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Evaluation of the Therapeutic Effect of Botulinum toxin A on Hallux Valgus Deformity and Pain

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Background: Hallux Valgus is a kind of Toes aberration where the Metatarsophalangeal joint that connects the big toe to the foot, leading to the inner side and a protrusion on the inner surface of toe arise. This study aimed to determine the effect of botulinum toxin A injection to reduce pain and deviation angle of the thumb in Hallux Valgus and to increase outcomes of treatment as an adjuvant therapy.

Material & methods: Randomized clinical study was performed on 18 patients at the Clinic of Physical Medicine and Rehabilitation, Isfahan University of Medical Sciences. In this study the Halgvs valgus angle (HVA) between the metatarsals (IMA) and cartilage distal metatarsal angle (DMAA) and pain was assessed before and after injection.

Results: Average of Hallux Valgus angle before and after Botox injections were $28/89 \pm 10/21$ and $21/56 \pm 8/22$ degrees and the angle deviation in the 6 months after treatment was significantly improved (p <0.001).

Conclusion: Injection of botulinum toxin A is a suitable and acceptable method to reform the skeleton deformities and also to reduce the pain in patients with Hallux valgus.

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Keywords: Hallux valgus, botulinum toxin A, Metatarsal bone, Pain.

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Real-time whole genome sequencing direct diagnosis of community-acquired bacterial meningitis

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Community-acquired bacterial meningitis (CABM) is a life-threatening condition whose prognosis is partially depends on the causative bacteria genotype, which requires efficient diagnosis, patient management and adequate treatment. Current routine point-of-care multiplex real-time PCR diagnosis of CABM allowed to detect the presence of the pathogen genome in the cerebrospinal fluid (CSF). This assay requires additional in-vitro investigation for pathogen genotyping and antibiotic-resistance tests. Here we proposed one-shot pathogen genotyping in a case of deadly Haemophilus influenzae (H. influenzae) meningitis. Real-time PCR diagnosed H. influenzae meningitis in a 22-year-old male patient immunized against H. influenzae b serotype, during his hospitalization following a more than six-meter fall. Using metagenomics real-time sequencing in parallel to real-time PCR, we detected the H. influenzae genome directly from the CSF sample in six hours workflow, in-silico susceptible to the antibiotic panel used in routine. Furthermore, BLAST analysis of the sequence encoding for a partial DUF417 domain-containing protein diagnosed a non-b serotype, non-typeable H. influenzae belonging to lineage H. influenzae 22.1-21. The Oxford Nanopore metagenomic next-generation sequencing approach could be considered for the point-of-care diagnosis of infectious meningitis, by direct identification of pathogenic genomes and their genotypes.

Biography

MORSLI Madjid, PhD, researcher at IHU Méditerranée Infection, Aix-Marseille Université, Marseille, France. The main research project focuses on the improvement of community-acquired meningitis diagnosis using both metagenomics next-generation sequencing and real-time metagenomics and its implementation at the Point-Of-Care laboratory.

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Viewing microbiota as a potential therapeutic target for cancer therapy

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Statement of the Problem: Can microbiota be seen as a potential therapeutic target in the host for cancer therapy?

Microbiota influences cancer directly- via proteins (metabolites and toxins), induces apoptosis via signaling pathways, stimulates the immune system, and is responsible for various risk factors associated with cancers, for example, pancreatic cancer. The microbiome can modulate the immune system and hence, cause carcinogenesis of different organs distant from the gut possibly because of increased systemic inflammatory response. Altered gut microbiota is associated with resistance to chemo drugs or immune checkpoint inhibitors (ICIs), whereas supplementation of distinct bacterial species restores responses to the anticancer drugs.

In pancreas cancer, if certain bacteria are removed, macrophages and T cells in the tumor get activated. Hence, to target cancer, the "microbiome", should be addressed as a therapeutic target. This can be done by genetically engineering the bacteria to carry genes whose products are involved in inherent metabolic pathways related to cancer. Then multiple ways to deliver an array of therapeutic proteins and drug compounds to cancer cells could be explored. Further, alteration of the microbiome indirectly using probiotics, fecal microbiota transplantation (FMT), diet alteration, etc. would also pave the way for cancer therapy

Key words: Allanblackia Floribunda, Suppositories, Paracetamol, Diclofenac

Biography

Arpita is an early-stage academic researcher. She has expertise in molecular biology techniques. Academic and research experience to date along with participation in various national and international conferences has provided her strong understanding of how the wet lab work is translated into a medically relevant form. Currently, she is working on a collaborative project between India and the UK entitled "ResPharm" which is an initiative to tackle Antimicrobial Resistance on a global front. The enteric lab is set in a clinical setting where she has gained expertise in the processing of samples (water, soil, stool, semen, urine). Further, she is training in bioinformatics and data analysis to be able to put shreds of evidence into perspective through the window frame of science.

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In silico and in vitro identification of pan-coronaviral main protease inhibitors from a large natural product library

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The main protease (Mpro or 3CLpro) in coronaviruses represents a promising, specific drug target since it is essential for the cleavage of the virus polypeptide with a unique cleavage site that does not exist in human host proteases. In this study, we explored the potential natural pan-coronavirus drugs using in vitro and in silico approaches and three coronavirus main proteases as treatment targets. The PyRx program was first used to screen 39,442 natural product-like compounds from the ZINC database and 121 preselected phytochemicals with known antiviral activity against SARS-CoV-2 Mpro. After assessment with the Lipinski's rule of 5, molecular docking was performed for the top 33 compounds of both libraries. Enzymatic assays were applied for the top candidates from both in silico approaches for testing their ability to inhibit the SARS-CoV-2 Mpro. Four compounds (hypericin, rosmarinic acid, isorhamnetin, luteolin) that most efficiently inhibited SARS-CoV-2 Mpro in vitro were then further tested for their efficacy to inhibit Mpro of SARS-CoV-1 and MERS-CoV as well. Microscale thermophoresis was performed to determine the dissociation constant (Kd) values to validate the binding of these active compounds to recombinant Mpro proteins of SARS-Cov-2, SARS-CoV-1, and MERS-CoV. The cytotoxicity of hypericin, rosmarinic acid, isorhamnetin, and luteolin was also assessed in human diploid MRC-5 lung fibroblasts using the resazurin cell viability assay to determine the therapeutic indices. Sequence alignment of Mpro of SARS-CoV-2 demonstrated 96.08%, 50.83%, 49.17%, 48.51%, 44.04%, and 41.06% similarity to Mpro of other human-pathogenic coronaviruses (SARS CoV-1, MERS-COV, HCoV-NL63, HCoV-OC43, HCoV-HKU1, and HCoV-229E, respectively). Molecular docking showed that 12 out of 121 compounds were bound to the SARS-CoV-2 Mpro with the same binding site at Mpro as the control inhibitor GC376. Enzyme inhibition assays revealed that hypericin, rosmarinic acid, isorhamnetin, and luteolin inhibited Mpro of SARS-CoV-2, while hypericin and isorhamnetin inhibited Mpro of SARS-CoV-1 and hypericin showed inhibitory effects towards Mpro of MERS-CoV. Microscale thermophoresis confirmed the binding of these compounds to Mpro with high affinity. Resazurin assays showed that rosmarinic acid and luteolin did not reveal significant cytotoxicity toward MRC-5 cells, whereas hypericin and isorhamnetin were slightly cytotoxic. We demonstrated that hypericin represents a potential novel pan-anti-coronaviral agent by binding to and inhibition of Mpro of several human-

3pathogenic coronaviruses. Moreover, isorhamnetin showed inhibitory effects towards SARS-CoV-2 and SARS-CoV-1 Mpro indicating that this compound may also reveal at least some pan-coronaviral potential. Luteolin revealed inhibitory effects against SARS-CoV-2 Mpro.

Biography

I have completed my Master in Clinical Biochemistry at Tarbiat Modares University in Iran and published 2 papers, and now I am doing a Ph.D. in Pharmaceutical Biology at, the Institute of Pharmaceutical and Biomedical Sciences, Johannes Gutenberg University, Mainz, Germany. I am interested in the molecular modes of action of small molecules, phytochemicals, and microbiological compounds with activity towards infectious diseases, cancer and Inflammation.

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Escherichia coli (e. Coli) associated hematogenous sternoclavicular joint osteomyelitis:arareconditionwithararecausativepathogenicmicroorganism

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Escherichia coli is the most common microorganism that causes urinary tract infections (UTIs), including acute prostatitis. However, E. coli osteomyelitis, especially ones that involve sternoclavicular joint, are rare hematogenous complications. We present a case of an immunocompetent man who presented with symptoms of UTI and right shoulder pain. Urine cultures and blood cultures grew E. coli. There was also radiographic evidence of a large prostatic abscess and a right sternoclavicular joint osteomyelitis. Our patient was treated with antibiotic and improved clinically. This case is noteworthy given the rarity of both the condition as well as the causative pathogenic agent. It is important for clinicians to be aware of E. coli sternoclavicular osteomyelitis in adults with preceding bacterial prostatitis.

Biography

Tyler Luu is an internal medicine resident at the Loyola University Chicago. He has a profound passion for infectious disease, His work in research has a focus on bacteriology, antibiotics and antibiotic stewardship.

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