RESEARCH NEWS SCAN

Databases for Antimicrobial Resistance Genes and Mobile Genetic Elements in Gut Microbiome

Anshul Sood

ABSTRACT

The human gut microbiota forms a large reservoir of antimicrobial resistance (AMR) genes. Also a number of these bacteria are endowed with metabolic potentials and added advantages which are often provided by mobile genetic elements (MGE). MGEs carry out extensive horizontal gene transfer (HGT) in gut and are believed to be agents of open source evolution. Regardless of their medical importance and biological significance, MGEs from the gut microbiome have not been methodically characterized. This research news scan highlights the Intestinal microbiome mobile element database (ImmeDB) associated with the collection, classification, and annotation of MGEs from gut microbiome using a novel "deletion-based" Split Read Insertion Detection (SRID) method. The database can help us screen already identified genomes for the validation and detection of new MGEs

Keywords: Antimicrobial resistance, Intestinal microbiome mobile element database, Mobile genetic elements, Split read insertion detection.

INTRODUCTION

Human microbiome comprises a huge diversity of microbes. The gut microbiota makes the most densely populated microbial ecosystem on earth. Though the microbiome wields various functions in human health, their high density within this ecosystem provides conditions to facilitate horizontal transfer of genetic elements including antimicrobial resistance (AMR) genes to potential pathogenic bacteria. It has been reported in the study that gut bacteria exchange resistance genes among themselves and the bacteria passing through the gut help them acquire and transmit AMR genes. This extensive horizontal gene transfer is mediated by mobile genetic elements (MGEs) in the gut microbiome. The MGEs are believed to be potent vectors for resistance, disease, and evolution. Not only they spread AMR but also benefit human health by conferring new metabolic capabilities to gut commensals. Regardless of their medical importance and biological significance, MGEs from the gut microbiome have not been methodically characterized.[1]

To date, different web resources, databases, and repositories are available online to study resistome, gene-based antibiograms, and MGE together with online bioinformatics tools used for sequence comparison, alignment, and annotation. Databases/repositories pertaining to the AMR include ARDB, CARD, ResFinder, LacED, ResFams, Patric, HMP, RED-DB, U-CARE, ARG-ANNOT, BLAD, CBMAR, Lahey Clinic, Institut Pasteur, Tetracycline MLS nomenclature, ABRES Finder, RAC, MvirDB etc. Different web resources to study MGE genomics include ACLAME, IS Finder DB, INTEGRALL, Islander DB, PlasMapper, Plasmid Genome Database, T4-like Phage Genomes, Gypsy Database of Mobile Genetic Elements.[2,3]

In November, 2017, a team of researchers from Massachusetts Institute of Technology in collaboration with other institutes found out a novel scheme termed as Split Read Insertion Detection (SRID) which helps identify the exact mobilizable unit of MGEs and thus provides a comprehensive analysis of MGEs in the gut microbiome. Exploiting the SRID method, the authors curated a database called ImmeDB (Intestinal microbiome mobile element database) (https://immedb.mit.edu/). The ImmeDB provides a rich and accurate annotation of MGEs from gut microbiome and also contains their collection and classification. The database comprises of 5600 putative MGEs which are further classified into seven classes:

1. Integrative conjugative elements
2. Integrative mobilizable elements
3. Prophages
4. Group II introns
5. Transposons
6. Unclassified genomic islands
7. Unclassified islets

PhD Student

Department of Medical Microbiology, Postgraduate Institute of Medical Education & Research, Chandigarh, India

Corresponding author: Anshul Sood, PhD Student Department of Medical Microbiology, Postgraduate Institute of Medical Education & Research, Chandigarh, India, e-mail: anshulsood02@gmail.com

All comprised MGEs are identified with a "deletion-based" method. This study reveals a phylum level niche-adaptive gene pool in gut microbiome.[4]

With the ever-increasing resistance and the advent of next generation sequencing, it has become necessarily important to update and amalgamate AMR and MGE data resources and repositories. Hitherto, there is no centralized and methodical platform for MGEs and AMR gene resource which hampers the information availability and accuracy resulting in information discrepancy across different databases. Therefore, there is a strong need to establish methodical web resources and make them available in public domain for better research and clinical outcomes.

REFERENCES

1. Schaik WV. The human gut resistome. Philos Trans R Soc Lond B Biol Sci 2015 June;370(1670):20140087.
2. Xavier BB, Das AJ, Cochrane G, De Ganck S, Kumar-Singh S, Aarestrup FM, Goossens H, Malhotra-Kumar S. Consolidating and exploring antibiotic resistance gene data resources. J Clin Microbiol 2016 Apr;54(4):851-859.
3. Frost LS, Leplae R, Summers AO, Toussaint A. Mobile genetic elements: the agents of open source evolution. Nat Rev Microbiol 2005 Sep;3(9):722-732.
4. Jiang X, Hall AB, Xavier RJ, Alm EJ. Comprehensive analysis of mobile genetic elements in the gut microbiome reveals a phylum-level niche-adaptive gene pool. bioRxiv preprint first posted online Nov. 6, 2017.