Anti microbial resistance (AMR) is a phenomenon where an organism is invulnerable to a given chemical and is therefore unaffected by treatment with that chemical agent. Although antibiotic resistance is a natural process, it has been enhanced by human use of antibiotics. There is significant concern and attention to the emergence of pathogenic strains resistant to these compounds. In the recent days we focus on the antibiotic resistance in the clinical environment and unnoticed about the fact that this phenomenon may took place in the natural environment also the environment can act as a reservoir of resistance. A holistic approach-involving human environments and natural environments are necessary to create lasting policy change to preserve antibiotics and understand antibiotic resistance.

An estimated 700 000 people die annually from infection with drug-resistant microbes, a figure that is projected to increase to about 10 million by 2050. Last year the United Nations declared antimicrobial resistance to be one of the biggest threats to global health. While there's no disagreement that action must be taken to combat the evolving drug-resistance crisis, just how to proceed remains a matter of debate.

For some, the logical step forward is to develop new antibiotics. The new drugs are needed to be marketed and need to be evaluated by clinical trials. If we take beta-lactam drug as an example the resistance to beta-lactam drug is the most threaten because till now it is the most potent antibiotics that our doctors routinely prescribed. Beta-lactams like penicillins, cephalosporins, carbapenems and monobactams constitute the therapy of choice for some well-established practices and infections. The main problem of new beta-lactam drug evaluation includes the diversity of Beta-Lactamase production which is responsible for the appearance of a large number of pathogenic bacterial strains exhibiting a high degree of resistance to beta-lactam antibiotics. A large number of enzymes have been described with very diverse primary structures and catalytic profiles. Nevertheless, all known three-dimensional structures of beta-lactamase reveals that they are 70-80 percent identical, they have 100 percent structural identity, 100 percent fold and motif identity, and active-site serine beta-lactamases exhibit a high degree of similarity with apparently equivalent chemical functionalities in the same strategic positions (primary active site identity). Instead of all these sequence, structural, motif, primary catalytic residue identity, this enzyme possesses a vast catalytic diversity. Even in a single organism

various diverse enzymes are found to perform the same function creating the pathogen most resistance to the last resort of the beta-lactam drugs even the beta-lactamase inhibitor drugs.

The awareness with this scenario is much more critical and needs awareness to the farm people and clinicians. With the effect in the mind to combat the drug resistance we are proposing the in vitro and in silico analysis to understand the enzyme beta-lactamase and to develop personalized medicine against the bacterial infection and several diagnostics parameter to implement the personalized medicine. The proposed project starts with specific class A beta-lactamase family of around 90 class A from different disease causing and general species of bacteria and with the help of structural bioinformatics tool we are classifying several diversion analysis among the all listed beta-lactamase. Next part of our project is to clone and purify all the listed beta-lactamase. A detail in vitro analysis will be carried out with this protein staring from the stability and activity of the enzyme towards library of beta-lactam drugs and its inhibitor. We will develop a perfect drug screening platform both in vivo and ex vivo to determine MIC of each drug and their combinations. Other part of the project includes chemical approach to design potential drug molecule against drug resistant beta-lactamase and in silico analysis of automated drug diagnostic development.