Hypervariable-Locus Melting Typing (HLMT): a novel, fast and inexpensive sequencing-free approach to pathogen typing based on High Resolution Melting (HRM) analysis

Matteo Perini 1; Aurora Piazza 2; Simona Panelli 1; Stella Papaleo 1; Alessandro Alvaro 1; Francesca Vailati 3; Marta Corbella 4; Francesca Saluzzo 5; Floriana Gona 6; Daniele Castelli 7, Claudio Farina 3; Piero Marone 4; Daniela Maria Cirillo 5; Annalisa Cavallero 7; Gian Vincenzo Zuccotti 1,8; Francesco Comandatore* 1.

1. Department of Biomedical and Clinical Sciences “L. Sacco”, Pediatric Clinical Research Center “Romeo and Enrica Invernizzi”, Università Di Milano, 20157 - Milan (Italy).
2. Department of Clinical, Surgical, Diagnostic and Pediatric Sciences, University of Pavia, 27100 - Pavia (Italy).
3. Microbiology Institute, A.S.S.T. “Papa Giovanni XXIII”, 24127 - Bergamo (Italy).
4. Microbiology and Virology Unit, Fondazione IRCCS Policlinico San Matteo, 27100 - Pavia (Italy).
5. Emerging Bacterial Pathogens Unit, Division of Immunology, Transplantation and Infectious Diseases, IRCCS San Raffaele Scientific Institute, 20132 - Milan (Italy).
6. Laboratory Microbiology and Virology -Ospedale San Raffaele Dibit, 2-San Gabriele 1, 20132 - Milan (Italy).
7. Laboratory of Microbiology, ASST Monza, San Gerardo Hospital, 20900 - Monza (Italy).
8. Department of Pediatrics, Children’s Hospital Vittore Buzzi, Università Di Milano, 20154 - Milan (Italy).

*corresponding author
francesco.comandatore@unimi.it
Via Giovanni Battista Grassi, 74, 20157 Milano
tel. +39 0250319826

Abstract

Objectives

Subspecies pathogen typing is a pivotal tool to detect the emergence of high-risk clones in hospital settings and to limit their spreading among patients. Unfortunately, the most used subspecies typing methods (i.e. Pulsed-field Gel Electrophoresis - PFGE, Multi-Locus Sequence Typing - MLST and Whole Genome Sequencing - WGS) are too expensive and time consuming to be suitable for real-time surveillance. Here we present Hypervariable-Locus Melting Typing (HLMT), a novel subspecies typing approach based on High Resolution Melting (HRM) analysis, which allows pathogen typing in a few hours and with ~5 euros per sample.

Methods

HLMT types the strains by clustering them using melting temperatures (HLMT-clustering) and/or by assigning them to Melting Types (MTs) on the basis of a reference dataset (HLMT-assignment). We applied HLMT (clustering and typing) to 134 *Klebsiella pneumoniae* strains collected during outbreaks or surveillance programs in four hospitals. Then, we compared HLMT typing results to PFGE, MLST and WGS.

Results

HLMT-clustering distinguished most of the *K. pneumoniae* high-risk clones with a sensitivity comparable to PFGE and MLST. It also drawed surveillance epidemiological curves comparable to those obtained by MLST, PFGE and WGS typing. Furthermore, the results obtained by HLMT-assignment were coherent to MLST for 96% of the typed strains with a Jaccard index of 0.912.

Conclusions

HLMT is a fast and scalable method for pathogen typing, suitable for real-time hospital microbiological surveillance. HLMT is also inexpensive and thus it is applicable to infection control programs in low-middle income countries.

Keywords:

Microbiological surveillance,

High Resolution Melting,

Outbreak reconstruction,

Low-middle income countries,

Real-time surveillance

Introduction

Healthcare-associated infections (HAIs) are a major burden for global public health [1]. The microbiological surveillance programs are pivotal to establish effective infection control strategies. In particular, subspecies typing is fundamental to detect the emergence of high-risk clones. The most used methods for subspecies bacterial typing are Pulsed Field Gel Electrophoresis (PFGE), Multi-Locus Sequence Typing (MLST) and Whole Genome Sequencing (WGS). All these methods require several hours (up to days) to be performed and this limits their application in nosocomial real-time surveillance programs.

High Resolution Melting (HRM) assay has been proposed as a suitable method for fast bacterial typing [2,3]. This technique measures the melting temperatures of qPCR amplicons, which depends on the GC content. HRM can even distinguish amplicons diverging for just one Single Nucleotide Polymorphism (SNP) and it is widely used to detect human allele variants [4]. HRM protocols designed on hypervariable genes are able to discriminate among bacterial clones within the same species [2,3], because their amplicons will melt at different temperatures (e.g. they differ in GC content). HRM is particularly promising for microbiological surveillance: it is fast (~5 hours to complete the analysis), discriminatory, inexpensive (~5 euros per sample) and it can be performed on the most common qPCR platforms [5].

Despite the numerous HRM protocols proposed so far for bacterial typing [2], the method is rarely applied in hospital settings for microbiological surveillance. Indeed, most protocols have been designed to distinguish only among the few clones used for protocol development, including only a fraction of the entire genetic variability of the

pathogen. Moreover, only a few algorithms and software are available to analyse HRM data for epidemiological purposes.

Recently, we developed a novel approach for HRM-based subspecies typing. We focused on hypervariable genes and implemented a tool (i.e. EasyPrimer) to facilitate HRM primers designing in this difficult context [3]. Additionally, we developed an algorithm to obtain robust, repeatable and portable pathogen typing using HRM data [5,6]. In this study we provide a comprehensive description of this novel approach that we named Hypervariable-Locus Melting Typing (HLMT). We applied HLMT in four nosocomial epidemiological investigations on *Klebsiella pneumoniae*, comparing its typing efficiency to PFGE, MLST and WGS.

Methods

Ethics Statement

This study uses bacterial isolates from human samples that were obtained as part of hospital routines. No extra human samples were obtained for this research. Therefore, informed consent (either written or verbal) was not required.

Isolates datasets

Four Italian hospitals were included in the study: “San Gerardo” Hospital in Monza (from here HSG), “IRCCS Fondazione Policlinico San Matteo” Hospital in Pavia (PSM), “ASST Papa Giovanni XXIII” Hospital in Bergamo (PG23) and “IRCCS San Raffaele” Hospital in Milan (OSR). The hospitals provided a total of 134 *Klebsiella pneumoniae* strains: i) HSG provided 10 strains isolated during an outbreak that involved 10 patients

in the oncohematology ward between 14/08/2018 and 24/09/2018 (HSG dataset); ii) PSM provided 24 strains isolated during an outbreak already investigated with Whole Genome Sequencing (WGS) and described by Ferrari and colleagues [7] (PSM dataset) (the original dataset consisted of 32 strains, but only 24 were successfully revitalized in this work); iii) PG23 hospital provided 20 strains isolated during an outbreak that involved 16 patients and nine hospital wards, between 07/05/2019 and 04/11/2019 (PG23 dataset); iv) OSR hospital provided all the 80 strains isolated during a one-year-long WGS surveillance in 2017 and already typed with WGS and PFGE by Gona and colleagues [8] (OSR dataset).

DNA extraction

For each of the 134 strains, the bacterial culture was subjected to two consecutive single colony selections on MacConkey agar, incubated overnight at 37 °C (Becton Dickinson, Franklin Lakes, NJ, USA). A single bacterial colony was then suspended in liquid medium, incubated overnight and the DNA was extracted using the DNeasy blood and tissue kit, following the manufacturer's instructions (Qiagen, Hilden, Germany).

Whole Genome Sequencing

The 104 *K. pneumoniae* strains isolated from PSM (n=24) and OSR (n=80) have been already subjected to WGS in previous studies [7,8]. The remaining 30 isolates (HSG and PG23 datasets) were subjected to WGS on the Illumina MiSeq platform, (Illumina, San Diego, CA, USA), after Nextera XT 2×250 bp paired-end library preparation. The

reads were quality-checked using FastQC and trimmed using Trimmomatic software [9]. SPAdes [10] was then used to assembly the pair-end reads.

WGS-based typing

The 15,699 public genome assemblies of *K. pneumoniae* present in the PATRIC database on 08/02/2021 for which the publication code was available (in accordance with Fort Lauderdale and Toronto agreements) were retrieved. Each of the four datasets was separately subjected to core SNPs calling as follows: i) each genome was compared to the retrieved PATRIC dataset using Mash [11] and the 50 most similar strains were included in the background dataset; ii) these selected PATRIC genomes were merged to the dataset genomes; iii) core SNP calling was performed on the merged genome dataset using Purple tool [8]. For each of the four datasets, the obtained core SNPs alignment was subjected to Maximum Likelihood (ML) phylogenetic analysis with 100 bootstraps using the software RAxML8 [12], after best model selection using ModelTest-NG [13] (GTR+G for HSG and PG23; TVM+G for PSM and OSR). For each of the four dataset, clusters were then identified, on the resulting trees, as the largest monophyla of dataset strains (not from PATRIC) with a bootstrap support >= 75.

Multi-Locus Sequence Typing and *wzi* alleles

K. pneumoniae clones are often defined combining the MLST profile and the *wzi* gene allele [14]. Multi-Locus Sequence Typing (MLST) profiles and the *wzi* alleles of the 134 genome assemblies were determined using Kleborate [15].

Pulsed Field Gel Electrophoresis Clustering

Pulsed Field Gel Electrophoresis (PFGE) clusters were described by Gona and

colleagues [8] on the 80 strains of the OSR dataset following digestion with XbaI enzyme and separation into a CHEF-DRIII electrophoretic system (BioRad, Hercules, California).

Hypervariable-Locus Melting Typing

HLMT includes two different typing strategies: HLMT-clustering and HLMT-assignment. HLMT-clustering groups the strains on the basis of melting temperatures without a reference dataset. HLMT-assignment classifies each strain into a Melting Type (MT) by comparing the strains melting temperatures to a reference dataset. The reference dataset used in this work was reconstructed using the 43 *K. pneumoniae* strains previously typed by HRM by Pasala and colleagues [5]: HLMT-clustering grouped the strains in seven clusters that we used to define seven Melting Types (MTs). For each MT, the reference melting temperatures were computed as the mid-range melting temperatures (the arithmetic mean of the highest and the lowest temperature) of the strains in that cluster. The MTs were then labelled using the name of the most relevant lineages of the strains that they contain. The reference dataset is available at https://skynet.unimi.it/wp-content/uploads/MeltingPlot/TemplateHLMT_ref_KPN_03-15-2021.xls. All the *K. pneumoniae* strains included in this work were subjected to High Resolution Melting (HRM) assays using the protocol described in Perini et al., 2020 [3]. For each of the four datasets, the obtained melting temperatures and the above-mentioned reference dataset were used to perform HLMT-clustering and HLMT-assignment analyses with MeltingPlot v2.0 tool [6] (available online at https://skynet.unimi.it/index.php/tools/MeltingPlot/).

Comparison of the typing results

HLMT results were compared to PFGE, MLST+*wzi* and WGS by means of heatmaps and correlation plots, produced using the R libraries gplots [16] and corrplot [17], respectively. Furthermore, the HLMT-assignment results were compared to MLST+*wzi* by Jaccard similarity index, computed using the R package clustelval. For each dataset, HLMT-clustering, MLST+*wzi* and WGS typing results were combined to the collection dates of the strains to obtain the epidemiological curves showing the prevalence of the clusters and groups over time [6]. Additionally, PFGE typing results were retrieved from Gona et al. 2020 [8] and used to obtain the relative epidemiological curves.

Data availability

Genome assemblies of the 30 strains sequenced in this work are available from the NCBI BioProject repository under project PRJEB44864 (ERP128959).

Results

Whole Genome Sequencing

The assembly statistics and the accession numbers of the 30 sequenced *K. pneumoniae* strains (10 of the HSG dataset and 20 of PG23 dataset) are reported in the Supplementary Table S1.

Typing methods results

Strains from the four datasets (HSG, PSM, PG23 and OSR) were typed by HLMT (clustering and assignment), MLST+*wzi* and WGS. Furthermore, the PFGE typing results of the 80 OSR dataset strains were retrieved from Gona and colleagues 2020

[8]. The results of HLMT, MLST+*wzi*, WGS and PFGE typing are reported in the Supplementary Table S1 and the core SNP-based phylogenetic trees used for WGS typing are shown in the Supplementary Figure S1.

Comparison of the typing methods

For each dataset, the HLMT-clustering results were compared to MLST+*wzi* and WGS: the graphical representation of the relative contingency tables are reported in Supplementary Figure S2 and Supplementary Figure S3, respectively. HLMT-clustering results were compared to PFGE for OSR dataset only (see Supplementary Figure S4).

The HLMT-assignment algorithm classifies the strains into Melting Types. This analysis was able to classify 120 out of the 134 strains (~90%) included in this study. Seven of these 120 strains (~6%) belonged to MLST+*wzi* profiles not included in the HLMT reference strains dataset used for the analyses (see Methods). This made it impossible to assess, for these seven strains, if the HLMT-assignment and MLST+*wzi* results were coherent. For 108 out of the remaining 113 strains (96%) the HLMT-assignment and MLST+*wzi* were coherent, with a Jaccard similarity index of 0.912. The HLMT-assignment results are reported in the Supplementary Table S1 and the correlation matrix plot of the HLMT-assignment vs MLST+*wzi* is shown in Figure 1.

For each dataset, the epidemiological curves obtained combining typing information (HLMT-clustering, MLST+*wzi*, WGS and PFGE) and isolation dates of the strains are shown in Figure 2.

Discussion

Hypervariable-Locus Melting Typing (HLMT) is an innovative approach to High Resolution Melting (HRM)-based typing: it makes it easier to design highly discriminatory HRM protocols and to perform reliable, robust, repeatable and portable HRM-based typing analyses. In this work we show the application of HLMT to the typing of *Klebsiella pneumoniae* in four real hospital scenarios, comparing the results with those obtained by more established approaches, as Whole Genome Sequencing (WGS), Multi-Locus Sequence Typing (MLST) and Pulsed-Field Gel Electrophoresis (PFGE). As summarised in Figure 3, the workflow of HLMT consists of three main parts: i) HLMT protocol design on hypervariable genes; ii) HRM experiments; iii) HRM data analysis for HLMT-clustering and HLMT-assignment.

HRM primer design

HRM is less sensitive than sequencing to discriminate among DNA sequences thus, to obtain a stronger signal, the HRM protocol should include more than one primer pair and it should be designed on hypervariable genes. Primer design on hypervariable genes is challenging because it requires the analysis of up to thousands of different gene alleles to identify conserved regions suitable for primer design. We already developed the EasyPrimer tool to automatically identify these gene regions [3].

HRM experiments

HLMT analysis can be performed using HRM data obtained from any HRM-capable qPCR platform. As shown by Pasala et al. [5] HLMT-clustering is highly repeatable when the experiments are performed on the same model of instrument.

HLMT-Clustering and HLMT-assignment

HLMT analysis includes two different strain typing methods: HLMT-clustering and HLMT-assignment. HLMT-clustering groups the strains on the basis of their melting temperatures using a graph-based clustering algorithm [6]. Strains with similar melting temperatures for all the primers included in the HLMT protocol are grouped together. This clustering approach recalls the PFGE clustering, where a hierarchical clustering algorithm groups the strains on the basis of their restriction patterns.

On the other hand, in HLMT-assignment each strain is assigned to a Melting Type (MT) by comparing each strain to a reference dataset. The dataset consists of melting temperatures of previously typed strains selected to represent the genetic variability of the pathogen (see methods).

The strength of HLMT-clustering over HLMT-assignment is that the clustering works even on strains belonging to lineages absent in the HLMT strains dataset. On the other hand, the HLMT-assignment results are portable and they can be shared among laboratories and/or they can be compared to previous HLMT experiments.

The use of multiple primer pairs makes HLMT-clustering and HLMT-assignment more powerful but it also makes the analyses trickier. To tackle this issue, we have already

developed MeltingPlot v2.0 tool [6] that automatically performs HLMT-clustering and HLMT-assignment analyses using HRM data.

HLMT protocol for K. pneumoniae

We already designed an HLMT protocol for *K. pneumoniae* typing [3]. In this work, we show the applicability of the method for hospital surveillance. More in detail, we followed the three steps of the workflow described in Figure 3: i) HRM protocol design has been already carried out by Perini et al. 2020 [3], selecting the hypervariable capsular gene *wzi* as target and designing two primer sets (called *wzi*-3 and *wzi*-4) analysing the hundreds *wzi* allele sequences available, using EasyPrimer tool; ii) HRM experiments were performed in this work; iii) HLMT-clustering and HLMT-assignment analyses were also performed in this work using the HLMT reference strains dataset (see methods) and the melting temperatures of the 134 strains of the four datasets, using MeltingPlot v2.0 tool.

We reconstructed the *K. pneumoniae* reference dataset naming the Melting Types as the most epidemiologically relevant clone(s) present in the MT, recalling the labelling approach used in MLST for Clonal Clusters (e.g. *K. pneumoniae* CC258).

HLMT-assignment analysis classified almost every strain in concordance with MLST+*wzi* (Figure 1), showing the portability and repeatability power of the method. Furthermore, despite HLMT-clustering is less sensitive than MLST+*wzi*, the method was able to discriminate the most epidemiologically relevant STs (i.e. ST258 *wzi*29, ST258 *wzi*154, ST307 *wzi*173 and ST11) (Supplementary Figure S2). Indeed, the HLMT-clustering epidemiological scenarios were highly consistent with those from the

other typing methods (Figure 2): the curves were very similar for HSG, PG23 and OSR datasets and HLMT-clustering was able to detect the emergence of the outbreak in PSM. These results show that HLMT is suitable for real-time epidemiological surveillance in hospital settings.

Applicability

The only two instruments required to perform HLMT are a HRM-capable qPCR platform and a standard Personal Computer (PC); the molecular biology skills required are also minimal. No bioinformatic skills are necessary because both HLMT-clustering and HLMT-assignment can be automatically performed online, using the free and user-friendly tool MeltingPlot.

When the strains metadata is available, MeltingPlot can be used to merge HLMT clusters and strains metadata (isolation date and location) to produce graphical descriptions of the epidemiological scenario under study. Lastly, HLMT allows to type large amounts of isolates in a few hours for a few euros per sample (Figure 4).

WGS is the most sensitive method for bacterial typing and, even if it is becoming the gold standard typing approach for several pathogen species, PFGE and MLST are applied more often in real-time hospital surveillance programs [18]. In this work we show that HLMT is four times faster than MLST and 33 times faster than PFGE, maintaining a sensitivity comparable to these typing methods. Moreover, the low cost of HLMT (~5 euros/isolate) makes it one of the most inexpensive sub-species pathogen typing methods available, being up to 20 times less expensive than MLST, PFGE and WGS (Figure 4). This makes HLMT suitable for epidemiological investigations in

real-time and for the development of low cost surveillance programs even in low and middle income countries.

Acknowledgements

Thanks to the Romeo ed Enrica Invernizzi Foundation.

Funding

None.

References

[1] Suetens C, Latour K, Kärki T, Ricchizzi E, Kinross P, Moro ML, et al. Prevalence of healthcare-associated infections, estimated incidence and composite antimicrobial resistance index in acute care hospitals and long-term care facilities: results from two European point prevalence surveys, 2016 to 2017. Euro Surveill 2018;23. https://doi.org/10.2807/1560-7917.ES.2018.23.46.1800516.

[2] Tamburro M, Ripabelli G. High Resolution Melting as a rapid, reliable, accurate and cost-effective emerging tool for genotyping pathogenic bacteria and enhancing molecular epidemiological surveillance: a comprehensive review of the literature. Ann Ig 2017;29:293–316. https://doi.org/10.7416/ai.2017.2153.

[3] Perini M, Piazza A, Panelli S, Di Carlo D, Corbella M, Gona F, et al. EasyPrimer: user-friendly tool for pan-PCR/HRM primers design. Development of an HRM protocol on *wzi* gene for fast *Klebsiella pneumoniae* typing. Sci Rep 2020;10:1307. https://doi.org/10.1038/s41598-020-57742-z.

[4] Vossen RHAM, Aten E, Roos A, den Dunnen JT. High-resolution melting analysis (HRMA): more than just sequence variant screening. Hum Mutat 2009;30:860–6. https://doi.org/10.1002/humu.21019.

[5] Pasala AR, Perini M, Piazza A, Panelli S, Di Carlo D, Loretelli C, et al. Repeatability and reproducibility of the *wzi* high resolution melting-based clustering analysis for *Klebsiella pneumoniae* typing. AMB Express 2020;10:217. https://doi.org/10.1186/s13568-020-01164-7.

[6] Perini M, Biffignandi GB, Di Carlo D, Pasala AR, Piazza A, Panelli S, et al. MeltingPlot, a user-friendly online tool for epidemiological investigation using High Resolution Melting data. BMC Bioinformatics 2021;22. https://doi.org/10.1186/s12859-021-04020-y.

[7] Ferrari C, Corbella M, Gaiarsa S, Comandatore F, Scaltriti E, Bandi C, et al.

Multiple KPC Clones Contribute to an Extended Hospital Outbreak. Front Microbiol 2019;10:2767. https://doi.org/10.3389/fmicb.2019.02767.
[8] Gona F, Comandatore F, Battaglia S, Piazza A, Trovato A, Lorenzin G, et al. Comparison of core-genome MLST, coreSNP and PFGE methods for *Klebsiella pneumoniae* cluster analysis. Microbial Genomics 2020;6. https://doi.org/10.1099/mgen.0.000347.
[9] Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics 2014;30:2114–20. https://doi.org/10.1093/bioinformatics/btu170.
[10] Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, et al. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 2012;19:455–77. https://doi.org/10.1089/cmb.2012.0021.
[11] Ondov BD, Treangen TJ, Melsted P, Mallonee AB, Bergman NH, Koren S, et al. Mash: fast genome and metagenome distance estimation using MinHash. Genome Biol 2016;17:132. https://doi.org/10.1186/s13059-016-0997-x.
[12] Stamatakis A. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 2014;30:1312–3. https://doi.org/10.1093/bioinformatics/btu033.
[13] Darriba D, Posada D, Kozlov AM, Stamatakis A, Morel B, Flouri T. ModelTest-NG: A New and Scalable Tool for the Selection of DNA and Protein Evolutionary Models. Mol Biol Evol 2020;37:291–4. https://doi.org/10.1093/molbev/msz189.
[14] Brisse S, Passet V, Haugaard AB, Babosan A, Kassis-Chikhani N, Struve C, et al. *wzi* Gene sequencing, a rapid method for determination of capsular type for *Klebsiella* strains. J Clin Microbiol 2013;51:4073–8. https://doi.org/10.1128/JCM.01924-13.
[15] Lam MMC, Wick RR, Watts SC, Cerdeira LT, Wyres KL, Holt KE. Genomic surveillance framework and global population structure for *Klebsiella pneumoniae*. bioRxiv 2021:2020.12.14.422303. https://doi.org/10.1101/2020.12.14.422303.
[16] Warnes GR, Bolker B, Bonebakker L, Gentleman R. gplots: Various R programming tools for plotting data. R Package Version 2009.
[17] Wei T, Simko V. R package “corrplot”: Visualization of a Correlation Matrix. (Version 0.88). Github n.d. https://github.com/taiyun/corrplot (accessed May 21, 2021).
[18] ECDC. ECDC strategic framework for the integration of molecular and genomic typing into European surveillance and multi-country outbreak investigations. Www.ecdc.europa.eu 2019. https://www.ecdc.europa.eu/en/publications-data/ecdc-strategic-framework-integration-molecular-and-genomic-typing-european (accessed June 15, 2021).

Figure Captions

Figure1: MLST+*wzi* vs HLMT-assignment correlation matrix

Correlation matrix between Multi-Locus Sequence Typing (MLST)+*wzi* typing and Hypervariable-Locus Melting Typing (HLMT)-assignment on the 134 strains analysed in the study. The pie charts indicate, for each MLST+*wzi* profile, the proportion of matches with the Melting Types (MT). Green pies show correct matches and the red ones the mismatches. Light blue pies show the strains belonging to MLST+*wzi* profiles absent in the reference dataset used to perform HLMT-assignment analysis. Gray pies show the strain that were classified as “Unassigned” by HLMT-assignment analysis.

Figure2: Epidemiological curves comparison

Epidemiological curves reconstructed using isolation dates and typing information obtained by HLMT-clustering, MLST+*wzi*, WGS and PFGE on the four dataset analysed in this study. Each line of the plot refers to a dataset while each column to a typing method. The colors used in the barplots correspond to the HLMT clusters.

Figure3: Hypervariable-Locus Melting Typing flow

Graphical representation of the flow of Hypervariable-Locus Melting Typing (HLMT). On the top, the three main steps of the HLMT method: HRM protocol design on hypervariable genes, HRM experiments and HRM data analysis for typing (HLMT-clustering and HLMT-assignment). On the bottom, the combination of HLMT typing and isolates metadata allow to perform epidemiological investigations, e.g.

epidemiological curves and patient timeline. Primer design, HLMT-clustering, HLMT-assignment and epidemiological curve production can be performed using on-line free user-friendly tools (namely: EasyPrimer for primer design and MeltingPlot v2.0 for the others).

Figure4: Timeline and costs of the typing methods

The timeline summarises the time required and the prices of Hypervariable-Locus Melting Typing (HLMT) (in green), Hypervariable-Locus Melting Typing (MLST), Whole Genome Sequencing (WGS) and Pulsed-Field Gel Electrophoresis (PFGE). The time required to perform each typing analysis, the relative typing definition and cost per sample are also reported.

Supplementary Figures Captions

FigureS1: WGS phylogenetic analysis

Maximum Likelihood phylogenetic trees of the four datasets used in this study (HSG, PSM, PG23, OSR). Each dataset was analysed with the closest genomes found in PATRIC online database. The WGS cluster of each genome used in this study is shown by the colors next to the strain name.

FigureS2: Contingency tables of HLMT-clustering vs MLST+*wzi*

For each of the four datasets analysed in this study (HSG, PSM, PG23, OSR), the HLMT clusters are compared to the MLST+*wzi* groups with a contingency table. Each

color represents a HLMT cluster. The gray color indicates the strains that the HLMT clustering algorithm classified as “Undetermined”.

FigureS3: Contingency tables of HLMT-clustering vs WGS

For each of the four datasets analysed in this study (HSG, PSM, PG23, OSR), the HLMT clusters are compared to the WGS clusters with a contingency table. Each color represents a HLMT cluster. The gray color indicates the strains that the HLMT clustering algorithm classifies as “Undetermined”.

FigureS4: Contingency table of HLMT-clustering vs PFGE

For the OSR dataset the HLMT clusters are compared to the PFGE clusters with a contingency table. Each color represents a HLMT cluster.

MLST+*wzi* vs HLMT-assignment

- Correct Matches
- Mismatches
- Missing reference strain
- Unassigned

		MT_ST258:512_wzi154	MT_ST307_wzi173---MT_ST147_wzi64	MT_ST11:101:15	MT_ST258_wzi29	MT_ST10_wzi95	MT_ST147_wzi64	Unassigned	TOTAL
ST512	wzi154	36						13	49
ST307	wzi173		37				5		42
ST258	wzi154	14							14
ST258	wzi29				8				8
ST101	wzi137			5					5
ST147	wzi95					4			4
ST15	wzi24			2					2
ST395	wzi2			2					2
ST11	wzi75			1					1
ST147	wzi64						1		1
ST149	wzi62	1							1
ST423	wzi8	1							1
ST45	wzi101			1					1
ST37	wzi96					1			1
ST3985	wziUNK					1			1
ST15	wzi89							1	1
	TOTAL	52	37	11	8	6	6	14	**134**

HLMT-clustering
MLST+wzi
WGS
PFGE
HSG
PSM
PG23
OSR
HLMT clusters
Cluster_01
Cluster_02
Cluster_05
Cluster_03
Cluster_04
Isolates
Months
ST512_wzi154
ST307_wzi173
ST512_wzi154_HSG_2
ST307_wzi173_HSG_1
ST258_wzi154
ST258_wzi154_PSM_3
ST512_wzi154_PSM_1
ST512_wzi154_PSM_2
ST258_wzi29
ST147_wzi95
ST307_wzi173_PG23_4
ST258_wzi29_PG23_2
ST147_wzi95_PG23_5
ST307_wzi173_OSR_6
ST307_wzi173_OSR_7
ST101_wzi137
ST101_wzi137_OSR_3
ST258_wzi154_OSR_11
ST512_wzi154_OSR_10
ST512_wzi154_OSR_2
ST512_wzi154_OSR_8
ST512_wzi154_OSR_9
B
D
C
A

Hypervariable Locus Melting Typing - HLMT

Typing

HRM protocol design

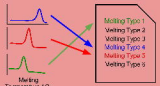
Select **hypervariable genes** and design primers using **EasyPrimer**

easy primer

HRM experiments

HLMT-ASSIGNMENT

Melting temperatures are compared to the reference dataset to get **portable results**

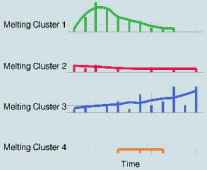


HLMT-CLUSTERING

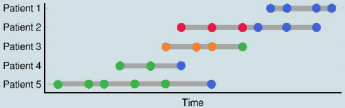
Melting temperatures are used to find **clusters** of isolates

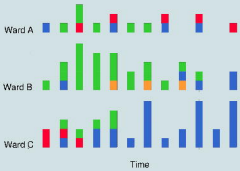
MELTINGPLOT

Typing + metadata

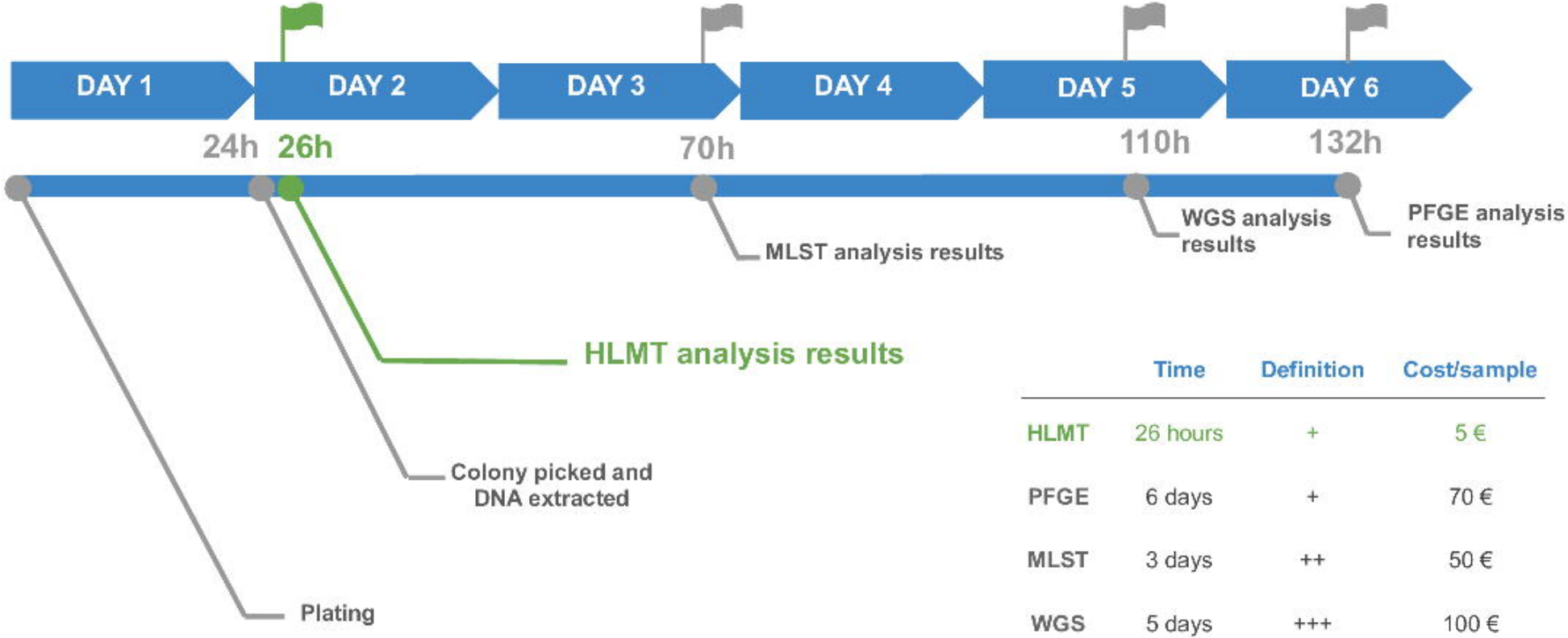


Epidemiological investigation





MELTINGPLOT



	Time	Definition	Cost/sample
HLMT	26 hours	+	5 €
PFGE	6 days	+	70 €
MLST	3 days	++	50 €
WGS	5 days	+++	100 €