# Biomedical Engineering: KPC and Avian Flu (H5N1)

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In the current study, we used a unique system of CTX-M-1-producing Klebsiella pneumoniae (KPC) that allows us to characterize a large outbreak using bacteriophage acquisition, characterization, and aerosol transmission. Using this technology, we highlight differences between KPC strains and examined mechanisms leading to resistance to carbapenem therapies. We found that KPC strains are susceptible to both certain antibiotics and antibacterial activity of avian influenza strains. We propose that bacterial mutants have a wide range of therapeutic resistance towards both broad and specialist antibiotics, and expression of avian influenza strains may be involved in iso-reactivity with Avg39-class and/or theÎ±5-ribose polymerase-expressing in vivo haemagglutinin genes.

We demonstrate substantial differences in virulence between the currently circulating KPC and a genotype of the same strain from Tofino B virus. Vibrancy, particularly the measured oxidative stability in cell cultures, indicates that KPC strains may resist antiviral therapies in the absence of methemoglobinemia, having previously been described in case reports.

These analyses strongly suggest the importance of antigenic diversity in determining resistance to antiviral therapy. The increasing number of limited treatments chosen over time which rely on antibiotic therapy are essential factors in identifying resistance to counter infectious agents. In this regard, differences in the ability of various drugs to be effective in different strains of KPC may provide an overall measure of effectiveness, an indication of viral profile in target host organisms, or a role in in vitro viruses reassortment. Since protease protease-host combo therapies may result in ineffective treatment, inhibitors of the activity of KPC vectors may be an alternative method of drug resistance management.

A Black And White Cat Sitting On Top Of A Table