



Research article

The role of the surface smear microbiome in the development of defective smear on surface-ripened red-smear cheese

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Supplementary

Table S1. Related to Figure 3. Relative abundances of 16S rDNA amplicons determined by next-generation sequencing of cheese smear samples.

Phylum	Genus	Unpacked	Vacuum film-prepacked	Vacuum
		14413 reads	non-defective 7708 reads	film-prepacked defective 7910 reads
		Relative abundance (%)		
		rDNA	rDNA	rDNA
	other taxa (n = 105) ^a	7.19	9.80	9.27
<i>Firmicutes</i>	<i>Staphylococcus</i>	16.83	14.22	4.20
	<i>Alkalibacterium</i>	3.50	6.23	1.64
	<i>Facklamia</i>	2.14	2.71	1.98
	<i>Lactobacillus</i>	1.42	0.19	0.09
	<i>Sporosalibacterium</i>	0.07	0.65	0.21
<i>Actinobacteria</i>	<i>Corynebacterium</i>	17.92	21.95	24.73
	<i>Brevibacterium</i>	4.74	4.46	1.18
	<i>Brachybacterium</i>	1.33	1.50	0.63
	<i>Agrococcus</i>	0.95	0.40	0.52
	<i>Pseudoclavibacter</i>	1.67	2.11	0.68
	<i>Leucobacter</i>	12.13	5.76	3.55
	<i>Humibacter</i>	3.17	2.74	0.73
	<i>Trueperella</i>	0.42	0.80	0.33
	<i>Bogoriella</i>	0.44	0.54	0.25
<i>Proteobacteria</i>	<i>Halomonas</i>	5.63	10.56	16.92
	<i>Psychrobacter</i>	0.86	2.26	8.53
	<i>Herbaspirillum</i>	3.58	5.70	7.40
	<i>Sphingomonas</i>	1.28	1.80	2.25
	<i>Fulvimonas</i>	0.03	1.35	0.10
<i>Bacteroidetes</i>	<i>Sphingobacterium</i>	1.37	1.06	5.27
	<i>Hydrotalea</i>	0.00	0.00	1.73
	<i>Marinifilum</i>	0.00	0.09	0.86
<i>Tenericutes</i>	<i>Asteroleplasma</i>	0.00	0.00	0.75
<i>Crenarchaeota</i>	<i>Thermocladium</i>	9.37	1.60	1.74
	<i>Sulfurisphaera</i>	0.17	0.09	0.63
<i>Euryarchaeota</i>	<i>Methanohalobium</i>	3.75	1.41	3.26
	<i>Methanomicrobium</i>	0.03	0.00	0.56

^aSummary of the relative abundances of taxa revealing less than 0.5% of total reads in each of the smear samples analyzed.

Table S2. Related to Figure 4. Relative abundances of 16S rRNA reads determined by next-generation sequencing of cheese smear samples.

Phylum	Genus	Unpacked	Vacuum	Vacuum
		2774 reads	film-prepacked	film-prepacked
			non-defective	defective
		2774 reads	2518 reads	2285 reads
Relative abundance (%)				
		rRNA	rRNA	rRNA
	other taxa (n = 28) ^a	2.81	4.13	4.38
<i>Firmicutes</i>	<i>Staphylococcus</i>	1.66	17.00	2.84
	<i>Alkalibacterium</i>	0.65	4.13	1.36
	<i>Facklamia</i>	0.43	1.43	0.70
	<i>Salirhabdus</i>	0.00	0.75	0.00
	<i>Sporanaerobacter</i>	0.00	1.19	0.48
<i>Actinobacteria</i>	<i>Corynebacterium</i>	22.06	26.25	21.66
	<i>Brevibacterium</i>	29.45	14.18	17.77
	<i>Brachybacterium</i>	13.70	5.36	5.60
	<i>Agrococcus</i>	7.43	3.22	4.03
	<i>Clavibacter</i>	2.92	1.15	4.81
	<i>Plantibacter</i>	2.52	2.86	3.28
	<i>Pseudoclavibacter</i>	2.34	2.58	3.33
	<i>Nesterenkonia</i>	2.09	2.50	2.28
	<i>Klugiella</i>	1.33	3.02	4.42
	<i>Curtobacterium</i>	1.80	0.56	4.29
	<i>Microbacterium</i>	1.01	1.07	1.18
	<i>Georgenia</i>	0.87	0.44	0.61
	<i>Millisia</i>	0.94	1.31	1.05
	<i>Mycetocola</i>	0.87	0.91	1.62
	<i>Leucobacter</i>	0.61	0.24	2.36
	<i>Serinibacter</i>	0.47	1.55	1.53
	<i>Actinobaculum</i>	0.43	0.75	1.01
	<i>Frigoribacterium</i>	0.25	0.00	1.97
	<i>Arcanobacterium</i>	0.00	0.83	0.83
	<i>Quadrisphaera</i>	0.25	0.71	0.48
	<i>Subtercola</i>	0.50	0.24	0.35
	<i>Zimmermannella</i>	0.36	0.32	0.53
	<i>Salinibacterium</i>	0.18	0.28	0.70
	<i>Zhihengliuella</i>	0.00	0.52	0.48
<i>Proteobacteria</i>	<i>Halomonas</i>	1.77	0.32	2.41
	<i>Psychrobacter</i>	0.29	0.20	1.66

^aSummary of the relative abundances of taxa revealing less than 0.5% of total reads in each of the smear samples analyzed.



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