted to the mature sourdough ecosystem.**

Type 1 Starter: *Saccharomyces cerevisiae*

S. cerevisiae is fully compatible with Type 1 ecology and can dominate mature "bakery" starters.

In the von Gastrow mature bakery dataset, *S. cerevisiae* was the dominant yeast in 30.4% of starters, including 12 starters also dominated by *F. sanfranciscensis*. Although *Kazachstania* was more frequently dominant, this study demonstrates that *S. cerevisiae* dominance is compatible with mature Type 1 ecology.

Therefore, the distinction is not that *S. cerevisiae* is incompatible with Type 1 starters. Rather, *Kazachstania* is simply the **more characteristic microbial differentiator** when comparing mature Type 1 starters with the broader household population.

The table therefore states: ***S. cerevisiae* can dominate Type 1 starters, but is less characteristic than *Kazachstania* spp.**

Type 1 Starter: *Fructilactobacillus sanfranciscensis*

This is one of the strongest microbial signposts in the entire model.

Across the Type 1 literature, *F. sanfranciscensis* is repeatedly associated with continuously propagated starters. It frequently is the overwhelmingly dominant bacterial species. The von

Gastrow mature bakery cohort demonstrates this pattern particularly clearly, while other Type 1 studies provide additional support.

Its prevalence in mature bakery starters contrasts sharply with its rarity in newly created starters and its low prevalence among household starters.

Frequent propagation, infrequent refrigeration, and long-term microbial selection appear to strongly favor this organism.

The table therefore describes *F. sanfranciscensis* as the **hallmark bacterium of mature Type 1 starters, strongly selected by frequent propagation.**

Reversion

Reversion: *Kazachstania humilis* and other *Kazachstania* spp.

Unlike the preceding cells, the Reversion column describes **directional and transitional change from an established Type 1 condition**, not a stable endpoint.

Observational studies associate different maintenance practices with different *Kazachstania* communities. Michel et al. (2023), for example, found differences in dominant yeasts between artisanal bakery and "farmer-baker" sourdough starters, although the study did not track individual starters through a maintenance change.

Wardhana et al. (2026) provides direct experimental evidence. Under prolonged refrigerated storage with feeding every three weeks, *M. humilis* (formerly *K. humilis*) was no longer recovered from one established starter after week 15, while it persisted in the other through week 39.

These contrasting outcomes show that persistence is possible but not guaranteed. The table therefore uses deliberately cautious language: ***Kazachstania* may decline in dominance with less rigorous maintenance or other stressors.**

Reversion: *Saccharomyces cerevisiae*

This remains one of the more inferential cells in the model.

In this study, *S. cerevisiae* represented 40.7% of the source starter's yeast population and 78.0% in my starter after 14 months of separate maintenance. If the source starter retained a profile similar to the original shared culture, this difference would be consistent with *S. cerevisiae* gaining dominance under my less intensive maintenance routine. Without baseline DNA measurements, however, the direction of change cannot be determined.

The marked differences between Type 1 and Household microbial profiles and their associated maintenance practices provide a broad basis for inferring this possible pathway. As a starter transitions away from Type 1 toward a Household profile, we can assume the characteristic Type 1 community diminishes while a Household community emerges. The greater prevalence of *S. cerevisiae* dominance in the Household dataset suggests that its increasing dominance would be consistent with this transition.

Together, these observations support a plausible pathway rather than a demonstrated transition. The table therefore states cautiously: **S. cerevisiae may gain dominance when Type 1 maintenance is relaxed.**

Reversion: *Fructilactobacillus sanfranciscensis*

Long-term studies document **remarkable persistence** of *F. sanfranciscensis* under changed maintenance conditions. Whether that persistence accompanies a broader shift away from a Type 1 microbial community remains less directly established.

Both Pham et al. and the Auerbach study provide striking examples of *F. sanfranciscensis* persistence**.** In the Pham retired-baker case, it remained dominant after approximately 15 years of reduced-frequency household maintenance. In the Auerbach comparison, it dominated both branches of a starter maintained separately for approximately 20 years. These cases demonstrate that an established *F. sanfranciscensis* population can persist for decades, including under maintenance substantially different from intensive bakery propagation.

Wardhana et al. (2026) tested an unusually substantial departure from routine Type 1 maintenance: feeding only once every three weeks, with refrigeration at 4°C between feedings. *F. sanfranciscensis* persisted in one starter throughout the 39-week study, but was displaced in the cultured bacterial population of the other starter around week 12. These contrasting outcomes illustrate both its capacity for persistence and the possibility of displacement under substantially altered maintenance conditions.

For that reason, the table states that ***F. sanfranciscensis* is persistent and may decline or be displaced under substantially altered maintenance conditions.**

Importantly, this does **not** imply that disappearance is immediate or inevitable. The available evidence instead suggests that yeast composition may respond more quickly to altered maintenance while an established *F. sanfranciscensis* population can, in some lineages, persist for many years.

Classification Note

The value of understanding the occurrence of organisms is not that any one species provides an absolute diagnostic test. The usefulness comes from the **constellation of signpost** readings.

The strongest Type 1-like fingerprint is an established starter dominated by *F. sanfranciscensis* together with a characteristic Type 1 yeast community, particularly *Kazachstania* spp. That combination is common enough among mature bakery starters to represent a recognizable ecological pattern, yet rare among the household starters in the Landis dataset.

My analysis finds this pairing of *Kazachstania* spp. as the most abundant yeast and F. *sanfranciscensis* as the most abundant bacterium in **approximately 3.8% of the Landis household population**, giving the pattern useful discriminatory power.

The Maturity Map should therefore be read as an ecological framework rather than a taxonomy. The microbial signposts show where a starter appears to be within that continuum; they do not impose rigid boundaries between stages.

Appendix L: Sources and References

Published Research

Landis et al. (2021)

The diversity and function of sourdough starter microbiomes

Large-scale study of approximately 500 primarily household sourdough starters. This is the **principal source for the Household** microbial population used throughout this paper, including species diversity, recurring species patterns, co-occurrence analysis, the Walkdown, and the Landis sample-size adjustment.

DOI: **10.7554/eLife.61644**
Link: *Landis et al. study*

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von Gastrow et al. (2023)

Microbial community dispersal from wheat grains to sourdoughs: A contribution of participatory research

Study comparing microorganisms in wheat grains, flour, bakery environments, and mature sourdoughs. The population of 46 sourdough starters provides the **principal "Type 1"** comparison dataset used in this paper. It is also important evidence that many microorganisms characteristic of mature sourdoughs are not readily detected in the grains and flours from which they originate.

DOI: **10.1111/mec.16630**
Link: *von Gastrow et al. study*

Michel et al. (2023)

Artisanal and farmer bread making practices differently shape fungal species community composition in French sourdoughs

Examines yeast communities associated with different French bread-making practices. Particularly useful for understanding how maintenance practices select different *Kazachstania* and *Saccharomyces* populations and as evidence for **movement away from characteristic Type 1** yeast patterns under changed maintenance conditions.

DOI: **10.24072/pcjournal.237**
Link: *Michel et al. study*

Gänzle et al. (2023)

The quest for the perfect loaf of sourdough bread continues: Novel developments for selection of sourdough starter cultures

Reviews the microbial ecology of sourdough starters, highlighting the **remarkable consistency of microbial communities in traditional Type 1** sourdoughs across different geographic regions

and baking traditions. Identifies *F. sanfranciscensis* as a characteristic dominant bacterium and *K. humilis* as a frequently dominant yeast. Particularly useful as independent support for the distinctive Type 1 microbial profile described in this paper, demonstrating that these recurring species patterns are well established in the scientific literature.

DOI: **10.1016/j.ijfoodmicro.2023.110421**
Link: *Gänzle et al. review*

Sanmartín et al. (2024)

Bioprospecting of sourdough microbial species from artisan bakeries in the city of Valencia

Examines the microbial communities of ten mature Type 1 sourdoughs from artisan bakeries in Valencia, Spain. Identifies *F. sanfranciscensis*, *S. cerevisiae*, and *K. humilis* as prominent species while documenting the **influence of maintenance conditions** and associations between maintenance conditions and microbial communities, fermentation performance, and aroma. Particularly useful as independent evidence of characteristic Type 1 microbial communities and the influence of maintenance conditions on yeast populations, fermentation performance, and aroma.

DOI: **10.1016/j.fm.2024.104474**
Link: *Sanmartín et al. study*

Taheri et al. (2025)

The role of flour type and feeding schedule on the sourdough microbiome

Experimental study following **18 newly created starters** for 28 days using three flour types and two feeding schedules. Provides species-level evidence of microbial succession during new-starter development and is particularly important to the discussion of *Kazachstania*, *S. cerevisiae*, *F. sanfranciscensis*, and the differences between flour microbiota and mature starter microbiota.

DOI: **10.1128/spectrum.02380-25**
Link: *Taheri et al. study*

McKenney et al. (2023)

Sourdough starters exhibit similar succession patterns but develop flour-specific climax communities

Experimental study following **40 newly created starters** made from ten different flours. Identified repeatable stages of bacterial succession and approximately Day-10 functional maturity while showing that mature communities could differ according to flour.

DOI: **10.7717/peerj.16163**
Link: *McKenney et al. study*

Reese et al. (2020)

Influences of Ingredients and Bakers on the Bacteria and Fungi in Sourdough Starters and Bread

Study of new sourdough starters created by 18 bakers from 14 countries using standardized ingredients and a common recipe. Researchers found microbial overlap among flour, starters, and **bakers' hands,** suggesting possible exchange between bakers and their starters. This study informs the discussion of microbial arrival during new-starter formation; it did not test microbial replacement in established starters.

DOI: **10.1128/mSphere.00950-19**
Link: *Reese et al. study*

Lattanzi et al. (2013)

The lactic acid bacteria and yeast microbiota of eighteen sourdoughs used for the manufacture of traditional Italian sweet leavened baked goods

Study of 18 traditional Italian mother sourdoughs used for products such as Panettone and Pandoro. Provides an important additional Type 1 cohort. *F. sanfranciscensis* was highly prevalent, while *S. cerevisiae* was the dominant yeast in most samples, illustrating that mature Type 1 sourdoughs do not require *K. humilis* dominance.

DOI: **10.1016/j.ijfoodmicro.2013.02.010**
Link: *Lattanzi et al. 2013 study*

Lattanzi et al. (2014)

Assessment of comparative methods for storing type-I wheat sourdough

Experimental study examining **refrigerated, frozen, and dried storage** of laboratory-prepared sourdoughs inoculated with selected strains and propagated to functional maturity before storage, followed by reactivation. Provides evidence that some microbes can persist through storage even when fermentation performance and microbial community composition change. Other microbes are impacted by various storage methods.

DOI: **10.1016/j.lwt.2014.06.032**
Link: *Lattanzi et al. 2014 study*

Minervini et al. (2012)

Lactic acid bacterium and yeast microbiotas of 19 sourdoughs used for traditional/typical Italian breads: Interactions between ingredients and microbial species diversity

Survey of traditional Italian bread sourdoughs examining their lactic acid bacteria and yeast populations and relationships with **ingredients, especially flour type, and production practices**. Used as additional evidence for the microbial structure and diversity of traditionally maintained bakery sourdoughs.

DOI: **10.1128/AEM.07721-11**
Link: *Minervini et al. traditional Italian bread study*

Minervini et al. (2012)

Influence of artisan bakery- or laboratory-propagated sourdoughs on the diversity of lactic acid bacterium and yeast microbiotas

Seven mature Type I sourdoughs were propagated for 80 days **under bakery and laboratory conditions**. Demonstrates that changing the propagation environment can alter established microbial communities even when the originating sourdough is the same.

DOI: **10.1128/AEM.00572-12**
Link: *Minervini et al. bakery-versus-laboratory study*

Minervini et al. (2015)

House microbiotas as sources of lactic acid bacteria and yeasts in traditional Italian sourdoughs

Examined flour, air, walls, storage boxes, mixers, and sourdoughs in four bakeries. Provides evidence that the bakery environment can act as a **reservoir for sourdough organisms** and that dominant sourdough organisms can also become established throughout the bakery environment.

DOI: **10.1016/j.fm.2015.06.009**
Link: *Minervini et al. house microbiota study*

Minervini et al. (2018)

Wheat endophytic lactobacilli drive the microbial and biochemical features of sourdoughs

Examines microorganisms associated with wheat and their potential contribution to developing sourdough communities. Used in the discussion of **where sourdough organisms originate** and how flour-associated organisms contribute to early community assembly.

DOI: **10.1016/j.fm.2017.09.006**
Link: *Minervini et al. 2018 study*

Minervini et al. (2019)

Tap water is one of the drivers that establish and assembly the lactic acid bacterium biota during sourdough preparation

Controlled study comparing ten Italian tap waters used to propagate a mature sourdough and develop new starters, with flour and fermentation conditions held constant. **Water influenced** the assembly of lactic acid bacteria communities in new starters, while the mature starter's lactic acid bacteria species and strain composition remained largely unchanged over nine days. Supports the distinction between environmental influences during starter establishment and

resistance to change in an established community. The persistence findings concern lactic acid bacteria over a short observation period, rather than long-term stability of the entire microbiome.

DOI: *10.1038/s41598-018-36786-2*
Link: *Minervini et al. study (open access)*

Calabrese et al. (2022)

Metabolic framework of spontaneous and synthetic sourdough metacommunities to reveal microbial players responsible for resilience and performance

Detailed molecular study of eight spontaneous sourdoughs from the Puratos Sourdough Library and experimentally reconstructed communities. Provides unusually **detailed species-level data** and evidence regarding dominant, subdominant, and satellite organisms and community resilience.

DOI: **10.1186/s40168-022-01301-3**
Link: *Calabrese et al. study*

Pham et al. (2024)

Does strain-level persistence of lactobacilli in long-term back-slopped sourdoughs inform on domestication of food-fermenting lactic acid bacteria?

Longitudinal analysis of established bakery sourdoughs sampled over periods as long as 19 years. Particularly important to this paper is Sourdough C, which split into commercial and household-maintained **('retired baker')** descendants after 2009. Provides **unusually strong evidence for long-term strain persistence** as well as a natural experiment involving a major change in maintenance intensity.

DOI: **10.1128/aem.01892-24**
Link: *Pham et al. study*

Gänzle, Ehmann & Hammes (1998)

Modeling of Growth of *Lactobacillus sanfranciscensis* and *Candida milleri* in Response to Process Parameters of Sourdough Fermentation

Classic experimental study modeling the effects of temperature, pH, acids, salt, and other environmental variables on *L. sanfranciscensis* and *Candida milleri* (also known as *K. humilis* and *M. humilis*). Particularly important to the discussion of **temperature as a selective pressure** in sourdough ecosystems.

DOI: **10.1128/AEM.64.7.2616-2623.1998**
Link: *Gänzle et al. 1998 study*

Gänzle & Ripari (2016)

Composition and function of sourdough microbiota: From ecological theory to bread quality

Ecological synthesis explaining sourdough community assembly in terms of **selection, dispersal, drift, and adaptation.** Particularly useful to the Maturity Map framework and its emphasis on intensive, long-term propagation selecting microorganisms specifically adapted to the sourdough environment.

DOI: **10.1016/j.ijfoodmicro.2016.05.004**
Link: *Gänzle and Ripari review*

Carbonetto et al. (2020)

Interactions between *Kazachstania humilis* Yeast Species and Lactic Acid Bacteria in Sourdough

Experimental study examining how *K. humilis*, *S. cerevisiae*, and sourdough lactic acid bacteria affect one another's growth and fermentation. Shows that organisms can coexist and ferment effectively together **without necessarily helping one another** grow under tested conditions.

DOI: **10.3390/microorganisms8020240**
Link: *Carbonetto et al. study*

Urien et al. (2019)

Fungal Species Diversity in French Bread Sourdoughs Made of Organic Wheat Flour

Survey of fungal communities in 14 French sourdoughs from **bakers and farmer-bakers**, using culture-based identification and DNA metabarcoding. *Kazachstania* species dominated most sourdoughs, with *K. humilis* associated mainly with baker-like practices and other *Kazachstania* species with farmer-baker-like practices. Supports the diversity of sourdough yeast communities and their association with bread-making practices. This was a comparison among existing starters, rather than a longitudinal demonstration of yeast replacement following a maintenance change.

DOI: *10.3389/fmicb.2019.00201*
Link: *Urien et al. study (open access)*

Boiocchi et al. (2017)

Insect frass in stored cereal products as a potential source of *Lactobacillus sanfranciscensis* for sourdough ecosystem

Identified insect frass (droppings) as a potential **natural reservoir of *F. sanfranciscensis***, supporting insects as a possible route of introduction into sourdough.

DOI: *10.1111/jam.13546*
Link: *Boiocchi et al. study*

Rogalski, Ehrmann & Vogel (2020)

Role of *Kazachstania humilis* and *Saccharomyces cerevisiae* in the strain-specific assertiveness of *Fructilactobacillus sanfranciscensis* strains in rye sourdough

Experimental study demonstrating that **interactions** among *F. sanfranciscensis* and sourdough yeasts can be **strain-specific.** Used to support the caution that species-level DNA results do not reveal all of the ecological interactions occurring below the species level.

DOI: **10.1007/s00217-020-03535-7**
Link: *Rogalski et al. study*

Sánchez-Adriá et al. (2023)

Technological and acid stress performance of yeast isolates from industrial sourdough

Compared sourdough yeast isolates for **CO_2 production**, acid tolerance, and other technological characteristics. Used in discussing why a change in yeast species composition cannot automatically be translated into a predictable change in starter rising power; fermentation performance also varies substantially among strains.

DOI: **10.1016/j.lwt.2023.114957**
Link: *Sánchez-Adriá et al. study*

Siragusa et al. (2009)

Taxonomic structure and monitoring of the dominant population of lactic acid bacteria during wheat flour sourdough type I propagation using *Lactobacillus sanfranciscensis* starters

Experimental study following ten newly prepared wheat sourdoughs for ten days: nine inoculated individually with different *F. sanfranciscensis* strains and one flour-and-water control. ***S. cerevisiae* was the dominant** yeast in all sourdoughs, supporting its potential to become dominant **early in starter development**. The study also demonstrates strain-level selection: six introduced bacterial strains declined substantially, while other *F. sanfranciscensis* strains persisted. It did not establish the source of *S. cerevisiae* or demonstrate species-level loss of *F. sanfranciscensis*.

DOI: 10.1128/AEM.01524-08
Link: *Siragusa et al. study*

Böcker, Stolz & Hammes (1995)

Neue Erkenntnisse zum Ökosystem Sauerteig und zur Physiologie der sauerteigtypischen Stämme *Lactobacillus sanfrancisco* und *Lactobacillus pontis*

Foundational sourdough ecology paper associated with the Type I, Type II, and Type III classification system. Provides **historical context for the definition** of traditional continuously propagated Type I sourdoughs.

Getreide, Mehl und Brot **49**, 370–374.
Link: *Böcker et al. reference record*

Aiki et al. (2025)

Rapid counting of *Kazachstania humilis* and *Saccharomyces cerevisiae* in sourdough by deep learning-based classifier

Study developing an automated method for measuring the relative abundance of two common sourdough yeasts. Researchers repeatedly refreshed sourdough at 25°C, 30°C, and 35°C and observed dramatic differences in yeast composition. *K. humilis* represented approximately 25% of the yeast population at 25°C but less than 1% at 30°C and 35°C. This provides direct experimental evidence that **maintenance temperature can strongly influence** yeast dominance during repeated feeding cycles. Particularly relevant to the Selection and Maintenance conditions of the proposed Maturity Map.

DOI: **10.1016/j.mimet.2025.107183**

Link: *Aiki et al. study*

Aiki et al. (2026)

Comparison of microbiological and bread-making properties of *Kazachstania humilis* and *Saccharomyces cerevisiae* isolated from sourdough

Study compares sourdough isolates of two common yeast species and their effects on fermentation and bread quality. *S. cerevisiae* demonstrated **greater gas production** and leavening ability under the tested conditions, producing bread with higher specific volume. The findings contrast with earlier studies in which selected *K. humilis* strains outperformed *S. cerevisiae,* illustrating the importance of strain selection and fermentation conditions.

DOI: **10.3136/fstr.FSTR-D-26-00044**

Link: *Aiki et al. (2026) study*

Vogel, Müller, Stolz & Ehrmann (1996)

Ecology in sourdoughs produced by traditional and modern technologies

Early foundational description of how different production technologies select different sourdough microbial communities. Used as **historical support for the ecological basis of Type I** sourdough classification.

Advances in Food Science 18, 152–159.
Link: *Vogel et al. bibliographic record*

Wardhana et al. (2026)

Stability of *Fructilactobacillus sanfranciscensis–Maudiozyma humilis in* industrial sourdough

Study examining the long-term microbial stability of two established industrial Type 1 sourdough starters under infrequent feeding and refrigeration. Both starters initially contained *F. sanfranciscensis* and *M. humilis* (formerly *K. humilis*). Researchers compared a firm (60%

hydration) and semi-liquid (100% hydration) starter, including a 39-week experiment with feeding every three weeks and refrigeration at 4°C between feedings. The firm starter retained both characteristic species throughout the experiment, demonstrating **extraordinary persistence of the Type 1 microbial profile**. In contrast, the semi-liquid starter experienced bacterial species replacement and the eventual loss of culturable yeasts, demonstrating **loss of the characteristic Type 1 microbial profile**. The starters differed in hydration, feeding ratios, and other maintenance conditions, preventing attribution to any single factor. The contrasting outcomes provide evidence of both persistence and loss under prolonged, infrequent maintenance, making the study particularly relevant to the maintenance conditions influencing the proposed Maturity Map.

DOI: **10.1007/s00253-026-14018-2**
Link: *Wardhana et al. study*

Data Sources

Landis et al. Raw Dataset / Figshare

Sample-level bacterial and fungal abundance data associated with the Landis household sourdough study. Used directly in this paper for species-frequency calculations, recurring species patterns, the Walkdown, co-occurrence analyses, and the 10,000-draw n=46 sample-size adjustment.

Primary paper: Landis et al. (2021), The diversity and function of sourdough starter microbiomes.

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von Gastrow et al. Raw Data

Sample-level data associated with **Microbial community dispersal from wheat grains to sourdoughs**. Used for the mature bakery species-frequency analysis, recurring species patterns, and the Type 1 side of the Walkdown.

Primary paper: von Gastrow et al. (2023).

McKenney et al. Data Repository

Underlying data for the new-starter succession experiment.

Dryad DOI: **10.5061/dryad.bk3j9kdh3**
Link: *McKenney et al. Dryad dataset*

Personal Communications and Interviews

David Auerbach, personal communication (2026)
Direct correspondence concerning the history, provenance, maintenance practices, and long-term separation of the Auerbach starter lineage. Used in the long-term persistence case study.

Michael Gänzle, personal communication (2026)
Correspondence concerning Type 1 ecology, maintenance pressure, refrigeration, microbial persistence, reversion, historical starter interpretation, and the limitations of drawing conclusions from species-level DNA results.

Nancy Rubuliak, personal communication / interview (2026)
Detailed history of the starter described in the Pham et al. “Sourdough C” case, including bakery maintenance, retirement, relocation, household maintenance, loss and recovery of the original starter, and subsequent commercial and household descendants.

Eric Pallant, personal communication (2026)
Correspondence concerning historical sourdough starters, provenance, starter-age claims, and the difficulty of establishing continuity of very old starter lineages.

Michael Kalanty, personal communication / interview (2026)
Professional baker perspective concerning long-term bakery starter maintenance, traditional sourdough practices, and the practical ecology of continuously propagated starters.

Carrie Diulus, M.D., personal communication (2026)
Project-related scientific review and correspondence concerning interpretation of sourdough microbiome results.

Alain Marec, personal communication (2026)
Review and feedback from the perspective of a food scientist, baker, and educator.

Sabrina Spiezio, personal communication (2026)
Review and feedback from the perspective of a sourdough baker and food scientist.

Other Supporting Sources

Gänzle / Peter Reinhart: Johnson & Wales Symposium (2021)

Presentation by Michael Gänzle that helped shape my understanding of sourdough microbial ecology. Explains how repeated feeding selects for organisms suited to sourdough, why established communities can persist, and how maintenance conditions influence their stability. Provides an accessible foundation for several ecological ideas explored in this report.

Pallant, Eric: Sourdough Culture: A History of Bread Making from Ancient to Modern Bakers (2021)

Historical survey of sourdough baking that includes discussions with researchers Rob Dunn and Erin McKenney about the microbial origins of new starters, flour and kitchen environmental contributions, early microbial succession, and the potential stability of mature cultures (pp. 245–255). Used as contextual and historical background, with primary research studies providing the scientific evidence.

Myhrvold and Migoya, Modernist Bread (2017)

Comprehensive five-volume technical reference on the science and practice of bread making, including sourdough fermentation and microbiology. Influential in initially developing the author's foundational understanding of sourdough science (2020). Included as background research rather than as a source supporting specific findings in this paper.

Wink / Janjigian — “Flowers and flours” (2024)

Interview with Debra Wink by Andrew Janjigian, Wordloaf, January 24, 2024.

Discussion of possible environmental sources of sourdough microorganisms, particularly Debra Wink’s experiments inoculating new starters with flowers and other plant material.

Avery / Sourdough Home (2019) “Another Delicate Matter”

Public-facing analysis of DNA results from David Auerbach's sourdough starter and a descendant maintained separately for approximately 20 years. The comparison provides an unusual example of two starters sharing a common origin and sharing similar species profiles after prolonged separation. Used in the discussion of microbial persistence, divergence, and the limitations of starter age or shared ancestry as predictors of present-day microbial composition.

The Sourdough Journey Experiments and Observations (2019-2026)

The author's independent experiments include the creation and observation of new starters, controlled starter maintenance experiments, pressure vessel measurements of CO_2 production, pH tracking, refrigeration and vacation hold experiments, dough rising experiments, baking observations, and the two-starter DNA study reported in this paper.

A Note on the Use of Artificial Intelligence

I used ChatGPT extensively during the development of this report as a research assistant and analytical tool. It assisted with locating, organizing, and interpreting published research; analyzing published microbial datasets; exploring alternative explanations; and assisting with some copyediting and proofreading.

AI was an important tool in this process, but it was not infallible. I identified and corrected many errors in AI-generated research summaries, calculations, and interpretations. Important scientific claims were checked against original published sources, and I reviewed and reconciled quantitative analyses against the source datasets.

The scientific findings and interpretations presented in this report are grounded in the published research cited herein, the underlying datasets, and my own experimental observations and independent research. **AI-generated responses or general AI knowledge were not treated as independent scientific evidence**. Where AI assisted in interpreting or synthesizing research findings, the underlying published sources remained the basis for my evaluation of those interpretations.

The original ideas, experiments, observations, illustrations, independent research, correspondence with researchers and bakers, scientific interpretations, conclusions, and final editorial decisions are my own.

I take full responsibility for the accuracy and content of this report.

I produced this manuscript in Microsoft Word, including the use of its spelling, grammar, and proofreading tools.

Support The Sourdough Journey

If you found this paper helpful, please consider supporting **The Sourdough Journey** with a donation at *thesourdoughjourney.com/donate*

All of my research is independently funded through donations.

Your support helps make it possible for me to continue this work with more DNA studies and share the results with the sourdough community. Thank you for supporting independent sourdough research.

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For clarifications, corrections, FAQs, videos, additional information, and future updates to this paper, please visit *https://thesourdoughjourney.com/inside-the-invisible-world-of-sourdough-starters/*