# Characterisation of

# Shigella flexneri polysaccharide co-

polymerase (PCP) protein Wzz

Analysis of structure, function and protein interaction



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Submitted for the Degree of Doctor of Philosophy

Discipline of Microbiology and Immunology

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The University of Adelaide

August 2010

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### **ABSTRACT**

In *Shigella flexneri*, Wzz<sub>SF</sub> determines the lipopolysaccharides (LPS) O antigen (Oag) modal chain length of 11-17 repeat units (RUs). Wzz<sub>SF</sub> has two transmembrane regions, the N-terminal TM1 and the C-terminal TM2, and previous studies have shown that the TM2 region is important in Wzz function. The mechanism of Oag modal chain length regulation has not been revealed. Previous studies have probed the structure-function relationship of Wzz<sub>SF</sub> and have suggested that function is a result of the overall structure and not one particular region. Genetic evidence suggests that Wzz may form a complex with other Oag processing proteins, possibly with the Wzy polymerase.

This thesis describes in-frame linker mutagenesis of Wzz<sub>SF</sub>, and five classes of Wzz insertion (Wzz<sub>i</sub>) mutants with 5 amino acid insertions were identified: Class I (non-functional), Class II (conferred very short (VS) Oag chain length, 2-10 RUs), Class III (8-14 RUs), Class IV (11-19 RUs), and Class V (16-25 RUs). The susceptibility of strains expressing Wzz<sub>i</sub> mutants to colicin E 2 w as i nvestigated, and a correlation be tween r andom/VS LPS O ag modal chain length, and susceptibility to colicin E 2 was found. Chemical cross-linking analyses were conducted to assess Wzz oligomerisation and showed that high molecular weight proteins were easily detected in wild-type Wzz<sub>SF</sub> and mutants from Classes V, but not easily detected in Classes II and III, and only Wzz<sub>SF</sub>, Wzz<sub>i</sub> Class IV and Class V dimers were detected after heating to 100°C and in the presence of SDS, suggesting wild-type/longer LPS O ag modal chain length may be dependent on dimer stability.

The i nvolvement of the TM2 region in Wzz:Wzz i nteractions w as a lso investigated. *S. typhimurium* Wzz (Wzz<sub>ST</sub>) confers an LPS Oag modal chain length of Long-type (L-type) 19-30 RUs, and Wzz<sub>ST</sub> and Wzz<sub>SF</sub> have identical residues in the conserved residues of their TM2 regions. Wzz<sub>ST</sub> expression in Wzz de ficient *S. flexneri* strain confers an L-type LPS O ag

modal chain length, ho wever co-expression of Wzz<sub>ST</sub> with Wzz<sub>SF</sub> resulted in mono-modal LPS Oag m odal chain length. A pr eviously constructed W zz m utant w hich ha d t wo G305A/G311A substitutions in the TM2 region confers a VS LPS Oag modal chain length (3-8 RUs), however co-expression of Wzz<sub>G305A/G311A</sub> with wild-type Wzz<sub>SF</sub> resulted in LPS with a bimodal Oag chain length distribution (both wild-type 11-17 RUs, and VS-type 3-8 RUs). Strains expressing His<sub>6</sub>-Wzz<sub>SF</sub> and FLAG-tagged version of Wzz<sub>ST</sub>, Wzz<sub>SF</sub> and Wzz<sub>G305A/G311A</sub> were us ed in co-purification a ssays. Purified His<sub>6</sub>-Wzz<sub>SF</sub> and had FLAG-Wzz<sub>ST</sub> was in the eluted fraction, demonstrating that FLAG-Wzz<sub>ST</sub> interacted with His<sub>6</sub>-Wzz<sub>SF</sub>. H owever when His<sub>6</sub>-Wzz<sub>SF</sub> was pur ified from a s train co-expressing FLAG-Wzz<sub>G305A/G311A</sub>, very low amounts of the latter were detected in the elution fraction, indicating that H is<sub>6</sub>-Wzz<sub>SF</sub> interacted ve ry poorly with FLAG-Wzz<sub>G305A/G311A</sub>. These da ta i mplicate residues G305 and G311 in Wzz:Wzz interactions.

A fusion of the red fluorescent protein m Cherry to W zz<sub>SF</sub> was performed and showed the localisation of this protein was in the periphery regions of the cell, as determined by epifluorescence microscopy. Wzy was tagged with StrepTag-II at its amino terminal end; the resulting StrepII-Wzy protein was able to complement a wzy mutation, however the smooth LPS produced lacked any Oag modal chain length control. Two GFP<sup>+</sup>-tagged W zy fusion proteins were constructed, pGFP<sup>+</sup>-StrepII-Wzy, (with the *strepII* linker region between *gfp*<sup>+</sup> and wzy), and pGFP<sup>+</sup>-Wzy (*strepII* excised). GFP<sup>+</sup>-StrepII-Wzy had near wild-type Wzy functionality, and the complemented wzy mutant exhibited the wild-type trait of resistance to the lethal action of colicin E 2, but GFP<sup>+</sup>-StrepII-Wzy could not be detected by epifluorescence microscopy, and was poorly detectable by Western immunoblotting. GFP<sup>+</sup>-Wzy was partially functional and the complemented wzy mutant was susceptible to colicin E2, like the StrepII-Wzy complemented wzy mutant. GFP<sup>+</sup>-Wzy could be detected by both Western immunoblotting and e pi-fluorescence microscopy. These results implicate the N-terminal region of Wzy in Oag modal chain length determination.

#### **DECLARATION**

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

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Magdalene Papadopoulos

#### **ACKNOWLEDGEMENTS**

Firstly, I'd like to thank my supervisor, Associate Professor Renato Morona. Thank you for giving me the opportunity to learn from you, to grow and develop - and not just as a scientist. I am so grateful for your patience and understanding, and you will always have my sincerest affection, respect and admiration. Also, I would like to thank Luisa Van Den Bosch for helping me with techniques in the lab and for always cheering me up with that infectious smile of hers.

To other members of the lab including Gerald Murray, Leanne Purins, Alistair Standish, Kerrie G rabowicz, Marcin G rabowicz and T ony Focareta, thank you for the a dvice and expertise you provided, I sincerely appreciate it. To all past Honours students, you made the lab a joy to be a part of, and I thank you for that. I would also like to thank Chris Wong, Jamie Botten and the general staff, particularly Ros Hammond, Genny Drexel, Shirley Coad, Sergei Volgin, Shelley Pezy, Garry Penney and John Mackrill. Getting to know you has been a highlight of my time here. I would especially like to thank Martin Lennon for being one of the best friends I have encountered, and for introducing me to the very awesome hobby of running. We'll make it to another City to Bay, I'm sure. Special thanks also go to Min Teh, Damien Chong, Mabel Lum, Kim LeMessurier, Jai Denton, Sophia Tan, Campbell Strong, James 'Jiminion' Byrne, Georget Reaiche, Thomas Tu and particularly Elizabeth Tran, who has been more like a sister rather than a fellow student. I cannot express how valuable your friendship is to me. I will never forget any of you, and my apologies for the Saddle Club moment, but I think the bonds made by our experiences at MLS will keep us friends forever. Thanks a lso to the P aton lab for being excellent neighbours and fantastic company during morning tea. Thanks to Uwe Stroeher in particular, for being the go-to-guy. I think I'll put you on speed dial once I'm gone, just to be sure I can still ask questions from afar!

Very i mportantly, I would like to thank D amon T umes. Thank you for your love, your support, and for being there when I needed you the most.

And finally, I would like to thank my a mazing family. I am grateful to you for all your support and unwavering faith in me, not just as a student, but as a person. I love you all very much and could not have done this without you – of that, I am sure.  $\Sigma$  as  $\alpha \gamma \alpha \pi \dot{\omega}$ .

## **PUBLICATIONS**

Tocilj, A., Munger, C., Proteau, A., Morona, R., Purins, L., Ajamian, E., Wagner, J., **Papadopoulos, M.**, Van Den Bosch, L., Rubinstein, J.L., Fethiere, J., Matte, A. and Cygler, M. (2008) Bacterial polysaccharide co-polymerases share a common framework for control of polymer length. *Nat Struct Mol Biol* **15**, 130-138.

**Papadopoulos, M**. and Morona, R. (2010) Mutagenesis and chemical cross-linking suggest that Wzz dimer stability and oligomerization affect lipopolysaccharide O-antigen modal chain length control. *J Bacteriol* **192**, 3385-3393.

#### LIST OF ABBREVIATIONS

~ approximately

°C degree

% percentage

# number

 $\alpha$  alpha

 $\beta$  beta

γ gamma

 $\lambda$  lambda

μg; μl; μm microgram (s); microliter (s); micrometre (s)

aa amino acid

3D 3-dimensional

Å Amstrong

ACP acyl carrier protein

ABM actin based motility

Amp ampicillin

Arp actin-related protein

ATP adenosine triphosphate

bp base pairs

C-terminal carboxyl-terminal

Cat. number catalogue number

Cml chloramphenicol

CPS capsular polysaccharides

DDM D-dodecyl β-D maltoside

DMF dimethylformamide

DNA deoxyribonucleic acid

dNTP deoxynucleoside triphosphate

ECA enterobacterial common antigen

EDTA ethylene diamine tetra-acetic acid

EPS exopolysaccharides

FAE follicular associated epithelium

FITC fluorescein isothiocyanate

FP fluorescent protein

GlcNAc N-acetylglucosamine

h; min; sec hour (s); minutes (s); seconds (s)

Hep L-glycero-D-manno-heptose

HEPES 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid

His<sub>6</sub> 6x histidine

IM inner membrane

Ipa invasion plasmid antigens

Ipg invasion plasmid gene

IPTG isopropyl-β-D-thiogalactopyranoside

IS insertion sequences

I-type intermediate type

Kan kanamycin

kb kilobase pairs

kDa kilodaltons

Kdo 3-deoxy-D-*manno*-oct-2-ulosonic acid

L litres

Lab laboratory

LB Luria-bertani

LPS lipopolysaccharides

Lpt lipopolysaccharides transport

L-type long type

Lys lysine

M; mM molar; millimolar (s)

mA milli-amps

mAb monoclonal antibody

M-cells Membraneous epithelial cells

mg; ml milligram (s); millilitre (s)

MOPS 3-(N-Morpholino)-propanesulfonic acid

MQ MilliQ water

*mxi-spa* membrane expression of Ipas-surface presentation of antigens

N-terminal amino terminal

N-WASP neural Wiskott-Aldrich syndrome protein

NEB New England Biolabs

Ni-NTA nickel-charged agarose

nm nanometre

nt nucleotide

Oag O antigen

OD600 optical density of 600 nm

OM outer membrane

Omp outer membrane protease

OSP outer surface protein

PBS phosphate buffered saline

PCP polysaccharide co-polymerase

PCR polymerase chain reaction

PFO perfluoro-octanoic acid

PMN polymorphonuclear cells

R resistance

Rha rhamnose

Rif rifampicin

R-LPS rough LPS

rpm revolutions per minute

RT room temperature

RU(s) repeat unit(s)

SAP shrimp alkaline phosphatase

SDS sodium dodecyl sulphate

SDS-PAGE SDS polyacrylamide gel electrophoresis

S-LPS smooth LPS

S-type short type

SR-LPS semi rough LPS

Sm streptomycin

SU-LPS semi unregulated LPS

TBS tris buffered saline

Tet tetracycline

Tp trimethoprim

TM transmembrane

Tris tris (hydroxymethyl) aminomethane

TTBS tween tris buffered saline

TTSS Type III secretion system

U units

UV ultraviolet

v/v volume per volume

V volts

VL-type very long type xi

VS-type very short type

w/v weight per volume

WM whole membrane

Wzz<sub>SF</sub> Shigella flexneri Wzz

Wzz<sub>ST</sub> Salmonella typhimurium Wzz

X-Gal 5'-bromo-4-chloro-3-indolyl- $\beta$ -D-galactopyranoside