Combating Infectious Diseases by Bioinformatics Approach

Manish Kumar [*]

Department of Biophysics, University of Delhi South Campus, New Delhi, India

Address for Correspondence: Manish Kumar; manish@south.du.ac.in

ABSTRACT: Beta-lactamases are a superfamily of enzymes, which degrade the β-lactam class of antibiotics. They are produced endogenously by the bacterial cells, which when exposed to the β-lactam class of antibiotics inactivate them by cleaving the β-lactam ring. Based on the presence or absence of metallic ligand, β-lactamases have been divided into two broad functional classes. β-Lactamases are a constitutively evolving and expanding superfamily of enzymes, which could be further subdivided on the basis of presence/absence of conserved motifs. Our work shows that they also contain family specific patterns/motifs which useful in recognizing and assigning newly discovered β-lactamases to one or the other family or subfamily. We have also developed a database Comprehensive Beta-lactamase Molecular Annotation Resource (CBMAR) that contains comprehensive information about different types of β-lactamases. Analysis of β-lactamase from *Yersinia enterocolitica* shows that not only the three-dimensional structure, other factors are also responsible for their production and efficacy. © 2014 iGlobal Research and Publishing Foundation. All rights reserved.