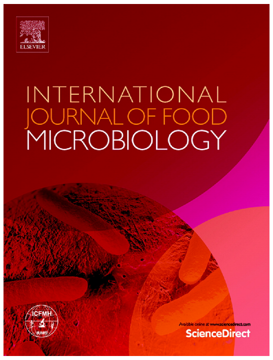
Accepted Manuscript



Comparative analysis of core genome MLST and SNP typing within a European Salmonella serovar Enteritidis outbreak

Madison E. Pearce, Nabil-Fareed Alikhan, Timothy J. Dallman, Zhemin Zhou, Kathie Grant, Martin C.J. Maiden

PII: S0168-1605(18)30074-6
DOI: doi:10.1016/j.ijfoodmicro.2018.02.023
Reference: FOOD 7830

To appear in: *International Journal of Food Microbiology*

Received date: 27 October 2017
Revised date: 23 February 2018
Accepted date: 27 February 2018

Please cite this article as: Madison E. Pearce, Nabil-Fareed Alikhan, Timothy J. Dallman, Zhemin Zhou, Kathie Grant, Martin C.J. Maiden , Comparative analysis of core genome MLST and SNP typing within a European Salmonella serovar Enteritidis outbreak. The address for the corresponding author was captured as affiliation for all authors. Please check if appropriate. Food(2017), doi:10.1016/j.ijfoodmicro.2018.02.023

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.

ACCEPTED MANUSCRIPT

Comparative analysis of core genome MLST and SNP typing within a European *Salmonella* serovar Enteritidis Outbreak

Authors: Madison E. Pearce[a,b*], Nabil-Fareed Alikhan[c], Timothy J. Dallman[d] Zhemin Zhou[c], Kathie Grant[d], Martin C. J. Maiden[a,b,]

*Corresponding Author: Madison.pearce@zoo.ox.ac.uk

Affiliations:

[a] Department of Zoology, University of Oxford, Peter Medawar Building for Pathogen Research, South Parks Road, Oxford, United Kingdom, OX1 3SY. Madison.Pearce@zoo.ox.ac.uk; Martin.Maiden@zoo.ox.ac.uk

[b] National Institute for Health Research, Health Protection Research Unit, Gastrointestinal Infections, University of Oxford

[c] Warwick Medical School, University of Warwick, Coventry, United Kingdom, CV4 7AL N-F.Alikhan@warwick.ac.uk; Zhemin.Zhou@warwick.ac.uk;

[d] Public Health England, Gastrointestinal Bacteria Reference Unit, 61 Colindale Avenue, London, United Kingdom, NW9 5EQ tim.dallman@phe.gov.uk; Kathie.Grant@phe.gov.uk

ACCEPTED MANUSCRIPT

Abstract

Multi-country outbreaks of foodborne bacterial disease present challenges in their detection, tracking, and notification. As food is increasingly distributed across borders, such outbreaks are becoming more common. This increases the need for high-resolution, accessible, and replicable isolate typing schemes. Here we evaluate a core genome multilocus typing (cgMLST) scheme for the high-resolution reproducible typing of *Salmonella enterica (S. enterica)* isolates, by its application to a large European outbreak of *S. enterica* serovar Enteritidis. This outbreak had been extensively characterised using single nucleotide

Download English Version:

https://daneshyari.com/en/article/8844207

Download Persian Version:

https://daneshyari.com/article/8844207

Daneshyari.com