**Original article**

**Markers of epidemiological success of methicillin-resistant *Staphylococcus aureus* (MRSA) isolates in European populations**

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**ABSTRACT**

OBJECTIVES – Methicillin-resistant *Staphylococcus aureus* (MRSA) infections impose a considerable burden on health systems, yet there is remarkable variation in the global incidence and epidemiology of MRSA. The MACOTRA consortium aimed to identify bacterial markers of epidemic success of MRSA isolates in Europe using a representative MRSA collection originating from France, the Netherlands and the United Kingdom.

METHODS – Operational definitions of success were defined in consortium meetings to compose a balanced strain collection of successful and sporadic MRSA isolates. Isolates were subjected to antimicrobial susceptibility testing and whole genome sequencing, genes were identified and phylogenetic trees constructed. Markers of epidemiological success were identified using genome-based time-scaled haplotypic density (THD) analysis and linear regression. Antimicrobial usage data from ESAC-Net was compared to national MRSA incidence data.

RESULTS - Heterogeneity of MRSA isolate collections across countries hampered the use of a unified operational definition of success, so country-specific approaches were used to establish the MACOTRA strain collection. Phenotypic antimicrobial resistance varied within related MRSA populations and across countries. In THD analysis, fluoroquinolone, macrolide and mupirocin resistance were associated with MRSA success, while gentamicin, rifampicin and trimethoprim resistance were associated with sporadicity. Usage of antimicrobials across 29 European countries varied substantially, and beta-lactam, fluoroquinolone, macrolide and aminoglycoside use correlated with MRSA incidence.

CONCLUSIONS - Our results are the strongest yet to associate MRSA antibiotic resistance profiles and antibiotic usage to incidence of infection and successful clonal spread, which varied by country. Harmonized isolate collection, typing, resistance profiling and alignment with antimicrobial usage over time will aid comparisons and further support country-specific interventions to reduce MRSA burden.

**INTRODUCTION**

Antimicrobial resistance (AMR) is considered to be the greatest threat to the future of modern medicine, and MRSA is estimated to be the most common cause of AMR associated deaths globally and second in Europe [1,2]. MRSA carriage is a risk factor for subsequent infection [3–5]. MRSA are resistant to virtually the full spectrum of beta-lactam antimicrobials due to the *mecA* carrying SCC*mec* mobile element acquired on multiple occasions into different *S. aureus* genetic lineages, resulting in a range of different MRSA clones. Approximately a dozen clones, often discriminated by their different lineage (also called clonal cluster (CC)) dominate the MRSA population globally. The dominant clone may differ in different geographic settings, and may even change over time [4,6,7]. Resistance to almost all classes of antimicrobials can be found in MRSA, although fully drug-resistant isolates are rare. Furthermore, the incidence of MRSA infection can vary widely between countries, but the reasons for these geographical differences are poorly understood.

Each country has developed distinct strategies for collecting, testing, typing and reporting of MRSA isolates [8]. This variation in approaches obstructs comparisons and proper aggregation of data and therefore thorough epidemiological analysis on an international level and could potentially hide or over-estimate common markers of successful clones across geographic settings. The implementation of whole genome sequencing analysis can aid international data comparison and can be used to search for genotypic markers of successful isolates.

France, the UK and the Netherlands represent countries with very differing incidences of MRSA infection, recently estimated at 48.13, 10.65 and 1.47 per 100 000 population, respectively [2]. Each country is dominated by different clones [9–11], with community isolates rare in the UK, and livestock isolates more prevalent in the Netherlands. Here we used two approaches to identify epidemiologically successful isolates in each country and searched for genetic and AMR biomarkers of success. Further analysis of resistance markers revealed associations between the usage of specific antimicrobial classes and MRSA incidence across 29 European countries, identifying potential targets for stewardship interventions.

**METHODS**

Full details are in the Supplementary Methods section.

***Operational definition and collection of successful and sporadic (unsuccessful) isolates***

Collaborators from each country, France, the Netherlands and the UK in the MACOTRA consortium (Combating MRSA; increasing our understanding of transmission success will lead to better control of MRSA), identified their country-specific epidemiological characteristics of MRSA success over time, which included incidence of infection and local typing methods. Where common criteria across countries could be identified this was used. The success selection criteria were designed to not be biased by lineage, antimicrobial resistance profile or any other biomarker.

***Whole genome sequencing and epidemiological clustering***

Whole genome sequencing used the Illumina MiSeq platform. Sequence reads were aligned to reference genomes (RefSeq NC\_002952 (CC30), NC\_017763 (CC22), NC\_002745 (CC5)). Phylogenetic reconstruction was performed using IQ-Tree v2.0.3. Genomes were also assembled using Shovill v1.0.9 and resistance genes identified using Abricate and the Comprehensive Antibiotic Resistance Database (CARD) database, virulence genes identified using the Virulence Factor Database (VFDB) database [12,13]. Genes associated with operational success were compared using Chi-squared tests at 5% significance threshold.

***Antimicrobial susceptibility testing***

EUCAST disk diffusion methodology [14] was used to test for sensitivity to 14 antibiotics using Oxoid disks (Basingstoke, UK). The distribution of phenotypic resistance and successful isolates in each country was compared using Chi-squared tests at 5% significance threshold.

***Time-scaled haplotypic density (THD) analysis***

We used the time-scaled haplotypic density (THD) method to examine the factors predicting epidemic success of MRSA based on genome sequences [15–17]. THD assigned relative indices of epidemic success, over a defined time period of 5 years, to each isolate in the dataset, on the basis of the branching density and distribution of genetic distances separating it from other isolates. Potential predictors of success, such as antimicrobial drug resistance patterns, were identified using linear regression models with THD indices as the response variable.

Genome wide association studies (GWAS) were performed using pyseer [18], using kmer and unitig approaches utilising the shovill derived denovo assembled genome sequences. Genes associated with THD success and resistance phenotypes were also determined using pyseer following kmer and unitig based approaches [18].

***AMR and antimicrobial usage across Europe***

The sum of estimated incidence of all infection types caused by MRSA was used to give an overall MRSA annual incidence per 100 000 population data across 29 European countries [2]. This was based on EARS-Net data adjusted for coverage and usage of diagnostics for the year 2015 [2]. Antimicrobial consumption data for 2015 was from ESAC-Net (ecdc.europa.eu) and expressed as defined daily dose (DDD) per 1000 inhabitants per day. The data for some countries was split into community and healthcare usage and sourced from national sales and reimbursement data. We tested both linear (shown here) and exponential trend associations (in Supplementary Methods), with an F test for significance: all data management and analysis is provided in the Supplementary 2 and as code in a Github repository: <https://github.com/gwenknight/mrsa_inf_abx>.

**RESULTS**

***Operational definition of epidemiologically successful and sporadic isolates***

National strategies for collecting, typing and reporting MRSA isolates in each country were found to be markedly different [8], necessitating some variation in inclusion criteria between countries (Supplementary 1). AMR resistance profiles were not used as selection criteria.

Representative isolates from France were selected from the collection of the French National Reference Centre for Staphylococcus (NRC), Lyon, France and previously typed using DNA array hybridization [19,20]. Eight representative clonal complexes (CC) were chosen and CC subtype clusters totalling >25% of the CC size labelled ‘successful’, while examples totalling <25% were labelled ‘sporadic’.

In the Netherlands, mandatory surveillance of all clinical and colonisation MRSA isolates is combined with epidemiological data and typing by multiple locus variable number-tandem repeat analysis (MLVA) at the Dutch National Institute for Public Health and the Environment (RIVM). Seven representative clonal types aligned with CCs were chosen, and random isolates from the most prevalent and least prevalent MLVA types with each clone were chosen as successful and sporadic isolates respectively. In addition, some isolates from populations involved in known outbreaks but from a different type as causing the outbreak were included as sporadic isolates.

In the UK, an isolate collection from St George’s University Hospital Trust, London that documented a shift in the dominant clones over time was utilised [9]. CC30 and CC22 account for most UK isolates and whole genome multi-locus sequence typing (wgMLST) phylogenetic trees were constructed and clusters with <15 wgMLST allelic differences were defined as successful. Examples of those that did not cluster were defined as sporadic, along with examples from another six CCs.

***Phylogenetically related isolates were identified across the three countries but differed in dominance and success***

Sequence data were submitted to the European Nucleotide Archive (EBI ENA) database with accession number PRJEB47238. Phylogenetic trees of 157 successful and 221 sporadic MRSA clearly identified the different CCs (Figure 1). Each of the three countries was dominated by isolates from different CCs. Clusters within sub-branches of each lineage were isolated suggesting dissemination into other countries (Figure 1, S3). Further analysis of CC22 and CC30, the most prevalent CCs, demonstrated that transmission of an isolate to another country did not generally lead to successful localised clusters (Supplementary Figures S1, S2).

***AMR profiles were highly variable and associated with country***

AMR phenotypes and genotypes varied substantially within CCs and across CCs (Figure 1), as well as between countries and operational definitions of success (Figure 2). France had a higher proportion of fusidic acid resistance and a lower proportion of gentamicin, mupirocin and trimethoprim resistance. The Netherlands had a higher proportion of tetracycline resistance and a lower proportion of tobramycin resistance. The UK had a higher proportion of fluoroquinolone, erythromycin, gentamicin, mupirocin, tobramycin and trimethoprim resistance and a lower proportion of tetracycline resistance (Supplementary Figure S4).

Within countries, success in France was associated with tobramycin resistance and sporadic isolates with clindamycin and tetracycline resistance. Success in the UK was associated with ciprofloxacin, gentamicin, rifampicin and tobramycin resistance and sporadic isolates with tetracycline resistance (Figure 2). Across the collection, successful isolates were associated with tobramycin resistance (Supplementary Table S3).

***Time-scaled haplotypic density (THD) analysis***

THD indices were assigned by genetic distance to other isolates in the collection (Supplementary Table S1) reflecting the rate of transmission and selection over time [15–17]. THD indices were higher in the UK, suggesting that successful isolates were closely related in this country (Figure 1, Supplementary Table S1). CC22 was the most successful clone overall (Figure 3b) and the dominant clone in the UK (Figure 1,3a).

The THD and operational definitions of success did not differ significantly between successful and sporadic isolates (2-sided Mann Whitney test, p = 0.42). However, after taking into account the country and CC of each strain as random effects in a mixed-effect linear regression, operational success predicted slightly higher THD values (17.5% increase, 95% CI, 6.7 to 29.4%, p = 0.001). These findings indicate that the operational definitions of success failed to capture the epidemic success of a given isolate among the global MRSA population, most likely due to the country-specific definitions; however, operational definitions correctly predicted epidemic success within the same lineage and country.

Then, we leveraged THD indices to examine AMR with epidemic success. We constructed univariate and multivariable models of the THD success index as a function of the inhibition zone diameters for 7 antimicrobial drugs. All models were adjusted for variations across countries and CCs using random intercepts. In multi-variable analysis, the THD success index correlated positively with ciprofloxacin, erythromycin and mupirocin, and negatively with gentamicin, rifampicin and trimethoprim (Figure 3c).

Genome-wide association study (GWAS) using pyseer to identify mutations and account for lineage variation did not reveal any markers of success. Pyseer correctly identified the most common mutations associated with phenotypic resistance (Supplementary Figure S5). A search for known virulence genes using VFDB identified *tst* (toxic shock syndrome toxin) although prevalence was low (Supplementary Table S1, Supplementary data).

***AMR incidence and antimicrobial usage across Europe***

MRSA incidence of infection varied widely between 29 countries across Europe, ranging from an estimated 1.47 cases in the Netherlands to 102 cases in Portugal per 100,000 persons per year (Figure 4, Supplementary Figures S7, S8). Similarly, antimicrobial usage is markedly different across countries (Supplementary Figures S9-S12). We compared antimicrobial usage with MRSA incidence across European countries to further explore MRSA selection by antibiotics.

MRSA incidence correlated with total beta-lactam usage in 29 countries (Figure 5a, Supplementary Figures S16-S19). Specific associations were found between combinations of penicillins, including beta-lactamase inhibitors in the community and hospitals, and 3rd generation cephalosporins in the community. Countries with higher use of beta-lactamase sensitive penicillins in the community had lower MRSA incidence.

We also identified a correlation between MRSA incidence and fluoroquinolone usage (Figure 5b, Supplementary Figures S20-S23). We note that Portugal is an outlier in our data with very high MRSA incidence. When excluding Portugal from analysis, additional correlations were found between MRSA incidence with macrolide use in the community and aminoglycoside use in hospitals (Figure 5b, Supplementary Figures S24-S27, S31-S32). Correlations between MRSA incidence and other classes of antimicrobials were not significant (Supplementary Data pages 14-55)

**DISCUSSION**

In this project we brought together isolates from three European countries with varying MRSA incidence. Surprisingly, we found that harmonizing a definition and unifying data analysis for epidemic success was extremely challenging. We explored the internationally differing MRSA surveillance programs, strain collections, typing methods and uses of data [8]. THD analysis confirmed that our operational definitions of success in each country did not completely match or capture epidemic success. A unified framework for MRSA sampling is needed to establish cohesive sample and data collections, such as common reasons for collecting isolates and sources of isolates, harmonised typing and accessible strains, which we discuss further in an accompanying paper [8]. This would allow a direct comparison between clonal types of differing incidence and success in different locations.

The high variation in MRSA incidence and in CC types in European countries indicates differing selection pressures based on geographical factors. Identifying markers of selection in successful isolates in different countries will be key to designing effective interventions to reduce selection.

Comprehensive phylogenetic analysis by GWAS did not identify mutations associated with success. Despite using pyseer, the complex lineage structure of MRSA may have confounded the analysis. This method does not include most of the antibiotic resistances which in MRSA are due to resistance genes carried on mobile genetic elements. A THD analysis was more nuanced assigning indices for success. This approach allowed CC22 to clearly be identified as the most successful clone, despite samples being chosen across a range of CCs.

Across the collection, an antibiotic resistance phenotype was associated with THD success for ciprofloxacin, macrolides and mupirocin (Figure 3). Success was not associated with gentamicin, rifampicin and trimethoprim resistance. This pattern does not simply align with CC22 AMR profiles, or with resistance profiles in the UK MRSA, and demonstrates that CCs across the strain collection and all three countries contributed to this finding.

If certain antimicrobial resistances were particularly associated with success, we might expect the antimicrobials to be used at higher frequency in areas where these resistances have become prevalent. We used standardised data and estimates across 29 countries of Europe to answer this question. Firstly, we demonstrated that beta-lactam use was correlated with MRSA incidence and specifically, this could be narrowed down to penicillins combined with beta-lactam inhibitors in both hospitals and the community. Additionally, there was correlation with 3rd generation cephalosporin use in the community. Importantly, higher usage of beta-lactamase sensitive penicillins in the community was correlated with a lower MRSA incidence, likely due to their effectiveness when MRSA incidence is low. These results may provide suggestions as to which beta-lactams could be targeted by stewardship interventions and in which locations.

Beyond beta-lactams, fluoroquinolone use (including ciprofloxacin) correlated with MRSA incidence across Europe. Resistance to fluoroquinolones due to stable point mutations is common in successful clones, and reduction of ciprofloxacin usage has previously been implicated in MRSA incidence decline in UK hospitals [9], while resistance was identified as a key selected epidemiological marker using phylogenetic methods [17, 21]. Fluoroquinolone antimicrobials are particularly secreted onto the skin and mucous membranes [22], influencing the colonising microbiome, and presumably selecting a host reservoir of MRSA.

Macrolide resistance was also implicated as having association with successful MRSA, despite the instability of the resistance gene in MRSA populations [9,21,23]. Genes are typically carried on plasmids and transposons with high incidence of gain and loss in experimental and phylogenetic studies [23]. High frequency of resistance in MRSA suggests active selection. Usage of macrolides in the community correlated with MRSA incidence in Europe and further studies should focus on the proportion of resistant MRSA which may vary across countries.

While mupirocin resistance was identified as a marker of success, the incidence is relatively low, and there is limited previous evidence for mupirocin resistance contributing to epidemiological success. Similarly, *tst* gene (encoding for the Toxic shock syndrome toxin (TSSST)) carriage was implicated in success, but incidence was also low [24]. Aminoglycoside resistance was less prevalent in successful MRSA, though use in hospitals was associated with MRSA incidence, and we can speculate the large plasmids carrying such resistances may be a burden to colonising strains. Rifampicin resistance mutations are also rare, possibly due to fitness cost [25].

MRSA isolates showed evidence of recent spread from one country to others, but limited spread in the new location. However, the study was hampered by under-sampling to evidence this. Our recent mathematical modelling has suggested that dominant local clones have a particular advantage in outcompeting introduced clones, particularly when antimicrobial resistance genes are unstable [10].

All epidemiological studies are limited and biased by the isolates chosen to study. Here we attempted to power our study by selecting successful versus unsuccessful/sporadic isolates, which was hampered by un-harmonized collections. However, the very different strain collections from three different countries hampered our analysis [8]. The choice of isolates may have skewed our THD analysis. THD is a method that benefits from large strain collections, and future studies could investigate global populations assigning success and utilising comparisons with genotypic AMR.

This study highlights the wide variation in antimicrobial resistance incidence in MRSA populations in the France, UK and the Netherlands, as well as in usage of antimicrobials. Furthermore, there are alignments with the use of particular antimicrobial classes and MRSA infection incidence across Europe. Stewardship programmes to reduce infection incidence can be hampered if they focus on restricting antimicrobial usage that is not selective. The data presented here may allow targeted interventions, particular in locations where MRSA is prevalent. Further studies to investigate the antibiotic resistance profiles of MRSA in a wider range of locations, combined with the impact of changing antimicrobial usage over time, will support the design of enhanced stewardship interventions.

**Figure Legends**

Figure 1. Phylogenetic tree of the collection showing CCs, country and operational success. Two panels aligned to the tree show the Resistant (R), Susceptible (S), Intermediate (I) and Unknown (U) status of each drug for each isolate, and the Presence (P) and Absence (A) of known resistance genes from the CARD database. Further details of the isolates are in Supplementary Table S1.

Figure 2. AMR resistance varied between successful and sporadic isolates within countries. AMR association is marked as \*: p=< 0.05 ; \*\*: p=< 0.01 ; \*\*\*: p=< 0.001 by Chi2 test.

Figure 3. Genome-based analysis of markers of epidemiological success. Shown are the distributions of THD success indices across countries (A) and clonal complexes (B). Panel C shows pointwise estimates (dots) and 95% confidence intervals (bars) of the coefficients of regression models predicting THD indices with antimicrobial resistance, expressed as units of 2-fold reduction of inhibition zone diameters. Models were either unadjusted (blue bars) or adjusted (multi-variable, red bars). In multivariable regression, THD success indices were predicted by higher ciprofloxacin, erythromycin and mupirocin resistance, and by susceptibility to gentamicin, rifampicin and trimethoprim.

Figure 4. Median infection incidence in 29 European countries due to MRSA in 2015 as estimated by Cassini *et al.* [25] for five infection types (colours) and total (point) with 97.5-102.5% confidence ranges. The five infection types are: bloodstream infections (BSI), urinary tract infections (UTI), respiratory tract infections (RESP), surgical site infections (SSI), and other infections (OTH).

Figure 5. Antimicrobial usage in 29 European countries is associated with MRSA infection incidence. A. Beta-lactam (ATC code classes: “J01C” and “J01D”) usage in the community, hospitals or combined. B. For other antibiotics, associations were seen with fluoroquinolones (“J01MA”), Macrolides (“J01FA”) and aminoglycosides (“J01G”) (here the outlier of Portugal was excluded). See supplementary 2 for all antibiotics. Significant trends are highlighted with a red R^2 and p-value (p<0.05). Shaded cells indicate summary classes of antibiotics – those that are sums of other columns (Supplementary Table S1). Shaded areas around the blue trend line are the 95% confidence level interval for predictions from a linear model.

**Statement of contribution**

Conceptualisation and supervision: MCV, GMK, AAW, JPR, JAL. Funding: MCV, GL, JAL. Data generation and analysis: VOB, AG, GMK, LMS, KL, MT, APAH, MK, MCV, AAW, JPR, JAL. Methodology of strain collection: VOB, AG, GMK, LMS, AB, WJBvW, GL, FV, MCV, AAW, JPR, JAL. Strain collection: VOB, AG, LMS, APAH, MT, JPR, JAL. Sequencing and bioinformatics: AAW, KL, AG, JPR. Phenotypic antimicrobial resistance analysis: AG. THD: JPR. Antibiotic usage analysis: GMK, AG, JAL. MACOTRA consortium member intellectual input: VB, AG, GMK, LMS, AB, SJdV, ASdV, APAH, MEK, WJBvW, GL, FV, MCV, AAW, JPR, JAL. Writing: VOB, AG, GMK, LMS, MCV, AAW, JPR, JAL. Review and agreement with the final version of the manuscript: all authors

**Conflict of Interest**

Nothing to declare.

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**REFERENCES**

[1] Murray CJ, Ikuta KS, Sharara F, Swetschinski L, Robles Aguilar G, Gray A, et al. Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis. Lancet 2022;399:629–55. https://doi.org/10.1016/S0140-6736(21)02724-0.

[2] Cassini A, Högberg LD, Plachouras D, Quattrocchi A, Hoxha A, Simonsen GS, et al. Attributable deaths and disability-adjusted life-years caused by infections with antibiotic-resistant bacteria in the EU and the European Economic Area in 2015: a population-level modelling analysis. Lancet Infect Dis 2019;19:56–66. https://doi.org/10.1016/S1473-3099(18)30605-4.

[3] Bode LGM, Kluytmans JAJW, Wertheim HFL, Bogaers D, Vandenbroucke-Grauls CMJE, Roosendaal R, et al. Preventing Surgical-Site Infections in Nasal Carriers of *Staphylococcus aureus*. N Engl J Med 2010;362:9–17. https://doi.org/10.1056/NEJMoa0808939.

[4] DeLeo FR, Otto M, Kreiswirth BN, Chambers HF. Community-associated meticillin-resistant *Staphylococcus aureus*. Lancet 2010;375:1557–68. https://doi.org/10.1016/S0140-6736(09)61999-1.

[5] Wertheim HF, Melles DC, Vos MC, van Leeuwen W, van Belkum A, Verbrugh HA, et al. The role of nasal carriage in *Staphylococcus aureus* infections. Lancet Infect Dis 2005;5:751–62. https://doi.org/10.1016/S1473-3099(05)70295-4.

[6] Enright MC, Robinson DA, Randle G, Feil EJ, Grundmann H, Spratt BG. The evolutionary history of methicillin-resistant *Staphylococcus aureus* (MRSA). Proc Natl Acad Sci 2002;99:7687–92. https://doi.org/10.1073/pnas.122108599.

[7] Stefani S, Chung DR, Lindsay JA, Friedrich AW, Kearns AM, Westh H, et al. Meticillin-resistant *Staphylococcus aureus* (MRSA): global epidemiology and harmonisation of typing methods. Int J Antimicrob Agents 2012;39:273–82. https://doi.org/10.1016/j.ijantimicag.2011.09.030.

[8] Baede VO, David MZ, Andrasevic AT, Blanc DS, Borg M, Brennan G, et al. MRSA surveillance programmes worldwide: moving towards a harmonised international approach. Int J Antimicrob Agents 2022;59:106538. https://doi.org/10.1016/j.ijantimicag.2022.106538.

[9] Knight GM, Budd EL, Whitney L, Thornley A, Al-Ghusein H, Planche T, et al. Shift in dominant hospital-associated methicillin-resistant *Staphylococcus aureus* (HA-MRSA) clones over time. J Antimicrob Chemother 2012;67:2514–22. https://doi.org/10.1093/jac/dks245.

[10] de Vos AS, de Vlas SJ, Lindsay JA, Kretzschmar MEE, Knight GM. Understanding MRSA clonal competition within a UK hospital; the possible importance of density dependence. Epidemics 2021;37:100511. https://doi.org/10.1016/j.epidem.2021.100511.

[11] Gustave C-A, Tristan A, Martins-Simões P, Stegger M, Benito Y, Andersen PS, et al. Demographic fluctuation of community-acquired antibiotic-resistant *Staphylococcus aureus* lineages: potential role of flimsy antibiotic exposure. ISME J 2018;12:1879–94. https://doi.org/10.1038/s41396-018-0110-4.

[12] Seemann T. Shovill v1.0.9 2020. https://github.com/tseemann/shovill.

[13] Seemann T. Abricate 2020. https://github.com/tseemann/abricate.

[14] The European Committee on Antimicrobial Susceptibility Testing (EUCAST). Antimicrobial susceptibility testing EUCAST disk diffusion method Version 7.0. 2019. https://www.eucast.org/ast\_of\_bacteria/previous\_versions\_of\_documents.

[15] Rasigade J-P, Barbier M, Dumitrescu O, Pichat C, Carret G, Ronnaux-Baron A-S, et al. Strain-specific estimation of epidemic success provides insights into the transmission dynamics of tuberculosis. Sci Rep 2017;7:45326. https://doi.org/10.1038/srep45326.

[16] Wirth T, Bergot M, Rasigade J-P, Pichon B, Barbier M, Martins-Simoes P, et al. Niche specialization and spread of *Staphylococcus capitis* involved in neonatal sepsis. Nat Microbiol 2020;5:735–45. https://doi.org/10.1038/s41564-020-0676-2.

[17] Wirth T, Wong V, Vandenesch F, Rasigade J. Applied phyloepidemiology: Detecting drivers of pathogen transmission from genomic signatures using density measures. Evol Appl 2020;13:1513–25. https://doi.org/10.1111/eva.12991.

[18] Lees JA, Galardini M, Bentley SD, Weiser JN, Corander J. pyseer: a comprehensive tool for microbial pangenome-wide association studies. Bioinformatics 2018;34:4310–2. https://doi.org/10.1093/bioinformatics/bty539.

[19] Monecke S, Slickers P, Ehricht R. Assignment of *Staphylococcus aureus* isolates to clonal complexes based on microarray analysis and pattern recognition. FEMS Immunol Med Microbiol 2008;53:237–51. https://doi.org/10.1111/j.1574-695X.2008.00426.x.

[20] Rasigade J-P, Leclère A, Alla F, Tessier A, Bes M, Lechiche C, et al. *Staphylococcus aureus* CC30 Lineage and Absence of *sed,j,r*-Harboring Plasmid Predict Embolism in Infective Endocarditis. Front Cell Infect Microbiol 2018;8:187. https://doi.org/10.3389/fcimb.2018.00187.

[21] Holden MTG, Hsu L-Y, Kurt K, Weinert LA, Mather AE, Harris SR, et al. A genomic portrait of the emergence, evolution, and global spread of a methicillin-resistant *Staphylococcus aureus* pandemic. Genome Res 2013;23:653–64. https://doi.org/10.1101/gr.147710.112.

[22] Høiby N, Jarløv JO, Kemp M, Tvede M, Bangsborg JM, Kjerulf A, et al. Excretion of ciprofloxacin in sweat and multiresistant *Staphylococcus epidermidis*. Lancet 1997;349:167–9. https://doi.org/10.1016/S0140-6736(96)09229-X.

[23] McCarthy AJ, Loeffler A, Witney AA, Gould KA, Lloyd DH, Lindsay JA. Extensive Horizontal Gene Transfer during *Staphylococcus aureus* Co-colonization In Vivo. Genome Biol Evol 2014;6:2697–708. https://doi.org/10.1093/gbe/evu214.

[24] Durand G, Bes M, Meugnier H, Enright MC, Forey F, Liassine N, et al. Detection of new methicillin-resistant *Staphylococcus aureus* clones containing the toxic shock syndrome toxin 1 gene responsible for hospital- and community-acquired infections in France. J Clin Microbiol 2006;44:847–53. https://doi.org/10.1128/JCM.44.3.847-853.2006.

[25] O’Neill AJ, Huovinen T, Fishwick CWG, Chopra I. Molecular genetic and structural modeling studies of *Staphylococcus aureus* RNA polymerase and the fitness of rifampin resistance genotypes in relation to clinical prevalence. Antimicrob Agents Chemother 2006;50:298–309. https://doi.org/10.1128/AAC.50.1.298-309.2006.