Formalist features determining the tempo and mode of evolution in *Pseudomonas fluorescens* SBW25

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Abstract

In order to explain the adaptive process, it is necessary to understand the generation of heritable phenotypic variation. For much of the history of evolutionary biology, the production of phenotypic variation was believed to be unbiased, and adaptation the primary outcome of selection acting on randomly generated variation (mutation). While true, 'internal' features of organisms may also play a role by increasing the rate of mutation at specific loci, or rendering certain genes better able to translate mutation into phenotypic variation. This thesis, using a bacterial model system, demonstrates how these internal features – localised mutation rates and genetic architectures – can influence the production of phenotypic variation.

Previous work involving the bacterium *Pseudomonas fluorescens* SBW25 has shown that mutations at three loci, *wsp, aws* and *mws*, can cause the adaptive wrinkly spreader (WS) phenotype. For each locus, the causal mutations are primarily in negative regulators of di-guanylate cyclase (DGC) activity, which readily convert mutation into the WS phenotype. Mutations causing WS at other loci were predicted to arise, but to do so with less frequent types of mutation. The data presented in this thesis confirms this prediction. My work began with the identification and characterisation of a single rare WS-causing mutation: an in-frame deletion that generates a translational fusion of genes *fadA* and *fwsR*. The fusion couples a DGC (encoded by *fwsR*) to a membrane-spanning domain (encoded by *fadA*) causing relocalisation of the DGC to the cell membrane and the WS phenotype. This is one of the few examples of adaptation caused by gene fusion and protein relocation in a real-time evolution experiment. I next took an experimental evolution approach to isolate further rare WS types and characterized these, revealing a range of rarely taken mutational pathways to WS. Lastly, I describe an example of extreme molecular parallelism, in which a cell chaining phenotype is caused – without exception – by a single nucleotide substitution within the gene *nlpD*, despite multiple mutational pathways to this phenotype. Characterisation of different *nlpD* mutants suggests this molecular parallelism is caused by a high local mutation rate, possibly related to the initiation of transcription within this gene.

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Table of Contents

Table of Abbreviations

Abbreviation	Meaning
ACP	Acetylated cellulosic polymer
ALI	Air-liquid interface
BLAST	Basic local alignment search tool
bp	Base pair
c-di-GMP	bis-(3′-5′)-cyclic dimeric guanosine monophosphate
CCF	Cross correlation function
CFU	Colony forming units
DGC	Di-guanylate cyclase
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic Acid
dNTP	Dinucleotide triphosphate
EE	Experimental evolution
FAD	Fatty acid desaturase
FS	Fuzzy Spreader
g	Gravity or gram
GFP	Green fluorescent protein
Gm	Gentamicin
h	Hour
HT	Homopolymeric tract
IWS	Independent wrinkly spreader
ISWS	Independent slow wrinkly spreader
Km	Kanamycin
kb	kilobase
KB	King’s B medium
LB	Lysogeny broth
LSWS	Large spreading wrinkly spreader
M-W-W	Mann-Whitney-Wilcoxon
MCs	Microcosms
min	Minute
4MU	7-hydroxy-4-methylcoumarin
4MUG	4-methylumbelliferyl-b-d-galactoside
NF	Nitrofurantoin
ORF	Open reading frame
OD	Optical density
PCR	Polymerase chain reaction
PDE	Phosphodiesterase
RBS	Ribosome binding site
REE	Reverse evolution experiment
RNA	Ribonucleic acid
rpm	Revolutions per minute
RT-qPCR	Reverse transcription quantitative real-time PCR

Abbreviation	Meaning
SE	Standard error
SM	Smooth morphotype
SOC	Super optimal broth with catabolic repressor
SREE	Slow reverse evolution experiment
SWS	Slow wrinkly spreader
TAM	Transcription associated mutation
Tc	Tetracycline
TFB	Transformation buffer
TIAM	Transcription initiation associated mutation
TMD	Transmembrane domain
WGS	Whole genome sequencing
WS	Wrinkly spreader
WSS	Wrinkly spreader structural locus
WT	Wild type
X-gal	5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside