

Accepted Manuscript

Whole genome sequencing (WGS) options for bacterial strain typing and epidemiological analysis based on single nucleotide polymorphism (SNP) vs gene-by-gene-based approaches

A.C. Schürch, S. Arredondo-Alonso, R.J.L. Willems, R.V. Goering

PII: S1198-743X(17)30710-3

DOI: [10.1016/j.cmi.2017.12.016](https://doi.org/10.1016/j.cmi.2017.12.016)

Reference: CMI 1158

To appear in: *Clinical Microbiology and Infection*

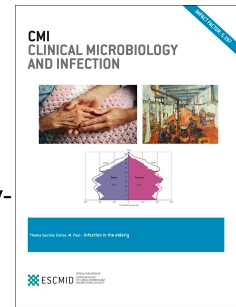
Received Date: 6 July 2017

Revised Date: 21 November 2017

Accepted Date: 22 December 2017

Please cite this article as: Schürch AC, Arredondo-Alonso S, Willems R JL, Goering RV, Whole genome sequencing (WGS) options for bacterial strain typing and epidemiological analysis based on single nucleotide polymorphism (SNP) vs gene-by-gene-based approaches, *Clinical Microbiology and Infection* (2018), doi: 10.1016/j.cmi.2017.12.016.

This is a PDF file of an unedited manuscript that has been accepted for publication. As a service to our customers we are providing this early version of the manuscript. The manuscript will undergo copyediting, typesetting, and review of the resulting proof before it is published in its final form. Please note that during the production process errors may be discovered which could affect the content, and all legal disclaimers that apply to the journal pertain.



1 For AA publication CLM-17-12189 - revised

2

3 Mini-review for Clinical Microbiology and Infection

4 **Whole genome sequencing (WGS) options for bacterial strain typing and epidemiological**
5 **analysis based on single nucleotide polymorphism (SNP) vs gene-by-gene-based approaches**

6

7 Authors:

8 A.C. Schürch¹, S. Arredondo-Alonso¹, R.J.L. Willems¹, R.V. Goering²

9

10 Affiliation: ¹ Department of Medical Microbiology, University Medical Center, Utrecht, ²

11 Creighton University School of Medicine, Omaha, NE

12

13

14

15 Corresponding author: RV Goering: RICHARDGOERING@creighton.edu

16

17 **Running title:** approach and analysis options for WGS-based bacterial strain typing

18

19 **Key words:** whole genome sequencing, SNP, cgMLST, core genome, accessory genome, pan-
20 genome, relatedness threshold

21

22

23 **Transparency Declaration:** The authors report no conflicts of interest relevant to this article.

Download English Version:

<https://daneshyari.com/en/article/8744841>

Download Persian Version:

<https://daneshyari.com/article/8744841>

[Daneshyari.com](https://daneshyari.com)