Copper Tolerance of Listeria monocytogenes strain DRDC8

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Presentation of Figures and Tables

All figures and tables referenced in this thesis are placed at the end of relevant chapters. This has been done to minimise the impact of large numbers of figures and tables on document flow and as an aid to interpretation of results and discussion sections of each chapter.

Table of Contents

Chapter 1: Introduction	1
1.1 Introduction	1
1.2 Characteristics of <i>L. monocytogenes</i>	2
1.3 Listeriosis	3
1.3.1 Listeriosis in Animals	4
1.3.2 Listeriosis in Humans	6
1.3.3 Transmission of Infection to Humans	8
1.4 Intracellular Invasion and Infection	9
1.4.1 Virulence Determinants	10
1.4.2 Environmental Control of Gene Expression	12
1.5 Ecology of L. monocytogenes	13
1.5.1 L. monocytogenes in the Farm Environment	15
1.5.2 L. monocytogenes in the Food-processing Environment	16
1.5.3 Association of <i>L. monocytogenes</i> with Protozoa	17
1.6 Mechanisms of Adaptation and Survival	19
1.7 Genomics of <i>Listeria</i> species	20
1.7.1 Genome Analysis	21
1.7.2 Plasmid Analysis	22
1.8 Cation Transport and Homeostasis	24
1.8.1 P-type ATPases	24
1.8.2 Copper Ion Homeostasis	25
1.9 Copper Transport in L. monocytogenes strain DRDC8	30
1.9.1 Significance of ctpA for Virulence of L. monocytogenes	32
1.9.2 Genes Accessory to <i>ctpA</i> mediated Copper Transport	34
1.9.3 Distribution of ctpA in L. monocytogenes isolates	36
1.9.4 ctpA is encoded on Plasmid DNA	36
1.10 Hypothesis and Aims	38
Chapter 2: Materials and Methods	59
2.1 Chemicals and Reagents	59
2.2 Bacterial strains and Plasmids	59

2.3 Bacterial Growth Media	59
2.4 Maintenance of Bacterial strains	60
2.5 Preparation of Tris-HCL Buffered Phenol	60
2.6 Centrifugation	61
2.7 DNA Extraction Procedures	61
2.7.1 Bacterial Plasmid DNA Isolation	61
2.7.2 Preparation of Bacterial Genomic DNA	64
2.7.3 Bacteriophage DNA extraction	65
2.8 DNA Analysis and Manipulation	65
2.8.1 DNA Quantification	65
2.8.2 Restriction Endonuclease Digestion of DNA	65
2.8.3 Agarose Gel Electrophoresis of DNA	66
2.8.4 Determination of DNA Fragment Size	66
2.8.5 Isolation of DNA Fragments from Agarose Gels	66
2.8.6 Precipitation of DNA	67
2.8.7 Dephosphorylation of DNA	67
2.8.8 Ligation Reactions	67
2.8.9 In vitro Cloning	68
2.9 Chemical Transformation of E. coli	68
2.9.1 Preparation of Competent Cells	68
2.9.2 Transformation Procedure	68
2.10 Electro-transformation of <i>Listeria monocytogenes</i>	69
2.10.1 Preparation of Electro-competent Cells	69
2.10.2 Electroporation Procedure	69
2.11 Bacterial Conjugation	69
2.12 Southern Hybridisation Analysis	70
2.12.1 Southern Transfer	70
2.12.2 DIG-11-UTP Labelling of DNA Probes	70
2.12.3 Hybridisation	70
2.12.4 Detection	71
2.13 Oligonucleotides	71
2.14 Polymerase Chain Reaction (PCR)	72

	2.14.1 Standard PCR Conditions	.72
	2.14.2 Amplification of Plasmid DNA using TempliPhi TM	.72
2	.15 Purification of PCR Products and other DNA fragments	.72
2	.16 Dye Terminator Sequence Analysis	.72
	2.16.1 PCR Products and Plasmid DNA	.72
	2.16.2 TempliPhi TM Amplified DRDC8 Plasmid DNA	.73
	2.16.3 Computer Analysis of Sequence Data	.73
2	.17 Listeria Antibodies	.74
	2.17.1 Immuno-fluorescence Microscopy of <i>L. monocytogenes</i> Cells	.74
	2.17.2 L. monocytogenes Serotype Analysis	.74
2	.18 Curing L. monocytogenes Plasmid DNA	.75
2	.19 MIC of Heavy Metal Cations	.75
	2.19.1 Statistical Analysis	.75
2	.20 Bacterial Growth Experiments	.75
2	.21 Cell Culture	.76
	2.21.1 Cell Lines	.76
	2.21.2 Growth Conditions and Culture Media	.76
	2.21.3 Preparation of Glass Coverslips	.76
	2.21.4 Tissue Culture Monolayer Invasion Assay	.76
2	.22 Isolation of Bacteriophage from L. monocytogenes DRDC8	.77
	2.22.1 Induction of Bacteriophage	.77
	2.22.2 Purification of Bacteriophage	.77
	2.22.3 Transfection of <i>L. monocytogenes</i> with Bacteriophage Preparations	.78
2	.23 Protein Overexpression	.78
2	.24 Preparation of whole Cell Lysates	.79
2	.25 SDS-PAGE	.79
2	.26 Purification of His-tagged Protein	.80
2	.27 Protein Mass Spectrometry Sequencing	.80
2	.28 Determination of Protein Concentration	.81
2	.29 Gel Shift Analysis	.82
	2.29.1 Labelling of DNA	.82
	2.29.2 Binding Reaction	.82

	2.29.3 Electrophoresis and Transfer	82
	2.29.4 Detection	83
C	Chapter 3: Analysis of Plasmid DNA of L. monocytogenes strain DRDC8	97
	3.1 Introduction	97
	3.2 Experimental design	98
	3.3 Results	99
	3.3.1 ctpA is encoded by Plasmid DNA	99
	3.3.2 ctpA is not encoded on Bacteriophage	100
	3.3.3 Plasmid pCT100 is Non-conjugative	101
	3.3.4 Identification of the Putative ORF <i>cutR</i>	103
	3.3.5 Partial Nucleotide Sequence Analysis of Plasmid pCT100	104
	3.3.6 Sequence Analysis and Annotation	106
	3.3.7 Significant Features of Plasmid pCT100	121
	3.4 Discussion	124
	3.4.1 L. monocytogenes strain DRDC8 carries ctpA on Plasmid DNA	124
	3.4.2 Features of Plasmid pCT100 from Sequence Analysis	125
	3.4.3 Distribution of the Copper Gene Cluster in isolates of L. monocytogenes	129
	3.5 Conclusions	130
C	Chapter 4: Mutagenesis of Genes implicated in Copper Ion Tolerance	170
	4.1 Introduction	170
	4.2 Experimental design	171
	4.3 Results	172
	4.3.1 Construction of <i>erm</i> Insertion Mutations	172
	4.3.2 Construction of <i>L. monocytogenes</i> Allelic Replacement Mutants	174
	4.3.3 Confirmation of Allelic Replacement Mutants	175
	4.3.4 Isolation of Plasmid-cured Variants of DRDC8	181
	4.3.5 Response of <i>L. monocytogenes</i> strains to Cation Stress	182
	4.4 Discussion	184
	4.5 Conclusions	192
C	Chapter 5: Purification and Functional Analysis of the pCT0017 Protein	223
	5.1 Introduction	223
	5.2 Experimental design	224

5.3 Results	225
5.3.1 Overexpression and Purification of pCT0017 Protein	225
5.3.2 Gel Shift Assay Analysis	227
5.4 Discussion	231
5.5 Conclusions	235
Chapter 6: General Discussion	256
6.1 Introduction	256
6.2 Plasmid-encoded Genes are Important for Environmental Survival of L .	
monocytogenes strain DRDC8	257
6.3 Chromosomal and Plasmid Genes are Involved in Copper Tolerance in	
L. monocytogenes strain DRDC8	261
6.4 Exposure of <i>L. monocytogenes</i> to Copper in the Environment	265
6.5 Future Directions	268
6.6 Conclusions	270
Chapter 7: References	273

List of Figures

Figure 1.1: The intracellular life cycle of L. monocytogenes in a host cell	48
Figure 1.2: Genetic organisation of the <i>L. monocytogenes</i> pathogenicity island	49
Figure 1.3: Model of the regulation of the <i>cop</i> operon in <i>E. hirae</i>	50
Figure 1.4: Schematic representation of the [Zn(II)CopY] ₂ - DNA interaction with	the E .
hirae cop operon promoter region	51
Figure 1.5: Growth of L. monocytogenes ctpA mutants in BHI broth containing 5µ	ıM of the
cation chelating agent, 8-hydroxyquinoline.	52
Figure 1.6: Growth of <i>ctpA</i> positive and <i>ctpA</i> negative <i>L. monocytogenes</i> isolates	in BHI
broth containing 10mM CuSO ₄	53
Figure 1.7: Course of infection by L. monocytogenes ctpA mutants in the liver of i	mice54
Figure 1.8: Genetic organisation of putative ORFs encoded by DRDC8 plasmid D	NA55
Figure 1.9: Comparison of the genetic arrangement of ORFs pCT0017, pCT0018,	
pCT0019 and ctpA of L. monocytogenes strain DRDC8 and genes that encode sim-	ilar
proteins in Lactobacillus salivarius subsp. UCC118 and Streptococcus pneumonia	e R656
Figure 1.10: Organisation of cop-like operons in different Gram-positive bacteria.	57
Figure 1.11: Typical PCR amplification of ctpA from L. monocytogenes isolates	58
Figure 3.1: Restriction enzyme digestion of plasmid pCT100	132
Figure 3.2: Gel electrophoresis and Southern hybridisation analysis of pCT100	133
Figure 3.3: PCR analysis of bacteriophage DNA extracts.	134
Figure 3.4: PCR amplification of <i>ctpA</i> from putative transconjugants DNA	135
Figure 3.5: Multiple amino acid sequence alignment.	136
Figure 3.6: Restriction digestion and Southern hybridisation analysis of pCT200.	137
Figure 3.7: Construction of plasmids pFB186 and pFB190.	139
Figure 3.8: Genetic map of 37.279 kbp of plasmid pCT100.	141
Figure 3.9: Nucleotide and deduced amino acid sequence of ORF pCT0001	143
Figure 3.10: Nucleotide and deduced amino acid sequence of ORF pCT0005	145
Figure 3.11: Nucleotide and deduced amino acid sequence of ORF pCT0006	147
Figure 3.12: Nucleotide and deduced amino acid sequence of ORF pCT0007	148
Figure 3.13: Nucleotide and deduced amino acid sequence of ORF pCT0015	149
Figure 3.14: Nucleotide and deduced amino acid sequence of ORF pCT0016	150

Figure 3.15: Nucleotide and deduced amino acid sequence of ORF pCT0024	.152
Figure 3.16: Nucleotide and deduced amino acid sequence of ORF pCT0025	.153
Figure 3.17: Nucleotide and deduced amino acid sequence of ORF pCT0026	.155
Figure 3.18: Nucleotide and deduced amino acid sequence of ORF pCT0027	.156
Figure 3.19: Nucleotide and deduced amino acid sequence of ORF pCT0028	.157
Figure 3.20: Nucleotide and deduced amino acid sequence of ORF pCT0029	.158
Figure 3.21: Nucleotide and deduced amino acid sequence of ORF pCT0030	.159
Figure 3.22: Nucleotide and deduced amino acid sequence of ORF pCT0031	.160
Figure 3.23: Nucleotide and deduced amino acid sequence of ORF pCT0032	.162
Figure 3.24: DNA regions conserved between plasmids pCT100, pLI100 and pLM80.	.163
Figure 3.25: PCR amplification of the ctpA gene from L. monocytogenes isolates	.165
Figure 3.26: PCR amplification of ORF pCT0025 from <i>L. monocytogenes</i> isolates	.166
Figure 3.27: Genetic map of the replication regions of plasmids pAD1 and pAW63 and	d the
putative replication region of plasmid pCT100.	.167
Figure 3.28: Nucleotide sequence of the pCT100 putative plasmid replication region	.168
Figure 4.1: PCR mutagenesis of ORFs pCT0017, pCT0018, pCT0019 and cutR	.194
Figure 4.2: Construction of <i>erm</i> insertion mutations.	.196
Figure 4.3: Restriction digestion of plasmids pCT750, pCT751, pCT752 and pCT755.	.198
Figure 4.4: Construction of plasmids pKS950, pKS951, pKS952 and pKS955	.199
Figure 4.5: PCR analysis of the putative pCT0017::erm mutant strain DSE950	.200
Figure 4.6: PCR analysis of strain DSE950.	.202
Figure 4.7: Southern hybridisation analysis of strain DSE950.	.204
Figure 4.8: PCR analysis of the putative mutant strains DSE951 and DSE952	.206
Figure 4.9: Southern hybridisation analysis of pCT0018::erm strain DSE951	.209
Figure 4.10: Southern hybridisation analysis of pCT0019::erm strain DSE952	.211
Figure 4.11: PCR analysis of the putative <i>cutR</i> :: <i>erm</i> mutant strain DSE955	.213
Figure 4.12: Southern hybridisation analysis of cutR::erm strain DSE955	.214
Figure 4.13: PCR analysis of plasmid-cured strains DSE201PL and DSE955PL	.216
Figure 4.14: MIC of CuSO ₄ for <i>L. monocytogenes</i> strains	.218
Figure 4.15: MIC of 8-hydroxyquinoline for <i>L. monocytogenes</i> strains	.219
Figure 4.16: MIC of CdSO ₄ for <i>L. monocytogenes</i> strains.	

Figure 5.1: Construction of pCTCF	236
Figure 5.2: Construction of the pCT0017 expression vector pETCF	237
Figure 5.3: SDS-PAGE of cell lysates of <i>E. coli</i> BL21 [pETCF]	239
Figure 5.4: SDS-PAGE of affinity purified His-tagged pCT0017* protein.	240
Figure 5.5: Titration of purified pCT0017* protein.	241
Figure 5.6: Interaction of pCT0017* protein with DRDC8 DNA.	242
Figure 5.7: Interaction of pCT0017* protein with DNA fragment P4	244
Figure 5.8: Interaction of pCT0017* protein with DNA fragments P14, P24 and P34	245
Figure 5.9: Comparison of <i>cop</i> boxes of strain DRDC8 and other bacteria	247
Figure 5.10: Construction of CopBox1 and CopBox2.	249
Figure 5.11: Interaction of pCT0017* protein with CopBox1 and CopBox2	250
Figure 5.12: Effect of CuSO ₄ and CdSO ₄ on pCT0017* protein binding to P4	251
Figure 5.13: Interaction of pCT0017* protein with CopBox1 and CopBox2 in the pres	ence
of CuSO ₄ .	253
Figure 5.14: Proposed model of copper-responsive gene regulation by pCT0017	255

List of Tables

Table 1.1:	Outbreaks of human food-borne listeriosis	40
Table 1.2:	Sequence data for <i>Listeria</i> species available in the GenBank database	41
Table 1.3:	Detection of plasmid DNA in isolates of Listeria monocytogenes	44
Table 1.4:	Summary of proteins encoded by Listeria plasmid genes.	45
Table 1.5:	ORFs flanking ctpA for L. monocytogenes strain DRDC8	46
Table 1.6:	Distribution of ctpA positive L. monocytogenes isolates identified by PCR	47
Table 2.1:	L. monocytogenes strains used in this study	84
Table 2.2:	E. coli strains used in this study	86
Table 2.3:	Plasmids used in this study	87
Table 2.4:	DNA markers used in this study	89
Table 2.5:	Protein markers used in this study	90
Table 2.6:	Oligonucleotides used for sequencing plasmid pCT100	91
Table 2.7:	Oligonucleotides used for L. monocytogenes mutant construction	93
Table 2.8:	Oligonucleotides used for protein overexpression and Gel shift analysis	95
Table 2.9:	Oligonucleotides used in this study to amplify gene fragments	96

Abstract

Listeria monocytogenes is one of the most important food-borne pathogens due to the severity of the disease it can cause. While the virulence factors required for effective colonisation and infection of mammalian hosts have been well described, other genes may modulate disease persistence. For L. monocytogenes strain DRDC8, the ctpA gene encodes a copper transporting P-type ATPase that apparently maintains intra-cellular copper ion homeostasis (Francis & Thomas, 1997a) and is also required for persistent infection of the liver and spleens of mice (Francis & Thomas, 1997b). However, the distribution of this gene is apparently limited to non-clinically derived environmental L. monocytogenes isolates (Bell, 2002). This may be explained by carriage of ctpA on plasmid DNA (Bell, 2002). Based on predictions of function and proximity to the ctpA gene (pCT0020), ORFs pCT0017, pCT0018, pCT0019 and ctpA were identified as a putative a cop-like operon involved in copper ion transport in L. monocytogenes (Bell, 2002).

Southern hybridisation analysis was used to confirm that the *ctpA* gene is carried on plasmid pCT100 in strain DRDC8. In addition, evidence to suggest that *ctpA* was encoded by bacteriophage DNA was not obtained. Furthermore, sequence analysis of DNA flanking *ctpA* identified ORFs that encode polypeptide sequences similar to proteins involved in plasmid replication and other plasmid-associated functions. Mating experiments provided evidence to show that plasmid pCT100 is not conjugative. This suggested that lateral transfer of this plasmid between cohabitating organisms may be limited.

Sequence analysis of a 37.279 kbp region of plasmid pCT100 from *L. monocytogenes* strain DRDC8 (GenBank Accession U15554) showed this plasmid had regions of gene content and organisation similar to that of other characterised *Listeria* plasmids, particularly plasmid pLI100 from *L. innocua* CLIP11262 and plasmid pLM80 from *L. monocytogenes* strain 4b H7858. Gene's common to these plasmids included those implicated in plasmid DNA replication, DNA transposition/insertion and heavy metal (cadmium) transport.

Sequence analysis of plasmid pCT100 also identified regions of DNA absent from other *Listeria* sequences. For example, a DNA region encoding a series of polypeptide

sequences similar to chromosomally-encoded proteins involved in copper transport in other Gram-positive bacteria was identified. The ORFs encoded by this region (pCT0017, pCT0018, pCT0019 and pCT0020 (*ctpA*), pCT0023, pCT0024, pCT0025, pCT0026, pCT0027) represent a novel cluster of genes implicated in copper homeostasis/tolerance that had not been previously described for other *Listeria* spp. PCR analysis was used to show that carriage of this copper gene cluster may be restricted to only some Australian *ctpA* positive *L. monocytogenes* isolates, typically of dairy and poultry origin.

In addition to these plasmid-encoded ORFs, PCR and sequence analysis identified a chromosomal ORF (*cutR*) also implicated in copper homeostasis/tolerance for strain DRDC8. *cutR* encodes a polypeptide similar to chromosomally-encoded copper-translocating P-type ATPases from other *Listeria* species.

The role of ORFs *cutR*, pCT0017, pCT0018 and pCT0019 in copper tolerance was assessed by comparison of the ability of wild type parent strain DRDC8 and variants containing independent mutations (pCT0017::*erm*, pCT0018::*erm*, pCT0019::*erm* or *cutR*::*erm*) to tolerate copper ion stress. The impact of loss of these genes (as a result of curing strain DRDC8 and *cutR*::*erm* derivatives of plasmid pCT100) on copper tolerance by DRDC8 was also examined. Minimal inhibitory concentration (MIC) and growth experiments showed that inactivation of *cutR*, pCT0018 or pCT0019, or removal of plasmid-encoded genes by curing DRDC8 of plasmid DNA, had a significant effect on copper tolerance. In addition, loss of plasmid DNA combined with disruption of *cutR* was shown to render cells completely incapable of growth in high levels of copper (14 mM CuSO₄). This data indicated that pCT0018, pCT0019 and *cutR* are involved in copper tolerance of *L. monocytogenes* strain DRDC8. MIC experiments also provided evidence to show that ORFs *cutR* and pCT0018 may play an additional role in tolerance to cadmium.

Interestingly, a *L. monocytogenes* mutant carrying an *erm* insertion within pCT0017 could not be constructed. However, evidence that showed that ORF pCT0017 encodes a CopY-like negative repressor protein directly implicated this ORF in copper tolerance. DNA gel shift experiments were used to show that pCT0017 protein binds to two '*cop* box-like' nucleotide sequences located upstream of the pCT0017 translation start site. Binding occurs in a copper-dependant manner that is consistent with published models of CopY-like protein function. Thus pCT0017 protein may regulate expression of

ORFs pCT0017, pCT0018, pCT0019 and *ctpA* in a copper responsive manner. This is consistent with the view that these ORFs form a *cop*-like operon involved in copper homeostasis.

In conclusion, *L. monocytogenes* strain DRDC8 displayed an exceptional tolerance to high concentrations of copper ions. The data obtained suggested that both chromosomal and plasmid-encoded genes are involved in copper homeostasis/tolerance of DRDC8. This particular strain may have acquired multiple genes involved in copper tolerance from a cohabitating Gram-positive bacterium in response to exposure to high levels of copper within the environment. Given that strain DRDC8 is an Australian dairy isolate, these genes may provide a selective advantage for survival of other *L. monocytogenes* strains in associated environments.

Declaration

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Francesca Y Bell

November, 2010

XV

Abbreviations

°C degrees Celsius

 $\begin{array}{ccc} \mu g & microgram/s \\ \mu L & microlitre/s \\ \mu M & micromolar \end{array}$

× g relative centrifugal force

aa amino acid/s

AP alkaline phoshatase

Amp ampicillin

ATP adenosine 5'-triphosphate

BHI Brain Heart Infusion

bp base pair

ca. circa = approximately

cf. confer = compare

CFU colony forming units

Cm chloramphenicol

Ctp copper transport protein

DIG digoxigenin

DIG-11-dUTP digoxigenin-11-uridine 5'triphosphate

DNA deoxyribonucleic acid

dNTP deoxyribonucleotide triphosphate

dsDNA double stranded deoxyribonucleic triphosphate

DTT dithiothreitol

EDTA ethylene-diamine-tetra-acetic-acid disodium salt

Em erythromycin

erm erythromycin resistance gene

EtBr ethidium bromide

g L⁻¹ grams per litre

h hour/s

HCL Hydrochloric acid

IPTG isopropyl-β-D-thio-galactopyranoside

IMVS The Institute of Medical and Veterinary Sciences

Kan kanamycin kbp kilobase/s kDA kilodalton/s

L litre/s

LA Luria agar

LB Luria Bertani broth

LIR left inverted repeat region of Tn917

LLO Listeriolysin O

M molar

mg milligram/s
min minute/s
mL millilitre/s
mM millimolar

mRNA messenger ribonucleic acid

NBT 4-Nitroblue tetrazolium chloride

ng nanogram(s)
nm nanometre(s)
nM nanomolar

OD optical density

O/N overnight

ONPG o-nitrophenyl-β-D-galactopyranoside

ORF open reading frame

PAGE polyacrylamide gel electrophoresis

PBS phosphate buffered saline

PCR Polymerase Chain Reaction

pM picomolar

rbs ribosome binding site

Rif rifampicin

RNA ribonucleic acid

RNase ribonuclease

RT room temperature

s second/s

SDS sodium dodecyl sulphate

SLCC Special *Listeria* Culture Collection

Sm streptomycin
Sp spectinomycin

spp. species

SSC standard saline citrate

TAE tris-acetate EDTA buffer

TE tris-EDTA buffer

UTP uridine 5'triphosphate

UV ultraviolet light

V volt/s/

vol volume/s

v/v volume per volume
w/v weight per volume
v/v volume/volume

X-gal 5-Bromo-4-chloro-3-indolyl-β-D-galactopyranoside

X-pho 5-Bromo-4-chloro-3-indolyl-phosphate

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