

Characterization of a trimethoprim/sulfamethoxazole-resistant *Stenotrophomonas maltophilia* clinical isolate from Bulgaria

S. Peykov^{1,2,3}, B. Kirov^{2,3,4,5}, M. Stancheva^{1,2}, T. Strateva⁶, D. Miteva¹

SCIENTIFIC CONFERENCE KLIMENT'S DAYS
(KD 2020)

5 November, 2020



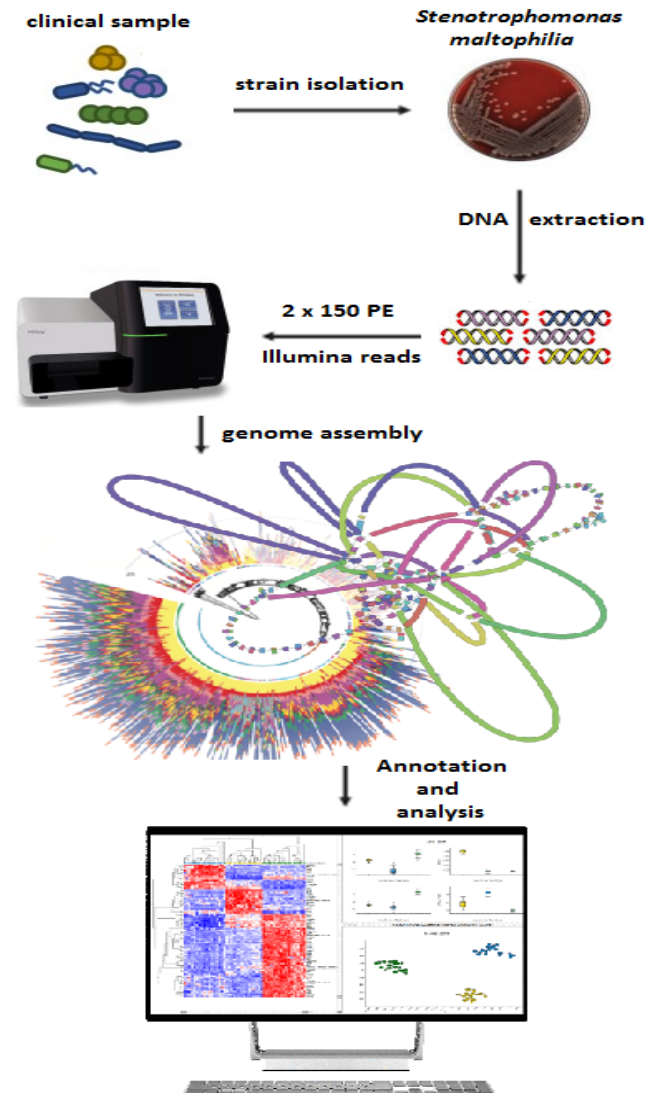
FACULTY OF BIOLOGY
SOFIA UNIVERSITY

1-University of Sofia “St. Kliment Ohridski”; 2- iGEM Bulgaria; 3- BioInfoTech Laboratory; 4- Sofia Tech Park; 5- Technical University of Sofia; 6- Medical University of Sofia

Abstract

Stenotrophomonas maltophilia is globally recognized as an emerging multidrug-resistant (MDR) pathogen in healthcare facilities, especially in the intensive care units (ICUs) where it predominantly causes respiratory tract infections, and less commonly urinary tract infections, wound and soft tissue infections, bacteraemia, sepsis, endocarditis, and meningitis. Here, we report the isolation of a trimethoprim/sulfamethoxazole (SXT)-resistant isolate, which was later identified to be class 1 integron-carrying strain. SXT has been recognized as the first-line agent for symptomatic *S. maltophilia* infections, therefore SXT resistance is a serious therapeutic challenge for clinicians.

Methodology



Results

Genome assembly quality metrics

Statistics without reference ≡ Shovill_on_data_65_and_data_6...

# contigs	87
# contigs (>= 0 bp)	93
# contigs (>= 1000 bp)	71
Largest contig	473 041
Total length	4 394 833
Total length (>= 0 bp)	4 396 839
Total length (>= 1000 bp)	4 383 926
N50	141 858
N75	72 925
L50	8
L75	19
GC (%)	66.76

Mismatches

# N's	0
# N's per 100 kbp	0

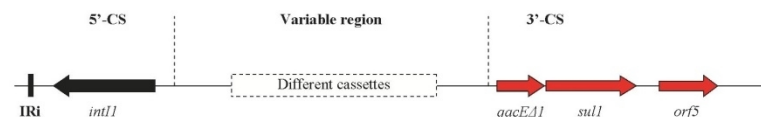
Multilocus sequence typing (MLST)

Locus	Identity	Coverage	Alignment Length	Allele Length	Gaps	Allele
atpD	100	100	531	531	0	atpD_116
gapA	100	100	558	558	0	gapA_165
guaA	100	100	552	552	0	guaA_124
mutM	100	100	465	465	0	mutM_176
nuoD	100	100	444	444	0	nuoD_4
ppsA	100	100	495	495	0	ppsA_163
recA	99.82	100	546	546	0	recA_137*

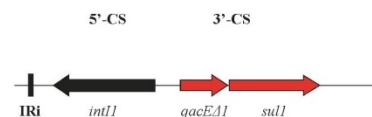
Class 1 integron



(a) Typical class 1 integron



(b) *S. maltophilia* SM148 class 1 integron



Funding

Работата е извършена в рамките на одобрено предложение за участие в конкурса по национална научна програма „МЛАДИ УЧЕНИ И ПОСТДОКТОРАНТИ“ (2019 г.) № КП-06-M21/10 със заглавие: “Разработка на нови методи и средства за изследване на ефективността на CRISPR-базирани базови редактори “