Phylogenomics of malaria and other apicomplexan parasites

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Apicomplexa are obligate intracellular parasites, many of which are responsible for diseases in human and other animals including malaria. They have small genomes, and have lost some distinct pathways which may contribute to pathogenecity and drug resistance. A comparative and phylogenomic analysis of 43 apicomplexa was conducted in the context of cellular, molecular, metabolic and evolutionary processes. Phylogenomic alignment was constructed by concatenating 522 genes from the core genome. We found significantly distinct relationships among hierarchical clusters of distance of phylogenomic, pairwise shared genes and pathways and only plasmodiums were found congruent among all the clusters. The number of some pathways varies substantially in different species, but some pathways remain almost same, with 41 pathways found in all species examined. Amino acid frequency in the whole genome is found highly variable compared to core genome and significantly correlated with GC (guanine-cytosine) content. Most of the malaria specific genes were found to be invasive. We have found significant correlations between proteome size and pathways in these organisms for metabolic pathways and informational genes. This data is consistent with the idea that information content of a genome exerts a selective pressure on genes necessary for genetic fidelity.

https://doi.org/10.1016/j.jiph.2018.10.104

Management of MERS CoV cluster in A hospital, Eastern Province, KSA

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Background: In August 2014, there was a report on striking rise in positive cases of MERS-CoV in A Hospital in Saudi Arabia (SA) after unprotected exposure to MERS-CoV patient. This report describes the outbreak investigation, finding and response.

Methods: Rapid response team was activated and mobilized to the medical institute. Epidemic investigation was conducted. Epidemiological data regarding patients and health care workers in relation to unprotected exposure was collected. Based on risk stratification, expanded surveillance among health care workers including housekeepers and maintenance was conducted. In addition, information about environmental and infection control measures implementation were collected. Gaps were identified, a plan to close gaps was initiated and implemented by rapid response team in collaboration with hospital' stakeholders and designated staff. The plan consist of many aspects including infection prevention and control education, infection control measures auditing, case finding and management. This was continued and audited for 14 days after last reported laboratory confirmed results.

Results: During surveillance period, 8 cases of HCWs (2 physicians, 6 nurses), and two patients in addition to the index case were positive to MERS CoV. One physician, and 2 patients had no direct contact with the index case. No additional cases were identified after implementation of infection prevention and control measures in the hospital.

Conclusions: The outbreak of MERS-CoV was contained after implementing infection prevention and control measures. Early case identification and risk stratification might played a major role in containing the cluster.

https://doi.org/10.1016/j.jiph.2018.10.105

A place for ceragenis and LL-37 peptide in treatment of urinary tract infections

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Background and purpose: Urinary tract infections (UTIs) are one of the most common causes of medical intervention. High recurrence rates and increasing antibiotic resistance among uropathogens constitute a large social and economic problem. The most common agent of UTIs is Gram-negative uropathogenic Escherichia coli (UPEC). We used a set of experiments to investigate whether combination of ceragenins (CSAs) with LL-37, a peptide that is naturally expressed in the urinary tract, can be an effective treatment against extra- and intracellular pathogens associated with UTIs.

Methodology: Extracellular activity of tested agents both alone and in combinations was evaluated using a killing assay. We also assessed the effects of LL-37 peptide and ceragenin CSA-131 against intracellular E. coli, a clinical isolate obtained from patients diagnosed with reoccurring UTIs. The CFU (CFU/ml) of the intracellular E. coli was determined from the dilution factor and was used to calculate the percentage of bacterial outgrowth.

Results: Our results indicate that the CSA-131 activity can be enhancing by presence of endogenous LL-37 peptide. Such a combination was found to be more effective in eliminating extra- and intracellular E. coli. The combination of CSA-131 with LL-37 killed approximately 65% and 79% of the intracellular E. coli at 5 μM and 10 μM concentrations, respectively. Moreover, 10 μM of CSA-131 with LL-37 completely eliminated the intracellular E. coli.

Conclusions: We suggest that combinations of natural LL-37 peptide with ceragenins, such as CSA-131, possess the potential to treat urinary tract infections caused by drug-resistant bacteria. Moreover, intracellular activity of these combinations appears to be well suited for treatment of recurrent UTIs.

This work was financially supported by the National Science Centre, Poland [UMO-2016/21/N/NZ6/02213 to UW].

https://doi.org/10.1016/j.jiph.2018.10.106

Reporting 4 Candida auris in National Guard Hospital, Riyadh/ Saudi Arabia

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Introduction: Candida auris was described initially in 2009 as a new species of the genus Candida in Japan, since then it has been reported to cause healthcare-associated infections, and hospital outbreaks from many countries in different continents. In 2016, the Center for Disease Control (CDC) and Public Health England have