

## Supplementary Materials

**Table S1.** Bacterial genera reported over time in aguamiel and pulque.

<i>Phylum</i>	<i>Genera</i>	<i>Matrix</i>	<i>Technique</i>	<i>Reference</i>
<i>Actinobacteria</i>	<i>Adlercreutzia</i>	Tailstock	Illumina Sequencing	Rocha et al., 2020
	<i>Cellulosimicrobium</i>	Aguamiel, Tailstock	Illumina Sequencing	Rocha et al., 2020
	<i>Corynebacterium</i>	Aguamiel, Tailstock	Illumina Sequencing	Rocha et al., 2020
	<i>Euzebia</i>	Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Luteimicrobium</i>	Tailstock	Illumina Sequencing	Rocha et al., 2020
<i>Bacteroidetes</i>	<i>Chryseobacterium</i>	Pulque	16S rRNA analysis	Escalante et al., 2008
	<i>Dysgonomonas</i>	Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Flavobacterium</i>	Pulque	16S rRNA analysis	Escalante et al., 2004
	<i>Prevotella</i>	Aguamiel	Illumina Sequencing	Rocha et al., 2020
<i>Chloroflexi</i>	<i>Ardenscatena</i>	Tailstock	Illumina Sequencing	Rocha et al., 2020
<i>Cyanobacteria</i>	<i>Halomicronema</i>	Aguamiel, Tailstock, Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Synechococcus</i>	Aguamiel, Pulque	Illumina Sequencing	Rocha et al., 2020
<i>Firmicutes</i>	<i>Bacillus</i>	Pulque, Aguamiel	16S rRNA analysis	Escalante et al., 2008
	<i>Clostridium</i>	Aguamiel, Tailstock	Illumina Sequencing	Rocha et al., 2020
	<i>Enterococcus</i>	Aguamiel	DGGE analysis	Villareal et al., 2019
	<i>Lactobacillus</i>	Pulque	16S rRNA analysis	Escalante et al., 2004
	<i>Lactococcus</i>	Aguamiel, Tailstock, Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Pediococcus</i>	Aguamiel	DGGE analysis	Villareal et al., 2019
	<i>Streptococcus</i>	Aguamiel	16S rRNA analysis	Escalante et al., 2008
	<i>Weissella</i>	Aguamiel, Tailstock, Pulque	Illumina Sequencing	Rocha et al., 2020
<i>Proteobacteria</i>	<i>Acetobacter</i>	Aguamiel, Tailstock, Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Acinetobacter</i>	Aguamiel	16S rRNA analysis	Escalante et al., 2008
	<i>Enterobacter</i>	Aguamiel, Pulque	16S rRNA	Enríquez et al., 2019
	<i>Erwinia</i>	Aguamiel	16S rRNA	Enríquez et al., 2019
	<i>Klebsiella</i>	Tailstock, Pulque	Illumina Sequencing	Rocha et al., 2020
	<i>Kluyvera</i>	Aguamiel, Pulque	16S rRNA analysis	Escalante et al., 2008
	<i>Pseudomonas</i>	Tailstock	Illumina Sequencing	Rocha et al., 2020
	<i>Zymomonas</i>	Pulque	16S rRNA amplicons	Escalante et al., 2008

**Table S2.** Relative abundance of 16S amplicons assigned to bacterial groups found in aguamiel, seedsamples, artisanal and commercial pulque.

Family	Genus	Aguamiel	Seed	Artisanal pulque	Commercial pulque
Bacteroidales S24-7	uncultured	0.05 ± 0.02	0.05 ± 0.1	0.05 ± 0.02	0.05 ± 0.01
Lactobacillaceae	<i>Lactobacillus</i>	5.07 ± 1.37	83.37 ± 2.95	63.61 ± 6.01	54.43 ± 6.97
Leuconostocaceae	<i>Leuconostoc</i>	49.36 ± 2.57	5.98 ± 0.92	14.06 ± 2.80	20.85 ± 4.43
Streptococcaceae	<i>Weissella</i>	0.00 ± 0.00	0.08 ± 0.07	0.15 ± 0.02	0.14 ± 0.03
	<i>Streptococcus</i>	22.33 ± 0.99	4.62 ± 1.99	14.03 ± 1.63	20.52 ± 3.01
	uncultured	0.01 ± 0.01	0.03 ± 0.01	0.06 ± 0.01	0.05 ± 0.00
Lachnospiraceae	NK4A136 group	0.01 ± 0.01	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.00
	uncultured	0.01 ± 0.01	0.03 ± 0.00	0.06 ± 0.00	0.05 ± 0.01
Erysipelotrichaceae	<i>Faecalibaculum</i>	0.01 ± 0.01	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.01
Acetobacteraceae	<i>Acetobacter</i>	0.02 ± 0.01	0.83 ± 0.16	2.95 ± 2.07	0.40 ± 0.05
	Other	0.00 ± 0.00	0.02 ± 0.01	0.08 ± 0.03	0.02 ± 0.01
Sphingomonadaceae	<i>Zymomonas</i>	0.00 ± 0.00	1.11 ± 0.95	2.81 ± 0.24	2.39 ± 0.86
Enterobacteriaceae	<i>Enterobacter</i>	0.04 ± 0.00	0.02 ± 0.01	0.01 ± 0.01	0.02 ± 0.01
	<i>Hafnia</i>	0.07 ± 0.00	0.01 ± 0.00	0.01 ± 0.00	0.01 ± 0.01
Moraxellaceae	<i>Acinetobacter</i>	22.83 ± 2.27	3.75 ± 1.38	2.05 ± 1.08	1.02 ± 0.16
Total		99.81	99.90	99.90	99.92