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Global monitoring of antimicrobial resistance based on metagenomics analyses of urban sewage

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Antimicrobial resistance (AMR) is a serious threat to global public health, but obtaining representative data on AMR for healthy human populations is difficult. Here, we use metagenomic analysis of untreated sewage to characterize the bacterial resistome from 79 sites in 60 countries. We find systematic differences in abundance and diversity of AMR genes between Europe/North-America/Oceania and Africa/Asia/South-America. Antimicrobial use data and bacterial taxonomy only explains a minor part of the AMR variation that we observe. We find no evidence for cross-selection between antimicrobial classes, or for effect of air travel between sites. However, AMR gene abundance strongly correlates with socioeconomic, health and environmental factors, which we use to predict AMR gene abundances in all countries in the world. Our findings suggest that global AMR gene diversity and abundance vary by region, and that improving sanitation and health could potentially limit the global burden of AMR. We propose metagenomic analysis of sewage as an ethically acceptable and economically feasible approach for continuous global surveillance and prediction of AMR.
Antimicrobial resistance (AMR) is a cross-cutting and increasing threat to global health\textsuperscript{1,2}, and it threatens to undermine decades of progress in the treatment of infectious diseases. AMR is a complex problem with multiple and interconnected drivers, which may include changing dynamics in travel, trade, climate change, and populations. Reliable information that accurately describes and characterizes the global occurrence and transmission of AMR is essential to address this challenge and to support national and global priority setting, public health actions, and treatment decisions.

Current surveillance of AMR is often focusing on a few pathogens only and mainly based on passive reporting of notypatatory laboratory results for specific pathogens isolated from human clinical infections\textsuperscript{1,2–5}. This procedure leads to significant time delays, often incomparable data, and a narrow pathogen spectrum not capturing all relevant AMR genes, where the major part might be present in the commensal bacterial flora of healthy individuals. However, obtaining fecal samples from healthy humans is logistically difficult.

From a surveillance point of view, urban sewage is attractive because it provides sampling material from a large and mostly healthy population, which otherwise would not be feasible to monitor. Globally, a rapidly increased proportion of the human population live in urban areas\textsuperscript{6} and an increasing proportion of especially transmissible resistance genes in a single sample. Moreover, the bacterial composition of sewage is complex and not only reflects human feces but also the changes occurring in the sewer. A comparison with publicly available metagenomic data, although generated using different DNA-purification methods, suggested that our urban sewage samples resemble more the human fecal microbiome than the animal fecal microbiome from chickens, pigs, or mice (Supplementary Fig. 5).

The total AMR gene abundances varied across sites and continents (Fig. 1b, Supplementary Data 4). The highest AMR gene levels were observed in African countries (average: 2034.3 fragments per kilo base per million fragments (FPKM)), although Brazil had the highest abundance of all (4616.9 FPKM). At the lower end of the spectrum were Oceania (New Zealand and Australia) (average: 529.5 FPKM). To the best of our knowledge, comparable data on the global occurrence of AMR genes of predominantly healthy people do not exist. In agreement with our findings, a previous study on the resistome from toilet waste from long-distance flights\textsuperscript{14} suggested that the AMR levels in South Asia were higher than in Europe. Data on AMR in bacteria isolated from clinical infections in humans, collected by the World Health Organization (WHO)\textsuperscript{3}, suggest a high prevalence of AMR in many developing countries, even though several of the national studies reported by the WHO give contradictory results\textsuperscript{4}.

A total of 1546 genera were detected across all samples (range: 942–1367 genera per sample), but a limited number of bacterial genera dominated (Supplementary Data 3, Supplementary Fig. 4). Several of the dominant bacterial genera were typical fecal, such as \textit{Faecalibacterium}, \textit{Bacteroides}, \textit{Escherichia}, \textit{Streptococcus}, and \textit{Bifidobacterium}. However, other highly abundant bacterial genera, such as \textit{Acidovorax} and \textit{Acinetobacter}, are most likely environmental bacteria. Thus, the bacterial composition of sewage is complex and does not only reflect human feces but also the changes occurring in the sewer. A comparison with publicly available metagenomic data, although generated using different DNA-purification methods, suggested that our urban sewage samples resemble more the human fecal microbiome than the animal fecal microbiome from chickens, pigs, or mice (Supplementary Fig. 5).

Metagenomic techniques, using short-read next-generation sequencing data, benefit from the ability to quantify thousands of especially transmissible resistance genes in a single sample. Moreover, it can provide additional information about the presence of bacterial species, pathogens, and virulence genes and the data can be reanalyzed if novel genes of interest are identified. It should, however, also be acknowledged that short-read metagenomics might provide limited information regarding the host of the genes or the genetic environment. Metagenomics has been found to be superior to conventional methods for AMR surveillance in pig herds\textsuperscript{13} and has also been utilized for the surveillance of global AMR gene dissemination through international flights\textsuperscript{14}. Additionally, an extensively shared resistome was observed across urban sewage samples within China\textsuperscript{15}, as well as between individuals and environmental samples in Lima, Peru\textsuperscript{16}. Interestingly, Pehrsson et al.\textsuperscript{16} showed that even though changes in the bacterial composition were observed between feces and sewage, this was not the case for AMR genes.

Here we use metagenomic analysis of untreated sewage to characterize the bacterial resistome from 79 sites in 60 countries. We find systematic differences in abundance and diversity of AMR genes between Europe/North-America/Oceania and Africa/Asia/South-America. Antimicrobial use data and bacterial taxonomy only explain a minor part of the AMR variation that we observe. However, AMR gene abundance strongly correlates with socio-economic, health, and environmental factors, which we use to predict AMR gene abundances in all countries in the world. Our findings suggest that global AMR gene diversity and abundance vary by region and that improving sanitation and health could potentially limit the global burden of AMR.

**Results**

**Global distribution of AMR genes.** Domestic sewage was collected from 79 sample locations, covering 7 geographical regions from 74 cities in 60 countries (Fig. 1a, Supplementary Data 1). Each sample was sequenced using Illumina HiSeq and the resulting data (>1.4 Tb) processed using MGmapper\textsuperscript{17}. The average number of reads per sample was 120 million reads (range: 8 million–398 million). An average of 0.03% of the reads were assigned to AMR genes, while on average 29%, 1%, 0.4%, and 0.2% were assigned to bacterial, protozoa, plants, and human genomic material, respectively (Supplementary Data 2). Sixty-eight percent of the reads could not be assigned to any reference sequence, and other metagenomic studies have also found larger number of un-mapped reads (42%–46%\textsuperscript{18}). Rarefaction of the reads mapping to bacterial genomes showed a tendency toward saturation in the sequence data (Supplementary Fig. 1).

Analyses of duplicate samples from separate days from eight sites showed a high degree of within-site reproducibility (Supplementary Fig. 2). Comparison of the data from the same countries showed much less (permutation test, \(p<0.0001\)) variance across sites within countries than across sites between different countries (Supplementary Fig. 3), which suggests that a single sample taken from one large city is representative of the overall occurrence of AMR in a country.

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A total of 1625 different AMR genes belonging to 408 gene groups were identified, including several that have emerged recently, such as \textit{CTX-M}, \textit{NDM}, \textit{mcr}, and \textit{optA} (Supplementary Data 4). Several different AMR genes might encode resistance to the same antimicrobial agent. Thus the relative abundance of AMR genes was aggregated to the corresponding antimicrobial class level for each sample to explore major trends across countries (Fig. 1c). AMR genes encoding resistance toward macrolides, tetracyclines, aminoglycosides, beta-lactams, and sulfonamides were the most abundant. Most samples from Europe and North America had a high relative proportion of macrolide resistance genes, while Asian
Fig. 1 Global sewage sampling sites and overview of antimicrobial resistance (AMR) abundance and composition. **a** Map of the sampling sites. **b** Boxplots of the total AMR fragments per kilo base per million fragments per sample, stratified by region. Each sample is represented by a dot with horizontal jitter for visibility. The horizontal box lines represent the first quartile, the median, and the third quartile. Whiskers denote the range of points within the first quartile – 1.5× the interquartile range and the third quartile + 1.5× the interquartile range. **c** Relative AMR abundance per antimicrobial class (AmGlyc aminoglycoside, Mac macrolide, Oxa oxazolidinone, Phen phenicol, Quin quinolone). **d** Relative abundance of the 15 most common AMR genes (mef(A) _10: mef(A)_10_AF376746).

and African samples had a large proportion of genes providing resistance to sulfonamides and phenicols. Fifteen AMR genes contributed >50% of the total AMR abundance (Fig. 1d). This proportion was especially prominent for Europe, North-America, and Oceania. None of the dominant AMR genes are known to be restricted to specific bacterial genera. We analyzed the AMR abundances on both the gene and antimicrobial class levels using both principal coordinate analyses (PCoAs) and heat maps (Fig. 2, Supplementary Fig. 6). With regard to the sample resistome dissimilarities, there was a clear geographical separation along the first principal coordinate of samples from...
Europe/North-America/Oceania and samples from Africa/Asia/South-America. Regional groupings explained 27% of the dissimilarity between sample resistomes (adonis2, \( p < 0.001 \); Fig. 2a). The separation among the groups was mainly driven by higher levels of resistance to tetracycline, aminoglycosides, beta-lactams, sulfonamides, and trimethoprim in the Africa/Asia/South America cluster, whereas macrolide resistance was more evenly distributed among all samples (Fig. 2b). A clearer clustering was observed based on regions, compared with clustering based on diet, income, or the Human Development Index (HDI) (Supplementary Figs. 6–7). A stronger regional separation was observed on the AMR class level, compared with the gene level (Fig. 2b, Supplementary Fig. 6). On the class level, a very clear separation of all samples in two groups was observed, where only a single European sample (Malta) did not cluster with all other samples from Europe/North America/Oceania (Fig. 2b). Furthermore, only one sample from Asia (Kazakhstan), one from the Middle East (Turkey), and one from South America (Galapagos Islands) clustered with the Europe/North-America/Oceania group.

Several alpha diversity indices for each sample resistome were calculated (Supplementary Fig. 8). The resistome median evenness was higher in African and Asian countries compared with resistomes from other geographical locations. Thus not only do these regions have a higher prevalence of AMR genes, but also a more equal distribution of the different AMR genes.

Analyses of the alpha diversity of the bacterial taxonomic composition showed less separation according to geographical regions compared with the AMR genes (Supplementary Figs. 9–11), and regions explained less of the variation in the resistome (adonis2, 27%) compared with the bacterial composition (adonis2, 17%). To test the degree to which bacterial genus-level composition of the microbiota is associated with the resistomes, Procrustes analyses were performed (Supplementary Fig. 12). We compared ordinations of the bacterial taxonomic composition with the resistome and found that they correlated significantly (protest, \( p < 0.001 \)).

**AMR genes and drug use association.** Several studies have shown that antimicrobial use (AMU) selects for AMR\(^{22,23}\) and that reducing AMU often results in reduced AMR\(^{24,25}\), except when there is interference between genetically linked AMR genes conferring resistance to different antimicrobial classes\(^{26}\). It has also been suggested that AMU explains only some of the variation\(^{22,23}\) and that other factors such as diet, cultural traditions and occupation also have an influence\(^{22,27}\).

In this study, the association between AMU and the occurrence of AMR in the sewage samples was estimated using a generalized linear mixed-effects model, with the counts of genes in the different antimicrobial classes as an outcome (Poisson) adjusting for sequencing depth and gene length. As AMU data, we included...
AMR genes (glmm, fi for resistance) and the total AMU (indirect selection via cross-resistance). As before, this model showed a significant increase in the abundance of AMR genes belonging to a specific antimicrobial class with increasing usage of that antimicrobial class, we found no significant effect of total usage of all antimicrobials on abundance of the different classes (Supplementary Fig. 13A, Supplementary Table 1). This suggests that, while AMU of a specific class is an important driver of AMR genes encoding resistance to that class, the effects of cross- and/or co-resistance appear to have a relatively minor contribution to AMR abundances. Furthermore, our model showed that the countries with a lower HDI (i.e., higher in rank) have lower abundances of AMR genes (glmm, p = 0.01) and that the number of passengers arriving in a country via flights has no effect on the abundance of AMR genes (glmm, p = 0.62).

A second (similar) model was developed to test the association between the abundance of AMR genes on the antimicrobial class level and the antimicrobial residue levels. Again we accounted for the potential effects of cross-resistance by fitting fixed effects of both residues of the antimicrobial class that a resistance gene primarily confers resistance to (direct selection for resistance) and the total antimicrobial residue levels (indirect selection via cross-resistance). As before, this model showed a significant increase in the abundance of AMR genes belonging to a specific antimicrobial class with increasing levels of drug residues of that antimicrobial class; however, we found no significant effect of total residue levels (Supplementary Fig. 13B). As with the previous model, this model also showed that the countries with a lower HDI (i.e., higher in rank) were less abundant in terms of AMU genes (glmm, p < 0.001), and that the number of passengers arriving in a country via flights had no effect on the abundance of AMR genes (glmm, p = 0.746), indicating that the results are robust.

Of interest is that there was no correlation between AMU and antimicrobial residue in our data (lm, R² = 0.00098, p = 0.55). One possible explanation for this could be that AMR abundances accumulates on a long timescale because of the average usage in a country (i.e., (long term) AMU impacts the level of resistance); however, on a much shorter timescale fluctuations in AMU will change the AMR composition (diversity) somewhat, which is captured by the residue levels, which can be interpreted as a (short) temporal snapshot of the actual usage.

Prediction of AMR based on population-level health data. We observed that AMU only explained a minor part of the occurrence of AMR across the world. In addition, AMU data are difficult to obtain and likely subject to limitations due to the lack of an effective prescription system in many countries. Measuring antimicrobial residue levels in sewage as a proxy for AMU is also associated with uncertainties and the rapid degradation in the environment of the heavily used beta-lactamase-sensitive antimicrobials makes it difficult to reliably measure them.

Because the HDI was strongly associated with AMR, in the results of our model, we hypothesized that a number of other factors could be either drivers or indicators for AMR. To investigate this further, we used 1503 variables from the World Bank’s Health, Nutrition and Population as well as Development indicator data sets collected between the years 2000 and 2016 for 259 countries and territories to study the potential association with the observed AMR gene abundances. Using country-specific variables, we were able to explain up to 89% of the observed variation across the samples (Supplementary Fig. 14, Supplementary Table 2). Most of the variables associated with AMR levels were related to sanitation and general health (Fig. 3, Supplementary Fig. 15, Supplementary Table 3). Subsequently, the identified variables were used to predict the occurrence of AMR in 259 countries and territories. The three countries predicted to have the lowest level of AMR were The Netherlands, New Zealand, and Sweden, whereas the highest predicted AMR levels were for Tanzania, Vietnam, and Nigeria (Fig. 4, Supplementary Data 5). The predicted global country-level resistance levels were multiplied with the latest national population estimate and used to create global maps of healthy human-associated AMR (Supplementary Fig. 16).

Discussion

A reliable base of evidence that accurately describes and characterizes the global burden and transmission of AMR is essential to support national and global priority setting, public health actions, and treatment decisions. Compared to samples directly obtained from humans, a major advantage of sewage is that such samples can be easily obtained and analyzed without ethical concerns. Thus, while current efforts to improve surveillance of AMR in human clinical pathogens should be continued, we do suggest that our study provides the foundation for a flexible, simple, affordable, and ethically acceptable global real-time surveillance of AMR that could be immediately implemented globally also in low- and middle-income countries. The study design can furthermore be used for other infectious disease agents.

Our study represents, to the best of our knowledge, the first attempt to monitor and predict the occurrence of AMR in the globally predominantly healthy human population. Even though the study suffers from the limitation that only a single sample was analyzed from each site, our study suggests a strong systematic separation of regions of the world according to AMR gene abundance with high-income countries in Europe/North-America/Oceania constituting one cluster and low-income countries in Africa/Asia/South-America constituting another cluster. This separation was mainly driven by a relatively high abundance of a limited number of AMR genes encoding macrolide resistance genes in Europe/North-America/Oceania, compared with a general high abundance of several different AMR genes from different classes in the rest of the world. The countries standing out as having the most divergent distribution of AMR genes were Vietnam, India, and Brazil, suggesting that these countries could be hot spots for emergence of novel AMR mechanisms.

In this study, we used metagenomics that benefit from the ability to quantify thousands of genes simultaneously and that the data can be reanalyzed if novel genes of interest are identified. However, other methodologies might also be useful such as culture and PCR-based methods that might have better sensitivity. Comparative studies evaluating the usefulness of various technologies, including evaluation of sensitivity, specificity, and number of targets detected, are warranted.

In our study, we have focused on total AMR abundance. However, the resistance to the different antimicrobial classes are not equally important neither are all AMR genes. Thus further studies could also benefit from addressing specific resistance genes.

An analysis of the same IQVIA AMU data from 2000 to 2015, as we have used here, was recently published, and even though a significant increase in AMU was observed, especially for countries in Africa, Asia, and South-America, the quantities are still below most countries in Europe and North-America. We could not in our study find significant associations between
obtainable AMU data and the concentrations of residues measured, but we did observe the highest concentrations of antimicrobial agents in the African samples, which could suggest that measuring residues in sewage could provide alternative data for monitoring AMU compared to obtainable sales data.

Historically, most strategies to reduce AMR have focused on reducing AMU, which relies upon AMR imparting a fitness cost on the bacterial host, an effect that has been relatively weak in horizontally transferred AMR genes compared with chromosomal mutations. Other factors, such as those related to

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**Fig. 3** World Bank variables significantly associated with the observed antimicrobial resistance abundances. Detailed information concerning the variables in a–r are presented in the same order in Supplementary Table 3

**Fig. 4** Global predictions of antimicrobial resistance (AMR) abundance in all countries and territories in the world. Map colored according to predicted abundance of AMR from light blue (low AMR abundance) to dark blue (high AMR abundance). Global resistance predictions for the 259 countries and territories are shown in Supplementary Data 5.
transmission, including infection control, sanitation, access to clean water, access to assured quality antimicrobials and diagnostics, travel, and migration, have also been suggested to contribute significantly to AMR. In this study, we found that, irrespective of the diversity of AMR genes, the total AMR abundance was highly correlated with a limited number of World Bank variables, mainly concerning sanitation and health. In contrast, human air travel had no significant influence on AMR abundance. Importantly, this suggests that the total AMR abundance is mainly influenced by local/national parameters, and even though all AMR genes might rapidly disseminate and be found in all corners of the world, local selection is required for them to reach appreciable frequencies. These findings suggest that improving sanitation, health, and perhaps education as part of the Sustainable Development Goals [www.un.org/sustainabledevelopment/sustainable-development-goals/] would be effective strategies for limiting the global burden of AMR.

Methods
Ethics. It was confirmed that this and similar studies using human sewage in accordance with the Danish Act on scientific ethical treatment of health research (Journal no.: H-14013582) do not require approval from ethical committees.

Collection of urban sewage samples. The National Food Institute, Technical University of Denmark (DTU Food) launched an open invitation 25 September 2015 seeking potential collaborators to participate in the pilot study of the Global Sewage Surveillance Project (GSSP). The invitation was sent by electronic mail to the following networks and individual research collaborators for further dissemination: WHO Global Foodborne Infections Network (GEN) [http://www.who.int/foodint/en/], WHO Advisory Group on Integrated Surveillance of Antimicrobial Resistance (AGISAR) [http://www.who.int/foodsafety/areas_work/antimicrobial-resistance/agisar/en/], European Union Reference Laboratory for AMR network [www.eurl-ar.eu/], and to the European Food- and Waterborne Diseases and Zoonoses Network (FWD-Net) [http://ecdc.europa.eu/en/about-us/partnerships-and-networks/disease-and-networks/disease-and-laboratory-networks/fwd-net/].

Participation was cost neutral and managed by online registration that also included requests for proper packaging and sample containers and the need to sign a material transfer agreement or similar approval agreement to protect any intellectual property rights. All expenses related to the shipments were paid by DTU Food, and the shipments complied with the IATA regulation as per SP A197 because the content of the parcels was identified as UN3082 “Environmentally hazardous substance, liquid, not otherwise specified” but did not exceed 5 L of sewage.

A protocol that instructed how to collect the urban sewage samples as well as epidemiological, demographic, and geographical information was provided to each participant in the study (Supplementary Data 8). Participants were requested in conjunction with collecting the samples to submit via an online survey the captured information related to epidemiological, demographic, and geographical information as well as a digital image of the sampling site, if possible the GPS coordinates of the sampling location, the temperature of the sample at the time of sampling, pH of the sewage, and storage temperature of sample. From each location, on 2 consecutive days between 25 January and 5 February 2016, one representative, non-processed, unfiltered urban sewage sample of 2 L was collected from the respective main sewage pipeline(s) prior to the inlet of the wastewater treatment plant or from the main outlet to rivers or similar according to the protocol provided. Flow proportion sampling over 24 h was preferred.

Alternatively, three crude point samples were collected in a short time interval, i.e., at least 5 min between each individual sample, to ensure as much randomness as possible. The collected urban sewage was not treated, neither with additives nor DNA stabilizers and was recommended to be stored at −80 °C for at least 48 h prior to shipment to avoid the use of dry ice. The sample-specific data are provided in Supplementary Data 1 and an explanation of the content of this file provided as Supplementary Note 1.

Sample handling and DNA extraction. At DTU Food, a photograph of each sample container was taken upon arrival combined with a short remark describing the condition of the sample, e.g., solid frozen, liquid, coloration, etc. The samples of the first of the consecutive days were thawed for 12 h at approximately 20 °C before processing. After thawing, 250 mL of each sample were pelleted in a centrifuge at 10,000 × g for 10 min. The pellet was stored at −20 °C or −80 °C before DNA extraction and metagenomics analysis, and the supernatant was stored at −80 °C for sub-sampling of microbial residue and virus analysis. DNA was extracted from the sewage pellets according to an optimized protocol using the QIAamp Fast DNA Stool Mini Kit including twice the input material and initial bead beating. For each batch of DNA extractions, a DNA extraction blank control was processed in parallel with the sewage samples to monitor background DNA.

Whole-community sequencing. DNA was shipped on dry ice for library preparation and sequencing to the Oklahoma Medical Research Foundation (OMRF). DNA from all samples was mechanically sheared to a targeted fragment size of 300 bp using ultrasonication (Covaris E220evolution). Library preparation was performed with the NEXTflex PCR-free Library Preparation Kit (Bioo Scientific). The Bioo NEXTflex-96 adapter set (Bioo Scientific) was used, and in batches of roughly 60 files, the libraries were multiplexed and sequenced on the HiSeq3000 platform (Illumina), using 2 × 150-bp paired-end sequencing per flow cell. The raw sequencing data have been deposited at the European Nucleotide Archive under accession number ERP015409.

Trimming and mapping of sequencing reads. The reads were trimmed, including adaptor removal, using BBduk. [BBMap—Bushnell B. —https://sourceforge.net/projects/bbmap/] with a quality threshold at 20 and minimum length of 50 bp. Trimmed reads were used as input to the reference-based mapping and taxonomy-assignment tool MGmapper [17], which is based on BWA-MEM [53] version 0.7.12 and SAMTools [44] version 1.6. Reads were aligned against reference sequence databases for the best hit (Bestmode, i.e., a read can only map to 1 reference sequence). An acquired AMR gene database (ResFinder) [33] was used to annotate properly paired reads (MGmapper option fullmode) where each read pair had sequence coverage of at least 80% compared with the length of the trimmed reads. This was the only filter that was applied to discard a read pair. The AMR genes were of bacterial origin and could therefore align to both bacteria databases and the Resfinder database. To enable multiple database hits on a single read, the MGmapper option fullmode was used. For AMR genes, the Bestmode option in MGmapper for the most optimal abundance calculation. Genomic annotation was performed by identifying the best hit (MGmapper option bestmode) for a pair of reads when aligned against a range of reference sequence databases. Databases were primarily downloaded via NCBI genbank clade specific assembly_level. The other ftp site is a list of databases used by MGmapper includes: Human (GRCch38.p3), bacteria (closed genomes), MetaHITAssembly (PRJEB674—PRJEB1046), HumanMicrobiome (genomes assemblies), bacteria_draft, plasmid, archaea, virus, fungi, protozoa, vertebrates_mammals, vertebrates_other, invertebrates, plant, and nt. For the bacteria and bacteria_draft databases, sequences were selected from the assembly_summary.txt file, when annotated with the tags version_status='latest' and genome_rep='Full'. Furthermore, assembly_level='Complete genome' or 'Chromosome' were required for entries in the bacteria database and resfeg_category='representative genome' for entries in the bacteria_draft database. The plasmid database was constructed as the subset of bacteria and bacteria_draft databases having the word 'plasmid' in the fasta entry header line.

The total bacteria read count for a sample was calculated as the sum of read counts from each of the bacteria-related databases (bacteria, bacteria_draft, MetaHITAssembly, and HumanMicrobiome). The total fraction of unmapped reads for each sample sites were used to calculate the percentage of reads falling into Z-scores, i.e., the number of standard deviations from the mean. Setting an absolute Z-score threshold at 3 retained data from 79 sample sites. Data from Chad were excluded based on the Z-score threshold together with data from Gambia with suspiciously low resistance read counts; i.e., lower than those observed from DNA extraction control samples.

Bacterial and AMR gene distribution. Inspection of the count tables and the mapped reads distribution on the genomes revealed an overestimation of some genomes due to plasmids with high copy numbers. The issue only occurred in the included draft genomes, as the plasmid DNA were left out of the database with complete bacterial genomes. The distribution of mapped reads across contigs was expected to be evenly distributed, with some variation. The plasmids were revealed by large hit counts to specific contigs compared with the associated contigs in a draft genome. For each draft genome, the hits to each contig was normalized with respect to contig size. The median of the contig hits was found and the third quartile and the interquartile range was calculated. If a hit count was above the third quartile plus 1.5 times the interquartile range, then the hit count was interpreted as an overestimation and adjusted by replacing the hit count with the median.

Relative abundance of AMR genes and bacterial genera were calculated as FPKM. This was done to account for both sample-wise sequencing depth differences and size-dependence of reliability of observed genome assemblies. FPKM was calculated based on the adjusted sum of fragments assigned to a genome assembly, whether or not the genome was closed. For AMR genes, FPKM was calculated on each individual ResFinder reference sequence. FPKMs were subsequently summed up across categories to bacterial genera (NCBI taxid), drug class level (NCBI tax ID), and highly homologous AMR gene groups (CD-HIT-EST, 90% similarity) [38].

Within-site reproducibility. In order to test reproducibility of sewage samples, a dendrogram of resistome composition from all sewage samples including samples from eight sites that were double-sampled sewage was generated using Bray–Curtis
(BC) dissimilarities and hierarchical clustering (Supplementary Fig. 2). The replicated samples were taken by 2 days apart. The day 2 samples were taken twice. The day 2 samples were kept in freeze for 2 years prior sequencing. Samples from day 1 and day 2 were sequenced using the same DNA extraction and sequencing protocols. The replicated samples had higher resistome similarity to its own replicates and all eight sets of replicate samples were clustered with their own replicate. This result shows a strong reproducibility of sewage samples despite having different day of sampling and 2 years of storage. The repeats were not included in subsequent analyses.

**Within-country representativeness.** To assess whether samples from individual sites are representative of other sites in that country, we compared the BC dissimilarities for pairs of sites within the same country and in different countries for both resistome and bacteriome compositions. We assessed the significance of these differences using permutation tests. We permuted the country labels for each sample and reassessed the dissimilarities for pairs within their own country and in different countries with permuted labels. We repeated this procedure 10^6 times to build up a null distribution of the differences in dissimilarity within and among countries. We found that resistome dissimilarities were on average 34% higher for pairs of sites in different countries than for pairs of sites within the same country (permutation, p < 0.0001, Supplementary Fig. 3A and B). While the AMR gene abundance dissimilarities were 46% higher for pairs of sites in different countries than for pairs of sites within the same country (p < 0.0001, Supplementary Fig. 3C and D). These results show that there is less variance across sites within countries than across sites within different countries. Thus individual sites in this study are representative of other sites in that country.

**Sample composition comparison.** Metagenomes with the following accession numbers were downloaded from SRA (December 2017): ERR011089, ERR011114, ERR011344, ERR1104480, ERR1104481, ERR1121453, ERR1121455, ERR1121556, ERR1135427, ERR1135431, ERR1135437, ERR1135693, ERR1278103, ERR1278104, ERR1278105, ERR1414230, ERR1414260, ERR1527239, ERR1527240, ERR1527241, ERR1527247, ERR1527249, ERR1558700, ERR1559789, ERR1560016, ERR1560024, ERR1560100, ERR1655116, ERR1682090, ERR1682101, ERR1698980, ERR186217, ERR186217, ERR1950597, ERR1950599, ERR1950601, ERR469632, ERR469664, ERR469665, ERR675524, ERR675555, ERR675575, ERR675560, ERR1182251, ERR1202091, ERR1267395, ERR2175638, ERR2175725, ERR2175730, ERR2751194, ERR2891615, ERR2869168, ERR2869169, ERR2869170, ERR2869171, ERR2869172, ERR2869173, ERR2869174, ERR2869175, ERR2869176, ERR3605603, ERR3605634, ERR3673603, ERR3753605, ERR3753606, and ERR3753607. The quality of the data was assessed and if necessary adapters were removed and trimmed with a quality threshold at 20 and minimum length of 50 bp. All pairwise Jaccard distances of the aforementioned metagenomes, all global sewage samples, and the control samples were calculated with Mash35. The heat map was drawn in R 3.4.4 (pheatmap).

**Sample dissimilarities.** Matrices with relative abundances (FPKM) of AMR genes and bacterial genes were Hellinger-transformed using the decostand function in vegan. The BC dissimilarity matrices were then calculated using the vegdist function, also in vegan (Supplementary Data 6).

**Heat maps.** The relative abundances (FPKM) of AMR genes were log-transformed and visualized in a heat map (pheatmap), showing the 50 most abundant genes. The gene-wise dendrogram is based on Pearson product moment correlation coefficient (r) of FPKM values. The samples were clustered based on the aforementioned BC dissimilarity matrices, not just for the visualized genes, but all genes. Both dendrograms are the result of complete linkage clustering. The bacterial genera heat map was produced in the same way, while the AMR class-level heat map differs by using PPCM for hierarchical clustering of both AMR classes and samples. Continuous locations were included as metadata for both heat maps. For the AMR genes, we included World Bank income levels [http://apps.who.int/gho/data/node.dsd.1], GEMS country (http://www.who.int/gho/data/node.dsd.1) and the HDI (Supplementary Fig. 4A and B), while the bacteriome dissimilarities were calculated using the diversity function in the vegan package.

**Procrustes analysis.** The vegan package was used for comparing the resistome dissimilarities with the bacteriome dissimilarities. The protest function was used to scale and rotate the principal coordinates of the bacterial PCoA onto the principal coordinates of the resistome PCoA and testing the strength of the association.

**Graphics and statistics.** All plots and statistical analyses were carried out in Microsoft R Open 3.3.2.

**Correlation between AMU and external explanatory variables.** A multilevel Poisson model was developed to investigate the sources of variance for the abundance of AMU genes and the relationship between AMU and abundance of AMU genes found in the samples. The counts of the individual AMU genes in each of the samples (see “Collection of urban sewage samples” and “Whole-community sequencing” sections) aggregated at the antimicrobial class level was used as the dependent variable.

An observation-level random effect was used to model the over dispersion inherent to count data31. Because several samples were sequenced more than once on separate sequencing runs, we were able to estimate and correct for the noise in mean AMU gene abundance owing to the sampling process. Therefore, a categorical variable indicating which sample was used was included as a random effect (sample). A categorical variable identifying each location to allow for the estimation of variation in abundance of resistance genes between the different sampling locations (location) was included. Furthermore, a variable identifying the resistance class a resistance gene is included to estimate the variance due to differences in abundance between antimicrobial classes (class).

For the fixed effects, we included a measure of AMU at the country level. Data from the ECDC database (Supplementary Data 1) and data from the IMS database (Supplementary Data 2) were used to calculate a new variable from the two data sets. To this end, we used the data from the ECDC data set where available, to make up for missing values from the IMS data set by using a linear regression model. Because the data from the two data sets are highly correlated (r = 0.97, p < 0.01, Pearson’s product moment correlation), we could infer the (approximate) corresponding ECDC value from the IMS value for that particular country. The antimicrobial usage data were then log-transformed because it has been shown that many antimicrobial classes show high cross-resistance, where resistance to one antimicrobial class also confers resistance to another class, we accounted for the potential effects of cross-resistance by fitting effects of both the antimicrobial class that a resistance gene primarily confers resistance to (direct selection for resistance) and total AMU (indirect selection via cross-resistance). When building the total number of passengers arriving in a country in 2015 was used as a fixed effect in the model. Data on the number of passengers were extracted from the ICAO international flight database [https://portal.icao.int, downloaded April 2016] and log-transformed. Lastly, we included the United Nations HDI as a fixed effect. HDI data from 2015 were extracted for the United Nations Development Programme website and log-transformed and scaled before including them in the final model. The same model set-up was used to investigate the association between drug residue levels and AMR gene abundance. In this model, the data on the drug residues in the samples was included as a fixed effect instead of the AMU data. All other effects (random and fixed) were kept the same. Others models including temperature at the collection site at the day of sampling and Gross Domestic Product showed no significant association with AMR genes abundance (glmm’s, p > 0.05).

**Resistance prediction.** World Bank Health, Nutrition and Population as well as Development indicator data sets collected between the years 2000 and 2016 for 259 countries and territories were downloaded from http://databank.worldbank.org/data/home.aspx in October 2017 and used to formulate AMR predictive models. Imputations of missing data were conducted using the missForest R package, which is a random forest-based technique that is highly computationally efficient for high-dimensional data consisting of both categorical and continuous predictors. The final data set consisted of 1503 economic and health indicator variables (Supplementary Data 7). The most important variables predicting total resistance (FPKM) were selected from the World Bank data set and a recursive feature elimination method from the caret (Supplementary Table 2). The caret model was also run on all 1503 variables for comparison (Supplementary Data 4) and a good correlation was observed. The machine learning algorithms Support Vector Machine and random forest were compared for accuracy in predictions based on their R^2 and Root Mean Square Error44,45. Random forest was the best choice of model (Supplementary Table 2). Future work could be directed towards determining key features, especially where each of the features contributes little information46. The prediction model was trained for the 60 countries where resistance data were available from the current project followed by global predictions of resistance for all 239 countries and territories (Supplementary Data 3). Overfitting remains a major hurdle when applying predictive models especially involving many predictors. Breiman45 proved that random forest is protected from overfitting by the incorporation of out-of-bag (OOB) estimates and from the law of large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45. In the study of error estimates for large numbers. This followed from earlier proposals on the use of OOB estimates as a key part of estimation of generalization error44,45.
need for a set aside test set. OOB is the mean prediction error on each training sample

Random forests also aggregate many decision trees to limit overfitting as well as

equiv. This has an added advantage that, unlike cross-validation, where bias is

However, a ten-fold cross-validation was included during our model building by randomly partitioning model inputs into ten sets of roughly equal size followed by estimation of accuracy based on held-out samples. This held-out sample was each time returned to the training set and the procedure was repeated with the second subset held out and so forth. Cross-validation and checking for valid accuracy were also performed with an implication that accuracy scores reduce if there is overfitting and only "valid accuracy" is finally used.

Creation of global figures and maps. QGIS 2.18.11 using the cartogram package was used to create colored and distorted maps.

Analysis of tetracyclines, sulfonamides, macrolides, and quinolones. The analy-

For sample pretreatment, two 10-mL portions of each sample of sewage supernatant were weighed into separate 50-mL tubes, after which internal standards were

Calculation of defined daily dosages (DDD) based on residues. After con-

For the sulfonamides, the excluded drugs constitute 11%.

The concentrations of antimicrobial residues were transformed into DDDS of antimicrobials for systemic use using the WHO DDD database [www.who.cc/ndd_dldx.html]

Data availability: The raw sequencing data have been deposited at the European Nucleotide Archive under accession number ERP015409. Data on the number of passengers were obtained under license from the ICAO international flight database and is available from the authors with restrictions. Data on antimicrobial use were obtained from ECDC and IMShealth and the data used in our analyses are provided in supplementary Table 1. IMShealth data were obtained under license and has restricted use. All source data underlying the multivariate analyses, the machine learning and Figs. 1–4 and supplementary Figs. 1–16 are included in supplementary tables or supplementary data.

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F.M.A. conceived the idea and ensured the funding. F.M.A., R.S.H., and M.P.K. elaborated the idea and planned the study. R.S.H. conducted the sampling with assistance from J.A., A.A.-K., S.K., and J.K. and in collaboration with The Global Sewage Surveillance Project Consortium. S.I.P., M.S., T.Z., A.M.d.R.H., H.S., F.M.A., and P.M. generated the data and planned the analyses. P.M., P.N., O. Lukjancenko, T.R., B.V., L.M.K., D.N., R.S.K., P.T.L.C.C., J.K.V., P.L., C.A., G.C., O. Lund, T.H., M.W., H.V., T.-S.P., B.P., S.R., T.N.P., and F.M.A. performed the bioinformatics, statistical, and epidemiological analysis. F.M.A. wrote the first draft. All authors have seen and accepted the final version.

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