

高圧損傷菌の回復メカニズムの解析

— 高圧処理を利用した微生物制御技術の高度化に向けて —

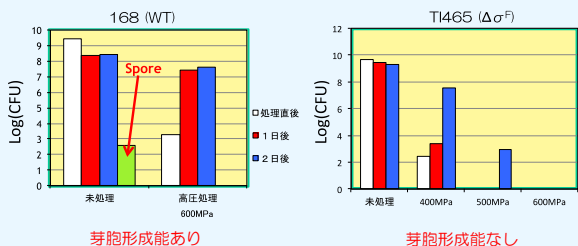
研究の内容

近年、高圧加工食品市場は急速に拡大していますが、高圧処理によって生じる細菌損傷についての知見はごくわずかです。本研究では、高圧処理により損傷した細菌の回復メカニズムを明らかにし、高圧処理を利用した微生物制御技術の高度化を目指しています。

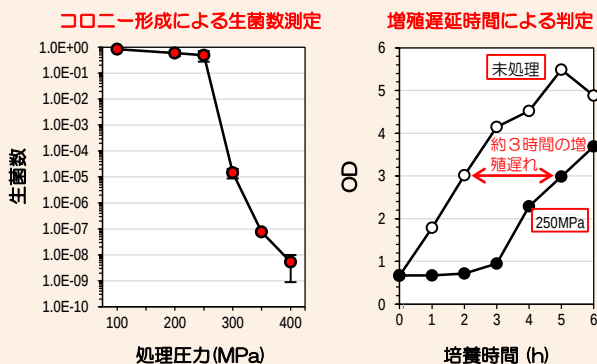
今後の展開

- 1) 様々な細菌の高圧損傷菌の特性の比較
- 2) 高圧損傷菌の回復メカニズムの解明

高圧処理後の生菌数の変動



枯草菌栄養細胞の圧力感受性



高圧損傷した枯草菌栄養細胞におけるトランスクリプトーム解析

Genes induced during recovery phase of HHP-injured cells

Gene	Operon	Gene product (function)	2h / 0h	4h / 0h	4h / 2h
ahpC	-	AhpC	(1.2.89)	(1.3.46)	(1.2.88)
ahpF	-	AhpF	(1.2.89)	(1.3.46)	(1.2.88)
ahpCF	-	AhpCF	(1.2.89)	(1.3.46)	(1.2.88)
bimBAA	bkd	Branched-chain alpha-keto acid dehydrogenase E1 subunit	(1.2.58)	(1.3.46)	(1.2.88)
clz	-	Citrate synthase II	(1.2.69)	(1.3.46)	(1.2.88)
csbD	-	General stress protein	(1.2.69)	(1.3.46)	(1.2.88)
gapB	gapB-speD	Glyceraldehyde-3-phosphate dehydrogenase	(1.2.47)	(1.3.46)	(1.2.88)
hsp	-	Heat shock protein	(1.2.47)	(1.3.46)	(1.2.88)
mntA	mntABCD	Manganese ABC transporter (membrane protein)	(1.2.89)	(1.3.46)	(1.2.88)
mntB	mntABCD	Manganese ABC transporter (ATP-binding protein)	(1.2.89)	(1.3.46)	(1.2.88)
pckA	-	Phosphoenolpyruvate carboxylase	(1.2.92)	(1.3.46)	(1.2.88)
rbaA	rbsRKDAB	Ribose ABC transporter (ATP-binding protein)	(1.3.16)	(1.3.46)	(1.2.88)
spoVG	-	Stage V sporulation protein G (spore cortex synthesis)	(1.3.32)	(1.3.46)	(1.2.88)
yitF	-	General stress protein	(1.3.16)	(1.3.46)	(1.2.88)
yagZ(mgsR)	-	Spx paralog controls a subregion within general stress response	(1.3.71)	(1.3.46)	(1.2.88)
vtxH	vtxGH2	General stress protein	(1.2.55)	(1.3.46)	(1.2.88)
vvyD	-	Dimerization of 70S ribosome	(1.4.45)	(1.3.46)	(1.2.88)
yweB	-	Unknown; putative cell wall binding protein	(1.3.27)	(1.3.46)	(1.2.88)
nsb	-	General stress protein	(1.2.72)	(1.3.46)	(1.2.88)
kzaA	-	Vegetative catalase 1	(1.4.06)	(1.3.46)	(1.2.88)
mntC	mntABCD	Manganese ABC transporter (membrane protein)	(1.3.40)	(1.3.46)	(1.2.88)
mntA	-	Metalloregulation DNA-binding stress protein; E. coli Dps homolog	(1.3.34)	(1.3.46)	(1.2.88)
srfAA	srfABCD	Surfactin synthetase	(1.2.45)	(1.2.60)	(1.2.60)
ybbB	-	Unknown	(1.4.72)	(1.3.16)	(1.3.16)
ybcA	-	General stress protein	(1.2.88)	(1.2.55)	(1.2.55)
ykzI	-	General stress protein	(1.3.94)	(1.3.76)	(1.3.76)
appC	appBC	Oligopeptide ABC transporter (permease)	(1.1.97)	(1.3.91)	(1.1.94)
phvA	rapA-phvA	Phosphatase RapA inhibitor	(1.1.84)	(1.3.76)	(1.1.92)
rapA	rapA-phvA	Response regulator aspartate phosphatase	(1.1.84)	(1.3.76)	(1.1.92)
ybcA	sktABCEFGH	Sporulation killing factor	(1.2.08)	(1.3.62)	(1.1.4)
yweF	-	Inducer of LrpS	(1.2.22)	(1.3.62)	(1.1.4)
mntD	mntABCD	Manganese ABC transporter	(1.2.65)	(1.3.88)	(1.3.18)
rhaX	rhaXC	Regulator of rhaC	(1.2.67)	(1.3.88)	(1.3.88)
srfAB	srfABCD	Surfactin synthetase	(1.2.59)	(1.3.88)	(1.3.88)
clpE	-	Clp ATPase	(1.3.30)	(1.4.07)	(1.3.45)
psfA	psfSCAB	Phosphate ABC transporter (permease)	(1.3.09)	(1.3.88)	(1.3.88)
mntD	-	Mannitol-1-phosphate 5-dehydrogenase	(1.3.40)	(1.3.88)	(1.3.88)
ahpC	-	AhpC	(1.2.89)	(1.3.88)	(1.3.88)
tuaG	tuaABCDEFGH	Biosynthesis of teichuronic acid; pho regulon	(1.2.39)	(1.3.88)	(1.3.88)

Genes repressed during recovery phase of HHP-injured cells

Gene	Operon	Gene product (function)	2h / 0h	4h / 0h	4h / 2h
ahpC	ahpCF	Alkyl hydroperoxide reductase (small subunit)	(1.3.94)	(1.3.94)	(1.3.94)
ahpF	ahpCF	Alkyl hydroperoxide reductase (large subunit)	(1.3.64)	(1.3.64)	(1.3.64)
bimBAA	bkd	Branched-chain alpha-keto acid dehydrogenase E1 subunit	(1.2.58)	(1.3.46)	(1.2.88)
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ybcA	-	General stress protein	(1.2.88)	(1.2.55)	(1.2.55)
ykzI	-	General stress protein	(1.3.94)	(1.3.76)	(1.3.76)
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srfAB	srfABCD	Surfactin synthetase	(1.2.59)	(1.3.88)	(1.3.88)
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tuaG	tuaABCDEFGH	Biosynthesis of teichuronic acid; pho regulon	(1.2.39)	(1.3.88)	(1.3.88)

The value in parentheses indicates the average value of log₂ Ratio between two independent microarray results.

Translation

Fur regulon

PerR regulon

MntR regulon

induced by iron limitation

induced by peroxide stress

induced by MntR limitation

参考文献

- 1) Kimura, K. et al. 2017. J. Biosci. Bioeng. 123. 698–706.
- 2) Inaoka, T. et al. 2017. Biosci. Biotechnol. Biochem. 81.1235–1240.