

Large-scale assessment of antimicrobial resistance marker databases for genetic phenotype prediction: a systematic review

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Background: Antimicrobial resistance (AMR) is a rising health threat with 10 million annual casualties estimated by 2050. Appropriate treatment of infectious diseases with the right antibiotics reduces the spread of antibiotic resistance. Today, clinical practice relies on molecular and PCR techniques for pathogen identification and culture-based antibiotic susceptibility testing (AST). Recently, WGS has started to transform clinical microbiology, enabling prediction of resistance phenotypes from genotypes and allowing for more informed treatment decisions. WGS-based AST (WGS-AST) depends on the detection of AMR markers in sequenced isolates and therefore requires AMR reference databases. The completeness and quality of these databases are material to increase WGS-AST performance.

Methods: We present a systematic evaluation of the performance of publicly available AMR marker databases for resistance prediction on clinical isolates. We used the public databases CARD and ResFinder with a final dataset of 2587 isolates across five clinically relevant pathogens from PATRIC and NDARO, public repositories of antibiotic-resistant bacterial isolates.

Results: CARD and ResFinder WGS-AST performance had an overall balanced accuracy of 0.52 (± 0.12) and 0.66 (± 0.18), respectively. Major error rates were higher in CARD (4.68%) than ResFinder (25.06%). However, CARD showed almost no very major errors (1.17%) compared with ResFinder (4.42%).

Conclusions: We show that AMR databases need further expansion, improved marker annotations per antibiotic rather than per antibiotic class and validated multivariate marker panels to achieve clinical utility, e.g. in order to meet performance requirements such as provided by the FDA for clinical microbiology diagnostic testing.

Introduction

Antimicrobial resistance (AMR) is a rising health threat estimated to cause 700 000 annual deaths, with 10 million annual casualties expected by 2050.¹ Appropriate antibiotic therapy improves patient outcomes and is a major factor in reducing the emergence of antibiotic resistance.^{2,3} Current clinical practice predominantly uses antibiotic susceptibility testing (AST) from bacterial culture, with long turnaround times ranging between 24 and 72 h, errors arising in inoculum preparation or culture conditions and limitations related to individual species–antibiotic combinations.^{3–5}

With the reduction in WGS costs and runtimes, several researchers have assessed WGS-based AST (WGS-AST) for clinical practice, for example in *Escherichia coli* and *Klebsiella pneumoniae*, as well as using different computational approaches.^{3,6–9}

The increasing availability of WGS data from clinical strains has helped to robustly identify antibiotic resistance determinants

and to curate them in dedicated databases.¹⁰ Public databases like the Comprehensive Antibiotic Resistance Database (CARD),¹¹ ResFinder¹² and its companion database PointFinder,¹³ ARG-ANNOT,¹⁴ as well as others, have emerged as AMR repositories and software tools have been developed for WGS-AST based on these databases.

Stoesser *et al.*³ and Zankari *et al.*¹³ used ResFinder and its sister database PointFinder for WGS-AST on clinical isolates of *E. coli*, *K. pneumoniae*, *Salmonella* and *Campylobacter jejuni*. They showed that *in silico* AMR predictions may suffer from high false-susceptible (false-negative) and/or false-resistant (false-positive) rates. In resistance phenotyping, a false-negative result is considered a very major error (VME) and a false-positive result a major error (ME). A VME might result in use of an ineffective therapeutic agent for treatment, leading to treatment failure; an ME might limit therapeutic options and complicate treatment. The more serious effect of VMEs is reflected in FDA stipulations for diagnostic

test approval, where the FDA requires VMEs <1.5% and MEs <3% for approval of a new AMR diagnostic test or device.¹⁵

As the coverage and quality of databases underlying WGS-AST are essential for clinically relevant AMR diagnostic tests,^{9,16} we evaluated the performance of public AMR marker reference databases for the prediction of resistance in bacterial isolates to spotlight current pitfalls and areas for improvement. Most studies that apply genotype to phenotype prediction focus on samples from a particular species or a single cohort. Here, we present a large-scale study encompassing bacterial isolates from multiple species and cohorts to investigate the utility of publicly available markers for AST prediction from WGS. To maximize the amount of data available for assessment, categorical phenotypes were used as provided by the public databases. A limitation may thus be that, with the increase of AMR, interpretive breakpoints have changed over time and isolates treated as susceptible may be considered resistant at present. As opposed to other studies that focus on smaller datasets or single pathogens together with expert manual curation of results,^{3,17} we evaluated the performance of AMR marker databases on a large and diverse dataset using default settings to assess the status quo and outline concrete steps to improve clinical utility of those databases without time-consuming result curation.

Materials and methods

Isolates and antibiotics collection

Assembled isolate genomes and categorical resistant/susceptible phenotypes as per the databases—filtered by antibiotics—were sourced from PATRIC (the Pathosystems Resource Integration Center) and NDARO (National Database of Antibiotic Resistant Organisms); accessed 31 January 2019. Details can be found in the [Supplementary data](#) (available as [Supplementary data](#) at JAC Online).

In silico phenotype prediction

CARD's Resistance Gene Identifier (RGI) 4.2.2 with the CARD database 3.0.1 was run with default settings for all isolates to predict resistance phenotypes. 'Perfect' and 'strict' hits as per CARD publication were included according to per model curated similarity cut-offs where a perfect hit is an exact match to the curated reference sequences and a strict hit is a previously unknown variant of known AMR genes.¹⁸

ResFinder 4.0 (git commit 0007df1) was installed and run using the ResFinder database (git commit bd77b98) for resistance phenotype prediction for all isolates with default settings (minimum coverage 60%; minimum sequence identity 90%). PointFinder (git commit bd50f0b) was run for *E. coli* isolates using the PointFinder database (git commit d1413d2) with the scheme for *E. coli*.

Evaluation of prediction performance

CARD and ResFinder predictions were compared against *in vitro* phenotypic AST results. CARD and ResFinder reported predicted phenotypes by antibiotic class. Observed phenotypes against individual antibiotics, as reported by PATRIC and NDARO, were mapped to predicted phenotypes by antibiotic class affiliation to evaluate prediction performance. For example, observed phenotypes for amikacin, gentamicin and tobramycin were mapped to CARD's predictions on aminoglycoside resistance.

Retrieved PATRIC and NDARO phenotypes were labelled as resistant/susceptible, in line with the resistance/susceptible prediction output from CARD and ResFinder. Evaluation of prediction performance was treated as a binary classification task; predicted phenotypes were compared with

observed phenotypes. An ME was defined as a resistant prediction discrepant with an observed susceptible phenotype; a VME was defined as a susceptible prediction discrepant with an observed resistant phenotype. To evaluate prediction performance, balanced accuracy (bACC)—the average of sensitivity and specificity—was used, which can be understood as the average accuracy obtained for each class, thus avoiding inflated performance statistics in the case of dataset class imbalance.^{19–21}

To evaluate PointFinder in combination with ResFinder for WGS-AST for the antibiotics ciprofloxacin, cefotaxime and ceftazidime in *E. coli*, an isolate was classified as resistant if either tool predicted resistance.

Evaluation of marker performance

We used the Antibiotic Resistance Ontology (ARO) provided by CARD to group detected CARD AMR markers, i.e. genes and variants, into AMR marker families. For example, all aminoglycoside nucleotide transferase (ANT) alleles were treated as a marker family, all TEM alleles as TEM β -lactamases and so on. The aim was to describe the effect of low-resolution annotations of marker-to-phenotype relationships on predictive performance. While considerable differences in activity exist for members of groups of, for example, β -lactamases, such as TEMs, SHVs and KPCs, those differences were not annotated conclusively and comprehensively for analysis on the allele level across evaluated databases.

For the evaluation, the predictive performance of every marker family for an associated antibiotic resistance listed by CARD ARO was independently evaluated on all isolates. Standard metrics such as sensitivity, specificity and positive predictive value (PPV) were calculated.

To assess the performance of entire AMR marker groups, marker families were further aggregated using resistance mechanism-related ontology terms that are close to the root term of CARD's ARO. This aggregation resulted in four 'marker groups' that covered all markers detected: (i) efflux-related AMR genes and mutations; (ii) β -lactamases; (iii) aminoglycoside-modifying enzymes (AMEs); and (iv) fluoroquinolone resistance-associated genes and mutations. Predictive performance of each marker group was calculated as the average performance of the marker families represented by the marker group for all species-antibiotic combinations evaluated above.

Mapping of ResFinder compound class predictions to compounds

We downloaded marker-phenotype associations available from ResFinder at https://bitbucket.org/genomicpidemiology/resfinder_db. Associations were used to predict antibiotic resistance using detected markers as per ResFinder output in analysed isolates per antibiotic rather than antibiotic class. Markers without phenotype associations for individual antibiotics were excluded.

Data availability statement

Genotype and phenotype data were downloaded from the public repositories NDARO and PATRIC and were publicly available at the time of this study.

Results

Selection of species and antibiotics

A total of 4278 isolate genomes and their resistance phenotypes were collected from PATRIC²² and NDARO,²³ two public repositories of microbial isolate data, for assessment of WGS-AST based on publicly available AMR markers from CARD¹¹ and ResFinder¹² (Table 1). Regarding antibiotic selection, 17 antibiotics were selected as representatives from penams, cephalosporins and other β -lactams,

tetracyclines, quinolones and aminoglycosides. Details regarding selection criteria that resulted in a final dataset size of 2587 isolates are listed in the [supplementary material](#).

Resistance phenotype prediction

Despite the large number of isolates per species, the proportion of resistant to susceptible isolates, as deposited in PATRIC/NDARO, was often skewed to either extreme for a given antibiotic. This strong class imbalance (Figure S2) was reported before by Drouin *et al.*²⁴ for PATRIC data. Therefore, averaged bACC was applied to assess resistance phenotype prediction

Table 1. The distribution of analysed isolates across different species

Pathogen/species	NDARO	PATRIC	Total	Selected
<i>A. baumannii</i>	220	492	712	663
<i>Enterobacter cloacae</i> complex	83	8	91	39
<i>E. coli</i>	185	1517	1702	563
<i>K. pneumoniae</i>	295	820	1115	668
<i>P. aeruginosa</i>	144	514	658	654
Total			4278	2587

for the five analysed species. Overall, bACC ranged from 0.50 to 0.73 (Figure 1).

ResFinder showed slightly better performance than CARD. CARD predictions suffered from overclassification and failure to identify susceptible isolates, where bACC ranged from a minimum of 0.13 for aztreonam resistance in *Acinetobacter baumannii* to a maximum of 0.51 for tobramycin resistance in the same species. Notably, CARD predicted all *E. coli* and *Pseudomonas aeruginosa* isolates to be resistant to all tested antibiotics, resulting in a bACC measure of 0.50 across all tested antibiotics ($n = 17$ and $n = 11$, respectively). In contrast, ResFinder predictions had a bACC of 0.49 for piperacillin/tazobactam resistance in *P. aeruginosa* but in many instances achieved a bACC of 1.00 (Figure 2). Across all antibiotic-species combinations, CARD's predictions showed an average bACC of 0.52 and ResFinder's predictions an average bACC of 0.66. CARD's predictions resulted in more MEs than ResFinder's predictions, with CARD's average ME rate at 0.42. ResFinder showed fewer MEs across all antibiotic-species combinations, where the average ME rate was 0.25.

We chose *E. coli* (Figure 3) for a detailed comparison of ResFinder and CARD prediction performance.²⁵ CARD and ResFinder results for the remaining species are in Tables S1 and S2. For *E. coli*, average bACC using ResFinder was 0.73 and average bACC using CARD was 0.50. Poor performance was mainly due to

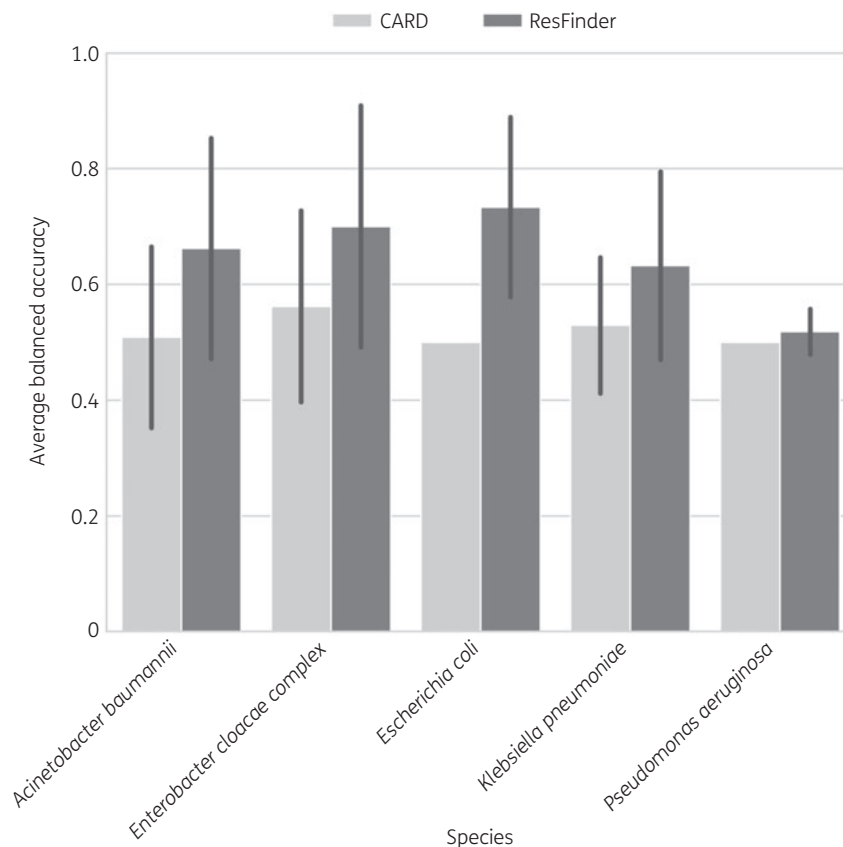


Figure 1. The bACC is shown for every species as the average of all bACCs for the species-antibiotic combinations mentioned in the main text. bACC was chosen as the evaluation criterion as it avoids performance inflation and provides a balanced representation of false-positive and false-negative rates even in the case of dataset class imbalance. Error bars indicate SD. CARD predicted all *E. coli* and *P. aeruginosa* isolates to be resistant to all tested antibiotics, resulting in a constant bACC of 0.5 and the absence of the error bars.

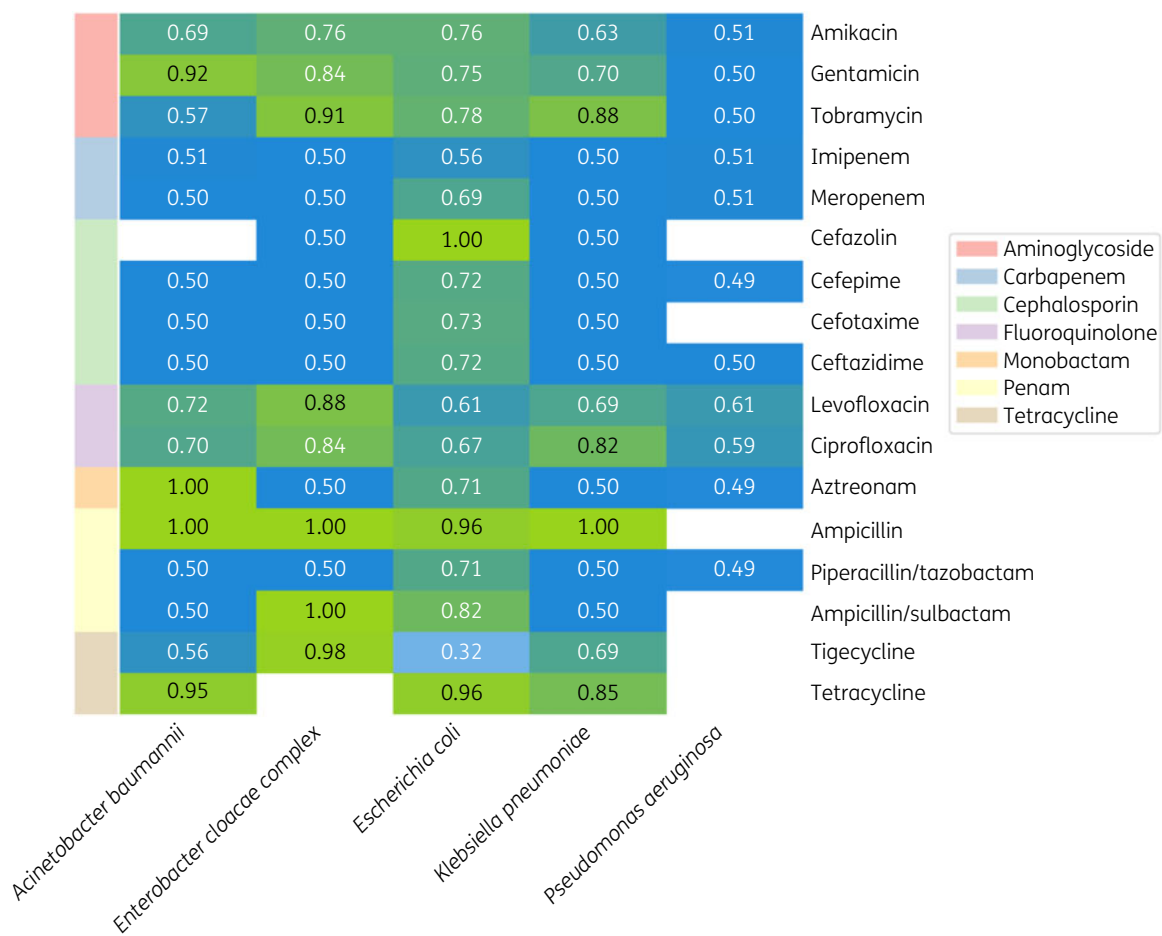


Figure 2. bACC measures using ResFinder. The heatmap shows analysed antibiotics versus pathogens. White rectangles represent species-antibiotic pairs that were not analysed due to absent or insufficient AST data.

high ME rather than VME rates. ResFinder predictions had an average ME rate of 29.76% and an average VME rate of 3.99% whereas CARD predictions had an average ME rate of 65.4% and no VMEs. ResFinder's predictions showed better overall performance than CARD except in the case of fluoroquinolones (Figure 3a and b).

ResFinder's bACC values of 0.67 for ciprofloxacin and 0.61 for levofloxacin were attributed to the fact that fluoroquinolone resistance is predominantly mediated by chromosomal mutations and ResFinder predictions are exclusively based on AMR genes.^{26,27} We combined results from ResFinder and PointFinder, the software developed by the ResFinder team to tackle chromosome mutation-mediated resistance. This approach could only be applied to *E. coli* as PointFinder's database was implemented only for *E. coli*, *Salmonella enterica* and *C. jejuni*.¹³ Combining predictions from ResFinder and PointFinder for ciprofloxacin resulted in improved prediction performance and a reduced VME rate from 16.5% to 0.5%. Despite abundant literature on *gyrA* and *parC* mutations mediating resistance to fluoroquinolones in general,²⁸ PointFinder exclusively associates *gyrA* and *parC* mutations with ciprofloxacin resistance; consequently levofloxacin resistance was not analysed (Figure 3c).

To further investigate CARD's high ME rates, we repeated the calculation excluding all predictions based on markers with efflux-

related resistance mechanisms. Efflux markers are highly affected by transcription regulation and detection by WGS is not always a sufficient indication of their contribution to AMR.^{29,30} This resulted in overall improvement in the performance of CARD's RGI for aminoglycoside and fluoroquinolone compounds (Figure 3d). However, for tetracyclines, VME rates increased, where many resistant isolates were predicted to be susceptible, in agreement with efflux-mediated resistance being the main resistance mechanism against tetracyclines.³¹ For results of using CARD predictions without efflux markers for all species, see Table S3.

AMR marker performance

To provide an overview of contributions of entire marker groups to WGS-AST, four groups were built from CARD's ARO: efflux-related markers, β -lactamases, AMEs and fluoroquinolone-resistance genes and mutations. For every group, we evaluated the contribution to the overall prediction of resistance phenotype using (i) PPV, i.e. the probability of a subject carrying a resistance marker being resistant, and (ii) specificity, i.e. the proportion of susceptible isolates that are correctly identified as such (Tables 2 and S4).

Efflux-related AMR markers from CARD were the most abundant marker class in terms of hits per isolate (Table S5). On

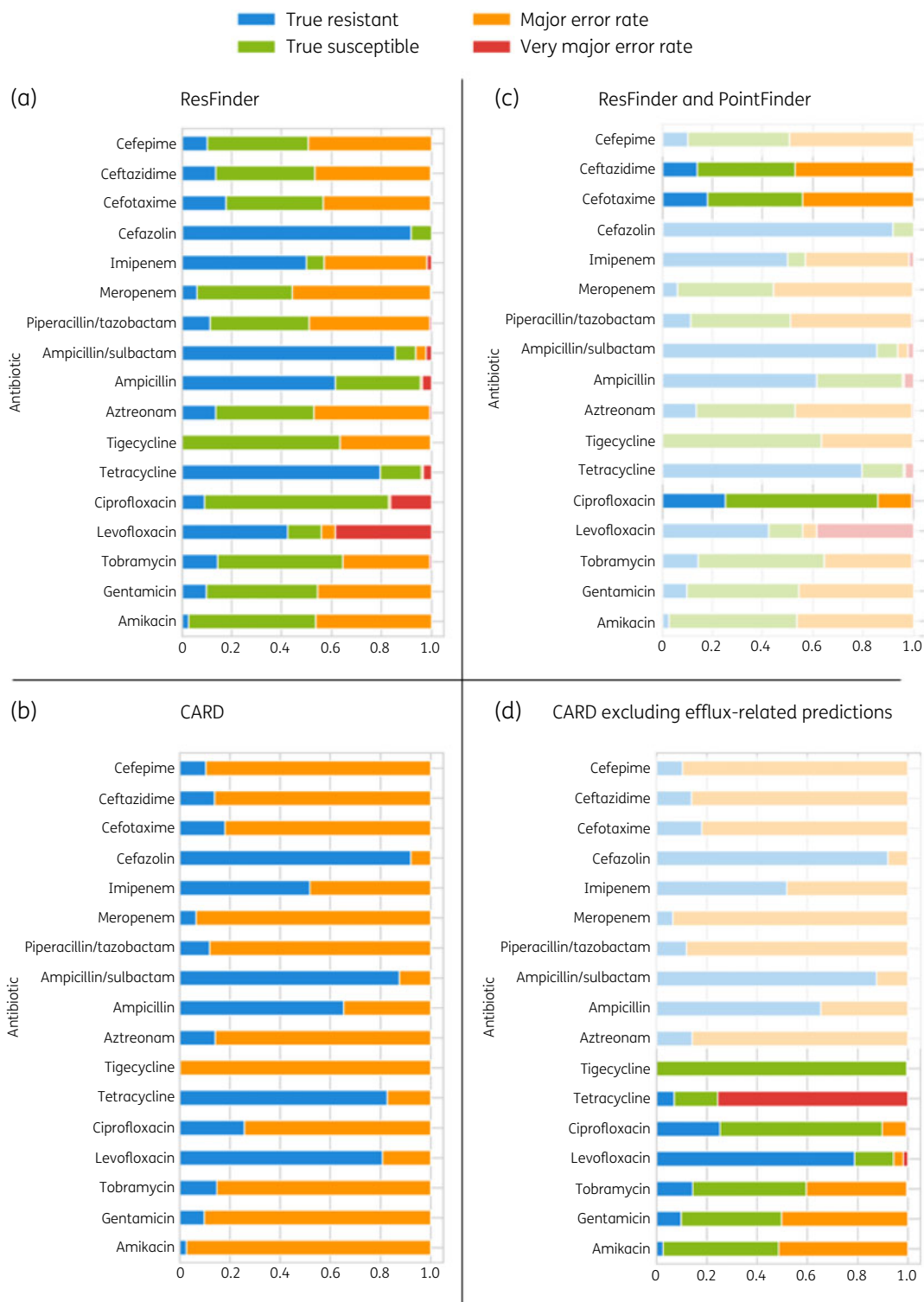


Figure 3. Evaluation of ResFinder and CARD (RGI) antibiotic resistance prediction performance on *E. coli*. (a) ResFinder prediction performance across 17 antibiotics. (b) CARD prediction performance across 17 antibiotics. (c) ResFinder and PointFinder prediction performance for ciprofloxacin, cefotaxime and ceftazidime. (d) CARD prediction performance excluding predictions based on markers related to efflux pump mechanism. ResFinder shows overall better prediction performance than CARD; PointFinder predictions improve ResFinder predictions and, excluding predictions based on efflux-related markers, improve CARD predictions except for tetracycline.

average, an isolate contained 30 hits related to ‘Antibiotic Efflux’ as per CARD ARO, significantly higher than the average hits of any other class. However, average specificity of an efflux-related AMR marker is lowest among marker families. *P. aeruginosa* isolates had the highest average number of efflux-related AMR determinants detected per isolate (mean = 44.66) compared with isolates from the remaining species (mean = 24.15), in agreement with studies demonstrating a major role of efflux pumps for *P. aeruginosa* resistance.^{32,33} In contrast, fluoroquinolone resistance genes and mutations show the highest specificity and PPV despite their low abundance (Figure S3). It should be noted that in addition to single-point mutations related to fluoroquinolone resistance, CARD also detects double mutations within the same gene, e.g. *gyrA* S83L/D87N, in line with scientific literature.³⁴ Increased resistance due to the presence of more than one mechanism simultaneously was not accounted for.

For the subsequent analysis, we focused on *K. pneumoniae*, another cause of highly threatening nosocomial infections.³⁵ With the rise of β -lactam (mainly meropenems and cephalosporins) and aminoglycoside resistance in *K. pneumoniae*,^{36,37} accurate and precise detection of resistance is of high clinical relevance and value. Despite identical resistance profiles of some β -lactamases

Table 2. Abundance and WGS-AST performance metrics of the four main marker families from CARD

Marker group	Average hits/sample	Average specificity	Average PPV
Efflux-related markers	30.30	0.12	0.52
β -Lactamases	2.61	0.66	0.76
AMEs	2.51	0.65	0.55
Fluoroquinolone resistance-associated genes and mutations	0.72	0.94	0.82

based on CARD ARO, we observed variability across some for resistance prediction against associated antibiotics (Figure 4).

Annotation level and prediction performance

To investigate the effect of a higher level of annotation detail, i.e. marker–compound annotation, we compared the predictions of ResFinder with default settings against ResFinder predictions mapped to individual compounds (see the Materials and methods section). In Figure 5, we show that compound-level annotations improved prediction performance for cephalosporins as well as aminoglycosides in *K. pneumoniae* samples.

Discussion

Ruppé et al.¹⁶ reviewed studies performing genotype to phenotype comparisons from AMR determinants from public databases in an approach similar to the one presented here. These studies, however, focused on one or two species, with smaller datasets not exceeding 400 samples and were mainly derived from a single location.^{10,12,38–40} According to Su et al.,⁴ including large, diverse test sets for development and evaluation of WGS-AST tools is critical. However, most studies have used a sample with limited geographic and temporal variability. By using datasets from PATRIC⁴¹ and NDARO,²³ comprised of genome assemblies and categorical resistant/susceptible phenotypes, we included a dataset from multiple clinically relevant species with diverse locations and collection times (Figure S1). A limitation may be that the study used categorical phenotypes as provided by the databases. With the increase of AMR, interpretive breakpoints have changed over time.⁴² For Enterobacteriaceae, for example, breakpoints (mg/L) for ciprofloxacin changed from susceptible (S) ≤ 1 , intermediate (I) = 2, resistant (R) ≥ 4 when first published by CLSI to S ≤ 0.25 , I = 0.5, R ≥ 1 in 2019. While S/I/R labels could have been recalculated, including only data with numerical MIC values, this would have drastically reduced the dataset. Moreover, breakpoint changes were expected not to affect the study’s main findings. This was validated exhaustively across all pathogen–compound pairs for which

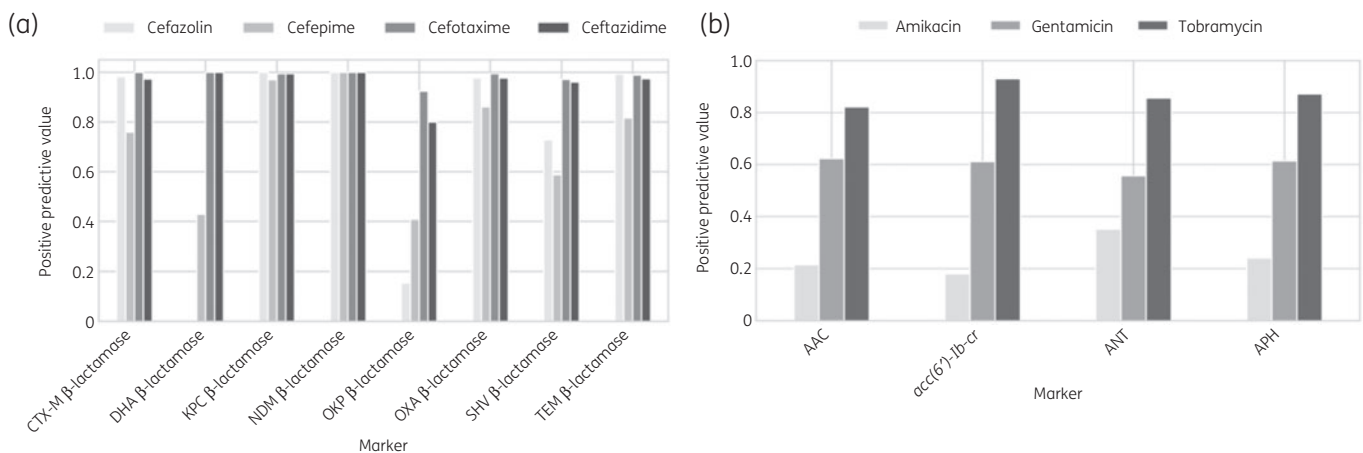


Figure 4. Differences in resistance profiles for β -lactamases and AMEs in *K. pneumoniae*. (a) KPC β -lactamases and NDM β -lactamases are consistently good predictors of resistance across all the analysed cephalosporins whereas OKP β -lactamases and CTX-M β -lactamases show variable resistance prediction performance. (b) AACs, aminoglycoside phosphotransferases (APHs) and ANTs consistently show lower PPVs for amikacin than tobramycin or gentamicin.

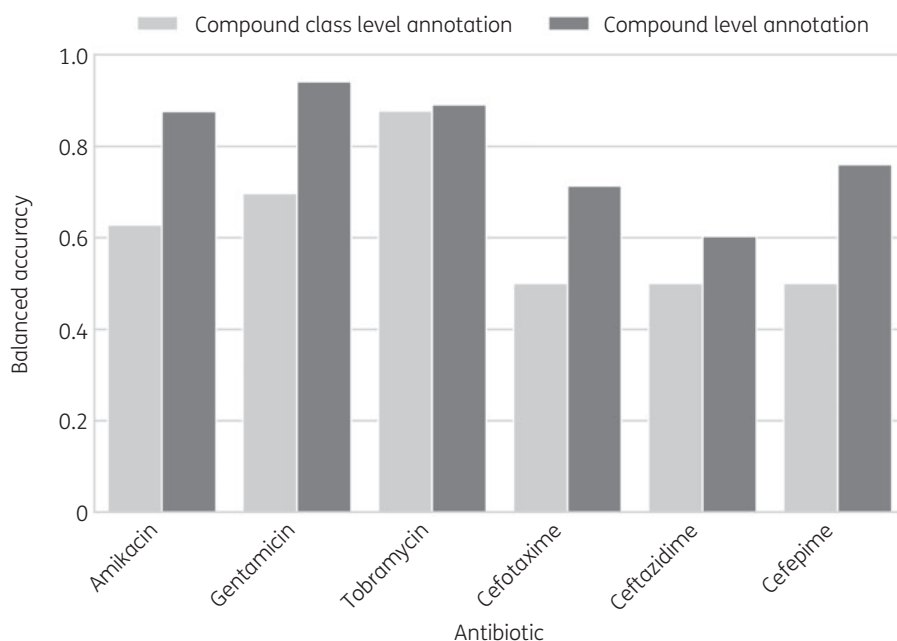


Figure 5. bACC of ResFinder predictions based on ResFinder compound-class-level annotation versus compound-level annotation in *K. pneumoniae* samples. Compound-level prediction consistently performs better and the increase in bACC ranges between 0.01 for tobramycin resistance prediction and 0.26 for cefepime resistance prediction.

numeric MIC data could be retrieved. Database labels as per submission and labels recalculated with breakpoints from 2019 were 95.6% concordant, while bACC of WGS-AST only differed by an average of 0.7%.

In this study, as well as others,¹⁶ culture-based AST is treated as the gold standard, being the primary method employed by clinical laboratories.⁴ However, culture-based AST has its own limitations. For example, a lack of reproducibility and comparability across laboratories and countries due to biological variability, as well as differences in technical staff training and standards provided by EUCAST and CLSI.^{43,44} Adopting WGS-AST, backed by standardized and validated sequencing and bioinformatics pipelines, represents an opportunity to eliminate errors due to experimental procedure and differences in laboratory conditions in addition to achieving comprehensive and more accurate results.^{4,9}

Our analysis highlighted factors that affect WGS-AST accuracy, starting at the databases, as shown by variable results from ResFinder and CARD. Poor performance reflected in our results was due to high rates of ME rather than VME. ResFinder prediction performance was improved by combination with PointFinder, in agreement with findings by Zankari *et al.*³⁸ that high VME rates for fluoroquinolones, for example, were due to the non-consideration of mutational events. Compared with ResFinder, CARD showed worse overall performance with lower specificity and higher ME rates, a result in agreement with a comparison carried out on Enterobacteriaceae by Pesesky *et al.*⁸ However, CARD's prediction performance for all antibiotic classes (except tetracyclines) improved upon removal of general AMR determinants such as efflux pumps and MEs were reduced significantly. These markers are likely to cause inaccurate predictions as they are affected by gene regulation where the presence of a gene detected by WGS is not

indicative of its expression due to weak promoters or low copy numbers.^{29,40,45} The aforementioned findings highlight two of the main challenges facing WGS-AST, namely: (i) the impact of reference databases on downstream results and hence the need for an exhaustive and up-to-date knowledgebase of AMR determinants that encompasses AMR genes and variants (chromosomal and acquired), their prevalence in individual bacterial species and metadata on compound activity and reported intrinsic resistance;^{9,16} and (ii) the high false-positive rate due to an inadequate understanding of aspects such as gene regulation, mutations in intergenic regions and *de novo* rRNA mutations. In the latter case, false positives may arise because naive detection of an AMR-related gene without considering the aforementioned aspects may not be sufficient to causally assume resistance. For example, gene expression is not considered.^{43,45} It is clear that these challenges must be addressed to approach the FDA requirements for a diagnostic test of MEs <3% and VMEs <1.5%.

Our results also highlighted that *P. aeruginosa* presents a particularly challenging case for WGS-AST, with its unique and complex resistome being tightly regulated by gene expression.⁴⁶ bACC ranged from 0.49 to 0.60, in agreement with Kos *et al.*⁴⁷ who showed that using WGS-based detection of functional genetic targets alone failed to explain observed resistance phenotypes in that species.

Another important factor affecting WGS-AST accuracy was the similarity/identity cut-off used for resistance gene identification. As our analysis explored the applicability of ResFinder in a standard manner, we used its default settings. This resulted in much lower accuracies than other studies applying a more stringent cut-off. For instance, Zankari *et al.*³⁸ used a more stringent cut-off in AMR gene identification ($\geq 98\%$) compared with our ResFinder default settings ($\geq 90\%$), which can explain the high rate of MEs (27.82%)

in our results. In another study by Thomas *et al.*,⁴⁰ applying a cut-off of $\geq 95\%$ together with focusing on a chosen subset of ResFinder markers yielded specificity levels approaching 100% for all antibiotic classes except aminoglycosides. Clausen *et al.*³⁹ claimed that the 98% sequence identity threshold, as recommended by Zankari *et al.*,³⁸ was tested to be the 'optimal threshold'. Our results here suggest that revisiting default parameters for ResFinder might be advisable.

A key factor determining WGS-AST accuracy was the annotation level of marker-phenotype relationships. Despite sharing an identical resistance profile on CARD, members of the same family of enzymes showed different performance in predicting resistance for different aminoglycosides in the case of AMEs or different cephalosporins in the case of β -lactamases. Individual members of these enzyme families interact differently with different members of the antibiotic class. For example, many members of the aminoglycoside acetyl transferase (AAC) class of AMEs confer resistance to gentamicin and tobramycin, but not amikacin.⁴⁸ Similarly, some members of the TEM class of β -lactamases are ESBLs, affecting all cephalosporins, whereas others are broad-spectrum β -lactamases that only affect early cephalosporins.^{49,50} Allele-specific compound resistance annotations and statistics on marker prevalence and performance, such as sensitivity and specificity, comprehensively applied across all AMR markers, despite being a determining factor for accurate phenotype prediction, are not currently available from any public AMR database.⁵¹ In addition, resistance against antibiotic classes may be affected by the simultaneous presence of multiple resistance mechanisms. Accumulation of AMR point mutations or genes can cause incremental MIC shifts, e.g. if mutations in *gyrA* and *parC* are present in combination with *qnr* or *aac(6')*-*Ib-cr* genes. Readily available data on those combinatorial marker-phenotype relationships would further improve WGS-AST accuracy.

A number of studies applied genotype to phenotype prediction while relying on a curated subset of markers from CARD, ResFinder and other resources and obtained better overall prediction performance. For instance, Stoesser *et al.*³ applied predictions relying on a curated in-house reference database that contained AMR determinants from ResFinder and other resources. Consequently, the sensitivity for predicting resistance for ~ 140 *E. coli* and *K. pneumoniae* clinical isolates was 0.96 and specificity was 0.97.³ Another study by Gordon *et al.*¹⁷ on a dataset of ~ 1000 *Staphylococcus aureus* clinical isolates predicted phenotype from genotype using a curated panel of AMR determinants based on a literature search that resulted in overall sensitivity and specificity of 0.97 and 0.99. A similar approach was applied in a recent study by Feldgarden *et al.*⁵² who used AMR Finder, a tool relying on a high-quality curated AMR gene reference database, combined with literature research on antibiotic resistance phenotypes. This resulted in predictions that are consistent with 98.4% of the actual phenotypes of 6242 isolates from four different species (mostly *S. enterica*).⁵² These studies highlight the effect of marker curation and high level of detail in phenotype-genotype annotation on WGS-based phenotype prediction.

Conclusions

To our knowledge, we have presented the first large-scale study to include a highly diverse dataset of thousands of bacterial isolates

from multiple species, locations and times. Results illustrate that databases such as CARD and ResFinder serve as reference databases on resistance markers and offer functionality to predict resistance phenotypes from single markers, but may not yield optimal results using default settings. In this context, several challenges in genetic phenotype prediction still exist. To achieve FDA requirements for clinical microbiology diagnostic testing below 3% MEs and 1.5% VMEs, current AMR databases need to: (i) be further curated and expanded, (ii) provide AMR marker annotations per antibiotic rather than antibiotic class, and (iii) use combinations of individual AMR markers selected for optimal diagnostic performance in experimentally validated multivariate panels.

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Transparency declarations

N.M., I.F. and S.B. are employees of Ares Genetics GmbH. A.E.P. is the Chief Executive Officer of Ares Genetics GmbH. The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest. All other authors: none to declare.

Author contributions

N.M., S.B., A.H. and A.E.P. designed the study. N.M. and I.F. analysed the data. N.M., S.B. and A.E.P. wrote the manuscript. All authors reviewed and approved the manuscript.

Supplementary data

[Supplementary Methods](#) and Results, Tables S1 to S6 and Figures S1 to S3 are available as [Supplementary data](#) at JAC Online.

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