

Table S1. Characteristics of the sourdough samples M1, M2, M3, and M4 collected from the four selected bakeries located in Sicily.

	M1	M2	M3	M4
Bakery location (city)	Maletto	Trapani	Palermo	Catania
Flour in chief sourdough	Maiorca	Maiorca	Maiorca	Maiorca
Hydration of sourdough (%)	87	75	82	73
No. of back-slopping steps before use	1	1	1	1
Temp (°C) of back-slopping ^a	22.5	21	23	22.6
Period (h) of back-slopping ^a	6h30	6h	11h	14h
Sourdough ^b (%)	43	16	15.1	33
Flour ^b (%)	37	44	49.4	39.4
Water ^b (%)	19	38	35	27
Salt ^b (%)	0.9	1.3	0.8	0.8
Kneading method ^c	Me	Me	Ma	Me
Total period of fermentation	4h30	6h50	4h45	4h20

^a Mature sourdough, after the last back-slopping

^b Percentage of total dough weight

^c Mechanically (Me) or manually (Ma)

^d For the second bread-making run, only wheat flour was used

Table S2. Overview of the 16S rRNA gene ARDRA profiles and clustering data based on (GTG)₅ rep-PCR.

Samples	Strains	16S ARDRA analysis		(GTG) ₅ rep-PCR	
		Restriction fragments (bp)	Pattern	Subcluster	Major cluster
M1	L7	313-305-246-110-100-90	B	S1	I
	L84, L89	313-305-246-110-100-90	B	S2	I
	L82	313-305-246-110-100-90	B	Singleton	II
	L83	313-305-246-110-100-90	B	Singleton	II
	L92, L96, L97	313-305-246-110-100-90	B	S3	II
	L90	313-305-246-110-100-90	B	S4	III
	L94	313-305-246-110-100-90	B	Singleton	III
	L88	313-305-246-110-100-90	B	Singleton	III
	L5, L6, L93	510-240-110-105-90	A	S5	III
	L4, L91, L95	510-240-110-105-90	A	S7	III
	L1, L2, L3	510-240-110-105-90	A	S9	III
M2	L10, L64, L69, L67, L77, L9, L11, L14, L8, L66	510-240-110-105-90	A	S5	III
	L74	510-240-110-105-90	A	S8	III
	L12, L13	510-240-110-105-90	A	S9	III
	L65	510-240-110-105-90	A	S10	III
	L68	510-240-110-105-90	A	Singleton	III
	L79	510-240-110-105-90	A	Singleton	III
	L73, L76, L78, L80, L72	313-305-246-110-100-90	B	S1	I
	L15	313-305-246-110-100-90	B	Singleton	I
	L75 L71	313-305-246-110-100-90	B	S2	I
	L81	310-310-220-212-115-90	C	Singleton	I
	L70	313-305-246-110-100-90	B	Singleton	III
M3	L50, L55, L56, L49, L52	313-305-246-110-100-90	B	S13	IV
	L21, L22, L19, L20, L16, L17, L23	510-240-110-105-90	A	S5	III
	L51	510-240-110-105-90	A	S7	III
	L59	510-240-110-105-90	A	S8	III
	L18	510-240-110-105-90	A	S9	III
	L58, L63, L53, L54, L61	510-240-110-105-90	A	S10	III
	L57, L62, L60	510-240-110-105-90	A	S11	III
M4	L43	313-305-246-110-100-90	B	Singleton	I
	L42, L44	313-305-246-110-100-90	B	S4	III
	L46	313-305-246-110-100-90	B	Singleton	III
	L30, L28, L29, L27, L26, L33, L38, L37, L39, L24, L25	510-240-110-105-91	A	S5	III
	L36, L47, L45, L35, L40, L41	510-240-110-105-91	A	S6	III
		510-240-110-105-91	A	S7	III

L31	510-240-110-105-91	A	S11	III
L32, L34, L48	510-240-110-105-91	A	S12	III

Restriction fragments were determined by simultaneously cutting 1500bp-long 16S rRNA gene amplicons with the endonucleases *AluI* and *MspI*. Fragments lower than 70 bp were omitted from the restriction analysis. Major clusters and subclusters were defined through (GTG)₅ rep-PCR analysis using 50 and 80.2% of similarity as cut-off values, respectively. Strains in bold were submitted to 16S rRNA gene sequencing.

Table S3. 16S rRNA gene sequencing results and BLAST search on NCBI RefSeq database (16S ribosomal RNA nucleotide sequence records for Bacteria and Archaea).

Sample	Strain code	Accession number	BLASTn search best hit				Description
			Max Score	Query cover (%)	E-value	Identity (%)	
M1	L7	OL314786	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L89	OL314807	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L82	OL314804	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L83	OL314803	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L97	OL314809	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L94	OL314808	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L88	OL314806	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
M2	L76	OL314801	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L15	OL314790	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L81	OL314803	2761	100	0.0	100	<i>L. rhamnosus</i> NBRC 3525(NR_113332.1)
	L10	OL314788	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L14	OL314789	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L68	OL314799	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L79	OL314802	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L70	OL314800	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
M3	L21	OL314792	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L22	OL314793	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L20	OL314791	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L49	OL314797	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L52	OL314798	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
M4	L42	OL314796	2651	100	0.0	100	<i>L. plantarum</i> NRRL B-14768 (NR_104573.1)
	L30	OL314794	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)
	L31	OL314795	2604	99	0.0	99.86	<i>L. brevis</i> DSM20054 (NR_116238.1)

Table S4. Overview of the ITS restriction patterns of sourdough yeast isolates.

Sample	Strain	Amplicon	Restriction profile		Yeast-id Best matching	Pattern code
			<i>HaeIII</i>	<i>HinfI</i>		
M1	Y1, Y2, Y3, Y8, Y12, Y66, Y67 , Y68, Y69, Y71, Y72, Y73, Y74, Y75, Y76, Y77, Y78, Y79	620	620	310-300	<i>W. anomalus</i> (100%)	A
	Y23	880	325-230-170-125	375-365-110	<i>S. cerevisiae</i> (100%)	B
	Y70	800	800	410-380	<i>T. delbrueckii</i> (100%)	C
M2	Y53, Y54, Y55, Y58 , Y26	880	325-230-170-125	375-365-110	<i>S. cerevisiae</i> (100%)	B
	Y10, Y13, Y22, Y56, Y57, Y59, Y60 , Y61, Y62, Y63, Y64, Y65	620	620	310-300	<i>W. anomalus</i> (100%)	A
	Y5	700	700	320-200-150	<i>C. boidinii</i> (73%)	D
M3	Y14, Y24, Y25, Y46	620	620	310-300	<i>W. anomalus</i> (100%)	A
	Y7 , Y9	450	350-100	310-310	<i>C. ethanolica</i> (83%)	E
	Y47 , Y51	800	800	410-380	<i>T. delbrueckii</i> (100%)	C
	Y21 , Y40 , Y41, Y42, Y43, Y44, Y48, Y49, Y50, Y52,	880	325-230-170-125	375-365-110	<i>S. cerevisiae</i> (100%)	B
M4	Y16, Y20, Y39	620	620	310-300	<i>W. anomalus</i> (100%)	A
	Y15 , Y17 , Y18 , Y19 , Y27 , Y28, Y29, Y30 , Y31, Y32, Y33, Y34, Y35, Y36, Y37, Y38	880	325-230-170-125	375-365-110	<i>S. cerevisiae</i> (100%)	B
	Y6 , Y11	630	420-130-80	310-310	<i>C. maritima</i> (100%)/ <i>C. zeylanoides</i> / <i>C. diddensiae</i> (100%)	F

Tentative yeast identification was obtained by using ITS restriction patterns as queries in Yeast ID databases (www.yeast-id.org). Strains in bold were submitted to sequencing of the 26S rDNA D1/D2 domain. All the fragment sizes are in bp. Fragments lower than 70 bp were omitted from the analysis.

Table S5. 26S rRNA D1/D2 region sequencing results and BLAST search on NCBI RefSeq database (28S ribosomal RNA Nucleotide sequence records).

ITS PCR-RFLP Pattern	Strain	Accession number	BLASTn search			
			Query cover (%)	E-value	Identity (%)	Best Hits
A	Y1	MN058031	100	0.0	100	<i>W. anomalus</i> strain CBS5759 (MK394130.1)
	Y67	MZ221134	100	0.0	100	<i>W. anomalus</i> strain CBS5759 (MH545921.1)
	Y56	MZ221130	100	0.0	100	<i>W. anomalus</i> strain CBS5759 (MH545921.1)
	Y59	MZ221132	100	0.0	100	<i>W. anomalus</i> strain CBS5759 (MH545921.1)
	Y60	MZ221133	100	0.0	100	<i>W. anomalus</i> strain CBS5759 (MH545921.1)
B	Y15	MN058035	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y17	MN058036	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y18	MN058037	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y19	MN058038	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y21	MN058039	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y23	MN058040	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y26	MN058041	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y27	MZ221124	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y30	MZ221125	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y40	MZ221126	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y50	MZ221128	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
	Y58	MZ221131	100	0.0	100	<i>S. cerevisiae</i> strain CEN.PK113-7D (CP0460921)
C	Y47	MZ221127	99	0.0	100	<i>T. delbrueckii</i> strain CBS2733 (KY109859.1)
	Y51	MZ221129	99	0.0	100	<i>T. delbrueckii</i> strain CBS2733 (KY109859.1)
	Y70	MZ221135	99	0.0	100	<i>T. delbrueckii</i> strain CBS2733 (KY109859.1)
D	Y5	MN058032	100	0.0	100	<i>C. boidinii</i> strain CBS6202 (KY106345.1)
E	Y7	MN058034	100	0.0	100	<i>P. kluyveri</i> strain CBS7275 (KY108826.1)
F	Y6	MN058033	100	0.0	100	<i>C. diddensiae</i> strain CBS2214 (MK394116.1)