

Supplementary Material

Chromatographic characterization and *in vitro* bioactivity evaluation of *Lactobacillus helveticus* hydrolysates upon fermentation of different substrates

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Table S1. Time sampling scheme for strain fermentation activity evaluation.

Strain	Time sampling (h)						
	12	36	60	72	120	280	400
<i>Lactococcus lactis</i> ssp. <i>lactis</i> (ref. 79, field strain)	x	x	x	x	x		
<i>Lactococcus lactis</i> ssp. <i>lactis</i> (ref. 81, field strain)	x	x	x	x	x		
<i>Lactobacillus casei</i> ssp. <i>casei</i> (ref. 80, filed strain)	x	x	x	x	x		
<i>Lactobacillus acidophilus</i> ATCC 4356 (ref. 618)	x	x	x	x	x		
<i>Lactobacillus acidophilus</i> LA 14 (ref. 1004)	x	x	x	x	x	x	x
<i>Lactobacillus acidophilus</i> (ref. 80/2, field strain)	x	x	x	x	x		
<i>Lactobacillus acidophilus</i> (ref. 80/3, field strain)	x	x	x	x	x		
<i>Lactobacillus helveticus</i> (ref. LH, field strain)	x	x	x	x	x	x	x
<i>Enterococcus faecium</i> UBEF-41 (ref. 1003)	x	x	x	x	x		
<i>Saccharomyces cerevisiae</i> var <i>boulardii</i> MTCC-5375 (ref. 1005)	x	x	x	x	x		

Table S2. Comparison between *L. acidophilus* (LA 14) and *L. helveticus* (LH) activity upon 72 h fermentation, reported as mean area values of reference peaks (measured in mV·s) $\pm$ standard deviation (SD), $n=3$ for each selected peak.

Peak t_r (min)	Peak Area	Peak Area
	LA-72h	LH-72h
4.80	0.00	1726.80 $\pm$ 49.12
5.50	3911.83 $\pm$ 47.25	11294.77 $\pm$ 90.69
9.48	86.41 $\pm$ 0.20	172.29 $\pm$ 16.80
13.15	622.45 $\pm$ 9.34	669.44 $\pm$ 25.53
13.58	570.08 $\pm$ 43.60	826.23 $\pm$ 33.72
16.20	47.49 $\pm$ 1.52	1055.96 $\pm$ 24.01
18.60	51.09 $\pm$ 3.25	334.28 $\pm$ 5.83
23.50	689.81 $\pm$ 49.88	1150.70 $\pm$ 28.40
30.86	153.43 $\pm$ 4.77	1318.87 $\pm$ 53.50

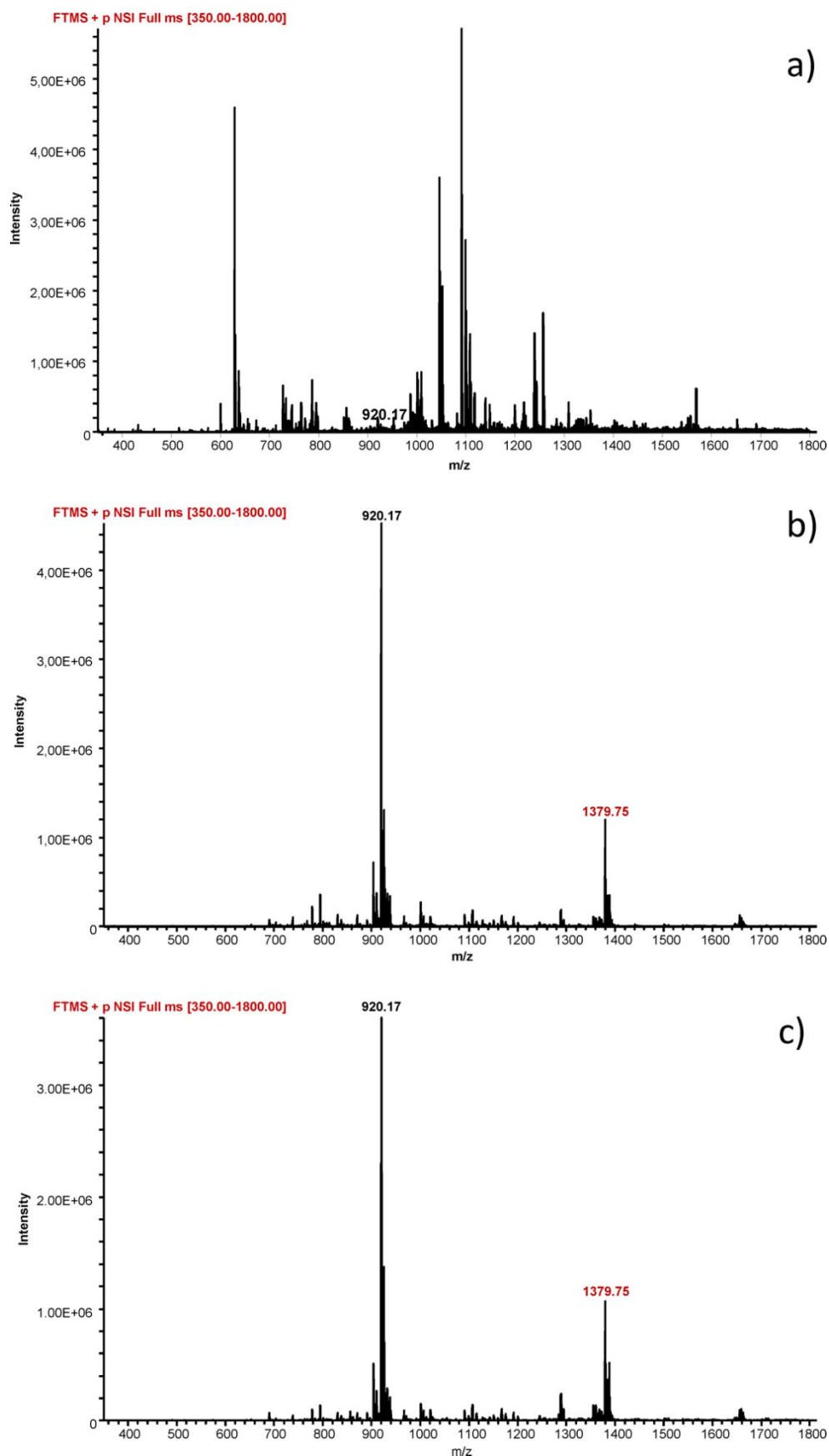


Figure S1. Full MS spectrum of the three samples **a)** SM-Substrate, **b)** SM-TCA, **c)** SM-Beads, related to the RT including the peak at 42.57 ± 0.16 min. The m/z of the newly formed peptides are highlighted in red.

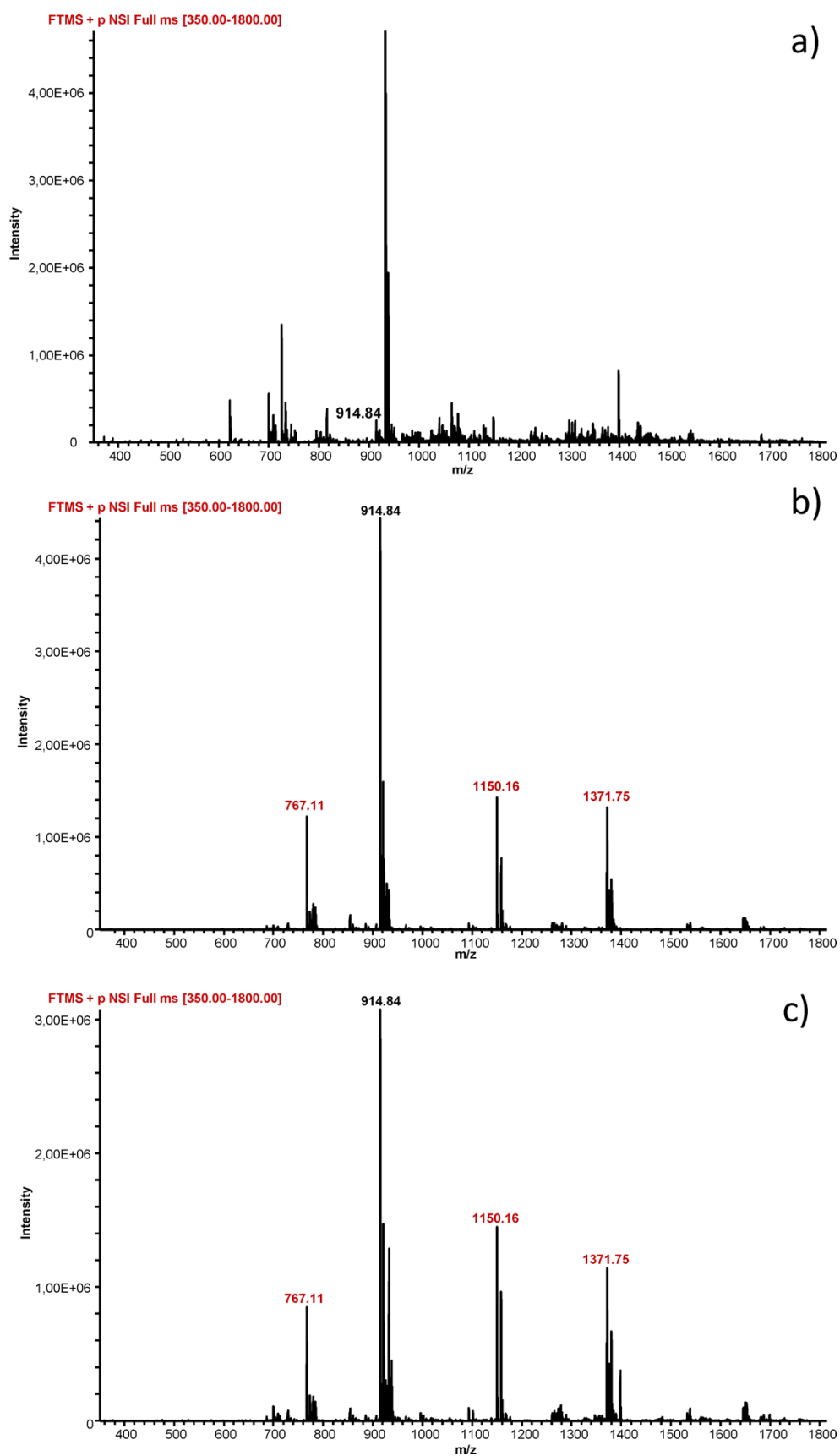


Figure S2. Full MS spectrum of the three samples **a)** SM-Substrate, **b)** SM-TCA, **c)** SM-Beads, related to the RT including the peak at 45.75 ± 0.19 min. The m/z of the newly formed peptides are highlighted in red.

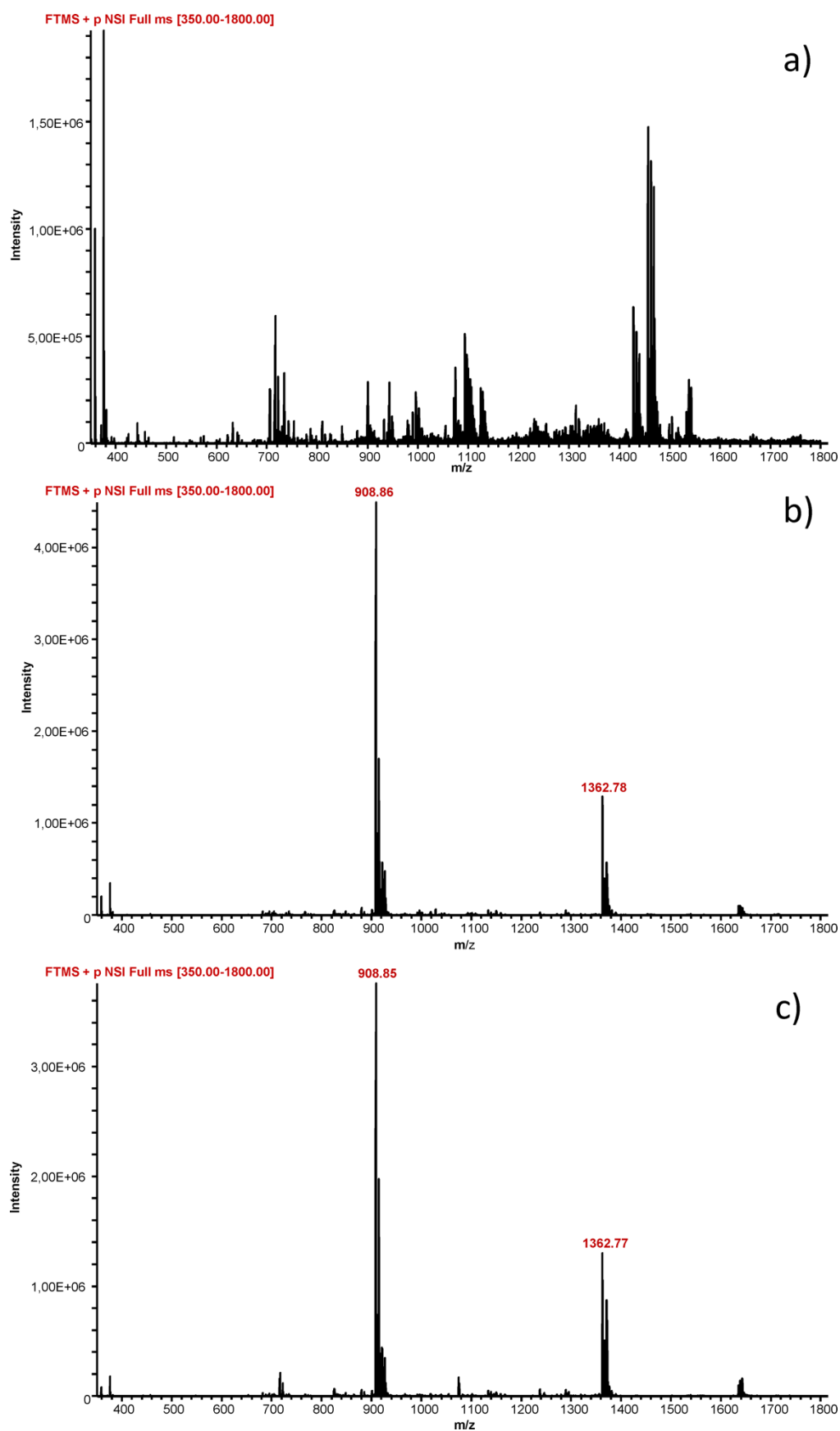


Figure S3. Full MS spectrum of the three samples **a)** SM-Substrate, **b)** SM-TCA, **c)** SM-Beads, related to the RT including the peak at at 47.12 ± 0.15 min. The m/z of the newly formed peptides are highlighted in red.



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