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Short Communication

Poverty and prevalence of antimicrobial resistance in invasive isolates

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SUMMARY

Objectives: To evaluate the association between the income status of a country and the prevalence of antimicrobial resistance (AMR) in the three most common bacteria causing infections in hospitals and in the community: third-generation cephalosporin (3GC)-resistant *Escherichia coli*, methicillin-resistant *Staphylococcus aureus* (MRSA), and 3GC-resistant *Klebsiella* species.
Methods: Using 2013–2014 country-specific data from the ResistanceMap repository and the World Bank, the association between the prevalence of AMR in invasive samples and the gross national income (GNI) per capita was investigated through linear regression with robust standard errors. To account for non-linear association with the dependent variable, GNI per capita was log-transformed.
Results: The models predicted an 11.3% (95% confidence interval (CI) 6.5–16.2%), 18.2% (95% CI 11–25.5%), and 12.3% (95% CI 5.5–19.1%) decrease in the prevalence of 3GC-resistant *E. coli*, 3GC-resistant *Klebsiella* species, and MRSA, respectively, for each log GNI per capita. The association was stronger for 3GC-resistant *E. coli* and *Klebsiella* species than for MRSA.
Conclusions: A significant association between GNI per capita and the prevalence of MRSA and 3GC-resistant *E. coli* and *Klebsiella* species was found. These results underscore the urgent need for new policies aimed at reducing AMR in resource-poor settings.

1. Introduction

The emergence of antimicrobial resistance (AMR) is a complex phenomenon and is intensified by selective pressure through antibiotic use in humans, animals, and agriculture.[1] The transmission of AMR to humans occurs from contact with animals (including food), other humans, and the environment.[1] Transmission is facilitated by several factors, including high population density, lack of access to clean water, suboptimal sewage systems, poor sanitation, and poor healthcare infection control practices, all of which are more common in low- and middle-income countries (LMIC).[1] In addition, with the increasing consumption of antimicrobials in humans, lack of regulation on antimicrobial use in farming, and pharmaceutical industry pollution, it may not be surprising that relatively higher levels of AMR among human pathogens are being reported from LMIC.[2,3] However, the association between the income status of a country and prevalence of AMR has not yet been published.

Escherichia coli, *Klebsiella* species, and *Staphylococcus aureus* are the most common bacteria causing infections in hospitals and in the community.[2] The aims of this study were (1) to evaluate the association between the income status of a country and the prevalence of AMR in the three most common bacteria isolated from invasive samples (third-generation cephalosporin (3GC)-resistant *E. coli*, methicillin-resistant *S. aureus* (MRSA), and 3GC-resistant *Klebsiella* species),[2] and (2) to estimate the overall prevalence of AMR among lower-middle-, upper-middle-, and high-income economies.

2. Methods

Data from the World Bank (gross national income (GNI) per capita) and from the ResistanceMap repository were used. ResistanceMap is a repository of reliable antimicrobial resistance data from hospitals and laboratory networks from around the world.[4]

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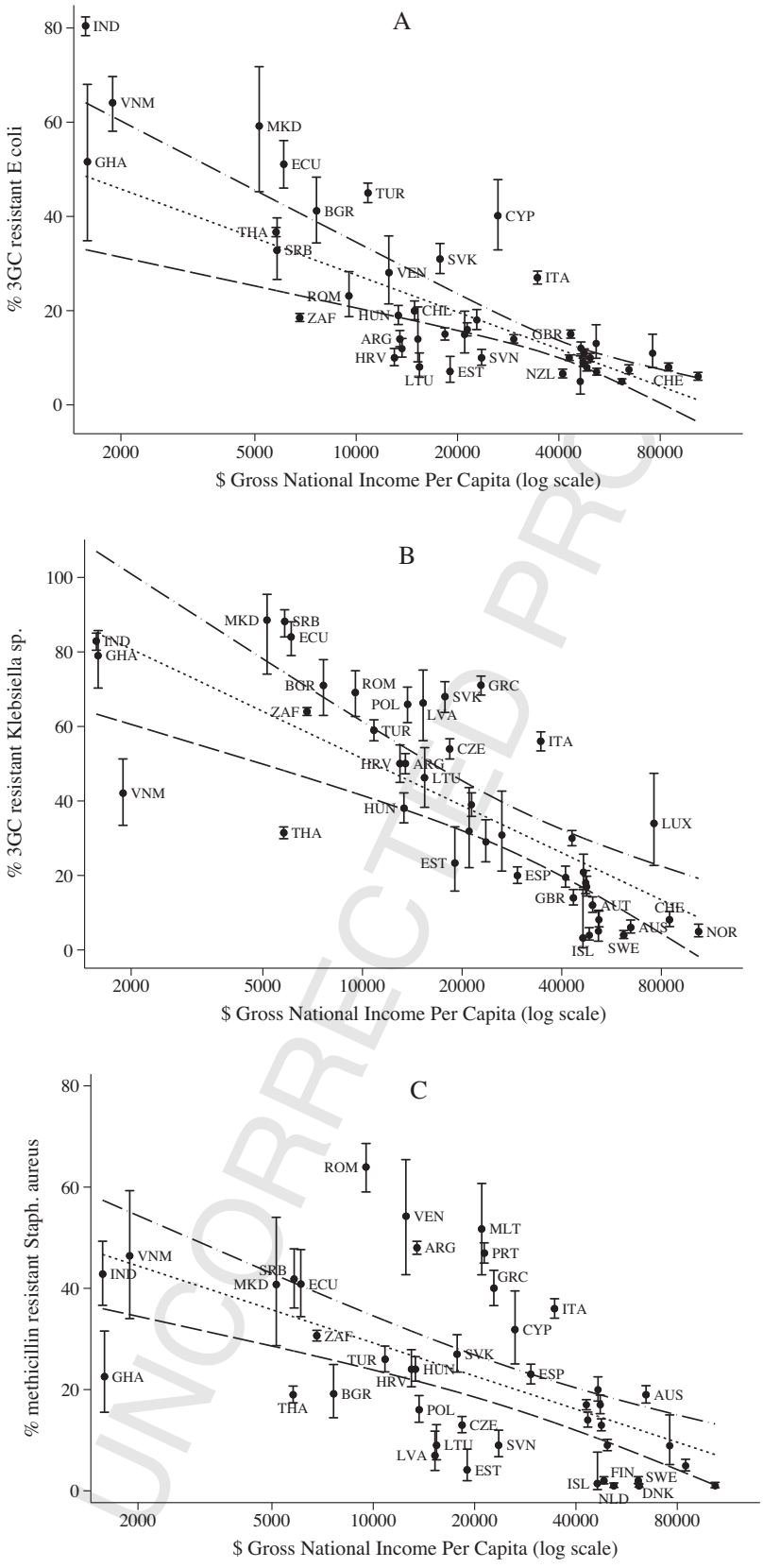

Figure 1. Prevalence of third-generation cephalosporin-resistant (3GCR) *Escherichia coli* (A), 3GCR *Klebsiella sp* (B), and methicillin-resistant *Staphylococcus aureus* (C) by gross national income per capita and predicted values with 95% confidence intervals according to a linear regression model.

All isolates of *E. coli*, *Klebsiella sp*, and *S. aureus* in the ResistanceMap database for 2013 and 2014 were selected. Countries with fewer than 30 samples and those for which samples came from a single hospital were excluded. Confidence intervals (CI) for proportions were estimated using the Wilson method. To facilitate the interpretation of the results, the proportion of isolates tested that were resistant was modeled as a continuous variable using linear regression with robust standard errors. GNI per capita was measured in US dollars according to 2014 World Bank data. To account for non-linear association with the dependent variable, GNI per capita was log-transformed. GNI per capita is presented on a log scale in the figures.

3. Results

The association between the percentage of 3GC-resistant *E. coli* and GNI per capita for the 45 countries that met the study criteria is presented in Figure 1A. The model predicted an 11.3% (95% CI 6.5–16.2%) decrease in the prevalence of 3GC-resistant *E. coli* for each log GNI per capita and was able to explain 65% of the variance ($R^2 = 0.6486$). When countries were grouped by their GNI per capita into high-, upper-middle-, and lower-middle-income economies, the predicted prevalence of 3GC-resistant *E. coli* was 11.5% (95% CI 9.2–13.8%), 30.7% (95% CI 19–42.4%), and 77.6% (95% CI 71.2–84.1%), respectively.

The association between the percentage of 3GC-resistant *Klebsiella sp* and GNI per capita for the 43 countries that met the study criteria is presented in Figure 1B. The model predicted an 18.2% (95% CI 11–25.5%) decrease in the prevalence of 3GC-resistant *Klebsiella sp* for each log GNI per capita and was able to explain 58% of the variance ($R^2 = 0.5745$). When countries were grouped by their GNI per capita into high-, upper-middle-, and lower-middle-income economies, the predicted prevalence of 3GC-resistant *Klebsiella sp* was 30.6% (95% CI 20.9–40.2%), 56.7% (95% CI 40.6–72.8%), and 78.9% (95% CI 69–88.7%), respectively.

The association between the percentage of MRSA and GNI per capita for the 43 countries that met the study criteria is presented in Figure 1C. The model predicted a 12.3% (95% CI 5.5–19.1%) decrease in the prevalence of MRSA for each log GNI per capita and was able to explain 41% of the variance ($R^2 = 0.4079$). When countries were grouped by their GNI per capita into high-, upper-middle-, and lower-middle-income economies, the predicted prevalence of MRSA was 19.2% (95% CI 10.2–28.3%), 29% (95% CI 22–36.1%), and 36.4% (95% CI 23.7–49%), respectively.

4. Discussion

The burden of bacterial infections is higher in LMIC,[5] and the present study results demonstrate that they have a higher prevalence of AMR too. This combination is likely to have devastating consequences for LMIC economies. First, infections caused by resistant organisms are associated with increased mortality and health costs.[2,6,7] Second, antibiotics that are effective against bacteria with AMR are more expensive and are not affordable for a substantial number of people living in resource-limited settings.[8] Third, increasing the use of effective antibiotics against bacteria with AMR will lead to higher resistance to last-resort antibiotics. In fact, carbapenem consumption is increasing at a rapid pace in poor economies,[9] leading to an increasing prevalence of carbapenem-resistant *E. coli* and *Klebsiella sp*.[3]

The association was stronger for 3GC-resistant *E. coli* and *Klebsiella sp* than for MRSA. This finding is consistent with the conditions that facilitate the transmission of AMR in developing countries. *E. coli* and *Klebsiella sp* are part of the human gut microbiota, and the spread of these organisms is facilitated by suboptimal sewage systems, poor sanitation, and a lack of access to clean water. Previous studies have demonstrated a high prevalence of AMR in surface water and ground water in developing countries.[1] Improving sewage systems and access to clean water is likely to have a greater impact on reducing the transmission of AMR in *E. coli* and *Klebsiella sp* than in contact-transmitted bacteria such as MRSA.

A strong association was found between the income status of a country and the prevalence of AMR in invasive isolates. The findings of this study underscore the urgent need for the implementation of policies to improve environmental sanitation, curb inappropriate antibiotic use, increase vaccination rates, improve laboratory capacity, and establish infection control, and for antimicrobial stewardship programs in healthcare facilities in developing countries.

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Conflict of interest: There are no conflicts of interest to disclose.

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