

Supplementary Materials:

Figure S1: Bacterial communities in coconut samples under different storage conditions through DGGE analysis

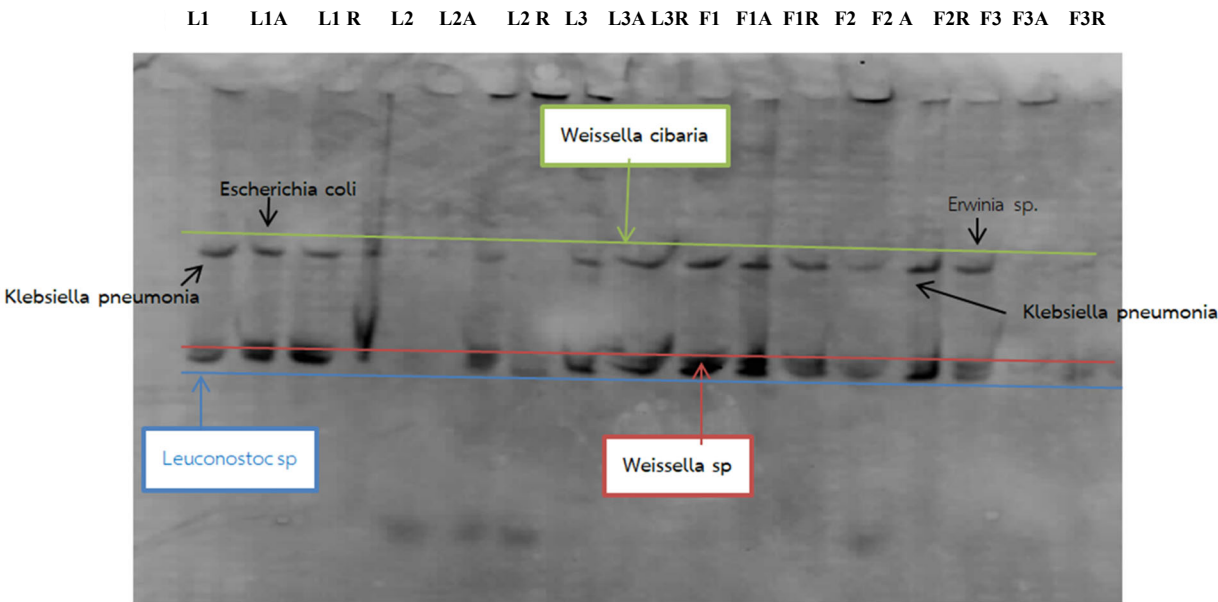


Table S1: Main microorganisms observed in every fresh and spoilage coconut waters under chilling and room temperature conditions by cultural plating

Code	identity	%homology	Accession number
B03	<i>Klebsiella pneumoniae</i>	291/99	MH203013.1
C03	<i>Klebsiella pneumoniae</i>	291/99	MH203013.1
D03	<i>Staphylococcus arlettae</i>	283/100	KF233798.1
E03	<i>Kluyvera cryocrescens</i>	291/100	LM655402.1
F03	proteobacterium	104/92	GQ863469.1
G03	<i>Enterobacter</i> sp.	291/99	KJ879990.1
H03	<i>Enterococcus faecium</i>	287/99	KT626391.1
A04	<i>Lactobacillus fermentum</i>	289/100	KX951727.1
B04	<i>Candida tropicalis</i>	364/98	KJ794698.1
C04	<i>Candida tropicalis</i>	377/98	KY106848.1
D04	<i>Candida tropicalis</i>	383/99	KJ794698.1
C02	<i>Candida tropicalis</i>	396/100	AF267497.1
B02	<i>Candida tropicalis</i>	390/99	GU373750.1

Figure S2: GC-MS analysis of dominant volatile compounds in coconut juice from processing sites (a), street vendor L1 with maturity stage of young; (b), street vendor L3 with maturity stage of mature; (c), street vendor L2; (d), industrial supplied F1; (e), industrial supplied F2; (f), industrial supplied F3.

