





Mapping Twenty Years of Antimicrobial Resistance Research Trends

Luz, Christian F; Niekerk, Magnus van; Keizer, Julia; Beerlage-de Jong, Nienke; Braakman-Jansen, Annemarie; Stein, Alfred; Sinha, Bhanu; Gemert-Pijnen, Lisette van; Glasner, Corinna

DOI: 10.1101/2021.03.01.433375

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version Publisher's PDF, also known as Version of record

Publication date: 2021

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA): Luz, C. F., Niekerk, M. V., Keizer, J., Beerlage-de Jong, N., Braakman-Jansen, A., Stein, A., Sinha, B., Gemert-Pijnen, L. V., & Glasner, C. (2021, Mar 1). Mapping Twenty Years of Antimicrobial Resistance Research Trends. https://doi.org/10.1101/2021.03.01.433375

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: https://www.rug.nl/library/open-access/self-archiving-pure/taverneamendment.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): http://www.rug.nl/research/portal. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Mapping Twenty Years of Antimicrobial Resistance Research Trends

C.F. Luz^{1*}, MD; J.M. van Niekerk^{1,2,3*}, MSc; J. Keizer², MSc; N. Beerlage-de Jong^{1,2}, PhD; L.M.A. Braakman-Jansen², PhD; A. Stein³, Prof; B. Sinha¹, Prof; J.E.W.C. van Gemert-Pijnen^{1,2}, Prof; C. Glasner¹, PhD

1 University of Groningen, University Medical Center Groningen, Department of Medical Microbiology and Infection Prevention, Hanzeplein 1, 9700RB Groningen, The Netherlands

2 University of Twente, Department of Psychology, Health and Technology, Centre for eHealth and Wellbeing Research, PO box 217, 7500AE Enschede, The Netherlands

3 University of Twente, Department of Earth Observation Science (EOS), Faculty of Geo-Information Science and Earth Observation (ITC), PO box 217, 7500AE Enschede, The Netherlands

* Equal contribution

Correspondence to:

Christian Luz, University of Groningen, University Medical Center Groningen, Department of Medical Microbiology and Infection Prevention, Hanzeplein 1 EB 80, 9713GZ Groningen, The Netherlands, Email: <u>c.f.luz@umcg.nl</u>, Telephone: +31 (0) 50 36 13480

Summary

Background

Antimicrobial resistance (AMR) is a global threat to health and healthcare. In response to the growing AMR burden, research funding also increased. However, a comprehensive overview of the research output, including conceptual, temporal, and geographical trends, is missing. Therefore, this study uses topic modelling, a machine learning approach, to reveal the scientific evolution of AMR research and its trends, and provides an interactive user interface for further analyses.

Methods

Structural topic modelling (STM) was applied on a text corpus resulting from a PubMed query comprising AMR articles (1999-2018). A topic network was established and topic trends were analysed by frequency, proportion, and importance over time and space.

Findings

In total, 88 topics were identified in 158616 articles from 166 countries. AMR publications increased by 450% between 1999 and 2018, emphasizing the vibrancy of the field. Prominent topics in 2018 were *Strategies for emerging resistances and diseases, Nanoparticles*, and *Stewardship*. Emerging topics included *Water and environment*, and *Sequencing*. Geographical trends showed prominence of *Multidrug-resistant tuberculosis (MDR-TB)* in the WHO African Region, corresponding with the MDR-TB burden. China and India were growing contributors in recent years, following the United States of America as overall lead contributor.

Interpretation

This study provides a comprehensive overview of the AMR research output thereby revealing the AMR research response to the increased AMR burden. Both the results and the publicly available interactive database serve as a base to inform and optimise future research.

Funding

INTERREG-VA EurHealth-1Health (202085); European Commission Horizon 2020 Framework

Research in context

Evidence before this study

Prior to this study, PubMed, Web of Science, Scopus, and IEEE Xplore were queried to find studies providing a conceptual overview of antimicrobial resistance (AMR) research over time and space. The search string included keywords ("antimicrobial" OR antibiotic*) AND (resistan*) AND ("science mapping" OR bibliometric OR scientometric) in the title and abstract and focused on articles published before 2019 without language restrictions. Few studies were found relying on scientometric and bibliometric methods to assess either subfields of AMR research (e.g., AMR among uropathogens) or AMR-related fields (e.g., microbiology). No studies were found that focus on the entire AMR field. Therefore, this science mapping study using topic modelling was performed to provide an overview of the AMR field by identifying and assessing topics, trends, and geographical differences over time.

Added value of this study

To the best of our knowledge, this study is the first to use a science mapping approach to provide a comprehensive overview of the entire AMR research field, covering over 150 thousand articles published between 1999 and 2018. Our findings revealed important (e.g., *Strategies for emerging resistances and diseases, Nanoparticles,* and *Stewardship*) and emerging (e.g., *Water and environment,* and *Sequencing*) topics in AMR research. Lastly, this study resulted in an interactive user interface where all data are presented for further analyses.

Implications of all the available evidence

Our comprehensive overview of the AMR field, including its conceptual structure, and temporal and geographical trends revealed the response of the research community to the AMR burden. The results and the openly available supporting data provide the base to guide future funding and research directions to tackle AMR.

Keywords: antimicrobial resistance; global health; research activity; geographic mapping; machine learning;

Introduction

Antimicrobial resistance (AMR) is challenging health and healthcare globally. The burden gradually increased over time and recent reports depict extreme predictions, although global estimates are difficult to derive.^{1,2} Previously well-treatable infections require new therapeutic strategies, while already difficult-to-treat diseases have developed extensive resistance, e.g., multidrug-resistant tuberculosis (MDR-TB). International policy bodies and governments have put AMR high on the political agenda and call for more research to ease the AMR rise.^{3,4} Hence, various dedicated research funding are increasing, the response in AMR research output (i.e., scientific evolution) remains unknown; a holistic view on the entire field and its structure is lacking.

Neither the AMR burden nor the appropriate financial resources are equally distributed.^{1,2} Thus, providing a comprehensive picture requires assessing geographical differences. The conceptual structure of AMR research is highly heterogeneous due to its cross-disciplinary nature, making it difficult to grasp the overall picture and interrelatedness of research topics.⁸ However, the structure of the AMR field is essential to identify temporal and geographical trends, assess funding effects, and help guide future research and funding.

Identifying research topics and trends within an entire field is challenging. The amount of publications can hardly be overseen by single individuals anymore. Few studies addressed trends in AMR-related research based on scientometric and bibliometric approaches (i.e., by quantitative means). They focused on the global research output on AMR among uropathogens, carbapenem resistance, AMR in the environment, and AMR history.^{9–12} Other studies aimed at broader levels by identifying research topics in microbiology between 1945-2016 and 2012-2016.^{13,14} These approaches were either too narrow by investigating merely parts of the AMR field or too broad to identify AMR and related subgroups. So far, no comprehensive study is available to provide information on global AMR research activities.

Data-driven, computational approaches can provide solutions to the challenge of identifying topics and trends in texts. Particularly, topic modelling has been used to study entire research fields before.¹⁵ Topic modelling is a statistical approach, which enables semi-automated topic discovery and exploration within texts.^{16,17} The underlying assumption is that a text consists of one or several topics made up of various words which are likely to co-occur and define the respective topic. Today's available computational resources allow for applying this unsupervised machine learning technique to large collections of documents.

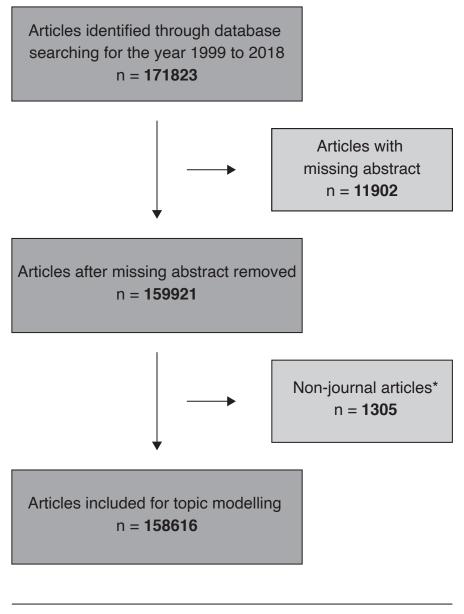
Studying the entire body of scientific literature on AMR in bacteria and fungi is unprecedented. Our study uses topic modelling to provide an overview of the AMR field by identifying and assessing topics, trends, and geographical differences over time. The study also lays the groundwork for further analyses by providing an interactive user interface, which provides guidance for future research directions in AMR.

Methods

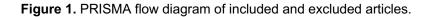
Data & Search String

Data was retrieved from the PubMed database using a comprehensive search string to reflect the entire AMR field accessed through the PubMed API.^{18–20} The search string was: ("Anti-Bacterial Agents"[Mesh] OR Anti-Bacterial*[tiab] OR antibacterial*[tiab] OR antibiotic*[tiab] OR antimicrobial*[tiab] OR antimycobacterial*[tiab] OR "Antifungal Agents"[Mesh] OR Anti-fungal*[tiab] OR "Antifungal Agents"[Mesh] OR "Intifungal Agents"[Mesh] OR "Microbial Sensitivity Tests"[Mesh]). The search results formed the text corpus of this study.

The extracted variables were: PMID number, author names, affiliations, title, abstract, journal, and database entry year. Records were included if they were published between 1999 and 2018, included an English abstract, and were not part of a set of exclusion criteria for article types (Figure 1). Records' citations were downloaded from the NCBI Entrez database.



*) Non-journal articles or any of type: Address, Autobiography, Bibliography, Biography, Corrected and Republished Article, Dataset, Directory, Duplicate Publication, Editorial, Festschrift, Interview, Lecture, Legal Case, Letter, News, Newspaper Article, Patient Education Handout, Portrait, Published Erratum, Video-Audio Media, Webcast



Data pre-processing

Title and abstract were merged into one text variable, excluding non-word and character strings with less than two characters. Generic and domain-specific (Appendix S1) stopwords were removed from the text.²¹ Finally, all text was stemmed using the snowball stemming

algorithm.²¹ First author countries were extracted from the affiliation data and complementary grouped into World Health Organization (WHO) regions.

Centrality measures can be used to quantify the extent to which articles influenced each other using network structures²². This study considered four measures of centrality (Degree, H-index, PageRank, and Eigenvector) to assess directional relationships of citations between the articles. The PageRank measure was used to determine the importance of countries and topics over time as it had the highest contribution according to principal component analysis.²³

Topic modelling

We used structural topic modelling (STM), which extends classical topic modelling (details in Appendix S2) and is available through the stm R package.^{20,24} STM modelling has previously been applied to identify topics in scientific literature.^{15–17} STM modelling is generative similar to latent Dirichlet allocation (LDA) but with the added benefit of including document-level covariates. We used publication year, citation count, PageRank, and first author country as document-level covariates. The output of a topic model is a collection of *bag-of-words* where each bag consists of words that constitute a topic.²⁵ We set a broad initial range for the number of bags/topics (*K*; range 15-205) and chose the optimal number by considering how well each number of topics represents the text corpus both quantitatively and qualitatively. The optimal number for *K* was identified by considering the semantic coherence and exclusivity per model of *K* topics and assessing the topics' interpretabilit.^{15–17}

Each model's output in the identified range of *K* was assessed. Two researchers (CFL, CG) independently assessed all topics based on the associated terms and generated a describing name per topic. Topic names were further refined by scanning titles and abstracts of five highly associated articles per topic and five important articles per topic by PageRank. No topic name was assigned if this process did not converge to a meaningful name. Consensus was reached when both researchers differed in their generated topic names. Five independent AMR researchers reviewed this process and verified the generated topic names. The final model was chosen based on the highest number of topics with an assigned topic name. Each article was assigned the topic name of the topic comprising the highest proportion of the article's text. Topics in the final model were inductively coded into thematic groups to navigate the results.

Topic investigation

Topics were assessed with two different objectives: 1) analysing topic relationships; 2) identifying trends by frequency, proportion, and PageRank (importance) over time and space. Topic relationships were assessed using two data sources: 1) within-text-corpus citations for the included publications; 2) topic co-occurrence per article. These data were clustered using 1) hierarchical clustering with Ward's minimum variance method and 2) topic correlation estimation.²⁶ Publication bursts, i.e., the least amount of years comprising 50% of all publications starting at the earliest year possible, were calculated per topic.

Data availability and interactive user interface

This study generated substantial amounts of data that enable detailed analyses. The results in this manuscript present only selected highlights from these data. To repeat this study's analyses and to enable further analyses, an interactive web-based application was developed (https://topicsinamr.shinyapps.io/amr_topics/). Additionally, individual articles can be searched and assessed and the topic model can be leveraged to evaluate texts from new articles not included in this study. Moreover, the data used and generated in this study is openly available under (https://osf.io/j3d65/). All analyses and the application development were performed in R.²⁰

Results

In total, 158616 articles were included, showing a steady increase over the past 20 years (8.5% nominal annual increase) (Figure 2). In 2018, 14547 articles were published, an increase of 450% compared to 1999. The topic modelling process using the optimal number of K= 95 topics resulted in 88 named topics, covering 152780 articles (96.3%). All topics sorted by thematic groups are presented in Figure 3, including trend lines in publication frequency, annual proportion, and PageRank. The cluster analysis based on topic co-occurrence correlation revealed a tightly connected network of the AMR field (Figure 4).

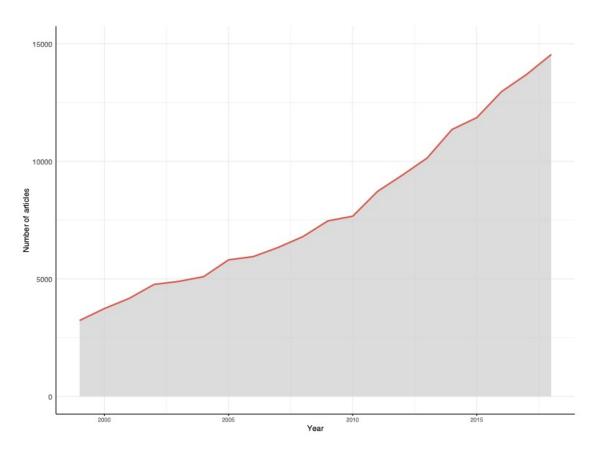


Figure 2. Total number of antimicrobial resistance (AMR) related publications indexed on PubMed per year (1999-2018) based on the applied search string: ("Anti-Bacterial Agents" [Mesh] OR Anti-Bacterial* [tiab] OR antibioticaterial* [tiab] OR antifungal Agents" [Mesh] OR Antifungal* [tiab] or anti-fungal* [tiab]) AND ("Drug Resistance" [Mesh] OR resistan* [tiab] OR "Microbial Sensitivity Tests" [Mesh]).

.

Topic name	Group	n	(%)	Trend (n)	Trend (%)	Trend (PageRank)
Bone, joint, tissue, and prosthetic infections	clinical	1327	0.9%	20 95	1.5 7.2	0.002 0.005
Case reports	clinical	35	2.3%	97 215	2.7	0.004 0.005
Clinical efficacy test	clinical	1486	1.0%	45 92	3 6.2	0.012
Community- acquired respiratory infections	clinical	1755	1.1%	103 🔨 36	5.9 2.1	0.028 📥 0.011
Diarrheal diseases	clinical	1333	0.9%	26 105	2 7.9	0.005 0.008
Longterm treatment outcome	clinical	939	0.6%	32 73	3.4 7.8	0.003 - 0.005
Ocular infections	clinical	931	0.6%	28 52	3 .6	0.006 0.004
PK/PD	clinical	2540	1.7%	33 223	1.3 8.8	0.005 0.016
Respiratory infections in chronic lung patients	clinical	677	0.4%	20	3	0.042 0.008
Risk factors and outcome in bacteraemia	clinical	2945	1.9%	41 266	1.4 9	0.042 0.028
Skin infection treatment	clinical	1001	0.7%	42 85	4.2	0.002 0.003
STD and neonatal infections	clinical	977	0.6%	15 81	1.5 - 8.3	0.003 - 0.005
Surgical site infections	clinical	1265	0.8%	24 116	1.9 9.2	0.003 0.005
Urinary tract infections	clinical	1573	1.0%	20 130	1.3 8.3	0.011 0.010
Active compound extration from plants	compound	35	2.3%	40 253	1.1 7.2	0.002
Alternative wound treatment	compound	1308	0.9%	16 177	1.2	0.002
Antimicrobial peptides	compound	2403	1.6%	55 221	2.3	0.007
Antimicrobials and cell wall interaction	compound	933	0.6%	13 133	1.4 14.3	0.023 0.007
Antimicrobials and microorganism cell membrane	compound	1700	1.1%	28 204	1.6	0.003 - 0.010

.

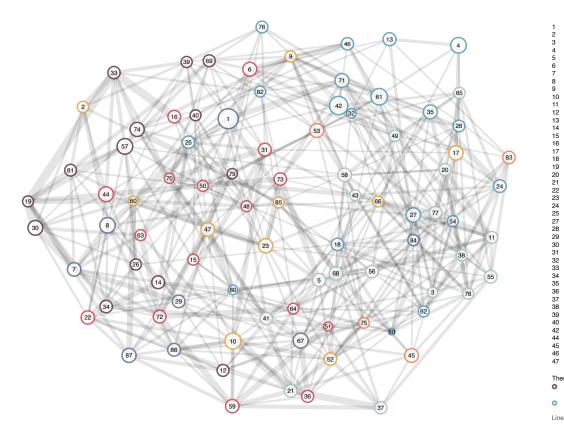
Antimicrobials and molecular interactions	compound	2645	1.7%	83 🚅 191	3.1 7.2	0.118 0.020
Essential oils	compound	1865	1.2%	13 164	0.7	0.002
Fluoroquinolones	compound	525	0.3%	26 15	5 2.9	0.003 0.005
Fusidic acid	compound	53	0.0%	3	5.7	0.002 - 0.003
Honey	compound	459	0.3%	6 45	1.3	0.002 0.004
Introduction of new antimicrobials	compound	1538	1.0%	36 92	2.3 6	0.010 .014
Isolation of new antimicrobial agents	compound	900	0.6%	22	2.49	0.002 0.004
Metal complex	compound	1239	0.8%	16	1.3	0.004 0.003
Nanoparticles	compound	42	2.8%	6 726	0.1	0.003 - 0.007
New compound synthesis	compound	5839	3.8%	128 - 419	2.2 ~~~~ 7.2	0.081
Novel molecular targets	compound	2400	1.6%	12 292	0.5	0.006 0.011
Probiotics	compound	1547	1.0%	15	1 9.9	0.005
Synergistic agents	compound	900	0.6%	13	1.4 •••••• 9.1	0.003 .007
Aquaculture	environment	810	0.5%	13 127	1.6	0.003
Biofilms	environment	2327	1.5%	13 245	0.6	0.007
Fungal diseases in plants	environment	1604	1.0%	25 146	1.6 9.1	0.009 0.005
Water and environment	environment	2348	1.5%	7 - 497	0.3 21.2	0.003 - 0.010
Antifungal susceptibility testing	method	1513	1.0%	37 4112	2.4 7.4	0.029 - 0.011
(Systematic) reviews	methods	1124	0.7%	4 156	0.4	0.011 0.008
Data modeling and estimation	methods	917	0.6%	12 114	1.3 - 12.4	0.006
MIC testing	methods	2227	1.5%	120 77	5.4 3.5	0.023 0.019
Microbial identification in blood cultures	methods	500	0.3%	7 - 31	1.46.2	0.002 0.003

Pre-clinical testing	methods	1001	0.7%	21 117	2.1	0.009
Purification of antimicrobial substances	methods	879	0.6%	17 85	1.9 9.7	0.002 0.004
Rapid antimicrobial susceptibility testing	methods	2578	1.7%	33 250	1.3 9.7	0.004 0.013
Sequencing	methods	1600	1.0%	2 - 317	0.1	0.003 - 0.013
Spectroscopy and compounds from natural resources	methods	2635	1.7%	52 188	2 7.1	0.003 - 0.005
Typing	methods	38	2.5%	94 282	2.4 7.3	0.021
Beta-lactamase	organism	885	0.6%	32 68	3.6	0.036
Candida species	organism	2413	1.6%	72 161	3 6.7	0.012 0.021
CoNS	organism	907	0.6%	20 58	2.2	0.003
CRE/CPE	organism	1734	1.1%	26 174	1.5 10	0.015
ESBL	organism	2103	1.4%	19 157	0.9	0.012
Escherichia coli	organism	367	0.2%	7 29	1.9	0.002
Helicobacter eradication	organism	1671	1.1%	95 96	5.7	0.008
Intracellular pathogens	organism	944	0.6%	31 84	3.3 8.9	0.008
MDR Acinetobacter	organism	913	0.6%	7 - 87	0.8	0.005 0.013
MDR-TB	organism	2971	1.9%	51 224	1.7	0.003 - 0.018
Oral flora & anaerobes	organism	895	0.6%	43 36	4.8 • 4	0.005 0.004
Salmonella	organism	1383	0.9%	23 97	1.7	0.086 0.010
Staphylococcus aureus	organism	1756	1.1%	24 93	1.4 5.3	0.006 0.020
Streptococcus pneumoniae and vaccination	organism	2070	1.4%	63 100	3 4.8	0.005 6.012
ТВ	organism	1581	1.0%	39 127	2.58	0.004 0.014
Vancomycin resistance	organism	629	0.4%	12	1.9	0.008 6000

Food contamination and preservation	strategy	1011	0.7%	14 9 6	9.5	0.020
Infection control	strategy	1687	1.1%	38 146	2.38.7	0.007 - 0.011
Institutional surveillance	strategy	2176	1.4%	47 165	2.2	0.003 0.016
International surveillance	strategy	1760	1.2%	43 188	2.4	0.006
Resistance patterns on hospital level	strategy	2519	1.6%	24 225	1 8.9	0.005 - 0.009
Resistance profiles in livestock and humans	strategy	3091	2.0%	42 341	1.4 11	0.013 - 0.016
Stewardship	strategy	3383	2.2%	51 523	1.5	0.012
Strategies for emerging resistances and diseases	strategy	7548	4.9%	137 - 784	1.8 10.4	0.029 0.057
Azole resistance	system	1033	0.7%	28 126	2.7	0.011 0.013
Bacterial growth conditions	system	957	0.6%	26 53	2.7	0.007 0.003
Bacterial persistence	system	918	0.6%	27 70	2.9 7.6	0.015
Biosynthetic gene cluster	system	714	0.5%	33 48	4.6 .7	0.040
Cell response to stress	system	1359	0.9%	20 152	1.5	0.003 - 0.008
Cytotoxicity	system	1072	0.7%	39 92	3.68.6	0.002 - 0.003
Efflux pumps	system	1693	1.1%	28 111	1.7 6.6	0.023
Gene expression	system	1624	1.1%	16 178	1 11	0.023 0.014
Genetic transformation	system	1757	1.2%	59 103	3.4 5.9	0.004 0.007
Host immune response	system	2139	1.4%	67 238	3.1 11.1	0.005
Host microbiota	system	2036	1.3%	9 289	0.4	0.004 0.021
Innate antimicrobial response in animals and humans	system	981	0.6%	11	1.1 6.2	0.003 0.006

Mobile genetic elements	system	1706	1.1%	30 - 117	1.8 6.9	0.033 - 0.022
Plasmids	system	1444	0.9%	20 223	1.4	0.004
Protein function in cellular pathways	system	1330	0.9%	41 -77	3.1 5.8	0.009
Resistance genes	system	1911	1.3%	41 107	2.1	0.009
Resistance mechanisms in Gram-positives	system	1445	0.9%	65 - 1000 54	4.5 - 3.7	0.034 👝 0.031

Figure 3. 88 named topics in the field of AMR sorted alphabetically and by thematic group. Total number of publications per topic and in percent of all publications is presented. Trends in publication frequency, annual proportion, and PageRank are displayed for the entire period 1999-2018.



Active comp Resistance Candida spain Institutional Stewardship Pre-clinical Typing Protein func Diarrheal di Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm tr Cell respons Mobile gene Streptococc Rapid antimicrobia Introduction STD and ne	gene cluster ound extraction fro genes scies surveillance) elesting tion in cellular path esases s acquired respirator pathogens reradication by and compounds seatment outcome ie to stress tic elements us pneumoniae an icrobial susceptibili is and microorgani of new antimicrobi	hwas bry infecti from na d vaccin lity testin ism cell	ions Itural resource Nation	3	49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 66 63 64 66 67 68 69 70 72	Antifungal susceptibility t MIC testing CoNS Azole resistance Oral flora & anaerobes Escherichia coli Sequencing Biofilms Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in livt Host microbials and to
Active comp Resistance Candida spain Institutional Stewardship Pre-clinical Typing Protein func Diarrheal di Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm tr Cell respons Mobile gene Streptococc Rapid antimicrobia Introduction STD and ne	ound extraction fro genes cicles surveillance) esting tion in cellular path seases s acquired respirator pathogens reradication y and compounds satment outcome is to stress tic elements us pneumoniae am icrobial susceptibili is and microorgani of new antimicrobia	hwas bry infecti from na d vaccin lity testin ism cell	ions Itural resource Nation	3	51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 66 66 66 68 69 70 72	CoNS Azole resistance Oral flora & anaerobes Escherichia coli Sequencing Biofilms Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticiles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbida
Resistance Candida spi Institutional Stewardship Pre-clinical Typing Protein func Diarrheal di Essential oil Community- Intracellular Besential oil Community- Intracellular Spectroscop Probiotics Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	genes socies surveillance besting tion in cellular path seases s acquired respirator pathogens reradication ny and compounds beatment outcome ie to stress tic elements us pneumoniae an ircobial susceptibili is and microorgani of new antimicrobi	hwas bry infecti from na d vaccin lity testin ism cell	ions Itural resource Nation	5	52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 72	Azole resistance Oral flora & anaerobes Escherichia coli Sequencing Biofilms Isolation of new antimicr Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbiata
Candida spe Institutional Stewardship Pre-clinical ' Typing Protein func Diarrheal di: Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm tr Cell respons Mobile gene Streptococc Rapid antim Antimicrobio Introduction STD and ne	icles surveillance) esting tion in cellular path esases s acquired respirator pathogens eradication y and compounds eatment outcome ie to stress tic elements us pneumoniae an icrobial susceptibili s and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	3	53 54 55 56 57 58 59 60 61 62 63 64 65 66 68 69 70 72	Oral flora & anaerobes Escherichia coli Sequencing Biofilms Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbida
Institutional Stewardship Pre-clinical Typing Protein func Diarrheal di Essential oil Community- Intracellular Helicobacte Spectrosco Probiotics Streptococc Robile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	surveillance lesting tion in cellular path seases acquired respirator pathogens reradication ay and compounds beatment outcome se to stress tic elements us pneumoniae and tic elements us pneumoniae and tic elements us and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	5	54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 72	Escherichia coli Sequencing Biofilms Isolation of new antimicre Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in livt Host microbiota
Stewardship Pre-clinical i Typing Protein func Diarrheal di Essential oli Essential oli Community- Intracellular Helicobacte Spectroscop Probiotics Longterm tr Cell respons Mobile gene Streptoococ Rapid antim Antimicrobia Introduction STD and ne	lesting tion in cellular path esases s acquired respirator pathogens reradication y and compounds eatment outcome ie to stress tio elements us pneumoniae an icrobial susceptibili is and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	3	55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 72	Sequencing Biofilms Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbida
Pre-clinical Typing Protein func Diarrheal di Essential oil Community Intracellular Helicobacte Spectroscop Probiotics Longterm tri Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	esting tion in cellular path seases s acquired respirator pathogens eradication yy and compounds eatment outcome ie to stress tic elements us pneumoniae an irrobial susceptibili us and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	3	56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 72	Biofilms Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in livt Host microbiota
Typing Protein func Diarrhead di Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm tr Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	in cellular path seases s acquired respirator pathogens reradication by and compounds seatment outcome se to stress tic elements us pneumoniae an icrobial susceptibili is and microorgani of new antimicrobi ontatal infections	ry infecti from na id vaccin lity testin ism cell	atural resource nation	3	57 58 59 60 61 62 63 64 65 66 67 68 69 70 72	Isolation of new antimicro Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbiota
Protein func Diarrheal dii Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm fro Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	seases s acquired respirator pathogens reradication by and compounds eatment outcome se to stress tic elements us pneumoniae an icrobial susceptibili us and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	3	58 59 60 61 62 63 64 65 66 67 68 69 70 72	Genetic transformation Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Diarrheal dis Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm trr Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	seases s acquired respirator pathogens reradication by and compounds eatment outcome se to stress tic elements us pneumoniae an icrobial susceptibili us and microorgani of new antimicrobi	ry infecti from na id vaccin lity testin ism cell	atural resource nation	5	59 60 61 62 63 64 65 66 67 68 69 70 72	Efflux pumps Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in livt Host microbiota
Essential oil Community- Intracellular Helicobacte Spectroscop Probiotics Longterm frr Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	s acquired respirator pathogens r eradication py and compounds eatment outcome set to stress tic elements us pneumoniae an icrobial susceptibili ls and microorgani of new antimicroor onatal infections	from na d vaccin lity testin lism cell	atural resource nation	3	60 61 62 63 64 65 66 67 68 69 70 72	Case reports Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in liv Host microbida
Community- Intracellular Helicobacte Spectroscop Probiotics Longterm fr Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	acquired respirator pathogens r eradication yy and compounds eatment outcome se to stress tic elements us pneumoniae ana icrobial susceptibili Isl and microorgani of new antimicrobi onatal infections	from na d vaccin lity testin lism cell	atural resource nation	3	61 62 63 64 65 66 67 68 69 70 72	Host immune response ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Intracellular Helicobacte Spectroscop Probiotics Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	pathogens eradication yy and compounds eatment outcome set to stress tic elements us pneumoniae and icrobial susceptibili Isl and microorgani of new antimicrobi onatal infections	from na d vaccin lity testin lism cell	atural resource nation	3	62 63 64 65 66 67 68 69 70 72	ESBL Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Helicobacte Spectroscop Probiotics Longterm tre Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	eradication y and compounds eatment outcome se to stress tic elements us pneumoniae and icrobial susceptibili Is and microorgani of new antimicrobio onatal infections	nd vaccin lity testin lism cell	nation	3	63 64 65 66 67 68 69 70 72	Microbial identification in Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Spectroscop Probiotics Longterm tri Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	by and compounds eatment outcome se to stress tic elements us pneumoniae and icrobial susceptibili uls and microorgani of new antimicrobii onatal infections	nd vaccin lity testin lism cell	nation	3	64 65 66 67 68 69 70 72	Nanoparticles Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Probiotics Longterm tre Cell respons Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	eatment outcome se to stress us pneumoniae and icrobial susceptibili uls and microorgani of new antimicrobi. onatal infections	nd vaccin lity testin lism cell	nation	3	65 66 67 68 69 70 72	Antimicrobials and cell w MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Longterm tre Cell response Mobile gene Streptococco Rapid antim Antimicrobia Introduction STD and ne	e to stress tic elements us pneumoniae and icrobial susceptibili uls and microorgani of new antimicrobio onatal infections	lity testin iism cell	ng		66 67 68 69 70 72	MDR Acinetobacter Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Cell respons Mobile gene Streptococcc Rapid antim Antimicrobia Introduction STD and ne	e to stress tic elements us pneumoniae and icrobial susceptibili uls and microorgani of new antimicrobio onatal infections	lity testin iism cell	ng		67 68 69 70 72	Beta-lactamase Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Mobile gene Streptococc Rapid antim Antimicrobia Introduction STD and ne	tic elements us pneumoniae and icrobial susceptibili uls and microorgani of new antimicrobia onatal infections	lity testin iism cell	ng		68 69 70 72	Cytotoxicity Purification of antimicrob Resistance profiles in live Host microbiota
Streptococc Rapid antim Antimicrobia Introduction STD and ne	us pneumoniae and icrobial susceptibili Ils and microorgani of new antimicrobi onatal infections	lity testin iism cell	ng		69 70 72	Purification of antimicrob Resistance profiles in live Host microbiota
Rapid antim Antimicrobia Introduction STD and ne	icrobial susceptibili Is and microorgani of new antimicrobio onatal infections	lity testin iism cell	ng		70 72	Resistance profiles in live Host microbiota
Antimicrobia Introduction STD and ne	Is and microorgani of new antimicrobi onatal infections	ism cell			72	Host microbiota
Introduction STD and ne	of new antimicrobi onatal infections		membrane			
STD and ne	onatal infections	lais				
					74	Bone, joint, tissue, and p
					76	Vancomycin resistance
	Is and molecular in	nteractio	ons		77	Novel molecular targets
Metal comp					78	CRE/CPE
Infection co					79	TB
	and outcome in ba	acteraen	nia		80	PK/PD
Staphylococ	cus aureus				81 82	Aquaculture
Honey						Alternative wound treatm
Clinical effic					83 84	Gene expression
Urinary trac						Bacterial growth conditio
Antimicrobia	i peptides				85	Respiratory infections in
Salmonella					86	Fluoroquinolones
Plasmids	··				87	Surgical site infections
		in anima	us and numans			Synergistic agents
						Fungal diseases in plants
		om naaiti	ine			Food contamination and Data modeling and estim
		in-positi	ive			International surveillance
						Resistance patterns on h
	sistence					Fusidic acid
MDH-1B					95	Fusicic acid
groups:						
cal C	environment	0	organism	0	system	
	methods	0	strategy			
	Innate antim Skin infectio Ocular infect Resistance i New compoi Bacterial per MDR-TB groups: al	Innate antimicrobial response Skin infection treatment Ocular infections Resistance mechanisms in gra New compound synthesis Bacterial persistence WDR-TB groups: al O environment bound O methods	Innate antimicrobial response in anima Skin inflection treatment Ocular infections Resistance mechanisms in gram-posit New compound synthesis Bacterial persistence MDR-TB groups: al o environment o	Innate antimicrobial response in animals and humans Skin inflection treatment Ocular infections Resistance mechanisms in gram-positive New compound synthesis Bacterial persistence WDR-TB groups: al O environment O organism	Innate antimicrobial response in animals and humans Skin inflections Coular infections Resistance mechanisms in gram-positive New compound synthesis Bacterial persistence WDR-TB groups: al O environment O organism O	Innate antimicrobial response in animals and humans 89 Skin inflection treatment 90 Ocular infections 91 Resistance mechanisms in gram-positive 92 New compound synthesis 93 Bacterial persistence 94 MDR-TB 95 groups: al O environment O organism O system

susceptibility testing tance anaerohes coli new antimicrobial agents nsformation s ne response entification in blood cultures als and cell wall interaction tobacter nase of antimicrobial substances profiles in livestock and humans biota tissue, and prosthetic infections n resistance cular targets wound treatment ession owth conditions infections in chronic lung patients olones e infections agents ases in plants mination and preservation ling and estimation al surveillance patterns on hospital level

Figure 4. Topic network in AMR research based on topic co-occurrence generated. The 88 topics names with their corresponding number are displayed. Colours are used to highlight the 7 thematic groups within the network: clinical (purple), environment (orange), organism (red), system (grey-blue), compound (light blue), methods (yellow), and strategy (dark blue). Line size within the network corresponds to correlation weight (more weight equals thicker lines) and node size corresponds to the proportion of published articles.

General trends

Time

The absolute number and proportion of articles per topic underwent various changes over the last 20 years (Figure 2 and Figure 3). The most prevalent and important topics (top three), changes in prevalence and importance over the last 20 years, and publication bursts are highlighted in Figure 5.

Prevalence, importance, publication bursts

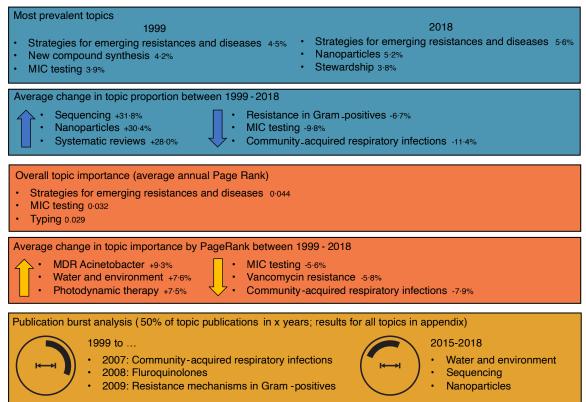
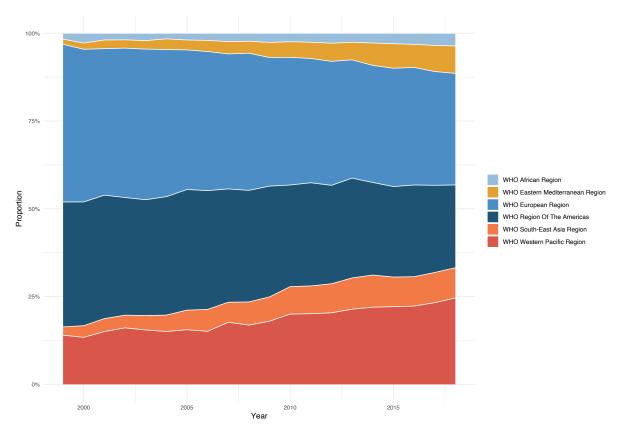


Figure 5. The most prevalent and important topics (top three) by: proportion of all published articles per year in 1999 and 2018 and average change (positive and negative) in proportion of all published articles between 1999 and 2018 (blue); average change (positive and negative) in topic importance (calculated PageRank) between 1999 and 2018 (orange); and publication bursts (period comprising 50% of all publications within one topic), longest and shortest intervals are shown (yellow).

Geography

WHO regions

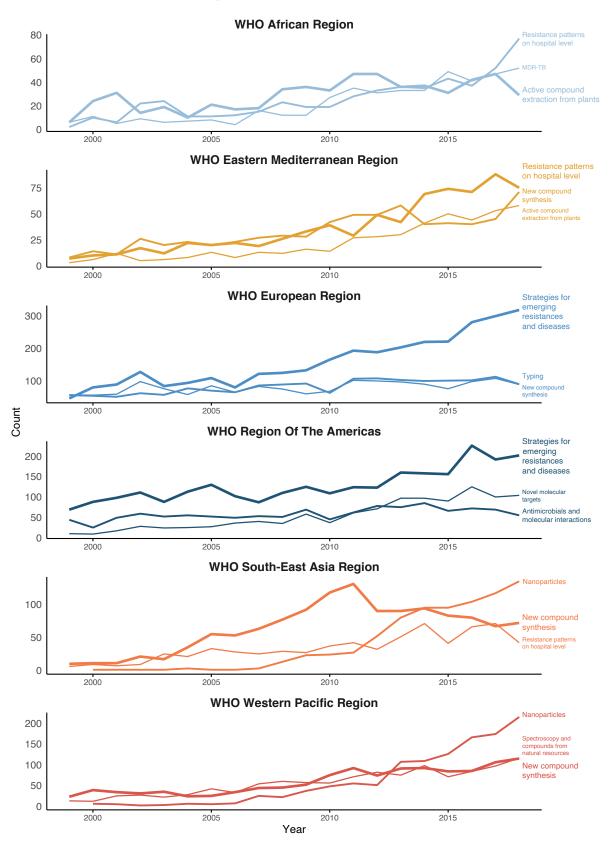
The first author's country of affiliation could be extracted for 153 879 articles (97.0%) and 166 unique countries. Based on the country names, the results were stratified by WHO regions. The WHO regions of the Americas and the European Region were the largest overall contributors. However, other regions steadily increased their proportion of articles over time (Figure 6).





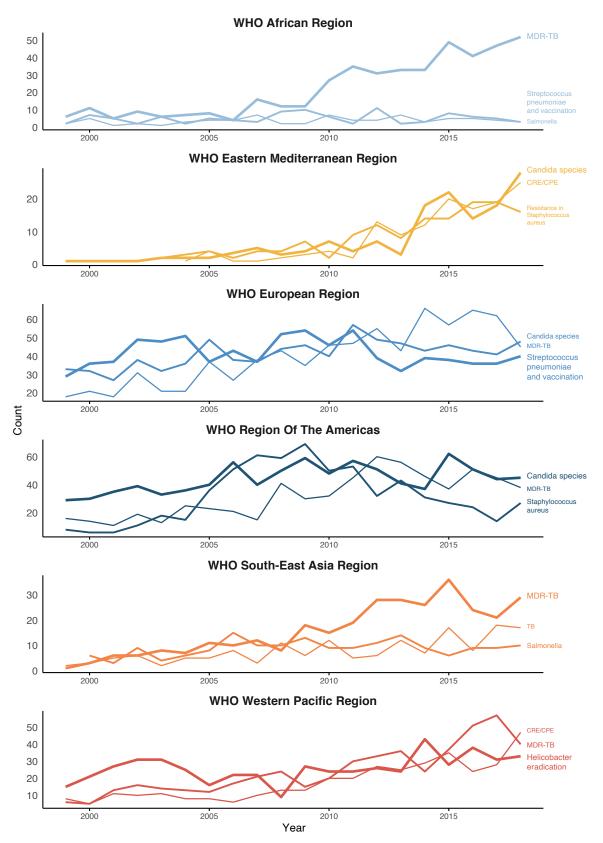
Varying patterns in the three most researched topics over time were observed per WHO region (Figure 7). While the European region and the region of the Americas focused strongly on *Strategies for emerging resistances and diseases,* the south-east Asian region and the western Pacific region demonstrated an increasing focus on *New compound synthesis* and *Nanoparticles. Resistance patterns on the hospital level* and *Active compound extraction from plants* were research priorities in the African and eastern Mediterranean region. Only the African region listed an organism-related topic (*MDR-TB*) among the top three topics. The importance of *MDR-TB* worldwide was further emphasized when assessing only organism-

related topics per WHO region (Figure 8). All regions but the eastern Mediterranean listed *MDR-TB* in the top three of all organism-related topics over time.



Cumulative top three organism-related topics per WHO region; line size and text size corresponds to total topic size.

Figure 7. Research priorities within WHO regions per year (1999-2018). Top three topics by overall count per WHO region; line size and text size correspond to the total number of publications per topic and region.



Cumulative top three organism-related topics per WHO region; line size and text size corresponds to total topic size.

Figure 8. Organism-related research priorities within WHO regions per year. Top three organismrelated topics by overall count per WHO region; line size and text size correspond to the total number of publications per topic and region.

Countries

At the country level, the United States of America (USA) contributed the most (ranked first in number of publications) to the body of AMR literature each year. However, China significantly increased its research output (n=2021 in 2018; +27·2% nominal annual increase), ranking second in 2018 after the USA (n=2092 in 2018; +4.9% nominal annual increase) and before India (n=1010 in 2018; +16·5% nominal annual increase). Regarding importance, according to PageRank per year, the USA led unchallenged throughout the years, followed by the United Kingdom (UK), France, Canada, Spain, and Germany (all countries in Appendix S6).

Thematic groups

For the following sections, results were stratified into thematic groups based on topic names (Figure 3). Each thematic group will be introduced in terms of topic representation and elaborated on in terms of nominal and relative increase/decrease over time, importance based on PageRanks, and contributing countries.

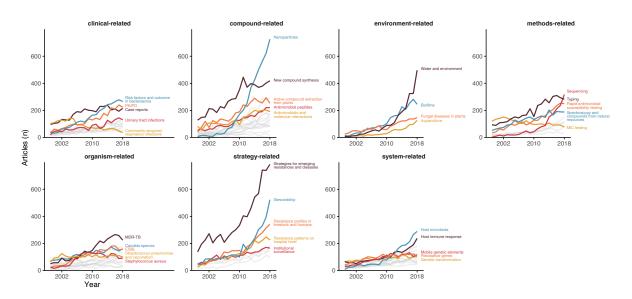


Figure 9. Five largest topics by total article count per thematic topic per year (1999-2018).

Clinical-related theme

The clinical-related theme represents 14 topics related to clinical infections. Most clinicalrelated topics showed a steady increase over time, except for *Community-acquired respiratory infections*, which decreased after 2004. The most researched topic in 2018 was *Risk factors and outcome in bacteraemia* (n=266 articles), which steadily increased both nominally (+11.5% annually) and relatively (+3.0% annually) over the past 20 years (Figure 9). The topic importance by PageRank also increased over that period (+2.6% annually). In 2018, the countries who contributed most to *Risk factors and outcome in bacteraemia* were the USA (18.1%), China (14.6%), and the Republic of Korea (7.3%).

Compound-related theme

New antimicrobials and new compound strategies are grouped in the compound-related theme (18 topics). All compound-related topics showed a nominal increase over time, while the topic *Nanoparticles* showed a particularly steep increase after 2006 (32.6% mean annual increase) (Figure 9). In 2018, China and India were the largest contributors to *Nanoparticles*, ranking first (21.6%) and second (17.2%), respectively. A similar trend was observed for *New compound synthesis*. The largest contributors for *Active compound extraction from plants* were India (12.8%), Brazil (9.9%), and South Africa (5.6%). The USA was the largest contributor to *Antimicrobial peptides* and *Antimicrobials and molecular interactions*, although China ranked first in *Antimicrobial peptides* after 2015.

Environment-related theme

The environment-related theme comprises the topics *Water and environment, Biofilms, Aquaculture,* and *Fungal diseases in plants. Water and environment* showed a remarkable increase over time (+18·4% annual increase in proportion), ranking fourth in absolute and relative numbers in 2018 and also increased in importance by PageRank (+7·6% annual increase) (Figure 9). China mainly drove this trend with an almost exponential increase in the number of annual publications. In 2018, China contributed 40·9% of all publications on this topic. Moreover, *Water and environment* was China's most researched topic after 2016. The topic was a driver for China's increasing contribution to the overall body of AMR literature. The USA ranked second $(12\cdot1\%)$ in *Water and environment* in 2018.

Methods-related theme

The methods-related theme represents 11 topics related to laboratory techniques and general research methodologies. *Typing* was the most prevalent method-related topic over 20 years

(2.5% overall) but fell behind *Sequencing* in 2018, which showed a substantial increase after 2009 (+29.5% annually) (Figure 9). In the PageRank analysis, *Typing* ranked third in 2018 and demonstrated steady importance over the years. *Sequencing* ranked lower in the PageRank than *Typing* but gained importance over the years (+5.7% annual increase). In 2018, articles contributing to *Typing* came predominantly from China (20.9%), Brazil (7.8%), and the Republic of Korea (5.0%). In the same year, the USA (17.4%) was leading in *Sequencing* studies before China (13.6%) and the UK (6.0%).

Organism-related theme

Topics with a clear association to a specific organism or pathogen are grouped in the organism-related theme (16 topics). Of these topics, *MDR-TB* was most prevalent over time, with a peak in relative proportion in 2012 (10.8% of all topics). *Staphylococcus aureus* displayed a short but prominent peak in 2007-2008. The topics which increased the most in terms of the annual change in proportion were *Escherichia coli* (+9.3%), *MDR Acinetobacter* (+9.0%), *ESBL* (+4.6%), *CRE/CPE* (+3.8%), and CoNS (+2.3%).

MDR-TB showed a distinct geographic distribution from the general trends in the AMR field. In 2018, most publications came from South Africa (11·6%), China (9·8%), and India (9·4%). Of the top ten countries with the highest burden of *MDR-TB*, according to the WHO, that were included in this study, 70% showed *MDR-TB* in their three most researched topics (Belarus, Kyrgyzstan, Republic of Moldova, Kazakhstan, Tajikistan, Uzbekistan, and Azerbaijan)²⁷.

Strategy-related theme

The strategy-related theme represents topics related to conceptual strategies against AMR (eight topics). By far, the most prevalent topic was *Strategies for emerging resistances and diseases*, which also prevailed overall in AMR research (4.9% of total). The topic showed close links with all other topics as an overarching topic (see also citation cluster analysis in Appendix S4). *Stewardship, Institutional surveillance,* and *International surveillance* were the following three most prevalent strategy-related topics overall.

Stewardship was the third most researched topic in 2018 ($3\cdot8\%$), showing a remarkable increase over time (+16·1% annually) and in particular after 2010. Next to the USA, the UK significantly increased its contribution to *Stewardship*, ranking first in the topic in 2018 (16·8%). Within the UK, *Stewardship* was the most researched topic in 2018 (13·5%). Similar trends were identified for Australia and France, where *Stewardship* ranked first and second in 2018, respectively.

International surveillance and Institutional surveillance also increased in overall proportion but to a reduced extent (+1.7% and +0.5% annually, respectively). The importance by PageRank decreased by -2.4% annually for International surveillance, in contrast to an annual +1.3% increase for Stewardship. The USA (17.3%), the UK (10.9%), and Australia (7.3%) were the main contributors to International surveillance. Institutional surveillance showed similar trends to international surveillance but with a more dominant role for the USA (21.1%) as the primary contributor. Despite these similarities, the importance by PageRank for Institutional surveillance and surveillance.

System-related theme

Molecular aspects and host characteristics are the focus of the 17 topics in the system-related theme. *Host microbiota* stood out with an annual nominal and relative increase of +24.0% and +14.5%, respectively (Figure 9). *Host microbiota* also gained importance over the years measured by PageRank (+6.3%). Other topics (*Mobile genetic elements, Efflux pumps, Resistance genes*, and *Genetic transformation*) did not show large variations in relative numbers over the years. The topics *Mobile genetic elements, Efflux pumps*, and *Resistance genes* were identified as important topics in terms of their PageRank over the years despite showing a steady decline. The USA was the largest contributor to most system-related topics, except for *Resistance genes* and *Mobile genetic elements*, where China was leading.

Discussion

This study mapped 20 years (1999-2018) of AMR research using data-driven text-based techniques (structural topic modelling). We identified 88 topics across 166 countries. Topics, trends, and geographical differences were assessed. AMR publications increased by 450% over the two decades, and grew by 129% between 2004 and 2013 compared to 48.9% for all PubMed publications over the same period.²⁸ The most prominent topics in 2018 were *Strategies for emerging resistances and diseases, Nanoparticles,* and *Stewardship*. Emerging topics included *Water and environment,* and *Sequencing*. Geographical trends highlighted the positive correlation between research on *MDR-TB* and the related MDR-TB burden.

AMR research geography

The research geography changed remarkably over time, mainly due to increased contributions from India and China. The USA remained the leading country but showed a slower increase

compared to other increasing countries. The geographical changes are similar to overall publication trends on PubMed, yet more pronounced.²⁸ For example, China increased its overall research output by 271% on PubMed (2004-2013) compared to 609% for AMR over the same time.²⁸

We identified research priorities on (supra-)national levels. Overall, the WHO European region and the region of the Americas produce much output on strategies and molecular aspects. *New compounds* and *Nanoparticles* were under focus in the South-East Asian and Western Pacific region. The African region is the only region listing an organism-specific topic, *MDR-TB*, in the top three researched topics. Considering organism-specific topics alone, *MDR-TB* played a significant role in most WHO regions and dominated organism-specific topics in the African region. It is positive to see that *MDR-TB* ranked high across AMR research output in the most affected countries. However, the overall trend for *MDR-TB* remained unchanged.

General topic overview

We identified 88 topics that cover the diversity in AMR with high granularity. Previous more limited studies validate parts of the identified topics and our results overlap with a study that assessed topics in microbiology.¹⁴ Another study also assessed themes in microbiology and identified broad themes (e.g., animal models).¹³ Our results offer a greater granularity and a more extensive variety of topics (not exclusively microbiological), which can be grouped into these existing microbiological themes. Organism-specific trends were verified in the existing literature. *Staphylococcus aureus* showed an increase after 2004 with a peak in 2007/2008 and a decrease thereafter, as also observed by a scientometric study.¹¹ Global surveillance data for methicillin-resistant *Staphylococcus aureus* (MRSA) also confirms this trend curve between the early 2000s and 2016.²⁹ Among methods-related topics, *Sequencing* stood out and can be referred to as a "hot topic" based on publication bursts and PageRank, as confirmed by another topic modelling study on bioinformatics.³⁰

Limitations

Our study has several limitations. Foremost, topic modelling requires a manual selection of the number of topics (K). A higher value of K topics could have revealed additional topics. Furthermore, the risk of misclassified articles can not be fully eradicated as topic names were assigned based on the largest topic proportion identified per article. We extracted AMR publications using a holistic search definition but only one database was queried. The applied AMR definition comprised bacteria or fungi, whereas viruses and parasites were not included.

Study inclusion was not limited by language as most indexed articles provide English titles and abstracts. Nevertheless, non-English publications might still be missing, potentially limiting geographical comparisons. Also, countries were determined by first author affiliation. This affiliation does not reflect the entire international network in the field. However, we hypothesize that the first authors might be closer to the geographic setting of the research focus.

Future research

The generated data of this study enables detailed insights. Topic trends can be compared at the national level (Appendix S7), which was beyond the scope of this study. Moreover, leveraging additional data sources such as economic, funding, or diseases burden data could be used to study correlation effects. These future studies can deepen our understanding of the AMR field and streamline efforts to tackle current and future challenges. To this extent, all data are publicly available (https://osf.io/j3d65/) accompanied by an interactive analysis tool [topicsinamr.shinyapps.io/amr_topics]. We encourage readers to use the presented results to guide their analyses.

Conclusion

We provide a comprehensive global map on important temporal and geographical trends in AMR over two decades. Using the entire AMR literature, an unprecedented data-driven approach identified several "hot" topics such as *Sequencing, Nanoparticles, Stewardship, Water and environment,* and *MDR-TB*. Simultaneously, the global research community has been changing and countries like China and India have become substantial contributors. This study and its publicly available data can be used to achieve a holistic view of the developments in the AMR field. Data on the global AMR burden is growing and information on AMR research funding is available. In the future, this can also be linked to data on global AMR research output, which has now been comprehensively assessed for the first time.

Acknowledgements

We thank Jan Arends, Matthijs S. Berends, Francis F. Cavallo, Marjolein Heuker, and Nico Meessen for supporting the topic review and validation process.

Funding

This research was supported by the INTERREG-VA (202085) funded project EurHealth-1Health (http://www.eurhealth1health.eu), part of a Dutch-German cross-border network supported by the European Commission, the Dutch Ministry of Health, Welfare and Sport, the Ministry of Economy, Innovation, Digitalisation and Energy of the German Federal State of North Rhine-Westphalia and the Ministry for National and European Affairs and Regional Development of Lower Saxony. In addition, this study was part of a project funded by the European Union's Horizon 2020 research and innovation programme under the Marie Sklodowska-Curie grant agreement 713660 (MSCA-COFUND-2015-DP "Pronkjewail").

Conflict of interests

We declare no conflict of interests.

References

- O'Neill J. Review on Antimicrobial Resistance: Tackling a crisis for the health and wealth of nations. London, 2014 https://amrreview.org/sites/default/files/AMR%20Review%20Paper%20-%20Tackling%20a%20crisis%20for%20the%20health%20and%20wealth%20of%20nati ons_1.pdf (accessed Feb 1, 2021).
- 2 Limmathurotsakul D, Dunachie S, Fukuda K, et al. Improving the estimation of the global burden of antimicrobial resistant infections. *Lancet Infect Dis* 2019; **19**: e392–8.
- 3 World Health Organization. Global Action Plan on Antimicrobial Resistance. Geneva, 2015 https://apps.who.int/iris/bitstream/handle/10665/193736/9789241509763_eng.pdf (accessed Feb 1, 2021).
- 4 OECD. Stemming the Superbug Tide. OECD Health Policy Studies 2018; : 224.
- 5 Joint Programming Initiative of Antimicrobial Resistance (JPIAMR). Mapping of AMR Research Funding. Stockholm, 2017 https://www.jpiamr.eu/wpcontent/uploads/2019/02/Mapping-of-AMR-research-funding-2017-report.pdf (accessed Feb 1, 2021).
- 6 Kostyanev T, Bonten MJM, O'Brien S, et al. The Innovative Medicines Initiative's New Drugs for Bad Bugs programme: European public-private partnerships for the development of new strategies to tackle antibiotic resistance. *J Antimicrob Chemother* 2016; **71**: 290–5.

- 7 Global Antibiotic Research & Development Partnership (GARDP). Activity Report 2018. Geneva, 2019 https://gardp.org/uploads/2019/08/GARDP-2018-Activity-Report.pdf (accessed Feb 1, 2021).
- 8 Vourc'h G, Brun J, Ducrot C, Cosson J-F, Le Masson P, Weil B. Using design theory to foster innovative cross-disciplinary research: Lessons learned from a research network focused on antimicrobial use and animal microbes' resistance to antimicrobials. *Veterinary and Animal Science* 2018; **6**: 12–20.
- 9 Sweileh WM, Al-Jabi SW, Zyoud SH, Sawalha AF, Abu-Taha AS. Global research output in antimicrobial resistance among uropathogens: A bibliometric analysis (2002-2016). *J Glob Antimicrob Resist* 2018; **13**: 104–14.
- 10 Sweileh WM, Shraim NY, Al-Jabi SW, Sawalha AF, AbuTaha AS, Zyoud SH. Bibliometric analysis of global scientific research on carbapenem resistance (1986-2015). *Ann Clin Microbiol Antimicrob* 2016; **15**: 56.
- 11 Brandt C, Makarewicz O, Fischer T, et al. The bigger picture: the history of antibiotics and antimicrobial resistance displayed by scientometric data. *Int J Antimicrob Agents* 2014; **44**: 424–30.
- Sweileh WM, Moh'd Mansour A. Bibliometric analysis of global research output on antimicrobial resistance in the environment (2000-2019). *Glob Health Res Policy* 2020; 5: 37.
- 13 Dehdarirad T, Sotudeh H, Freer J. Bibliometric mapping of microbiology research topics (2012-16): a comparison by socioeconomic development and infectious disease vulnerability values. *FEMS Microbiol Lett* 2019; **366**. DOI:10.1093/femsle/fnz004.
- 14 Moral-Munoz JA, Lucena-Antón D, Perez-Cabezas V, Carmona-Barrientos I, González-Medina G, Ruiz-Molinero C. Highly cited papers in Microbiology: identification and conceptual analysis. *FEMS Microbiol Lett* 2018; **365**. DOI:10.1093/femsle/fny230.
- 15 Bohr J, Dunlap RE. Key Topics in environmental sociology, 1990–2014: results from a computational text analysis. *Environmental Sociology* 2018; **4**: 181–95.
- 16 Chen X, Zou D, Cheng G, Xie H. Detecting latent topics and trends in educational technologies over four decades using structural topic modeling: A retrospective of all volumes of computer & education. *Comput Educ* 2020; : 103855.
- 17 Clare SM, Hickey GM. Modelling Research Topic Trends in Community Forestry. *Small-scale Forestry* 2019; **18**: 149–63.
- 18 Kovalchik S. RISmed: Download Content from NCBI Databases. 2017. https://CRAN.Rproject.org/package=RISmed (accessed Feb 1, 2021).
- 19 Fantini D. easyPubMed: Search and Retrieve Scientific Publication Records from PubMed. 2019. https://CRAN.R-project.org/package=easyPubMed (accessed Feb 1, 2021).
- 20 R Core Team. R: A Language and Environment for Statistical Computing v3.6.1. Vienna, Austria, 2019 https://www.R-project.org/ (accessed Feb 1, 2021).
- 21 Porter MF. Snowball: A language for stemming algorithms. 2001 https://snowballstem.org/texts/introduction.html (accessed Feb 1, 2021).
- 22 Oldham S, Fulcher B, Parkes L, Arnatkevic lūtė A, Suo C, Fornito A. Consistency and

differences between centrality measures across distinct classes of networks. *PLoS One* 2019; **14**: e0220061.

- 23 Page L, Brin S, Motwani R, Winograd T. The pagerank citation ranking: Bringing order to the web. Stanford, 1999.
- 24 Roberts M, Stewart B, Tingley D. stm: An R Package for Structural Topic Models. *Journal of Statistical Software, Articles* 2019; **91**: 1–40.
- 25 Blei DM, Ng AY, Jordan MI. Latent Dirichlet Allocation. *J Mach Learn Res* 2003; **3**: 993–1022.
- 26 Murtagh F, Contreras P. Algorithms for hierarchical clustering: an overview. WIREs Data Mining and Knowledge Discovery. 2012; **2**: 86–97.
- 27 World Health Organization. Global Tuberculosis Report 2019. Geneva, 2019 https://apps.who.int/iris/bitstream/handle/10665/329368/9789241565714-eng.pdf (accessed Feb 1, 2021).
- 28 Vardakas KZ, Tsopanakis G, Poulopoulou A, Falagas ME. An analysis of factors contributing to PubMed's growth. *J Informetr* 2015; **9**: 592–617.
- 29 Diekema DJ, Pfaller MA, Shortridge D, Zervos M, Jones RN. Twenty-Year Trends in Antimicrobial Susceptibilities Among Staphylococcus aureus From the SENTRY Antimicrobial Surveillance Program. *Open Forum Infect Dis* 2019; **6**: S47–53.
- 30 Hahn A, Mohanty SD, Manda P. What's Hot and What's Not? Exploring Trends in Bioinformatics Literature Using Topic Modeling and Keyword Analysis. In: Cai Z, Daescu O, Li M, eds. Bioinformatics Research and Applications. Springer International Publishing. Honolulu, 2017.