Emerging Infectious Diseases in Jordan (M. ulcerans)

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Background: Buruli ulcer is the third most common mycobacterial infection worldwide. It is endemic in tropical, subtropical, and temperate climates. It causes devastating disease with morbidity and mortality.

The treatment duration is long and the regimens considered are limited. Chronic cutaneous ulcers of mycobacterial etiology have been reported previously in Amman, but these were not associated with Mycobacterium ulcerans infection.

Methods: The case patient's initial diagnosis was based on chronological and morphological features, combined with appropriate diagnostic tests. The skin features were assessed histopathologically. Skin testing was positive for acid-fast bacilli (AFB), and M. ulcerans was identified by DNA strip test (GenoType Mycobacterium CM/AS, Hain Lifescience), which is based on a PCR technique targeting a 23S rRNA gene region, followed by reverse hybridization and a line probe technology.

Results: The skin mycobacterial infection was evaluated and verified as having a Mycobacterium marinum–M. ulcerans pattern in the GenoType CM assay. It was then counted as a pattern representing individual species and was resolved with the GenoType AS assay as having an M. ulcerans pattern. M. ulcerans DNA was isolated and amplified by PCR, and then detected against reverse hybridization probes in the strip assay.

Conclusions: An indigenous case of M. ulcerans (Buruli ulcer) is reported for the first time from Jordan and the surrounding region.

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UAE Gut Project "UAE Microbiome Project"

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Background: The Human Microbiome Project and other microbiome projects worldwide (American Gut Project, British Gut Project) have laid an important foundation for understanding our microbes that inhabits each of our bodies.

The "16S rRNA" sequencing was performed to characterize the complexity of microbial communities at each body sites microbiome.

The extent of microbial and molecular diversity in human stool remains unknowing our regions(ME and Africa).

Objectives: To discover the UAE Gut Microbiome Signature.

To discover the unique relationship between the UAE Gut Microbiome Signature and the Health and the Diseases.

To discover and pave the way of Personalized Medicine which is the Gold Stone of Future Medicine.

To stimulate the spirit of research & helping many researchers in Clinical Microbiology to enrich their research experience.

To help in stimulating publications in Microbiome Signature.

Methodology: Prepare the proper "Questionaire" which will be filled by the Participants.

Two Stool samples from each Participants will received by our "Molecular Biological Laboratory" to start study the "16SrRNA" in the samples.

In the initial phase of our Project we will start by 200 Participants.

If we do it in an international lab; each one will cost around 125$. Total cost equal to 25000$.

My Target to do the tests in Molecular Biological Unit (Next Generation Sequencing) in UAE.

Conclusion: "UAE Gut Microbiome Signature"

Our results will show uncover new molecules and kinds of molecular communities in the human stool metabolome; and examine emergent associations among the microbiome, metabolome, and the diversity of "diet" that are consumed.

The more we can understand the complex microbial ecosystems on which we depend, the more everyone will benefit.

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Discovery of Novel Molecules for the Treatment of Multidrug Resistant Superbugs

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Background and Purpose: Methicillin-resistant Staphylococcus aureus (MRSA) is a common cause of severe infections in health care facilities and the community. World health organization has included this bacteria in the list of top 12 pathogens causing high morbidity and mortality worldwide. Limited therapeutic options are currently available to treat MRSA infections. Novel antibacterial agents are urgently required to combat these resistant bacteria.

Methodology: Novel molecules with unique chemical scaffolds were designed and synthesised at the Sharjah Institute for Medical Research, University of Sharjah, UAE. These compounds were tested for antibacterial activities against both Gram-negative and Gram-positive bacteria. The compounds were also tested for activity against 10 multidrug-resistant Staphylococcus bacteria. Minimum inhibitory concentrations (MICs) of the compounds were determined using broth microdilution method. Bacteria were examined under the atomic force and fluorescent microscopes. Time-kill experiments were used to examine the rate of killing.

Results and Discussions: 18 novel compounds were found active against 10 multidrug-resistant bacteria of the genus Staphylococcus (MIC: 3.125–50 μg/ml) with 10–20 times more potent activity than ciprofloxacin. Killing was achieved after 30 minutes of exposure to the compounds (50–100 μg/ml), compared to 24 hours of exposure to ciprofloxacin (32 and 256 μg/ml). Rapid killing was confirmed by the fluorescent microscope with >70% bacterial death after 30 minutes treatment. Cell wall damage with leakage of intracellular components were evident by the atomic force microscope, indicating the possibility of the compound action on the cell wall. The compounds were also active in preventing biofilm formation by the multidrug-resistant bacteria. They were non-toxic and safe when tested against normal human cells and red blood cells, indicating their high safety for human consumption. Resistance was not developed against these compounds after several serial passages.

Conclusions: The discovered novel compounds represent promising lead drug candidates for treating multidrug-resistant bacterial infections.

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