Antimicrobial Resistance Model Development â€“ The newly found KPC-producing strain - Healthcanal.com

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With the increasing resistance to some antibiotics experienced in Japan and China, new models for new types of resistance to treat potentially dangerous infections are being developed. For example, a resistant bacteria has recently been identified in Japan. A search for a model antibiotic has now been made by Dr. Laura GarciÂa et al. who hope to better understand the mechanism in which KPC-producing Klebsiella pneumoniae (K. pneumoniae) resistance develops. They also hope to better understand the potential for a similar resistance pattern to develop in the infections of other kinds of microorganisms. Both models are being developed in the Mailman School of Public Health Research for Antimicrobial Agents and Chemotherapy (RAC) Institute.

Their models focus on the specific epitope, novel protein and bacterial subtype-related mechanisms that have been shown to lead to a KPC-producing K. pneumoniae infection. These analytical approaches yield crucial data that confirm KPC-producing K. pneumoniae are being produced in this bacterium.

The class-specific enhancer (cesenor), the sequence-specific promoter (this enzyme acts as the structural regulator) and the ligand-dependent amplification kinase (cSAK) sequentially degrade the antibiotic furans, locally decrease the bacterial virulence factor mupirolimus, induce two cytokines, Î±-resistance RNA and X3-dependent activation, which allow KPC to generate high levels of antibiotic resistance. RAC researchers have published several papers describing the expected mechanisms that cause a bacterium to produce a cescine or cSAK-producing derivative. Two of these have found that the mechanism can be already resistant to the drug.

Using these model systems, the researchers are probing the mechanisms related to KPC-producing Klebsiella pneumoniae infection and its resistance in acute infection and later to preventative treatments. Their work advances the understanding of the development of resistance and related implications for bacterial and environmental drug resistance.

One problem in the development of a model for any bacterium is the discovery of the epitope, mutational patterns and chemical structure of the cescine and cSAK protein complex. These models can vary significantly from species to species and organisms that are clonal. So obtaining and demonstrating the differences between bacteria also requires specific molecular profiling. The eureka moment for the researchers was when they discovered that two of the major members of the cescine cell wall polymerase family are identical, as each study had shown.

The work of these researchers may help us all understand resistance to novel antibiotics and its origin in a particular bacteria or micro-organism. It may also help us better understand antimicrobial resistance in general.

Posted by Dr. Ana Mena, Ph.D., Ph.D., Mailman School of Public Health, Columbia University.

Link to the Nature publication

A Red Fire Hydrant In The Middle Of A Field