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Perspective

Epidemiological Consideration: The Application of Quantitative Biology in the Analysis of Mortality Rates Affected by Antimicrobial Resistance

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Abbreviations AMR: antimicrobial resistance; hAMR: antimicrobial resistance via horizontal gene transfer; HGT: horizontal gene transfer

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Abstract

Antimicrobial resistance (AMR) combined with the lack of novel antibiotics poses an eminent threat to human survival and to the practicality of medical procedures that depend on antibiotics.

In the most basic terms, AMR will result in more untreatable illnesses and diseases subsequently accelerating mortality rates for those particular conditions. AMR will increase the cost of patient care and tax the already overburdened healthcare system, and will negatively impact individuals, families, and employers and the economy and society worldwide.

How AMR affects treatment and outcome in certain bacterial infections can be described in narrative form, such as: Elevated AMR increases disease and death. However, this brief narrative reveals little about other cofactors or how adjusting one cofactor may affect another cofactor, several cofactors or all cofactors. Thus, it is more practical to develop a mathematical model that depicts such cofactors and their correlations to more readily recognize and more aptly access the effects of AMR on human mortality.

Preface

The importance of biostatistical and mathematical models regarding antimicrobial resistance (AMR) cannot be overstated. Models help define the system being observed in order to study the influences of various components upon that system and to predict outcomes. From these models, conclusions and projections can be made and communicated succinctly and effectively.

Introduction

The human microbiome is one of the most densely populated ecosystems known to humankind. Due to this density, the proximity of cells in the human gut favors certain mechanisms of acquiring AMR, e.g., mutation and horizontal gene transfer (HGT). AMR via HGT is referred to herein as hAMR (antimicrobial resistance via horizontal gene transfer). Also, the human microbiome is an open system; thus, moment-to-moment, the human microbiome is involved in numerous encounters that may result in large populations of diverse cells becoming singularly resistant or cluster resistant to antibiotics. Devising biostatistical and mathematical models to depict the factorial correlations within this system is deemed fundamental [1-3].

The interpretation of a biostatistical model determines if variables are related and, according to the data, compute probability distribution; it can reveal if the variables are related in a statistically significant way, and if they are dependent and independent variables. A mathematical model incorporates and considers other formulae and determinants in the system, such as Combinatorics and Probability. The mathematical model helps explain a system and the correlations of the factors, and make predictions. Integrating biostatistical data into a mathematical model will result in a more realistic and dynamic paradigm. Developing biostatistical data, such as Combinatorics and Probability, for the Antibiotic-AMR-Mortality-Rate Model (below) is an extensive undertaking, and is well beyond the scope of this paper. Such an endeavor is left for future researchers and biostatisticians to explore and integrate.

Discussion

The following is a basic mathematical model (a formula in progress) to which other variables can be added if identified and considered consequential, and to which biostatistical summaries can be integrated into the model. The inclusion of subsequent variables and biostatistical summaries may assist in illustrating the interaction between biostatistical data and the mathematical model in this antibiotic-AMR-mortality-rate paradigm. Following is a rudimentary Antibiotic-AMR-Mortality-Rate Model of the effects of AMR on disease and death (mortality):

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$$\Sigma Dd_{bi} = Pr_{bi} - (Tx^{ab} + SpRc_{bi}); \text{ wherein } Tx^{ab} \propto k/rTx^{ab}$$

This preliminary model is surveying epidemiological considerations through the lens of quantitative biology (biostatistical and mathematical modeling). This model is concerned with AMR and its effect on disease and mortality in the human population. It is a working model, kept elemental by design, and represents a baseline to which other factors may be incorporated and biostatistical data overlaid. This Antibiotic-AMR-Mortality-Rate Model is deciphered as follows:

The sum total (Σ) of death (D) and disease (d) due to a specific bacterial infection $_{(bi)}$ is equal to (=) the prevalence (Pr) of that bacterial infection ($_{bi}$) minus (-) the successful antibiotic treatment of such bacterial infection (Tx^{ab}) minus (- times + equals -) the spontaneous nontreatment recovery ($SpRc_{bi}$) from such bacterial infection. It is primal to note that successful treatment with antibiotics (Tx^{ab}) is inversely proportional to cases not cured due to resistance to antibiotic treatment (rTx^{ab}). Thus, in short, as (rTx^{ab}) increases, (Tx^{ab}) decreases. Therefore, if given that ($SpRc_{bi}$) is constant, as (rTx^{ab}) increases, (Tx^{ab}) decreases, while prevalence of the bacterial infection (Pr_{bi}) increases resulting in an increase in disease and death caused by a bacterial infection (Dd_{bi}).

Conclusion

The implementation of biomedical research regarding an Antibiotic-AMR-Mortality-Rate Model is vital, including how bacteria evolve and diversify; DNA and genetic coding are elemental to this concern. Biostatistical and mathematical modeling are tools that provide meaningful data and interpretive formulations. The integration of biostatistical and mathematical models can elucidate more distinct findings, conclusions, and projections. In this Antibiotic-AMR-Mortality-Rate Model, all other factors remaining equal, any increase in AMR (through mutation and, particularly, via hAMR) will result in an increase in disease and death. This factorial relationship demonstrates the need to continually evaluate potential risks in the transference of AMR through the ingestion of antibiotics into the open system of the human microbiome. Also, it is fundamental to determine other consequential factors, probabilities, and proportions; and to develop more sophisticated and representative models by integrating associated and applicable biostatistical data [4-5].

The application of quantitative biology is instrumental in identifying factors and their effects on complex systems, and in addressing specific factors to achieve more favorable outcomes; in this case, the correlation between AMR and disease and mortality.

Conflict of Interest Statement

The author declares that this paper was written in the absence of any commercial or financial relationship that could be construed as a potential conflict of interest.

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Supplementary Note

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