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**Analysis of a *Helicobacter pylori* operon
incorporating flagellar export genes**

A thesis presented in partial fulfilment
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Abstract

Motility of *Helicobacter* species has been shown to be essential for successful colonization of the host. Previous studies indicated that the regulation of flagellar biosynthesis in the human gastric pathogen *Helicobacter pylori* differs from the suggested model for Gram-negative Enterobacteriaceae.

In this study, the organization of two *H. pylori* genes involved in export of flagellar structural proteins was investigated. A 7 kb fragment of the *H. pylori* 17874 genome was cloned. Sequence determination and analysis revealed a putative operon comprising an ORF of unknown function (ORF03), and genes for the isoleucyl-tRNA synthetase (*ileS*), an *Agrobacterium tumefaciens* VirB11 homolog (*virB11*), an ATPase involved in flagellum-specific protein export (*fliI*), a presumptive flagellar export channel component (*fliQ*), and a homolog of an enzyme necessary for cell wall biosynthesis (*murB*). The genetic organization of this region was found to be conserved in a panel of clinical *H. pylori* isolates, and in *H. pylori* 915 and SS1. The locus was also identified in the genome sequences of the *H. pylori* strains J99 and 26695.

Cotranscription of ORF03, *ileS*, *virB11*, *fliI*, *fliQ* and *murB* was demonstrated by RT-PCR. Primer extension experiments identified the major transcription start site, which coincided with the A residue of the initiation codon of ORF03. A promoter element was inferred that resembled the *E. coli* σ^{70} consensus sequence. In addition, a minor transcription start site was detected upstream from *ileS*.

Non-polar mutation of *virB11*, *fliI* and *fliQ* was generated by an allele replacement strategy. Engineered *H. pylori* *fliI* and *fliQ* mutant strains were completely aflagellate and nonmotile, whereas a *virB11* mutant still produced flagella and displayed slightly greater motility. The *fliI* and *fliQ* mutant strains produced severely reduced levels of flagellin and the hook protein FlgE, although reduction was less stable in the *fliI* mutant. Production of OMP4, a member of the outer membrane protein family identified in *H. pylori* 26695, was diminished in both the *virB11* and the *fliI* mutant. This suggested related functions of the putative virulence factor transport protein (VirB11) and the flagellar export component (FliI).

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Related Publications

Some of the material presented in this thesis has been published.

Porwollik, S., Noonan, B. & O'Toole, P.W. (1999). Molecular characterization of a flagellar export locus of *Helicobacter pylori*. *Infect Immun* 67:2060-2070.

Porwollik, S. & O'Toole, P.W. (1998). Molecular characterization of a flagellar export locus of *Helicobacter pylori*. *Gut* 43 (Suppl 2): A02/31

Abbreviations

A+T content of deoxyadenylate and deoxythymidylate in DNA

aa amino acid

ab antibody

ABI Applied Biosystems

AMV avian myeloblastosis virus

Ap ampicillin

APS ammonium persulphate

ATP adenosine triphosphate

BBH basal body-hook complex

BCIP 5-bromo-4-chloro-3-indolyl phosphate

BLAST basic local alignment search tool

BSA bovine serum albumine

cAMP cyclic adenosine monophosphate

CAP catabolite gene activator protein

CBA columbia base agar

cDNA complementary DNA

Cm chloramphenicol

colE1 colicin E1

CRP cyclic adenosine monophosphate receptor protein

CSPD disodium 3-(4-methoxy-spiro{1,2-dioxetane-3,2'-(5'-chloro)tricyclo[3.3.1.1.1]decan}-4-yl)phenyl phosphate

CTP cytidine triphosphate

dATP 2' deoxyadenosine triphosphate

DEPC diethylpyrocarbonate

dGTP 2' deoxyguanosine triphosphate

DIG digoxigenin

DNA deoxyribonucleic acid

DNase deoxyribonuclease

dNTP deoxynucleoside triphosphate

dTTP 2' deoxythymidine triphosphate

dUTP 2' deoxyuridine triphosphate

EDTA ethylenediaminetetraacetic acid

EPB electroporation buffer

f1 bacteriophage f1

F_{ab} variable sequence fragment of immunoglobulin

FSB final sample buffer
FP forward primer
G+C content of deoxyguanylate and deoxycytidylate in DNA
GSP general secretory pathway
GTP guanosine triphosphate
IL interleukin
IPTG isopropyl- β -D-galactoside
Kan kanamycin
LB Luria-Bertani broth
LBA Luria-Bertani agar
LPS lipopolysaccharide
MALT mucosa-associated lymphoid tissue
mcl monoclonal
MCS multicloning site
MOPS 3-(N-morpholino) propanesulphonic acid
n/a not applicable
NBT 4-nitro blue tetrazolium chloride
NCBI National Center for Biotechnology Information
Neo neomycin
OD optical density
ORF open reading frame
ori origin of replication
PBS phosphate-buffered saline
pcl polyclonal
PCR polymerase chain reaction
PEG polyethylene glycol
pI isoelectric point
PIR protein information resource
r resistant
RNA ribonucleic acid
RNase ribonuclease
RP reverse primer
rpm revolutions per minute
RT room temperature
RT-PCR polymerase chain reaction involving an initial reverse transcriptase step
SDS sodium dodecyl sulphate
SM-TBS skim milk powder in Tris-buffered saline

SV40 simian virus 40
TB terrific broth
TBS Tris-buffered saline
TEMED NNN'N' tetramethylethylenediamine
TIGR The Institute for Genomic Research
T_m melting temperature
TNF tumor necrosis factor
Tris tris(hydroxymethyl)methylamine
TSB tryptic soy broth
U unit
UTP uridine triphosphate
Vol volume
w/v weight per volume
X-gal 5-bromo-4-chloro-3-indolyl- β -D-galactoside

In addition, the conventional one-letter codes for amino acids, deoxyribonucleosides and ribonucleosides were applied:

amino acids: G, A, V, L, I, P, F, Y, W, S, T, C, M, N, Q, D, E, K, R, H for glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, tyrosine, tryptophan, serine, threonine, cysteine, methionine, asparagine, glutamine, aspartate, glutamate, lysine, arginine and histidine, respectively

deoxyribonucleosides: A, C, G, T for deoxyadenylate, deoxycytidylate, deoxyguanylate and deoxythymidylate, respectively

ribonucleosides: A, C, G, U for adenylate, cytidylate, guanylate and uridylate, respectively

Table of Contents

ABSTRACT	ii
ACKNOWLEDGMENTS	iii
RELATED PUBLICATIONS	iv
ABBREVIATIONS	v
TABLE OF CONTENTS	viii
LIST OF FIGURES	xii
LIST OF TABLES	xiv
1. INTRODUCTION	1
1.1 A BACTERIUM THAT CAUSES GASTRIC DISEASE: <i>HELICOBACTER PYLORI</i>	1
1.1.1 History and general features	1
1.1.2 <i>H. pylori</i> pathogenesis	3
1.1.2.1 Pathogenic factors	3
1.1.2.2 Clinical outcomes and treatment.....	7
1.1.3 The <i>H. pylori</i> genome	10
1.2 PROTEIN SECRETION SYSTEMS IN BACTERIA.....	12
1.3 FLAGELLAR BIOSYNTHESIS	19
1.3.1 Structure and assembly of a flagellum in Gram-negative bacteria.....	19
1.3.1.1 Flagellum morphology.....	19
1.3.1.2 Assembly of the flagellum	21
1.3.1.3 Regulation of flagellar gene expression.....	23
1.3.2 The flagellar protein export apparatus	26
1.3.3 Unique aspects of <i>H. pylori</i> flagellum biology.....	28
1.4 AIMS OF THIS STUDY.....	31
2. MATERIALS AND METHODS	33
2.1 BACTERIAL STRAINS, CULTURE AND STORAGE CONDITIONS	33
2.2 MEDIA AND SUPPLEMENTS.....	34
2.3 OLIGONUCLEOTIDE PRIMERS	35
2.4 VECTORS AND RECOMBINANT PLASMIDS.....	36
2.5 ANTISERA.....	38
2.6 DNA ISOLATION	38
2.6.1 Plasmid preparation.....	38
2.6.1.1 Easy plasmid minipreparation.....	38
2.6.1.2 Wizard plasmid minipreparation	39

2.6.1.3 High Pure plasmid preparation	39
2.6.1.4 ABI plasmid preparation.....	39
2.6.2 Preparation of genomic DNA from <i>Helicobacter</i>	40
2.7 DNA ANALYSIS METHODS.....	41
2.7.1 DNA agarose gel electrophoresis.....	41
2.7.2 DNA restriction endonuclease treatment.....	41
2.7.3 DNA quantification	42
2.7.4 Southern blotting and hybridization.....	42
2.7.5 DNA sequencing.....	44
2.8 DNA AMPLIFICATION BY POLYMERASE CHAIN REACTION (PCR)	46
2.9 CLONING PROCEDURES	46
2.9.1 DNA preparation	47
2.9.2 Ligation.....	47
2.9.3 Transformation	48
2.9.3.1 Preparation of competent bacterial cells.....	48
2.9.3.2 Transformation of <i>E. coli</i>	49
2.9.3.3 Transformation of <i>H. pylori</i>	49
2.10 GENERAL PRECAUTIONS FOR RNA WORK	50
2.11 RNA ISOLATION FROM <i>H. PYLORI</i> CELLS	50
2.11.1 Total RNA isolation using TRIzol.....	50
2.11.2 RNA isolation using density gradient ultracentrifugation.....	51
2.12 RNA ANALYSIS METHODS	52
2.12.1 RNA agarose gel electrophoresis.....	52
2.12.2 RNA quantification.....	52
2.12.3 Northern blotting and hybridization	52
2.12.3.1 Northern analysis using DIG-labelled DNA probes	53
2.12.3.2 Northern analysis using ECL™-labelled DNA probes.....	53
2.12.3.3 Northern analysis using radiolabelled DNA probes.....	54
2.12.3.4 Northern analysis using DIG-labelled riboprobes.....	54
2.12.4 Transcript analysis by RT-PCR.....	55
2.12.5 Transcript analysis by primer extension	56
2.13 PROTEIN SAMPLE PREPARATION.....	57
2.13.1 Whole cell lysates.....	57
2.13.2 Cell fractionation.....	58
2.14 PROTEIN ANALYSES	58
2.14.1 Protein quantification.....	58

2.14.2 Protein electrophoresis.....	59
2.14.3 Western blotting and hybridization	60
2.15 MICROSCOPY.....	61
2.15.1 Phase contrast microscopy	61
2.15.2 Electron microscopy.....	62
3. RESULTS	63
3.1 CLONING OF THE <i>HELICOBACTER PYLORI FLII</i> GENE	63
3.1.1 The λ ZAP excisant pHP042.....	63
3.1.2 Subcloning of an <i>H. pylori</i> DNA segment comprising <i>fliI</i>	64
3.2 SEQUENCE ANALYSIS OF THE pSP102 INSERT.....	69
3.2.1 Sequencing strategies.....	69
3.2.2 Identification of the genetic elements on the pSP102 insert.....	71
3.2.3 Further sequence features of the pSP102 insert.....	80
3.3 CONSERVATION OF THE PUTATIVE OPERON IN <i>H. PYLORI</i>	81
3.4 TRANSCRIPT ANALYSES.....	86
3.4.1 Transcript detection attempts by Northern blotting.....	86
3.4.2 RT-PCR transcript analysis.....	90
3.4.3 Promoter mapping by primer extension.....	92
3.5 KNOCKOUT MUTAGENESIS OF THE GENES OF THE EXPORT LOCUS	95
3.5.1 Allele replacement strategy.....	95
3.5.2 Preparation of the mutagenic constructs.....	97
3.5.2.1 The <i>virB11</i> mutagenic constructs pSP117 and pSP118.....	97
3.5.2.2 The <i>fliI</i> knockout plasmids pSP108 and pSP110.....	99
3.5.2.3 The <i>fliQ</i> disrupting plasmids pSP107 and pSP109.....	100
3.5.3 Generation of <i>H. pylori virB11</i> , <i>fliI</i> and <i>fliQ</i> mutants.....	100
3.6 NON-POLARITY OF THE MUTATIONS	102
3.7 PHENOTYPIC CHARACTERIZATION OF THE <i>H. PYLORI</i> MUTANTS	105
3.7.1 Growth characteristics.....	106
3.7.2 Motility	106
3.7.3 Flagellum production	107
3.7.4 Expression of structural flagellar components.....	107
3.7.4.1 Flagellin and FlgE expression patterns in subcellular fractions of <i>H. pylori</i>	107
3.7.4.2 Stability of the effects of the mutageneses on flagellar protein production.....	109
3.7.5 Production of <i>H. pylori</i> virulence factors.....	111
3.7.6 Expression of outer membrane proteins.....	114

4. DISCUSSION.....	116
4.1 MAJOR FINDINGS	116
4.2 CONTRIBUTION OF THIS STUDY TO THE FIELD	116
4.3 DISCUSSION OF THE EXPERIMENTAL DATA.....	120
4.3.1 The genetic organization of the investigated operon	120
4.3.2 Conservation of the operon in <i>H. pylori</i>	124
4.3.3 Transcriptional regulation of the operon.....	126
4.3.4 Successful mutagenesis of <i>H. pylori</i> 17874 <i>virB11</i> , <i>fliI</i> and <i>fliQ</i>	128
4.3.5 Phenotypic consequences of the <i>virB11</i> , <i>fliI</i> and <i>fliQ</i> knockout	130
4.4 FUTURE STUDIES.....	133
APPENDIX 1 Physical maps of the pHP and pSP series of plasmids.....	137
APPENDIX 2 The complete sequence of the pSP102 insert	149
REFERENCES	162

List of Figures

Figure 1.1. Electron micrograph of a mucosal biopsy with active chronic gastritis. ...	2
Figure 1.2. Schematic diagram of currently classified bacterial protein secretion systems.....	13
Figure 1.3. Model of the <i>Agrobacterium</i> T-complex transport apparatus.	18
Figure 1.4. Structure of the flagellum of a Gram-negative bacterium like <i>S. typhimurium</i> and <i>E. coli</i>	20
Figure 3.1. An internal segment of the <i>H. pylori</i> 17874 <i>fliI</i> gene has joined the rest of the pHP042 insert by scrambled cloning.....	65
Figure 3.2. Cloning of the <i>H. pylori</i> 17874 <i>fliI</i> gene.....	67
Figure 3.3. The <i>fliI</i> probe hybridized near the insert end of pSP101.	68
Figure 3.4. The 0.7 kb <i>Hind</i> III fragment of the pSP102 insert is contiguous with the pSP101 insert in the <i>H. pylori</i> 17874 genome.	70
Figure 3.5. Sequence determination of the pSP102 insert.	72
Figure 3.6. Comparison of the pSP102 insert with the corresponding regions from the <i>H. pylori</i> J99 and 26695 genomes.....	73
Figure 3.7. Similarity of <i>H. pylori</i> 17874 VirB11 to presumptive ATP binding nucleoprotein transport components.	76
Figure 3.8. Conserved sequence motifs in <i>H. pylori</i> 17874 FliI.....	78
Figure 3.9. Similarity in hydropathicity plots of <i>H. pylori</i> 17874 FliQ and components of type III protein export systems.	79
Figure 3.10. The genetic linkage of the components of the putative operon is conserved in <i>H. pylori</i>	82
Figure 3.11. The flanking regions of the putative operon are not strictly conserved in <i>H. pylori</i>	84

Figure 3.12. The components of the putative <i>H. pylori</i> operon are not conserved in <i>H. mustelae</i>	85
Figure 3.13. Transcript detection by Northern analysis using gene specific probes.....	89
Figure 3.14. ORF03, <i>ileS</i> , <i>virB11</i> , <i>fliI</i> , <i>fliQ</i> and <i>murB</i> are cotranscribed.....	91
Figure 3.15. Generation of defined cDNA fragments by primer extension.....	93
Figure 3.16. Transcription start sites and inferred promoters of the operon.	94
Figure 3.17. Schematic representation of the strategy for deletion-insertional knockout of <i>H. pylori</i> genes (allele replacement strategy).....	96
Figure 3.18. Schematic representation of the relevant genomic DNA regions in the <i>H. pylori</i> wild type and knockout mutants.....	98
Figure 3.19. PCR verification of <i>H. pylori</i> knockout mutants.....	103
Figure 3.20. The deletion-insertion mutations are non-polar.....	104
Figure 3.21. Electron micrographs of negatively stained preparations of <i>H. pylori</i> cells.	108
Figure 3.22. Altered flagellin and FlgE production levels in <i>H. pylori</i> <i>virB11</i> , <i>fliI</i> and <i>fliQ</i> mutants.	110
Figure 3.23. Influence of passage on flagellin and FlgE production levels in the <i>H. pylori</i> mutants.....	112
Figure 3.24. Expression of UreB, CagA and VacA is not altered in the <i>H. pylori</i> <i>virB11</i> , <i>fliI</i> and <i>fliQ</i> mutants compared to the 17874 wild type.	113
Figure 3.25. Influence of the knockout mutations on expression of two outer membrane proteins (HopB and OMP4) in <i>H. pylori</i>	115
Figure 4.1. Major results of the investigations presented in this thesis.....	117

List of Tables

Table 1.1. General features of protein secretion systems in Gram-negative bacteria. . .	14
Table 1.2. Presumed homologs in type III secretion systems and the flagellar protein export apparatus.....	28
Table 2.1. Bacterial strains.	33
Table 2.2. Media.....	34
Table 2.3. Media supplements and antibiotics.....	34
Table 2.4. Oligonucleotide primers.....	35
Table 2.5. Plasmids used in this study.....	37
Table 2.6. Antibodies.	38
Table 3.1. Restriction analysis of the two plasmid variants identified by the <i>fliI</i> probe.....	66
Table 3.2. Genetic elements present in the pSP102 insert.	74
Table 3.3. Summary of transcript detection attempts by Northern analysis.	88
Table 3.4. Mutagenesis of <i>H. pylori</i> by electroporation or natural transformation. . .	101
Table 3.5. Calculated PCR product sizes from <i>H. pylori</i> wild type and mutant genomic DNA.	102