Whole genome sequencing for foodborne disease surveillance Landscape paper



# Whole genome sequencing for foodborne disease surveillance Landscape paper



Whole genome sequencing for foodborne disease surveillance: landscape paper

ISBN 978-92-4-151386-9

#### © World Health Organization 2018

Some rights reserved. This work is available under the Creative Commons Attribution-NonCommercial-ShareAlike3.0 IGO licence (CC BY-NC-SA 3.0 IGO; https://creativecommons.org/licenses/by-nc-sa/3.0/igo).

Under the terms of this licence, you may copy, redistribute and adapt the work for non-commercial purposes, provided the work is appropriately cited, as indicated below. In any use of this work, there should be no suggestion that WHO endorses any specific organization, products or services. The use of the WHO logo is not permitted. If you adapt the work, then you must license your work under the same or equivalent Creative Commons licence. If you create a translation of this work, you should add the following disclaimer along with the suggested citation: "This translation was not created by the World Health Organization (WHO). WHO is not responsible for the content or accuracy of this translation. The original English edition shall be the binding and authentic edition".

Any mediation relating to disputes arising under the licence shall be conducted in accordance with the mediation rules of the World Intellectual Property Organization.

**Suggested citation.** Whole genome sequencing for foodborne disease surveillance: landscape paper. Geneva: World Health Organization; 2018. Licence: CC BY-NC-SA 3.0 IGO.

Cataloguing-in-Publication (CIP) data. CIP data are available at http://apps.who.int/iris.

**Sales, rights and licensing.** To purchase WHO publications, see http://apps.who.int/bookorders. To submit requests for commercial use and queries on rights and licensing, see http://www.who.int/about/licensing.

**Third-party materials.** If you wish to reuse material from this work that is attributed to a third party, such as tables, figures or images, it is your responsibility to determine whether permission is needed for that reuse and to obtain permission from the copyright holder. The risk of claims resulting from infringement of any third-party-owned component in the work rests solely with the user.

**General disclaimers**. The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

The mention of specific companies or of certain manufacturers' products does not imply that they are endorsed or recommended by WHO in preference to others of a similar nature that are not mentioned. Errors and omissions excepted, the names of proprietary products are distinguished by initial capital letters.

All reasonable precautions have been taken by WHO to verify the information contained in this publication. However, the published material is being distributed without warranty of any kind, either expressed or implied. The responsibility for the interpretation and use of the material lies with the reader. In no event shall WHO be liable for damages arising from its use.

Printed in Switzerland

# Contents

Acronyms and abbreviations	v
Acknowledgements	vi
Introduction	viii
1. Whole genome sequencing: the future of FBD surveillance and outbreak response	1
1.1 Public health surveillance	1
1.1.1 Subtyping of pathogens for surveillance and outbreak investigation	1
1.1.2 Comparison of WGS with traditional methods for real-time surveillance	2
1.1.3 WGS detects outbreaks taking place under the surveillance radar	2
1.2 Additional information from phylogenetic analysis	3
1.2.1 Outbreak investigation and source-finding	3
1.2.2 Source attribution	3
1.3 Predicting emerging threats	4
1.4 Monitoring antimicrobial resistance in foodborne pathogens	4
1.5 References	5
2. WGS as a tool to strengthen integrated surveillance	7
2.1 Overview of integrated foodborne disease surveillance	7
2.2 High accuracy matching of pathogens across the animal, food, environmental and human	1
sectors	7
2.3 Coordinating the use of WGS across public health, food safety and regulatory agencies	9
2.3.1 Organizational and cultural aspects	9
2.3.2 Technical and scientific aspects	10
2.4 References	12
3. Implementing WGS as a tool for public health in low- and middle- income countrie the main challenges	es: 13
3.1 Infrastructure	13
3.2 Costs	14
3.2.1 Overall cost	14
3.2.2 Consumables	14
3.2.3 Personnel	15
3.3 Bioinformatics	15

iii

3.4 Data sharing	16
3.4.1 Harmonization	16
3.4.2 Data ownership	17
3.4.3 Metadata and ontology	18
3.4.4 Data analysis	18
3.4.5 Trade implications	19
3.5 References	20
4. The current state of WGS technology and the supporting bioinformatic tools	21
4.1 WGS instrumentation and capacity	21
4.1.1 Short-read platforms	21
4.1.2 Long-read platforms	23
4.1.3 Summary	24
4.2. Bioinformatics of WGS data	25
4.2.1 Quality assurance, quality control and read preprocessing	26
4.2.2 Species identification	27
4.2.3 In silico typing and phenotype prediction	27
4.2.4 Whole genome molecular typing, allele calling and phylogenetic inference	28
4.2.5 Examples of bioinformatic tools	30
4.3 References	32
5. Use of WGS information by health professionals and risk managers: the need for	
cultural change	35
5.1 The role of microbiologists, bioinformaticians and epidemiologists	35
5.1.1 Molecular microbiologist	35
5.1.2 Bioinformatician	36
5.1.3 Epidemiologist	36
5.2 Integration of WGS, epidemiological, and clinical data	37
5.3 Standardization of data and information and controlled vocabulary	38
5.4 New paradigms of practice arising from developments in pathogen genomics	39
5.5 References	42

iv

# Acronyms and abbreviations

AMR	antimicrobial resistance
API	application program interface
CFSAN	Center for Food Safety and Applied Nutrition (USA)
CGE	Center for Genomic Epidemiology, Denmark Technical University (Denmark)
CLI	command line interface
EUCAST	European Committee on Antimicrobial Susceptibility Testing
FAO	Food and Agriculture Organization of the United Nations
FBD	foodborne disease
FDA	Food and Drug Administration (USA)
Gb	gigabase
GO	gene ontology
GUI	graphical user interface
HUS	haemolytic uraemic syndrome
IHR (2005)	International Health Regulations (2005)
INSDC	International Nucleotide Sequence Database Collaboration
IRIDA	Integrated Rapid Infectious Disease Analysis
IT	information technology
kb	kilobase
LIMS	laboratory information management system
MLST	multilocus sequence typing
MLVA	multilocus variable-number tandem-repeat analysis
NCBI	National Center for Biotechnology Information (USA)
NGS	next generation sequencing
OIE	World Organisation for Animal Health
ONT	Oxford Nanopore Technologies
PacBio	Pacific Biosciences
PFGE	pulsed-field gel electrophoresis
QA	quality assurance
QC	quality control
SBL	sequencing-by-ligation
SBS	sequencing-by-synthesis
SENASICA	Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria
SMRT	single-molecule real-time sequencing
SNP	single nucleotide polymorphism
SNVPhyl	single nucleotide variant phylogenomics
SRA	sequence read archive
STEC	Shiga-toxin-producing Escherichia coli
Stx	Shiga toxin
WGS	whole genome sequencing
WHO	World Health Organization

# Acknowledgements

The World Health Organization (WHO) expresses sincere thanks to all the authors and other reviewers of this paper.

### Contributing authors

David Aanensen, Imperial College London, London, England; Clara Amid, European Bioinformatics Institute European Molecular Biology Laboratory, Cambridge, England; Stephen Baker, Oxford University Clinical Research Unit, Ho Chi Minh, Viet Nam; Claudio Bandi, Università degli Studi di Milano, Milan, Italy; Eric W. Brown, United States Food and Drug Administration (FDA), Silver Spring, MD, United States of America (USA); Josefina Campos, Instituto Nacional de Enfermedades Infecciosas, Buenos Aires, Argentina; Guy Cochrane, European Bioinformatics Institute European Molecular Biology Laboratory, Cambridge, England; Francesco Comandatore, Università degli Studi di Milano, Milan, Italy; Tim Dallman, Public Health England, London, England; Xiangyu Deng, University of Georgia, Griffin, GA, USA; Gordon Dougan, Department of Medicine, University of Cambridge, Cambridge, England; Rita Finley, Public Health Agency of Canada, Guelph, Canada; Alejandra García Molina, SENASICA, Mexico City, Mexico; Peter Gerner-Smidt, Centers for Disease Control and Prevention, Atlanta, GA, USA; Sara Goodwin, Cold Spring Harbor, NY, USA; Tine Hald, Technical University of Denmark, Copenhagen, Denmark; Zhaila Isaura Santana Hernández, Servicio Nacional de Sanidad, Inocuidad y Calidad Agroalimentaria (SENASICA), Mexico City, Mexico; Kirsty Hope, New South Wales Ministry of Health, Canberra, Australia; William Hsiao, British Columbia Centre for Disease Control Public Health Laboratory, Vancouver, Canada; Claire Jenkins, Public Health England, London, England; Katherine Littler, Wellcome Trust, London, England; Ole Lund, Technical University of Denmark, Copenhagen, Denmark; Megge Miller, South Australian Department for Health and Ageing, Adelaide, Australia; Alejandra García Molina, SENASICA, Mexico City, Mexico; Jacob Moran-Gilad, Ben Gurion University of the Negev, Beer-Sheva and Israeli Ministry of Health, Jerusalem, Israel; Nicola Mulder, Institute of Infectious Disease and Molecular Medicine, University of Cape Town, Cape Town, South Africa; Celine Nadon, Public Health Agency of Canada, Ottawa, Canada; Eric Ng'eno, Kenya Medical Research Institute, Nairobi, Kenya; Collins Owuor, Kenya Medical Research Institute and Wellcome Trust Research Institute,

### 预览已结束, 完整报告链接和二维码如下:

https://www.yunbaogao.cn/report/index/report?reportId=5 25903

